CheckM: assessing the quality of microbial genomes rec and metagenomes

Genome Research

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Citation Report

#	Article	IF	Citations
4	Back to Basics â€“ The Influence of DNA Extraction and Primer Choice on Phylogenetic Analysis of Activated Sludge Communities. PLoS ONE, 2015, 10, e0132783.	1.1	437
5	Comparative genomics of Fructobacillus spp. and Leuconostoc spp. reveals niche-specific evolution of Fructobacillus spp.. BMC Genomics, 2015, 16, 1117.	1.2	53
6	Complete Genome Sequence of <i>Curtobacterium</i> sp. Strain MR_MD2014, Isolated from Topsoil in Woods Hole, Massachusetts. Genome Announcements, 2015, 3, .	0.8	3
7	Impact of library preparation protocols and template quantity on the metagenomic reconstruction of a mock microbial community. BMC Genomics, 2015, 16, 856.	1.2	79
8	Genomic resolution of linkages in carbon, nitrogen, and sulfur cycling among widespread estuary sediment bacteria. Microbiome, 2015, 3, 14.	4.9	316
9	Draft Genome Sequence of Desulfocarbo indianensis SCBM, a New Genus of Sulfate-Reducing Bacteria, Isolated from Water Extracted from an Active Coalbed Methane Gas Well. Genome Announcements, 2015, 3, .	0.8	2
10	Auxotrophy and intrapopulation complementary in the â€˜interactomeâ€™ of a cultivated freshwater model community. Molecular Ecology, 2015, 24, 4449-4459.	2.0	97
11	Metagenomic Chromosome Conformation Capture (3C): techniques, applications, and challenges. F1000Research, 2015, 4, 1377.	0.8	13
12	Comparative genomic analysis of multiple strains of two unusual plant pathogens: Pseudomonas corrugata and Pseudomonas mediterranea. Frontiers in Microbiology, 2015, 6, 811.	1.5	50
13	A Metagenomics-Based Metabolic Model of Nitrate-Dependent Anaerobic Oxidation of Methane by Methanoperedens-Like Archaea. Frontiers in Microbiology, 2015, 6, 1423.	1.5	170
14	Genomic Reconstruction of an Uncultured Hydrothermal Vent Gammaproteobacterial Methanotroph (Family Methylothermaceae) Indicates Multiple Adaptations to Oxygen Limitation. Frontiers in Microbiology, 2015, 6, 1425.	1.5	36
15	gbtools: Interactive Visualization of Metagenome Bins in R. Frontiers in Microbiology, 2015, 6, 1451.	1.5	49
16	Abundant toxin-related genes in the genomes of beneficial symbionts from deep-sea hydrothermal vent mussels. ELife, 2015, 4, e07966.	2.8	50
17	Genome Sequence of Bacillus mycoides B38V, a Growth-Promoting Bacterium of Sunflower. Genome Announcements, 2015, 3, .	0.8	9
18	Genome of Pseudomonas sp. FeS53a, a Putative Plant Growth-Promoting Bacterium Associated with Rice Grown in Iron-Stressed Soils. Genome Announcements, 2015, 3, .	0.8	2
19	Genome of Rhizobium sp. UR51a, Isolated from Rice Cropped in Southern Brazilian Fields. Genome Announcements, 2015, 3, .	0.8	5
20	Draft Genome Sequences of 24 Microbial Strains Assembled from Direct Sequencing from 4 Stool Samples. Genome Announcements, 2015, 3, .	0.8	5
21	Draft Genome Sequence of Anammox Bacterium â€œCandidatus Scalindua brodae,â€•Obtained Using Differential Coverage Binning of Sequencing Data from Two Reactor Enrichments. Genome Announcements, 2015, 3, .	0.8	46

#	ARTICLE	IF	CITATIONS
22	Ecological speciation in bacteria: reverse ecology approaches reveal the adaptive part of bacterial cladogenesis. Research in Microbiology, 2015, 166, 729-741.	1.0	37
23	Multi-omics of permafrost, active layer and thermokarst bog soil microbiomes. Nature, 2015, 521, 208-212.	13.7	467
24	Mechanosensitive channel MSL8 regulates osmotic forces during pollen hydration and germination. Science, 2015, 350, 438-441.	6.0	184
25	Nanoarchaeota, Their Sulfolobales Host, and Nanoarchaeota Virus Distribution across Yellowstone National Park Hot Springs. Applied and Environmental Microbiology, 2015, 81, 7860-7868.	1.4	63
26	Methane metabolism in the archaeal phylum Bathyarchaeota revealed by genome-centric metagenomics. Science, 2015, 350, 434-438.	6.0	677
27	Experimental Design and Bioinformatics Analysis for the Application of Metagenomics in Environmental Sciences and Biotechnology. Environmental Science & Technology, 2015, 49, 12628-12640.	4.6	72
28	Microbial Malaise: How Can We Classify the Microbiome?. Trends in Microbiology, 2015, 23, 671-679.	3.5	36
29	Whole-Genome Shotgun Sequence of the Keratinolytic Bacterium Lysobacter sp. A03, Isolated from the Antarctic Environment. Genome Announcements, 2015, 3, .	0.8	5
30	Complete nitrification by a single microorganism. Nature, 2015, 528, 555-559.	13.7	1,336
31	Complete nitrification by Nitrospira bacteria. Nature, 2015, 528, 504-509.	13.7	1,878
32	Draft Genome Sequence of Strain LSUCC0135, an Early Diverging Member of the Order <i>Methylophilales</i> in the Phylum <i>Betaproteobacteria</i>. Genome Announcements, 2016, 4, .	0.8	4
33	Complete Genome Sequence of a Cylindrospermopsin-Producing Cyanobacterium, Cylindrospermopsis raciborskii CS505, Containing a Circular Chromosome and a Single Extrachromosomal Element. Genome Announcements, 2016, 4, .	0.8	2
34	Genome Analysis of a Limnobacter sp. Identified in an Anaerobic Methane-Consuming Cell Consortium. Frontiers in Marine Science, 2016, 3, .	1.2	19
35	Draft Genome Sequences of Two Ralstonia pickettii Strains with Different Aminoglycoside Resistance Phenotypes. Genome Announcements, 2016, 4, .	0.8	4
36	Draft Genome Sequence of <i>Curtobacterium</i> sp. Strain UCD-KPL2560 (Phylum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182 Td (<i>A	0.8	5
37	Genomic Analysis Unravels Reduced Inorganic Sulfur Compound Oxidation of Heterotrophic Acidophilic<i>Acidicaldus</i>sp. Strain DX-1. BioMed Research International, 2016, 2016, 1-8.	0.9	4
38	DFAST and DAGA: web-based integrated genome annotation tools and resources. Bioscience of Microbiota, Food and Health, 2016, 35, 173-184.	0.8	194
39	A Phylogenomic Analysis of the Bacterial Phylum Fibrobacteres. Frontiers in Microbiology, 2015, 6, 1469.	1.5	125

#	ARTICLE	IF	CITATIONS
40	Microevolution Analysis of Bacillus coahuilensis Unveils Differences in Phosphorus Acquisition Strategies and Their Regulation. Frontiers in Microbiology, 2016, 7, 58.	1.5	17
41	Improved Environmental Genomes via Integration of Metagenomic and Single-Cell Assemblies. Frontiers in Microbiology, 2016, 7, 143.	1.5	24
42	Metagenomic Insights into the Uncultured Diversity and Physiology of Microbes in Four Hypersaline Soda Lake Brines. Frontiers in Microbiology, 2016, 7, 211.	1.5	161
43	Comparative Genomic Analysis Reveals a Diverse Repertoire of Genes Involved in Prokaryote-Eukaryote Interactions within the Pseudovibrio Genus. Frontiers in Microbiology, 2016, 7, 387.	1.5	36
44	Proteomic Stable Isotope Probing Reveals Biosynthesis Dynamics of Slow Growing Methane Based Microbial Communities. Frontiers in Microbiology, 2016, 7, 563.	1.5	34
45	Metagenomics Reveals Pervasive Bacterial Populations and Reduced Community Diversity across the Alaska Tundra Ecosystem. Frontiers in Microbiology, 2016, 7, 579.	1.5	66
46	Deep Subsurface Life from North Pond: Enrichment, Isolation, Characterization and Genomes of Heterotrophic Bacteria. Frontiers in Microbiology, 2016, 7, 678.	1.5	21
47	Genome-Centric Analysis of Microbial Populations Enriched by Hydraulic Fracture Fluid Additives in a Coal Bed Methane Production Well. Frontiers in Microbiology, 2016, 7, 731.	1.5	67
48	Capturing One of the Human Gut Microbiomeâ€™s Most Wanted: Reconstructing the Genome of a Novel Butyrate-Producing, Clostridial Scavenger from Metagenomic Sequence Data. Frontiers in Microbiology, 2016, 7, 783.	1.5	24
49	Not All Particles Are Equal: The Selective Enrichment of Particle-Associated Bacteria from the Mediterranean Sea. Frontiers in Microbiology, 2016, 7, 996.	1.5	36
50	â€œCandidatus Propionivibrio aalborgensisâ€: A Novel Glycogen Accumulating Organism Abundant in Full-Scale Enhanced Biological Phosphorus Removal Plants. Frontiers in Microbiology, 2016, 7, 1033.	1.5	97
51	Genomic and Transcriptomic Resolution of Organic Matter Utilization Among Deep-Sea Bacteria in Guaymas Basin Hydrothermal Plumes. Frontiers in Microbiology, 2016, 7, 1125.	1.5	49
52	How Clonal Is Clonal? Genome Plasticity across Multicellular Segments of a â€œCandidatus Marithrix sp.â€•Filament from Sulfidic, Briny Seafloor Sediments in the Gulf of Mexico. Frontiers in Microbiology, 2016, 7, 1173.	1.5	15
53	Culture Independent Genomic Comparisons Reveal Environmental Adaptations for Altiarchaeales. Frontiers in Microbiology, 2016, 7, 1221.	1.5	25
54	Genome Sequence of Pseudomonas koreensis CRS05-R5, an Antagonistic Bacterium Isolated from Rice Paddy Field. Frontiers in Microbiology, 2016, 7, 1756.	1.5	20
55	Genomic and Transcriptomic Evidence for Carbohydrate Consumption among Microorganisms in a Cold Seep Brine Pool. Frontiers in Microbiology, 2016, 7, 1825.	1.5	29
56	Gene Turnover Contributes to the Evolutionary Adaptation of Acidithiobacillus caldus: Insights from Comparative Genomics. Frontiers in Microbiology, 2016, 7, 1960.	1.5	35
57	Characterization and Genome Analysis of the First Facultatively Alkaliphilic Thermodesulfovibrio Isolated from the Deep Terrestrial Subsurface. Frontiers in Microbiology, 2016, 7, 2000.	1.5	62

#	Article	IF	Citations
58	Fuerstia marisgermanicae gen. nov., sp. nov., an Unusual Member of the Phylum Planctomycetes from the German Wadden Sea. Frontiers in Microbiology, 2016, 7, 2079.	1.5	49
59	Comparative Genomics of the Extreme Acidophile Acidithiobacillus thiooxidans Reveals Intraspecific Divergence and Niche Adaptation. International Journal of Molecular Sciences, 2016, 17, 1355.	1.8	39
60	Comparative Genomic Analysis of Sulfurospirillum cavolei MES Reconstructed from the Metagenome of an Electrosynthetic Microbiome. PLoS ONE, 2016, 11, e0151214.	1.1	20
61	Genomic characterization of the uncultured Bacteroidales family S24-7 inhabiting the guts of homeothermic animals. Microbiome, 2016, 4, 36.	4.9	533
62	Draft Genome Sequence of <i>Pseudoalteromonas</i> sp. Strain XI10 Isolated from the Brine-Seawater Interface of Erba Deep in the Red Sea. Genome Announcements, 2016, 4, .	0.8	4
63	The deepâ€sea glass sponge <scp><i>L</i></scp><i>ophophysema eversa</i> harbours potential symbionts responsible for the nutrient conversions of carbon, nitrogen and sulfur. Environmental Microbiology, 2016, 18, 2481-2494.	1.8	64
64	Potential Mechanisms for Microbial Energy Acquisition in Oxic Deep-Sea Sediments. Applied and Environmental Microbiology, 2016, 82, 4232-4243.	1.4	51
65	<i>Candidatus</i> Desulfofervidus auxilii, a hydrogenotrophic sulfateâ€reducing bacterium involved in the thermophilic anaerobic oxidation of methane. Environmental Microbiology, 2016, 18, 3073-3091.	1.8	115
66	Trace Metal Acquisition by Marine Heterotrophic Bacterioplankton with Contrasting Trophic Strategies. Applied and Environmental Microbiology, 2016, 82, 1613-1624.	1.4	51
67	A scalable assembly-free variable selection algorithm for biomarker discovery from metagenomes. BMC Bioinformatics, 2016, 17, 311.	1.2	10
68	Reconstruction of a Nearly Complete Pseudomonas Draft Genome Sequence from a Coalbed Methane-Produced Water Metagenome. Genome Announcements, 2016, 4, .	0.8	5
69	Metagenome-Assembled Genome Sequence of Pseudomonas stutzeri Strain CO183 Isolated from a Coalbed Methane Well. Genome Announcements, 2016, 4, .	0.8	0
70	Draft Genome Sequences of Two Benthic Cyanobacteria, <i>Oscillatoriales</i> USR 001 and <i>Nostoc</i> sp. MBR 210, Isolated from Tropical Freshwater Lakes. Genome Announcements, 2016, 4, .	0.8	1
71	Family-wide Structural Characterization and Genomic Comparisons Decode the Diversity-oriented Biosynthesis of Thalassospiramides by Marine Proteobacteria. Journal of Biological Chemistry, 2016, 291, 27228-27238.	1.6	11
72	Reconstructing a hydrogen-driven microbial metabolic network in Opalinus Clay rock. Nature Communications, 2016, 7, 12770.	5.8	120
73	acdc â€" Automated Contamination Detection and Confidence estimation for single-cell genome data. BMC Bioinformatics, 2016, 17, 543.	1.2	22
74	Reconstructing metabolic pathways of a member of the genus <i>Pelotomaculum</i> suggesting its potential to oxidize benzene to carbon dioxide with direct reduction of sulfate. FEMS Microbiology Ecology, 2017, 93, fiw254.	1.3	13
76	Draft Genome Sequence of Antarctic Methanogen Enriched from Dry Valley Permafrost. Genome Announcements, 2016, 4, .	0.8	2

#	ARTICLE	IF	CITATIONS
77	Whole genome sequencing identifies a novel species of the genus Capnocytophaga isolated from dog and cat bite wounds in humans. Scientific Reports, 2016, 6, 22919.	1.6	28
78	Draft Genome Sequence of the Anaerobic Ammonium-Oxidizing Bacterium â€œ <i>Candidatus</i> Brocadia sp. 40â€. Genome Announcements, 2016, 4, .	0.8	28
79	From Genomes to Phenotypes: Traitar, the Microbial Trait Analyzer. MSystems, 2016, 1, .	1.7	102
80	A catalogue of 136 microbial draft genomes from Red Sea metagenomes. Scientific Data, 2016, 3, 160050.	2.4	47
81	Identification and genome reconstruction of abundant distinct taxa in microbiomes from one thermophilic and three mesophilic production-scale biogas plants. Biotechnology for Biofuels, 2016, 9, 156.	6.2	120
82	A minimalistic microbial food web in an excavated deep subsurface clay rock. FEMS Microbiology Ecology, 2016, 92, fiv138.	1.3	29
83	Differences down-under: alcohol-fueled methanogenesis by archaea present in Australian macropodids. ISME Journal, 2016, 10, 2376-2388.	4.4	41
84	Genomic insights into a new acidophilic, copper-resistant<i>Desulfosporosinus</i>isolate from the oxidized tailings area of an abandoned gold mine. FEMS Microbiology Ecology, 2016, 92, fiw111.	1.3	39
85	Genomic insights into members of the candidate phylum Hyd24-12 common in mesophilic anaerobic digesters. ISME Journal, 2016, 10, 2352-2364.	4.4	62
86	Phylogenomic analysis of <i>Candidatus</i> â€˜Izimaplasmaâ€™ species: free-living representatives from a <i>Tenericutes</i> clade found in methane seeps. ISME Journal, 2016, 10, 2679-2692.	4.4	88
87	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. MBio, 2016, 7, .	1.8	78
88	High definition for systems biology of microbial communities: metagenomics gets genome-centric and strain-resolved. Current Opinion in Biotechnology, 2016, 39, 174-181.	3.3	30
89	Metagenomic Evidence for the Presence of Comammox <i>Nitrospira</i> -Like Bacteria in a Drinking Water System. MSphere, 2016, 1, .	1.3	229
90	Diversification and niche adaptations of <i>Nitrospina</i>-like bacteria in the polyextreme interfaces of Red Sea brines. ISME Journal, 2016, 10, 1383-1399.	4.4	85
91	Near-Complete Genome Sequence of Clostridium paradoxum Strain JW-YL-7. Genome Announcements, 2016, 4, .	0.8	3
92	Draft Genome Sequence of Methanohalophilus mahii Strain DAL1 Reconstructed from a Hydraulic Fracturing-Produced Water Metagenome. Genome Announcements, 2016, 4, .	0.8	4
93	Deep metagenome and metatranscriptome analyses of microbial communities affiliated with an industrial biogas fermenter, a cow rumen, and elephant feces reveal major differences in carbohydrate hydrolysis strategies. Biotechnology for Biofuels, 2016, 9, 121.	6.2	141
94	SAR11 bacteria linked to ocean anoxia and nitrogen loss. Nature, 2016, 536, 179-183.	13.7	160

#	ARTICLE	IF	CITATIONS
95	Genome Characteristics of Two Novel Type I Methanotrophs Enriched from North Sea Sediments Containing Exclusively a Lanthanide-Dependent XoxF5-Type Methanol Dehydrogenase. Microbial Ecology, 2016, 72, 503-509.	1.4	39
96	Aerobic Degradation of Sulfadiazine by <i>Arthrobacter</i> spp.: Kinetics, Pathways, and Genomic Characterization. Environmental Science & Technology, 2016, 50, 9566-9575.	4.6	134
97	Orenia metallireducens sp. nov. Strain Z6, a Novel Metal-Reducing Member of the Phylum Firmicutes from the Deep Subsurface. Applied and Environmental Microbiology, 2016, 82, 6440-6453.	1.4	25
98	Comparative Genomics of Syntrophic Branched-Chain Fatty Acid Degrading Bacteria. Microbes and Environments, 2016, 31, 288-292.	0.7	19
99	Enrichment of Root Endophytic Bacteria from Populus deltoides and Single-Cell-Genomics Analysis. Applied and Environmental Microbiology, 2016, 82, 5698-5708.	1.4	53
100	Near complete genome sequence of the animal feed probiotic, Bacillus amyloliquefaciens H57. Standards in Genomic Sciences, 2016, 11, 60.	1.5	16
101	Mobile genes in the human microbiome are structured from global to individual scales. Nature, 2016, 535, 435-439.	13.7	233
102	Thermophilic archaea activate butane via alkyl-coenzyme M formation. Nature, 2016, 539, 396-401.	13.7	279
103	Reconstructing metabolic pathways of hydrocarbon-degrading bacteria from the Deepwater Horizon oil spill. Nature Microbiology, 2016, 1, 16057.	5.9	173
104	Accurate binning of metagenomic contigs via automated clustering sequences using information of genomic signatures and marker genes. Scientific Reports, 2016, 6, 24175.	1.6	212
105	Genome-based microbial ecology of anammox granules in a full-scale wastewater treatment system. Nature Communications, 2016, 7, 11172.	5.8	373
106	Draft Genome Sequence of a Tropical Freshwater Cyanobacterium, <i>Limnothrix</i> sp. Strain P13C2. Genome Announcements, 2016, 4, .	0.8	3
107	Measurement of bacterial replication rates in microbial communities. Nature Biotechnology, 2016, 34, 1256-1263.	9.4	342
108	Metagenomic analysis and functional characterization of the biogas microbiome using high throughput shotgun sequencing and a novel binning strategy. Biotechnology for Biofuels, 2016, 9, 26.	6.2	248
109	Genomic characterization of a fructophilic bee symbiont Lactobacillus kunkeei reveals its niche-specific adaptation. Systematic and Applied Microbiology, 2016, 39, 516-526.	1.2	51
110	Methylotrophic methanogenesis discovered in the archaeal phylum Verstraetearchaeota. Nature Microbiology, 2016, 1, 16170.	5.9	459
111	Integrative microbial community analysis reveals full-scale enhanced biological phosphorus removal under tropical conditions. Scientific Reports, 2016, 6, 25719.	1.6	61
112	Genomic and enzymatic evidence for acetogenesis among multiple lineages of the archaeal phylum Bathyarchaeota widespread in marine sediments. Nature Microbiology, 2016, 1, 16035.	5.9	256

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113	Genomic inference of the metabolism of cosmopolitan subsurface Archaea, Hadesarchaea. Nature Microbiology, 2016, 1, 16002.	5.9	118
114	Whole genome sequence analysis indicates recent diversification of mammal-associated Campylobacter fetus and implicates a genetic factor associated with H2S production. BMC Genomics, 2016, 17, 713.	1.2	18
115	Draft Genome Sequence of Pyrodictium occultum PL19 T , a Marine Hyperthermophilic Species of Archaea That Grows Optimally at 105Â°C. Genome Announcements, 2016, 4, .	0.8	2
116	Draft Genome Sequence of Uncultured SAR324 Bacterium lautmerah10, Binned from a Red Sea Metagenome. Genome Announcements, 2016, 4, .	0.8	15
117	Recovering complete and draft population genomes from metagenome datasets. Microbiome, 2016, 4, 8.	4.9	254
118	Draft Genome Sequence of <i>Megasphaera</i> sp. Strain DJF_B143, an Isolate from Pig Hindgut Unable to Produce Skatole. Genome Announcements, 2016, 4, .	0.8	2
119	Draft Genome Sequence of Olsenella scatoligenes SK9K4 T , a Producer of 3-Methylindole (Skatole) and 4-Methylphenol (p -Cresol), Isolated from Pig Feces. Genome Announcements, 2016, 4, .	0.8	2
120	Draft Genome Sequence of â€œ <i>Candidatus</i> Methanomethylophilusâ€•sp. 1R26, Enriched from Bovine Rumen, a Methanogenic Archaeon Belonging to the <i>Methanomassiliicoccales</i> Order. Genome Announcements, 2016, 4, .	0.8	17
121	Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. ISME Journal, 2016, 10, 1589-1601.	4.4	226
122	Environmental Breviatea harbour mutualistic Arcobacter epibionts. Nature, 2016, 534, 254-258.	13.7	68
123	Description of Endozoicomonas ascidiicola sp. nov., isolated from Scandinavian ascidians. Systematic and Applied Microbiology, 2016, 39, 313-318.	1.2	27
124	Draft Genome Sequences of Two Novel <i>Acidimicrobiaceae</i> Members from an Acid Mine Drainage Biofilm Metagenome. Genome Announcements, 2016, 4, .	0.8	8
125	Single-cell genome sequencing: current state of the science. Nature Reviews Genetics, 2016, 17, 175-188.	7.7	1,134
126	Draft Genome Sequence of a Novel <i>Desulfobacteraceae</i> Member from a Sulfate-Reducing Bioreactor Metagenome. Genome Announcements, 2016, 4, .	0.8	8
127	Genomic reconstruction of a novel, deeply branched sediment archaeal phylum with pathways for acetogenesis and sulfur reduction. ISME Journal, 2016, 10, 1696-1705.	4.4	161
128	Draft Genome Sequences of Two Thiomicrospira Strains Isolated from the Brine-Seawater Interface of Kebrit Deep in the Red Sea. Genome Announcements, 2016, 4, .	0.8	3
129	Draft Genome Sequence of Thermodesulfovibrio aggregans TGE-P1 T , an Obligately Anaerobic, Thermophilic, Sulfate-Reducing Bacterium in the Phylum Nitrospirae. Genome Announcements, 2016, 4, .	0.8	3
130	Genome-Based Microbial Taxonomy Coming of Age. Cold Spring Harbor Perspectives in Biology, 2016, 8, a018085.	2.3	69

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131	Draft Genome Sequence of Neisseria gonorrhoeae Strain NG_869 with Penicillin, Tetracycline and Ciprofloxacin Resistance Determinants Isolated from Malaysia. Indian Journal of Microbiology, 2016, 56, 225-227.	1.5	1
132	Six <i>Pseudoalteromonas</i> Strains Isolated from Surface Waters of Kabeltonne, Offshore Helgoland, North Sea. Genome Announcements, 2016, 4, .	0.8	9
133	Metagenomic Signatures of Bacterial Adaptation to Life in the Phyllosphere of a Salt-Secreting Desert Tree. Applied and Environmental Microbiology, 2016, 82, 2854-2861.	1.4	38
134	Draft Genome Sequence of a Strictly Anaerobic Dichloromethane-Degrading Bacterium. Genome Announcements, 2016, 4, .	0.8	13
135	Comparative Genomics of Candidate Phylum TM6 Suggests That Parasitism Is Widespread and Ancestral in This Lineage. Molecular Biology and Evolution, 2016, 33, 915-927.	3.5	119
136	Chloroflexi CL500-11 Populations That Predominate Deep-Lake Hypolimnion Bacterioplankton Rely on Nitrogen-Rich Dissolved Organic Matter Metabolism and C ₁ Compound Oxidation. Applied and Environmental Microbiology, 2016, 82, 1423-1432.	1.4	57
137	EffectiveDBâ€"updates and novel features for a better annotation of bacterial secreted proteins and Type III, IV, VI secretion systems. Nucleic Acids Research, 2016, 44, D669-D674.	6.5	172
138	MetaQUAST: evaluation of metagenome assemblies. Bioinformatics, 2016, 32, 1088-1090.	1.8	447
139	ProDeGe: a computational protocol for fully automated decontamination of genomes. ISME Journal, 2016, 10, 269-272.	4.4	65
140	Unraveling the microbial processes of black band disease in corals through integrated genomics. Scientific Reports, 2017, 7, 40455.	1.6	36
141	Endozoicomonas genomes reveal functional adaptation and plasticity in bacterial strains symbiotically associated with diverse marine hosts. Scientific Reports, 2017, 7, 40579.	1.6	207
142	MetaSort untangles metagenome assembly by reducing microbial community complexity. Nature Communications, 2017, 8, 14306.	5.8	52
143	Ecotype diversification of an abundant Roseobacter lineage. Environmental Microbiology, 2017, 19, 1625-1638.	1.8	17
144	Asgard archaea illuminate the origin of eukaryotic cellular complexity. Nature, 2017, 541, 353-358.	13.7	882
145	Draft Genome of Scalindua rubra, Obtained from the Interface Above the Discovery Deep Brine in the Red Sea, Sheds Light on Potential Salt Adaptation Strategies in Anammox Bacteria. Microbial Ecology, 2017, 74, 1-5.	1.4	73
146	Genomic reconstruction of multiple lineages of uncultured benthic archaea suggests distinct biogeochemical roles and ecological niches. ISME Journal, 2017, 11, 1118-1129.	4.4	79
147	New insights into marine group III Euryarchaeota, from dark to light. ISME Journal, 2017, 11, 1102-1117.	4.4	72
148	Singleâ€cell genomics based on Raman sorting reveals novel carotenoidâ€containing bacteria in the Red Sea. Microbial Biotechnology, 2017, 10, 125-137.	2.0	72

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149	Adaptive Evolution of Extreme Acidophile Sulfobacillus thermosulfidooxidans Potentially Driven by Horizontal Gene Transfer and Gene Loss. Applied and Environmental Microbiology, 2017, 83, .	1.4	48
150	A novel archaeal species belonging to Methanoculleus genus identified via de-novo assembly and metagenomic binning process in biogas reactors. Anaerobe, 2017, 46, 23-32.	1.0	63
151	Mixed transmission modes and dynamic genome evolution in an obligate animalâ€"bacterial symbiosis. ISME Journal, 2017, 11, 1359-1371.	4.4	35
152	High quality draft genome sequence of Janthinobacterium psychrotolerans sp. nov., isolated from a frozen freshwater pond. Standards in Genomic Sciences, 2017, 12, 8.	1.5	28
153	Syntrophic linkage between predatory <i>Carpediemonas</i> and specific prokaryotic populations. ISME Journal, 2017, 11, 1205-1217.	4.4	21
154	Scaffolding bacterial genomes and probing host-virus interactions in gut microbiome by proximity ligation (chromosome capture) assay. Science Advances, 2017, 3, e1602105.	4.7	110
155	Methylamine as a nitrogen source for microorganisms from a coastal marine environment. Environmental Microbiology, 2017, 19, 2246-2257.	1.8	50
156	Microbial communities in pyrene amended soilâ€"compost mixture and fertilized soil. AMB Express, 2017, 7, 7.	1.4	17
157	Predominance and Metabolic Potential of Halanaerobium spp. in Produced Water from Hydraulically Fractured Marcellus Shale Wells. Applied and Environmental Microbiology, 2017, 83, .	1.4	64
158	Chemolithotrophic processes in the bacterial communities on the surface of mineral-enriched biochars. ISME Journal, 2017, 11, 1087-1101.	4.4	121
159	Towards long-read metagenomics: complete assembly of three novel genomes from bacteria dependent on a diazotrophic cyanobacterium in a freshwater lake co-culture. Standards in Genomic Sciences, 2017, 12, 9.	1.5	53
160	Infection control in the new age of genomic epidemiology. American Journal of Infection Control, 2017, 45, 170-179.	1.1	90
161	Draft genome sequence of Streptomyces sp. strain F1, a potential source for glycoside hydrolases isolated from Brazilian soil. Brazilian Journal of Microbiology, 2017, 48, 612-614.	0.8	1
162	Sputum DNA sequencing in cystic fibrosis: non-invasive access to the lung microbiome and to pathogen details. Microbiome, 2017, 5, 20.	4.9	100
163	Metagenomic and Metatranscriptomic Analyses Reveal the Structure and Dynamics of a Dechlorinating Community Containing Dehalococcoides mccartyi and Corrinoid-Providing Microorganisms under Cobalamin-Limited Conditions. Applied and Environmental Microbiology, 2017, 83, .	1.4	29
164	Origin of microbial biomineralization and magnetotaxis during the Archean. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2171-2176.	3.3	98
165	SAR202 Genomes from the Dark Ocean Predict Pathways for the Oxidation of Recalcitrant Dissolved Organic Matter. MBio, 2017, 8, .	1.8	168
166	A submarine volcanic eruption leads to a novel microbial habitat. Nature Ecology and Evolution, 2017, 1, 144.	3.4	42

#	ARTICLE	IF	CITATIONS
167	Metagenome sequencing and 98 microbial genomes from Juan de Fuca Ridge flank subsurface fluids. Scientific Data, 2017, 4, 170037.	2.4	71
168	Metagenomics and CAZyme Discovery. Methods in Molecular Biology, 2017, 1588, 255-277.	0.4	19
169	The low diverse gastric microbiome of the jellyfish <i>Cotylorhiza tuberculata</i> is dominated by four novel taxa. Environmental Microbiology, 2017, 19, 3039-3058.	1.8	62
170	Genome Sequence of Dehalobacter sp. Strain TeCB1, Able To Respire Chlorinated Benzenes. Genome Announcements, 2017, 5, .	0.8	4
171	The novel bacterial phylum Calditrichaeota is diverse, widespread and abundant in marine sediments and has the capacity to degrade detrital proteins. Environmental Microbiology Reports, 2017, 9, 397-403.	1.0	39
172	Tracking microbial colonization in fecal microbiota transplantation experiments via genome-resolved metagenomics. Microbiome, 2017, 5, 50.	4.9	78
173	Isolation, Biosynthesis and Chemical Modifications of Rubterolones Aâ€“F: Rare Tropolone Alkaloids from <i>Actinomadura</i> sp. 5â€2. Chemistry - A European Journal, 2017, 23, 9338-9345.	1.7	39
174	Draft Genome Sequence of Uncultured Upland Soil Cluster <i>Gammaproteobacteria</i> Gives Molecular Insights into High-Affinity Methanotrophy. Genome Announcements, 2017, 5, .	0.8	18
175	Binning_refiner: improving genome bins through the combination of different binning programs. Bioinformatics, 2017, 33, 1873-1875.	1.8	75
176	Microbial community function in the bleaching disease of the marine macroalgae <i>Delisea pulchra</i>. Environmental Microbiology, 2017, 19, 3012-3024.	1.8	42
177	The metabolic potential of the single cell genomes obtained from the Challenger Deep, <scp>M</scp>ariana <scp>T</scp>rench within the candidate superphylum <scp>P</scp>arcubacteria (<scp>OD</scp>1). Environmental Microbiology, 2017, 19, 2769-2784.	1.8	88
178	BusyBee Web: metagenomic data analysis by bootstrapped supervised binning and annotation. Nucleic Acids Research, 2017, 45, W171-W179.	6.5	84
179	Short-chain alkanes fuel mussel and sponge Cycloclasticus symbionts from deep-sea gas and oil seeps. Nature Microbiology, 2017, 2, 17093.	5.9	80
180	Impact of drinking water treatment and distribution on the microbiome continuum: an ecological disturbance's perspective. Environmental Microbiology, 2017, 19, 3163-3174.	1.8	56
181	Genomic and phenotypic analyses of Pseudomonas psychrotolerans PRS08-11306 reveal a turnerbactin biosynthesis gene cluster that contributes to nitrogen fixation. Journal of Biotechnology, 2017, 253, 10-13.	1.9	12
182	Iron-Dependent Enzyme Catalyzes the Initial Step in Biodegradation of <i>N</i> -Nitroglycine by Variovorax sp. Strain JS1663. Applied and Environmental Microbiology, 2017, 83, .	1.4	11
183	Succession in the petroleum reservoir microbiome through an oil field production lifecycle. ISME Journal, 2017, 11, 2141-2154.	4.4	136
184	Comparative genomic analysis reveals the environmental impacts on two Arcticibacter strains including sixteen Sphingobacteriaceae species. Scientific Reports, 2017, 7, 2055.	1.6	27

#	ARTICLE	IF	CITATIONS
185	Genomic characterization of two novel SAR11 isolates from the Red Sea, including the first strain of the SAR11 Ib clade. FEMS Microbiology Ecology, 2017, 93, .	1.3	15
186	Energy and carbon metabolisms in a deep terrestrial subsurface fluid microbial community. ISME Journal, 2017, 11, 2319-2333.	4.4	119
187	Unexpected genomic features in widespread intracellular bacteria: evidence for motility of marine chlamydiae. ISME Journal, 2017, 11, 2334-2344.	4.4	34
188	<i>Crenothrix</i> are major methane consumers in stratified lakes. ISME Journal, 2017, 11, 2124-2140.	4.4	146
189	Draft Genome Sequences of Dermacoccus nishinomiyaensis Strains UCD-KPL2534 and UCD-KPL2528 Isolated from an Indoor Track Facility. Genome Announcements, 2017, 5, .	0.8	2
190	Draft Genome Sequences of Three Nontypeable Strains of Haemophilus influenzae, C188, R535, and 1200, Isolated from Different Types of Disease. Genome Announcements, 2017, 5, .	0.8	3
191	Metabolic network analysis reveals microbial community interactions in anammox granules. Nature Communications, 2017, 8, 15416.	5.8	489
192	Genomic Evidence that Methanotrophic Endosymbionts Likely Provide Deep-Sea Bathymodiolus Mussels with a Sterol Intermediate in Cholesterol Biosynthesis. Genome Biology and Evolution, 2017, 9, 1148-1160.	1.1	28
193	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. Nature Biotechnology, 2017, 35, 676-683.	9.4	222
194	Genome Sequence of Geothermobacter sp. Strain EPR-M, a Deep-Sea Hydrothermal Vent Iron Reducer. Genome Announcements, 2017, 5, .	0.8	5
195	Niche partitioning of diverse sulfur-oxidizing bacteria at hydrothermal vents. ISME Journal, 2017, 11, 1545-1558.	4.4	168
196	Complete genome sequence of Achromobacter insolitus type strain LMG 6003T, a pathogen isolated from leg wound. Pathogens and Disease, 2017, 75, .	0.8	3
197	Integrated metabolism in spongeâ€“microbe symbiosis revealed by genome-centered metatranscriptomics. ISME Journal, 2017, 11, 1651-1666.	4.4	118
198	Genome Reduction and Microbe-Host Interactions Drive Adaptation of a Sulfur-Oxidizing Bacterium Associated with a Cold Seep Sponge. MSystems, 2017, 2, .	1.7	35
199	Hidden diversity revealed by genome-resolved metagenomics of iron-oxidizing microbial mats from LÅâ€™ihi Seamount, Hawaiâ€™i. ISME Journal, 2017, 11, 1900-1914.	4.4	51
200	Comammox in drinking water systems. Water Research, 2017, 116, 332-341.	5.3	163
201	On the origins of oxygenic photosynthesis and aerobic respiration in Cyanobacteria. Science, 2017, 355, 1436-1440.	6.0	344
202	Whole-Community Metagenomics in Two Different Anammox Configurations: Process Performance and Community Structure. Environmental Science & Technology, 2017, 51, 4317-4327.	4.6	98

#	Article	IF	Citations
203	Comparative genomics analysis of five Psychrobacter strains isolated from world-wide habitats reveal high intra-genus variations. Extremophiles, 2017, 21, 581-589.	0.9	9
204	Spontaneous mutations of a model heterotrophic marine bacterium. ISME Journal, 2017, 11, 1713-1718.	4.4	22
205	The trajectory of microbial single-cell sequencing. Nature Methods, 2017, 14, 1045-1054.	9.0	120
206	Ecophysiology of Freshwater Verrucomicrobia Inferred from Metagenome-Assembled Genomes. MSphere, 2017, 2, .	1.3	87
207	Draft Genome Sequences of Two Unclassified Bacteria, Sphingomonas sp. Strains IBVSS1 and IBVSS2, Isolated from Environmental Samples. Genome Announcements, 2017, 5, .	0.8	1
208	Draft Genome Sequences of Two Uncultured Armatimonadetes Associated with a Microcystis sp. () Tj ETQq1 1 0.784314 rgBT /Overlo	0.8	1
209	Simulations predict microbial responses in the environment? This environment disagrees retrospectively. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8947-E8949.	3.3	5
210	A patchwork pathway for oxygenaseâ€•independent degradation of side chain containing steroids. Environmental Microbiology, 2017, 19, 4684-4699.	1.8	28
211	Metabolic Roles of Uncultivated Bacterioplankton Lineages in the Northern Gulf of Mexico â€œDead Zoneâ€• MBio, 2017, 8, .	1.8	80
212	Draft Genome Sequences of Two Unclassified Chitinophagaceae Bacteria, IBVUCB1 and IBVUCB2, Isolated from Environmental Samples. Genome Announcements, 2017, 5, .	0.8	1
213	Genomic diversification of giant enteric symbionts reflects host dietary lifestyles. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7592-E7601.	3.3	64
214	Transient exposure to oxygen or nitrate reveals ecophysiology of fermentative and sulfateâ€•reducing benthic microbial populations. Environmental Microbiology, 2017, 19, 4866-4881.	1.8	26
215	Candidatus Dactylopiibacterium carminicum, a Nitrogen-Fixing Symbiont of Dactylopius Cochineal Insects (Hemiptera: Coccoidea: Dactylopiidae). Genome Biology and Evolution, 2017, 9, 2237-2250.	1.1	19
216	Bioinformatics for NGS-based metagenomics and the application to biogas research. Journal of Biotechnology, 2017, 261, 10-23.	1.9	84
217	An investigation into the taxonomy of â€œ Bacillus aminovorans â€•and its reclassification to the genus Domibacillus as Domibacillus aminovorans sp. nov.. Systematic and Applied Microbiology, 2017, 40, 458-467.	1.2	13
218	Metabolic Network Analysis and Metatranscriptomics Reveal Auxotrophies and Nutrient Sources of the Cosmopolitan Freshwater Microbial Lineage acI. MSystems, 2017, 2, .	1.7	21
219	Pan-genomic and transcriptomic analyses of Leuconostoc mesenteroides provide insights into its genomic and metabolic features and roles in kimchi fermentation. Scientific Reports, 2017, 7, 11504.	1.6	55
220	Community-like genome in single cells of the sulfur bacterium Achromatium oxaliferum. Nature Communications, 2017, 8, 455.	5.8	31

#	ARTICLE	IF	CITATIONS
221	Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. Nature Microbiology, 2017, 2, 1533-1542.	5.9	1,465
222	Genome-Enabled Insights into the Ecophysiology of the Comammox Bacterium â€œ <i>Candidatus</i> Nitrospira nitrosaâ€. MSystems, 2017, 2, .	1.7	119
223	Examination into the taxonomic position of Bacillus thermotolerans Yang et al., 2013, proposal for its reclassification into a new genus and species Quasibacillus thermotolerans gen. nov., comb. nov. and reclassification of B. encimensis Dastager et al., 2015 as a later heterotypic synonym of B. badius. Systematic and Applied Microbiology, 2017, 40, 411-422.	1.2	14
224	Genomes of rumen bacteria encode atypical pathways for fermenting hexoses to shortâ€chain fatty acids. Environmental Microbiology, 2017, 19, 4670-4683.	1.8	41
225	Genetic diversity of marine anaerobic ammoniumâ€oxidizing bacteria as revealed by genomic and proteomic analyses of â€˜<i>Candidatus</i> Scalindua japonicaâ€™. Environmental Microbiology Reports, 2017, 9, 550-561.	1.0	29
226	Metagenomic analysis reveals a green sulfur bacterium as a potential coral symbiont. Scientific Reports, 2017, 7, 9320.	1.6	29
227	Metabolic Reconstruction and Modeling Microbial Electrosynthesis. Scientific Reports, 2017, 7, 8391.	1.6	117
228	Draft Genome Sequences of Nine Cyanobacterial Strains from Diverse Habitats. Genome Announcements, 2017, 5, .	0.8	11
229	Ninety-nine <i>de novo</i> assembled genomes from the moose (<i>Alces alces</i>) rumen microbiome provide new insights into microbial plant biomass degradation. ISME Journal, 2017, 11, 2538-2551.	4.4	120
230	Uncultivated microbes in need of their own taxonomy. ISME Journal, 2017, 11, 2399-2406.	4.4	572
231	High-Quality Draft Genome Sequence of Lactobacillus casei Strain Z11, Isolated from a Human Adult Intestinal Biopsy Sample. Genome Announcements, 2017, 5, .	0.8	3
232	dRep: a tool for fast and accurate genomic comparisons that enables improved genome recovery from metagenomes through de-replication. ISME Journal, 2017, 11, 2864-2868.	4.4	1,309
233	Contamination of the Arctic reflected in microbial metagenomes from the Greenland ice sheet. Environmental Research Letters, 2017, 12, 074019.	2.2	41
234	Improved genome recovery and integrated cell-size analyses of individual uncultured microbial cells and viral particles. Nature Communications, 2017, 8, 84.	5.8	169
235	Metabolic pathway and cell adaptation mechanisms revealed through genomic, proteomic and transcription analysis of a Sphingomonas haloaromaticamans strain degrading ortho-phenylphenol. Scientific Reports, 2017, 7, 6449.	1.6	25
236	Draft Genome Sequence of Pseudoruegeria sp. SK021, a Representative of the Marine Roseobacter Group, Isolated from North Sea Sediment. Genome Announcements, 2017, 5, .	0.8	3
237	Evidence of microbial rhodopsins in <scp>A</scp>ntarctic <scp>D</scp>ry <scp>V</scp>alley edaphic systems. Environmental Microbiology, 2017, 19, 3755-3767.	1.8	17
238	Metabolic potential and <i>in situ</i> activity of marine Marinimicrobia bacteria in an anoxic water column. Environmental Microbiology, 2017, 19, 4392-4416.	1.8	40

#	Article	IF	Citations
239	Grape pomace compost harbors organohalide-respiring <i>Dehalogenimonas</i> species with novel reductive dehalogenase genes. ISME Journal, 2017, 11, 2767-2780.	4.4	118
240	Enrichment of anaerobic nitrate-dependent methanotrophic â€˜Candidatus Methanoperedens nitroreducensâ€™ archaea from an Italian paddy field soil. Applied Microbiology and Biotechnology, 2017, 101, 7075-7084.	1.7	110
241	Chemical dispersants enhance the activity of oil- and gas condensate-degrading marine bacteria. ISME Journal, 2017, 11, 2793-2808.	4.4	114
242	Singleâ€cell sequencing unveils the lifestyle and CRISPRâ€based population history of <i>Hydrotalea</i> sp. in acid mine drainage. Molecular Ecology, 2017, 26, 5541-5551.	2.0	8
243	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. Nature Biotechnology, 2017, 35, 725-731.	9.4	1,512
244	Genetic adaptation of microbial populations present in high-intensity catfish production systems with therapeutic oxytetracycline treatment. Scientific Reports, 2017, 7, 17491.	1.6	20
245	Metagenome Sequence of a Microbial Community from the Gold Mine Tailings in the Kuzbass Area, Russia. Genome Announcements, 2017, 5, .	0.8	5
246	Draft Genome Sequence of Chloracidobacterium sp. CP2_5A, a Phototrophic Member of the Phylum Acidobacteria Recovered from a Japanese Hot Spring. Genome Announcements, 2017, 5, .	0.8	19
247	Atmospheric trace gases support primary production in Antarctic desert surface soil. Nature, 2017, 552, 400-403.	13.7	290
248	Major role of nitrite-oxidizing bacteria in dark ocean carbon fixation. Science, 2017, 358, 1046-1051.	6.0	229
249	Assessing species biomass contributions in microbial communities via metaproteomics. Nature Communications, 2017, 8, 1558.	5.8	211
250	Draft Genome Sequences of a Novel Lineage of Armatimonadetes Recovered from Japanese Hot Springs. Genome Announcements, 2017, 5, .	0.8	31
251	Diverse Marinimicrobia bacteria may mediate coupled biogeochemical cycles along eco-thermodynamic gradients. Nature Communications, 2017, 8, 1507.	5.8	99
252	Ammoniaâ€oxidising archaea living at low pH: Insights from comparative genomics. Environmental Microbiology, 2017, 19, 4939-4952.	1.8	107
253	Mimicking microbial interactions under nitrateâ€reducing conditions in an anoxic bioreactor: enrichment of novel Nitrospirae bacteria distantly related to <i>Thermodesulfovibrio</i>. Environmental Microbiology, 2017, 19, 4965-4977.	1.8	60
254	Vitamin and Amino Acid Auxotrophy in Anaerobic Consortia Operating under Methanogenic Conditions. MSystems, 2017, 2, .	1.7	28
255	Integrated view of <i>Vibrio cholerae</i> in the Americas. Science, 2017, 358, 789-793.	6.0	128
256	Detection of misidentifications of species from the Burkholderia cepacia complex and description of a new member, the soil bacterium Burkholderia catarinensis sp. nov.. Pathogens and Disease, 2017, 75, .	0.8	70

#	ARTICLE	IF	CITATIONS
257	Massively parallel whole genome amplification for single-cell sequencing using droplet microfluidics. Scientific Reports, 2017, 7, 5199.	1.6	102
258	ICoVeR â€“ an interactive visualization tool for verification and refinement of metagenomic bins. BMC Bioinformatics, 2017, 18, 233.	1.2	22
259	Draft genome sequences of eight bacteria isolated from the indoor environment: Staphylococcus capitis strain H36, S. capitis strain H65, S. cohnii strain H62, S. hominis strain H69, Microbacterium sp. strain H83, Mycobacterium iranicum strain H39, Plantibacter sp. strain H53, and Pseudomonas oryzihabitans strain H72. Standards in Genomic Sciences, 2017, 12, 17.	1.5	9
260	Genomics insights into production of 2-methylisoborneol and a putative cyanobactin by Planktothricoides sp. SR001. Standards in Genomic Sciences, 2017, 12, 35.	1.5	8
261	Chemosynthetic symbionts of marine invertebrate animals are capable of nitrogen fixation. Nature Microbiology, 2017, 2, 16195.	5.9	151
262	Quantitative Metaproteomics Highlight the Metabolic Contributions of Uncultured Phylotypes in a Thermophilic Anaerobic Digester. Applied and Environmental Microbiology, 2017, 83, .	1.4	67
263	Genome reduction in an abundant and ubiquitous soil bacterium â€˜Candidatus Udaeobacter copiosusâ€™. Nature Microbiology, 2017, 2, 16198.	5.9	168
264	High-resolution characterization of the human microbiome. Translational Research, 2017, 179, 7-23.	2.2	55
265	The antibiotic resistome of swine manure is significantly altered by association with the <i>Musca domestica</i> larvae gut microbiome. ISME Journal, 2017, 11, 100-111.	4.4	101
266	Metagenomics of Two Severe Foodborne Outbreaks Provides Diagnostic Signatures and Signs of Coinfection Not Attainable by Traditional Methods. Applied and Environmental Microbiology, 2017, 83, .	1.4	54
267	Draft Genome Sequence of <i>Sphingomonas</i> sp. Strain Sph1(2015), Isolated from a Fouled Membrane Filter Used to Produce Drinking Water. Genome Announcements, 2017, 5, .	0.8	0
268	Reconstructed genomes of novel Dehalococcoides mccartyi strains from 1,2,3,4-tetrachlorodibenzo-p-dioxin-dechlorinating enrichment cultures reveal divergent reductive dehalogenase gene profiles. FEMS Microbiology Ecology, 2017, 93, .	1.3	13
269	Organismal and spatial partitioning of energy and macronutrient transformations within a hypersaline mat. FEMS Microbiology Ecology, 2017, 93, .	1.3	23
270	Genomic insights into potential interdependencies in microbial hydrocarbon and nutrient cycling in hydrothermal sediments. Microbiome, 2017, 5, 106.	4.9	168
271	Towards enhanced and interpretable clustering/classification in integrative genomics. Nucleic Acids Research, 2017, 45, e169-e169.	6.5	1
272	Genomic characterization reconfirms the taxonomic status of <i>Lactobacillus parakefiri</i>. Bioscience of Microbiota, Food and Health, 2017, 36, 129-134.	0.8	2
273	Revealing the genomic differences between two subgroups in <i>Lactobacillus gasseri</i>. Bioscience of Microbiota, Food and Health, 2017, 36, 155-159.	0.8	8
274	Genome Sequence of Lactobacillus paracasei Strain LC-Ikematsu, Isolated from a Pineapple in Okinawa, Japan. Genome Announcements, 2017, 5, .	0.8	0

#	Article	IF	Citations
275	Draft Genome Sequence of <i>Bacillus</i> sp. FMQ74, a Dairy-Contaminating Isolate from Raw Milk. Genome Announcements, 2017, 5, .	0.8	0
276	Draft Genome Sequence of the Planktic Cyanobacterium Tychonema bourrellyi, Isolated from Alpine Lentic Freshwater. Genome Announcements, 2017, 5, .	0.8	6
277	Draft Genome Sequence of Streptococcus caviae Strain Cavy grass 6 ^T , Isolated from Domesticated Guinea Pig Fecal Samples. Genome Announcements, 2017, 5, .	0.8	0
278	Biotechnological Potential of Cold Adapted Pseudoalteromonas spp. Isolated from â€˜Deep Seaâ€™ Sponges. Marine Drugs, 2017, 15, 184.	2.2	20
279	Chaperone-Usher Pili Loci of Colonization Factor-Negative Human Enterotoxigenic Escherichia coli. Frontiers in Cellular and Infection Microbiology, 2016, 6, 200.	1.8	15
280	Metagenomic Binning Recovers a Transcriptionally Active Gammaproteobacterium Linking Methanotrophy to Partial Denitrification in an Anoxic Oxygen Minimum Zone. Frontiers in Marine Science, 2017, 4, .	1.2	44
281	Three Novel Species with Peptidoglycan Cell Walls form the New Genus Lacunisphaera gen. nov. in the Family Opitutaceae of the Verrucomicrobial Subdivision 4. Frontiers in Microbiology, 2017, 8, 202.	1.5	75
282	Comparative Genome Analysis of Three Thiocyanate Oxidizing Thioalkalivibrio Species Isolated from Soda Lakes. Frontiers in Microbiology, 2017, 8, 254.	1.5	53
283	Untangling Genomes of Novel Planctomycetal and Verrucomicrobial Species from Monterey Bay Kelp Forest Metagenomes by Refined Binning. Frontiers in Microbiology, 2017, 8, 472.	1.5	70
284	Isolation and Characterization of Dehalobacter sp. Strain TeCB1 Including Identification of TcbA: A Novel Tetra- and Trichlorobenzene Reductive Dehalogenase. Frontiers in Microbiology, 2017, 8, 558.	1.5	22
285	Genome-Centric Analysis of a Thermophilic and Cellulolytic Bacterial Consortium Derived from Composting. Frontiers in Microbiology, 2017, 8, 644.	1.5	61
286	Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). Frontiers in Microbiology, 2017, 8, 682.	1.5	409
287	Comparative Genomics Unravels the Functional Roles of Co-occurring Acidophilic Bacteria in Bioleaching Heaps. Frontiers in Microbiology, 2017, 8, 790.	1.5	17
288	A Metagenomic Approach to Cyanobacterial Genomics. Frontiers in Microbiology, 2017, 8, 809.	1.5	98
289	The Dark Side of the Mushroom Spring Microbial Mat: Life in the Shadow of Chlorophototrophs. II. Metabolic Functions of Abundant Community Members Predicted from Metagenomic Analyses. Frontiers in Microbiology, 2017, 8, 943.	1.5	100
290	Unexpected Dominance of Elusive Acidobacteria in Early Industrial Soft Coal Slags. Frontiers in Microbiology, 2017, 8, 1023.	1.5	32
291	Novel Pelagic Iron-Oxidizing Zetaproteobacteria from the Chesapeake Bay Oxicâ€"Anoxic Transition Zone. Frontiers in Microbiology, 2017, 8, 1280.	1.5	72
292	Exploring Microdiversity in Novel Kordia sp. (Bacteroidetes) with Proteorhodopsin from the Tropical Indian Ocean via Single Amplified Genomes. Frontiers in Microbiology, 2017, 8, 1317.	1.5	7

#	Article	IF	Citations
293	Genome Sequencing Reveals the Potential of Achromobacter sp. HZ01 for Bioremediation. Frontiers in Microbiology, 2017, 8, 1507.	1.5	43
294	Reclassification of Paenibacillus riograndensis as a Genomovar of Paenibacillus sonchi: Genome-Based Metrics Improve Bacterial Taxonomic Classification. Frontiers in Microbiology, 2017, 8, 1849.	1.5	27
295	Benefits of Genomic Insights and CRISPR-Cas Signatures to Monitor Potential Pathogens across Drinking Water Production and Distribution Systems. Frontiers in Microbiology, 2017, 8, 2036.	1.5	15
296	Genomic Comparison of Two Family-Level Groups of the Uncultivated NAG1 Archaeal Lineage from Chemically and Geographically Disparate Hot Springs. Frontiers in Microbiology, 2017, 8, 2082.	1.5	19
297	Reconstruction of Diverse Verrucomicrobial Genomes from Metagenome Datasets of Freshwater Reservoirs. Frontiers in Microbiology, 2017, 8, 2131.	1.5	68
298	Ecogenomics and Taxonomy of Cyanobacteria Phylum. Frontiers in Microbiology, 2017, 8, 2132.	1.5	99
299	Rokubacteria: Genomic Giants among the Uncultured Bacterial Phyla. Frontiers in Microbiology, 2017, 8, 2264.	1.5	142
300	The Draft Genome of the Non-Host-Associated<i>Methanobrevibacter arboriphilus</i>Strain DH1 Encodes a Large Repertoire of Adhesin-Like Proteins. Archaea, 2017, 2017, 1-9.	2.3	7
301	Metagenome of the Siberian Underground Water Reservoir. Genome Announcements, 2017, 5, .	0.8	9
302	Draft Genome Sequences of Two Unclassified Bacteria, Hydrogenophaga sp. Strains IBVHS1 and IBVHS2, Isolated from Environmental Samples. Genome Announcements, 2017, 5, .	0.8	0
303	Assessing biosynthetic potential of agricultural groundwater through metagenomic sequencing: A diverse anammox community dominates nitrate-rich groundwater. PLoS ONE, 2017, 12, e0174930.	1.1	26
304	Genomic and transcriptomic analyses reveal adaptation mechanisms of an Acidithiobacillus ferrivorans strain YL15 to alpine acid mine drainage. PLoS ONE, 2017, 12, e0178008.	1.1	34
305	Development of a real-time PCR for detection of Staphylococcus pseudintermedius using a novel automated comparison of whole-genome sequences. PLoS ONE, 2017, 12, e0183925.	1.1	20
306	Methods for analyzing next-generation sequencing data IX.Genome annotation, visualization, and registration to DDBJ . Japanese Journal of Lactic Acid Bacteria, 2017, 28, 3-11.	0.1	0
307	Lokiarchaea are close relatives of Euryarchaeota, not bridging the gap between prokaryotes and eukaryotes. PLoS Genetics, 2017, 13, e1006810.	1.5	136
308	DESMAN: a new tool for de novo extraction of strains from metagenomes. Genome Biology, 2017, 18, 181.	3.8	152
309	Metagenomic analysis reveals potential interactions in an artificial coculture. AMB Express, 2017, 7, 193.	1.4	17
310	Huanglongbing impairs the rhizosphere-to-rhizoplane enrichment process of the citrus root-associated microbiome. Microbiome, 2017, 5, 97.	4.9	177

#	Article	IF	Citations
311	Dietary energy drives the dynamic response of bovine rumen viral communities. Microbiome, 2017, 5, 155.	4.9	81
312	Genome sequence of the sulfur-oxidizing Bathymodiolus thermophilus gill endosymbiont. Standards in Genomic Sciences, 2017, 12, 50.	1.5	32
313	Draft genome sequence of Dethiobacter alkaliphilus strain AHT1T, a gram-positive sulfidogenic polyextremophile. Standards in Genomic Sciences, 2017, 12, 57.	1.5	16
314	Genomic insights into the thiamin metabolism of Paenibacillus thiaminolyticus NRRL B-4156 and P. apiarius NRRL B-23460. Standards in Genomic Sciences, 2017, 12, 59.	1.5	5
315	Improving contig binning of metagenomic data using $$ {d}_2^S $$ oligonucleotide frequency dissimilarity. BMC Bioinformatics, 2017, 18, 425.	1.2	18
316	Metagenome-Assembled Genome Sequences of <i>Acetobacterium</i> sp. Strain MES1 and <i>Desulfovibrio</i> sp. Strain MES5 from a Cathode-Associated Acetogenic Microbial Community. Genome Announcements, 2017, 5, .	0.8	3
317	Draft Genome Sequence of <i>Pseudomonas</i> sp. BDAL1 Reconstructed from a Bakken Shale Hydraulic Fracturing-Produced Water Storage Tank Metagenome. Genome Announcements, 2017, 5, .	0.8	3
318	BinSanity: unsupervised clustering of environmental microbial assemblies using coverage and affinity propagation. PeerJ, 2017, 5, e3035.	0.9	139
319	Homoacetogenesis in Deep-Sea <i>Chloroflexi</i> , as Inferred by Single-Cell Genomics, Provides a Link to Reductive Dehalogenation in Terrestrial <i>Dehalococcoidetes</i>. MBio, 2017, 8, .	1.8	31
320	Optimizing and evaluating the reconstruction of Metagenome-assembled microbial genomes. BMC Genomics, 2017, 18, 915.	1.2	59
321	phyloSkeleton: taxon selection, data retrieval and marker identification for phylogenomics. Bioinformatics, 2017, 33, 1230-1232.	1.8	18
322	Draft Genome Sequence of Arthrobacter sp. Strain UCD-GKA (Phylum Actinobacteria). Genome Announcements, 2017, 5, .	0.8	3
323	High-Quality Draft Genome Sequence of â€œ <i>Candidatus</i> Methanoperedens sp.â€•Strain BLZ2, a Nitrate-Reducing Anaerobic Methane-Oxidizing Archaeon Enriched in an Anoxic Bioreactor. Genome Announcements, 2017, 5, .	0.8	22
324	Draft Genome Sequence of the Pelagic Photoferrotroph <i>Chlorobium phaeoferrooxidans</i>. Genome Announcements, 2017, 5, .	0.8	28
325	Current Scenario on Application of Computational Tools in Biological Systems. , 2018, , 1-12.		6
326	Draft Genome Sequence of the Antimycin-Producing Bacterium Streptomyces sp. Strain SM8, Isolated from the Marine Sponge Haliclona simulans. Genome Announcements, 2018, 6, .	0.8	18
327	A virus or more in (nearly) every cell: ubiquitous networks of virusâ€“host interactions in extreme environments. ISME Journal, 2018, 12, 1706-1714.	4.4	94
328	Gene expression and ultrastructure of mesoâ€•and thermophilic methanotrophic consortia. Environmental Microbiology, 2018, 20, 1651-1666.	1.8	90

#	ARTICLE	IF	CITATIONS
329	Comparative genomics sheds light on niche differentiation and the evolutionary history of comammox <i>Nitrospira</i>. ISME Journal, 2018, 12, 1779-1793.	4.4	249
330	Gut bacteria selectively promoted by dietary fibers alleviate type 2 diabetes. Science, 2018, 359, 1151-1156.	6.0	1,521
331	Genome-resolved metagenomics identifies genetic mobility, metabolic interactions, and unexpected diversity in perchlorate-reducing communities. ISME Journal, 2018, 12, 1568-1581.	4.4	82
332	Landscape topography structures the soil microbiome in arctic polygonal tundra. Nature Communications, 2018, 9, 777.	5.8	105
333	Peatland <i>Acidobacteria</i> with a dissimilatory sulfur metabolism. ISME Journal, 2018, 12, 1729-1742.	4.4	168
334	Oxidation of organic electron donor by denitratation: Performance, pathway and key microorganism. Chemical Engineering Journal, 2018, 343, 554-560.	6.6	36
335	Metagenomic binning reveals the functional roles of core abundant microorganisms in twelve full-scale biogas plants. Water Research, 2018, 140, 123-134.	5.3	122
336	Dual Role of Humic Substances As Electron Donor and Shuttle for Dissimilatory Iron Reduction. Environmental Science & Technology, 2018, 52, 5691-5699.	4.6	116
337	A methanotrophic archaeon couples anaerobic oxidation of methane to Fe(III) reduction. ISME Journal, 2018, 12, 1929-1939.	4.4	266
338	Fast Metagenomic Binning via Hashing and Bayesian Clustering. Journal of Computational Biology, 2018, 25, 677-688.	0.8	5
339	Genomic insights into the Agromyces-like symbiont of earthworms and its distribution among host species. FEMS Microbiology Ecology, 2018, 94, .	1.3	9
340	Mechanisms of Persistence of the Ammonia-Oxidizing Bacteria <i>Nitrosomonas</i> to the Biocide Free Nitrous Acid. Environmental Science & Technology, 2018, 52, 5386-5397.	4.6	52
341	Genome Sequences of Apibacter spp., Gut Symbionts of Asian Honey Bees. Genome Biology and Evolution, 2018, 10, 1174-1179.	1.1	27
342	Cultivation and genomics of the first freshwater SAR11 (LD12) isolate. ISME Journal, 2018, 12, 1846-1860.	4.4	123
343	Metabolic potential and <i>in situ</i> transcriptomic profiles of previously uncharacterized key microbial groups involved in coupled carbon, nitrogen and sulfur cycling in anoxic marine zones. Environmental Microbiology, 2018, 20, 2727-2742.	1.8	18
344	Hospitalized Premature Infants Are Colonized by Related Bacterial Strains with Distinct Proteomic Profiles. MBio, 2018, 9, .	1.8	34
345	Obtaining high-quality draft genomes from uncultured microbes by cleaning and co-assembly of single-cell amplified genomes. Scientific Reports, 2018, 8, 2059.	1.6	48
346	Free-living bacteria and potential bacterial pathogens in sewage treatment plants. Applied Microbiology and Biotechnology, 2018, 102, 2455-2464.	1.7	47

#	ARTICLE	IF	CITATIONS
347	Recent advances in reconstructing microbial secondary metabolites biosynthesis in Aspergillus spp.. Biotechnology Advances, 2018, 36, 739-783.	6.0	61
348	Comparative genomic inference suggests mixotrophic lifestyle for Thorarchaeota. ISME Journal, 2018, 12, 1021-1031.	4.4	86
349	Draft Genome Sequence of <i>Endozoicomonas acroporae</i> Strain Acr-14 ^T , Isolated from <i>Acropora</i> Coral. Genome Announcements, 2018, 6, .	0.8	10
350	Partnership of <i>Arthrobacter</i> and <i>Pimelobacter</i> in Aerobic Degradation of Sulfadiazine Revealed by Metagenomics Analysis and Isolation. Environmental Science & Technology, 2018, 52, 2963-2972.	4.6	26
351	Draft Genome Sequence of <i>Telmatospirillum siberiense</i> 26-4b1, an Acidotolerant Peatland Alphaproteobacterium Potentially Involved in Sulfur Cycling. Genome Announcements, 2018, 6, .	0.8	13
352	Genomic insights into metabolic potentials of two simultaneous aerobic denitrification and phosphorus removal bacteria, Achromobacter sp. GAD3 and Agrobacterium sp. LAD9. FEMS Microbiology Ecology, 2018, 94, .	1.3	31
353	The reconstruction of 2,631 draft metagenome-assembled genomes from the global oceans. Scientific Data, 2018, 5, 170203.	2.4	449
354	Lysogeny is prevalent and widely distributed in the murine gut microbiota. ISME Journal, 2018, 12, 1127-1141.	4.4	140
355	Performance and genome-centric metagenomics of thermophilic single and two-stage anaerobic digesters treating cheese wastes. Water Research, 2018, 134, 181-191.	5.3	56
356	Community proteogenomics reveals the systemic impact of phosphorus availability on microbial functions in tropical soil. Nature Ecology and Evolution, 2018, 2, 499-509.	3.4	116
357	Insights into the metabolic functioning of a multipartner ciliate symbiosis from oxygenâ€depleted sediments. Molecular Ecology, 2018, 27, 1794-1807.	2.0	29
358	Salinivibrio kushneri sp. nov., a moderately halophilic bacterium isolated from salterns. Systematic and Applied Microbiology, 2018, 41, 159-166.	1.2	19
359	Genomic features of bacterial adaptation to plants. Nature Genetics, 2018, 50, 138-150.	9.4	480
360	The complex resistomes of Paenibacillaceae reflect diverse antibiotic chemical ecologies. ISME Journal, 2018, 12, 885-897.	4.4	15
361	In vitro and in silico characterisation of Lactobacillus paraplantarum D2-1, a starter culture for soymilk fermentation. International Journal of Food Sciences and Nutrition, 2018, 69, 857-869.	1.3	8
362	Genomeâ€enabled metabolic reconstruction of dominant chemosynthetic colonizers in deepâ€sea massive sulfide deposits. Environmental Microbiology, 2018, 20, 862-877.	1.8	41
363	Genomic insights into the <i>Acidobacteria</i> reveal strategies for their success in terrestrial environments. Environmental Microbiology, 2018, 20, 1041-1063.	1.8	228
364	Draft Genome Sequences of <i>Pseudomonas putida</i> UV4 and UV4/95, Toluene Dioxygenase-Expressing Producers of <i>cis</i> -1,2-Dihydrodiols. Genome Announcements, 2018, 6, .	0.8	4

#	ARTICLE	IF	CITATIONS
365	Draft Genome Sequence of the Predatory Marine Bacterium <i>Halobacteriovorax</i> sp. Strain JY17. Genome Announcements, 2018, 6, .	0.8	2
366	Vibrio coralliirubri sp. nov., a new species isolated from mucus of red coral (Corallium rubrum) collected at Procida island, Italy. Antonie Van Leeuwenhoek, 2018, 111, 1105-1115.	0.7	18
367	Studying microbial functionality within the gut ecosystem by systems biology. Genes and Nutrition, 2018, 13, 5.	1.2	31
368	Correcting for 16S rRNA gene copy numbers in microbiome surveys remains an unsolved problem. Microbiome, 2018, 6, 41.	4.9	514
369	Co-cultivation of the strictly anaerobic methanogen Methanosarcina barkeri with aerobic methanotrophs in an oxygen-limited membrane bioreactor. Applied Microbiology and Biotechnology, 2018, 102, 5685-5694.	1.7	16
370	Comparative genomic analysis of Geosporobacter ferrireducens and its versatility of anaerobic energy metabolism. Journal of Microbiology, 2018, 56, 365-371.	1.3	8
371	Draft Genome Sequence of <i>Rhodococcus</i> sp. Strain NCIMB 12038, a Naphthalene-Degrading Bacterium. Genome Announcements, 2018, 6, .	0.8	1
372	Genome biology of a novel lineage of planctomycetes widespread in anoxic aquatic environments. Environmental Microbiology, 2018, 20, 2438-2455.	1.8	57
374	Stable Isotope Probing for Microbial Iron Reduction in Chocolate Pots Hot Spring, Yellowstone National Park. Applied and Environmental Microbiology, 2018, 84, .	1.4	46
375	Microbial community and metagenome dynamics during biodegradation of dispersed oil reveals potential key-players in cold Norwegian seawater. Marine Pollution Bulletin, 2018, 129, 370-378.	2.3	91
376	Draft Genome Sequences of Novel <i>Pseudomonas</i> , <i>Flavobacterium</i> , and <i>Sediminibacterium</i> Species Strains from a Freshwater Ecosystem. Genome Announcements, 2018, 6, .	0.8	4
377	GraftM: a tool for scalable, phylogenetically informed classification of genes within metagenomes. Nucleic Acids Research, 2018, 46, e59-e59.	6.5	130
378	Finished Genome Sequence of a Polyurethane-Degrading Pseudomonas Isolate. Genome Announcements, 2018, 6, .	0.8	1
379	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. Nature Biotechnology, 2018, 36, 359-367.	9.4	414
380	Discovery of enzymes for toluene synthesis from anoxic microbial communities. Nature Chemical Biology, 2018, 14, 451-457.	3.9	47
381	Closed Genome Sequence of Phytopathogen Biocontrol Agent <i>Bacillus velezensis</i> Strain AGVL-005, Isolated from Soybean. Genome Announcements, 2018, 6, .	0.8	1
382	Microbiome Dynamics in a Large Artificial Seawater Aquarium. Applied and Environmental Microbiology, 2018, 84, .	1.4	33
383	New approach for studying mobile genes using metagenomic analysis. Oral Diseases, 2018, 24, 494-496.	1.5	0

#	ARTICLE	IF	CITATIONS
384	The Enigmatic Genome of an Obligate Ancient Spiroplasma Symbiont in a Hadal Holothurian. Applied and Environmental Microbiology, 2018, 84, .	1.4	38
385	Planctomycetes attached to algal surfaces: Insight into their genomes. Genomics, 2018, 110, 231-238.	1.3	39
386	Genomes of Novel Microbial Lineages Assembled from the Sub-Ice Waters of Lake Baikal. Applied and Environmental Microbiology, 2018, 84, .	1.4	91
387	DNA-SIP based genome-centric metagenomics identifies key long-chain fatty acid-degrading populations in anaerobic digesters with different feeding frequencies. ISME Journal, 2018, 12, 112-123.	4.4	88
388	Excess labile carbon promotes the expression of virulence factors in coral reef bacterioplankton. ISME Journal, 2018, 12, 59-76.	4.4	58
389	Acetoclastic <i>Methanosaeta</i> are dominant methanogens in organic-rich Antarctic marine sediments. ISME Journal, 2018, 12, 330-342.	4.4	70
390	Nutrient and acetate amendment leads to acetoclastic methane production and microbial community change in a nonâ€producing Australian coal well. Microbial Biotechnology, 2018, 11, 626-638.	2.0	30
391	Ecological and genomic profiling of anaerobic methane-oxidizing archaea in a deep granitic environment. ISME Journal, 2018, 12, 31-47.	4.4	59
392	A dynamic microbial community with high functional redundancy inhabits the cold, oxic subseafloor aquifer. ISME Journal, 2018, 12, 1-16.	4.4	148
393	Metagenomics-guided analysis of microbial chemolithoautotrophic phosphite oxidation yields evidence of a seventh natural CO ₂ fixation pathway. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E92-E101.	3.3	115
394	Metagenomic binning and association of plasmids with bacterial host genomes using DNA methylation. Nature Biotechnology, 2018, 36, 61-69.	9.4	116
395	Contrasting patterns of genome-level diversity across distinct co-occurring bacterial populations. ISME Journal, 2018, 12, 742-755.	4.4	76
396	Localized high abundance of Marine Group II archaea in the subtropical Pearl River Estuary: implications for their niche adaptation. Environmental Microbiology, 2018, 20, 734-754.	1.8	53
397	Rice Paddy Nitrospirae Carry and Express Genes Related to Sulfate Respiration: Proposal of the New Genus â€œCandidatus Sulfobiumâ€• Applied and Environmental Microbiology, 2018, 84, .	1.4	83
398	A novel Chromatiales bacterium is a potential sulfide oxidizer in multiple orders of marine sponges. Environmental Microbiology, 2018, 20, 800-814.	1.8	27
399	Metabolic versatility of a novel N₂â€fixing Alphaproteobacterium isolated from a marine oxygen minimum zone. Environmental Microbiology, 2018, 20, 755-768.	1.8	29
400	Spatially distinct, temporally stable microbial populations mediate biogeochemical cycling at and below the seafloor in hydrothermal vent fluids. Environmental Microbiology, 2018, 20, 769-784.	1.8	71
401	The enigmatic SAR202 cluster up close: shedding light on a globally distributed dark ocean lineage involved in sulfur cycling. ISME Journal, 2018, 12, 655-668.	4.4	101

#	Article	IF	Citations
402	Phylogeny and genomics of SAUL, an enigmatic bacterial lineage frequently associated with marine sponges. Environmental Microbiology, 2018, 20, 561-576.	1.8	32
403	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
404	A bacterial pioneer produces cellulase complexes that persist through community succession. Nature Microbiology, 2018, 3, 99-107.	5.9	38
405	On the bright side of a forest pest-the metabolic potential of bark beetles' bacterial associates. Science of the Total Environment, 2018, 619-620, 9-17.	3.9	25
406	Insights from the Genomes of Microbes Thriving in Uranium-Enriched Sediments. Microbial Ecology, 2018, 75, 970-984.	1.4	17
407	Metagenomic Protocols and Strategies. , 2018, , 15-54.		7
408	Metagenomes from deep Baltic Sea sediments reveal how past and present environmental conditions determine microbial community composition. Marine Genomics, 2018, 37, 58-68.	0.4	52
409	Evidence for H₂ consumption by uncultured <i>Desulfobacterales</i> in coastal sediments. Environmental Microbiology, 2018, 20, 450-461.	1.8	51
410	Freshwater carbon and nutrient cycles revealed through reconstructed population genomes. PeerJ, 2018, 6, e6075.	0.9	64
411	Draft Genome Sequence of â€œ Candidatus Moanabacter tarae,â€•Representing a Novel Marine Verrucomicrobial Lineage. Microbiology Resource Announcements, 2018, 7, .	0.3	9
412	Draft Genome Sequence of â€œ <i>Candidatus</i> Spirobacillus cienkowskii,â€•a Pathogen of Freshwater <i>Daphnia</i> Species, Reconstructed from Hemolymph Metagenomic Reads. Microbiology Resource Announcements, 2018, 7, .	0.3	13
413	The Phylogenomic Diversity of Herbivore-Associated <i>Fibrobacter</i> spp. Is Correlated to Lignocellulose-Degrading Potential. MSphere, 2018, 3, .	1.3	38
414	Draft Genome Sequences of Mycolicibacter senuensis Isolate GF74 and Mycobacterium colombiense Isolates GF28 and GF76 from a Swine Farm in Japan. Microbiology Resource Announcements, 2018, 7, .	0.3	16
415	Assessment of urban microbiome assemblies with the help of targeted in silico gold standards. Biology Direct, 2018, 13, 22.	1.9	10
416	Draft Genome Sequence of â€œ Candidatus Bathyarchaeotaâ€•Archaeon BE326-BA-RLH, an Uncultured Denitrifier and Putative Anaerobic Methanotroph from South Africaâ€™s Deep Continental Biosphere. Microbiology Resource Announcements, 2018, 7, .	0.3	11
417	Draft Genome Sequence of Bacillus safensis Strain JG-B5T, Isolated from a Uranium Mining Waste Pile. Microbiology Resource Announcements, 2018, 7, .	0.3	1
418	Read cloud sequencing elucidates microbiome dynamics in a hematopoietic cell transplant patient. , 2018, 2018, 234-241.		2
419	CLAME: a new alignment-based binning algorithm allows the genomic description of a novel Xanthomonadaceae from the Colombian Andes. BMC Genomics, 2018, 19, 858.	1.2	2

#	ARTICLE	IF	CITATIONS
420	High-Quality Draft Single-Cell Genome Sequence of the NS5 Marine Group from the Coastal Red Sea. Genome Announcements, 2018, 6, .	0.8	10
422	Parallel Evolution of Genome Streamlining and Cellular Bioenergetics across the Marine Radiation of a Bacterial Phylum. MBio, 2018, 9, .	1.8	27
423	Draft genome sequences of â€˜Candidatus Chloroploca asiaticaâ€™ and â€˜Candidatus Viridilinea mediisalinaâ€™, candidate representatives of the Chloroflexales order: phylogenetic and taxonomic implications. Standards in Genomic Sciences, 2018, 13, 24.	1.5	56
424	Quantifying and comparing bacterial growth dynamics in multiple metagenomic samples. Nature Methods, 2018, 15, 1041-1044.	9.0	40
425	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelersâ€™ diarrhea. Microbiome, 2018, 6, 201.	4.9	20
426	Expansive microbial metabolic versatility and biodiversity in dynamic Guaymas Basin hydrothermal sediments. Nature Communications, 2018, 9, 4999.	5.8	205
427	Characterisation of the British honey bee metagenome. Nature Communications, 2018, 9, 4995.	5.8	51
428	The draft genome sequence of â€œNitrospira lentaâ€•strain BS10, a nitrite oxidizing bacterium isolated from activated sludge. Standards in Genomic Sciences, 2018, 13, 32.	1.5	28
429	Analysis of the Genome and Metabolome of Marine Myxobacteria Reveals High Potential for Biosynthesis of Novel Specialized Metabolites. Scientific Reports, 2018, 8, 16600.	1.6	40
430	The gill-associated microbiome is the main source of wood plant polysaccharide hydrolases and secondary metabolite gene clusters in the mangrove shipworm Neoteredo reynei. PLoS ONE, 2018, 13, e0200437.	1.1	18
431	Metagenomics-Based, Strain-Level Analysis of Escherichia coli From a Time-Series of Microbiome Samples From a Crohn's Disease Patient. Frontiers in Microbiology, 2018, 9, 2559.	1.5	37
432	The first world swimming championships of roseobactersâ€”Phylogenomic insights into an exceptional motility phenotype. Systematic and Applied Microbiology, 2018, 41, 544-554.	1.2	23
433	Genomic and in-situ Transcriptomic Characterization of the Candidate Phylum NPL-UPL2 From Highly Alkaline Highly Reducing Serpentinized Groundwater. Frontiers in Microbiology, 2018, 9, 3141.	1.5	31
434	Single cell genomic and transcriptomic evidence for the use of alternative nitrogen substrates by anammox bacteria. ISME Journal, 2018, 12, 2706-2722.	4.4	45
435	Draft Genome Sequence of â€œCandidatus Izimaplasma sp.â€•Strain ZiA1, Obtained from a Toluene-Degrading and Iron-Reducing Enrichment Culture. Microbiology Resource Announcements, 2018, 7, .	0.3	2
436	Development of a Genetic System for Marinobacter atlanticus CP1 (sp. nov.), a Wax Ester Producing Strain Isolated From an Autotrophic Biocathode. Frontiers in Microbiology, 2018, 9, 3176.	1.5	26
437	Genome Sequences and Comparative Analysis of Two Extended-Spectrum Extensively-Drug Resistant Mycobacterium tuberculosis Strains. Frontiers in Pharmacology, 2018, 9, 1492.	1.6	2
438	Draft Genome Sequence of the Extremely Desiccation-Tolerant Cyanobacterium Gloeocapsopsis sp. Strain AAB1. Genome Announcements, 2018, 6, .	0.8	12

#	ARTICLE	IF	CITATIONS
439	Genome Sequence of <i>Geothermobacter</i> sp. Strain HR-1, an Iron Reducer from the LÅâ€˜ihi Seamount, Hawaiâ€™i. Genome Announcements, 2018, 6, .	0.8	2
440	Genotypic differences between strains of the opportunistic pathogen Corynebacterium bovis isolated from humans, cows, and rodents. PLoS ONE, 2018, 13, e0209231.	1.1	11
441	Draft Genome Sequence of a Divergent Anaerobic Member of the Chloroflexi Class Ardenticatenia from a Sulfidic Hot Spring. Genome Announcements, 2018, 6, .	0.8	13
442	Enrichment and Genomic Characterization of a N2O-Reducing Chemolithoautotroph From a Deep-Sea Hydrothermal Vent. Frontiers in Bioengineering and Biotechnology, 2018, 6, 184.	2.0	6
443	Genomic Insight Into the Predominance of Candidate Phylum Atribacteria JS1 Lineage in Marine Sediments. Frontiers in Microbiology, 2018, 9, 2909.	1.5	35
444	Complement Susceptibility in Relation to Genome Sequence of Recent Klebsiella pneumoniae Isolates from Thai Hospitals. MSphere, 2018, 3, .	1.3	25
445	Comparative Genomics and Proteomic Analysis of Assimilatory Sulfate Reduction Pathways in Anaerobic Methanotrophic Archaea. Frontiers in Microbiology, 2018, 9, 2917.	1.5	33
446	Insights Into Limnothrix sp. Metabolism Based on Comparative Genomics. Frontiers in Microbiology, 2018, 9, 2811.	1.5	5
447	Metatranscriptomic and Thermodynamic Insights into Medium-Chain Fatty Acid Production Using an Anaerobic Microbiome. MSystems, 2018, 3, .	1.7	69
448	GLOSSary: the GLobal Ocean 16S subunit web accessible resource. BMC Bioinformatics, 2018, 19, 443.	1.2	4
449	High throughput in situ metagenomic measurement of bacterial replication at ultra-low sequencing coverage. Nature Communications, 2018, 9, 4956.	5.8	95
450	Poplar phyllosphere harbors disparate isoprene-degrading bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 13081-13086.	3.3	69
451	Supragingival Plaque Microbiome Ecology and Functional Potential in the Context of Health and Disease. MBio, 2018, 9, .	1.8	58
452	Metabolism and Occurrence of Methanogenic and Sulfate-Reducing Syntrophic Acetate Oxidizing Communities in Haloalkaline Environments. Frontiers in Microbiology, 2018, 9, 3039.	1.5	48
453	Introduction to Bioinformatics in Microbiology. Learning Materials in Biosciences, 2018, , .	0.2	5
454	Full Shotgun DNA Metagenomics. Learning Materials in Biosciences, 2018, , 163-175.	0.2	1
455	Comparative Genomic Analysis of Members of the Genera<i>Methanosphaera</i>and<i>Methanobrevibacter</i>Reveals Distinct Clades with Specific Potential Metabolic Functions. Archaea, 2018, 2018, 1-9.	2.3	17
456	Identification of metabolite and protein explanatory variables governing microbiome establishment and re-establishment within a cellulose-degrading anaerobic bioreactor. PLoS ONE, 2018, 13, e0204831.	1.1	0

#	ARTICLE	IF	CITATIONS
457	Metagenome Assembly and Contig Assignment. Methods in Molecular Biology, 2018, 1849, 179-192.	0.4	0
458	Active Crossfire Between Cyanobacteria and Cyanophages in Phototrophic Mat Communities Within Hot Springs. Frontiers in Microbiology, 2018, 9, 2039.	1.5	29
459	Cyclopropane-Containing Fatty Acids from the Marine Bacterium Labrenzia sp. 011 with Antimicrobial and GPR84 Activity. Marine Drugs, 2018, 16, 369.	2.2	25
460	Biogeochemical Cycling by a Low-Diversity Microbial Community in Deep Groundwater. Frontiers in Microbiology, 2018, 9, 2129.	1.5	35
461	Review: The application of omics to rumen microbiota function. Animal, 2018, 12, s233-s245.	1.3	31
462	Metagenomics Reveals Microbial Diversity and Metabolic Potentials of Seawater and Surface Sediment From a Hadal Biosphere at the Yap Trench. Frontiers in Microbiology, 2018, 9, 2402.	1.5	80
463	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
464	Comprehensive simulation of metagenomic sequencing data with nonâ€uniform sampling distribution. Quantitative Biology, 2018, 6, 175-185.	0.3	2
465	Genome-Based Analysis Reveals the Taxonomy and Diversity of the Family Idiomarinaceae. Frontiers in Microbiology, 2018, 9, 2453.	1.5	48
466	Metagenomic analyses highlight the symbiotic association between the glacier stonefly <i>Andiperla willinki</i> and its bacterial gut community. Environmental Microbiology, 2018, 20, 4170-4183.	1.8	25
467	A metagenomics roadmap to the uncultured genome diversity in hypersaline soda lake sediments. Microbiome, 2018, 6, 168.	4.9	120
468	Microbiome Analysis. Methods in Molecular Biology, 2018, , .	0.4	13
469	Subsampled Assemblies and Hybrid Nucleotide Composition/Differential Coverage Binning for Genome-Resolved Metagenomics. Methods in Molecular Biology, 2018, 1849, 215-225.	0.4	2
470	Detection of the carbapenemase gene blaVIM-5 in members of the Pseudomonas putida group isolated from polluted Nigerian wetlands. Scientific Reports, 2018, 8, 15116.	1.6	20
471	Genomic Characterization of Extended-Spectrum Cephalosporin-Resistant Salmonella enterica in the Colombian Poultry Chain. Frontiers in Microbiology, 2018, 9, 2431.	1.5	27
472	Draft Genome Sequences of Two Bacillus sp. Strains and Four Cellulomonas sp. Strains Isolated from Heavy-Metal-Contaminated Soil. Microbiology Resource Announcements, 2018, 7, .	0.3	2
473	Hidden in plain sightâ€"highly abundant and diverse planktonic freshwater Chloroflexi. Microbiome, 2018, 6, 176.	4.9	130
474	Complete genome sequence reveals evolutionary dynamics of an emerging and variant pathovar of Xanthomonas euvesicatoria. Genome Biology and Evolution, 2018, 10, 3104-3109.	1.1	8

#	Article	IF	Citations
475	Draft genome sequences of Cylindrospermopsis raciborskii strains CS-508 and MVCC14, isolated from freshwater bloom events in Australia and Uruguay. Standards in Genomic Sciences, 2018, 13, 26.	1.5	4
476	Isolation and genomic characterization of six endophytic bacteria isolated from Saccharum sp (sugarcane): Insights into antibiotic, secondary metabolite and quorum sensing metabolism. Journal of Genomics, 2018, 6, 117-121.	0.6	8
477	The Tree of Life. Grand Challenges in Biology and Biotechnology, 2018, , 55-99.	2.4	8
478	High-quality genome sequences of uncultured microbes by assembly of read clouds. Nature Biotechnology, 2018, 36, 1067-1075.	9.4	103
479	Precision identification of diverse bloodstream pathogens in the gut microbiome. Nature Medicine, 2018, 24, 1809-1814.	15.2	158
480	High-Quality Draft Single-Cell Genome Sequence Belonging to the Archaeal Candidate Division SA1, Isolated from Nereus Deep in the Red Sea. Genome Announcements, 2018, 6, .	0.8	6
481	Bacterial Survival Strategies in an Alkaline Tailing Site and the Physiological Mechanisms of Dominant Phylotypes As Revealed by Metagenomic Analyses. Environmental Science & Technology, 2018, 52, 13370-13380.	4.6	112
482	Genomic Description of â€˜Candidatus Abyssubacteria,â€™ a Novel Subsurface Lineage Within the Candidate Phylum Hydrogenedentes. Frontiers in Microbiology, 2018, 9, 1993.	1.5	36
483	Metabolic Interactions of a Chain Elongation Microbiome. Applied and Environmental Microbiology, 2018, 84, .	1.4	93
484	MetaWRAPâ€"a flexible pipeline for genome-resolved metagenomic data analysis. Microbiome, 2018, 6, 158.	4.9	1,098
485	The genome of a novel isolate of Prochlorococcus from the Red Sea contains transcribed genes for compatible solute biosynthesis. FEMS Microbiology Ecology, 2018, 94, .	1.3	5
486	Dynamics of microbial populations mediating biogeochemical cycling in a freshwater lake. Microbiome, 2018, 6, 165.	4.9	40
487	Automatic identification of optimal marker genes for phenotypic and taxonomic groups of microorganisms. PLoS ONE, 2018, 13, e0195537.	1.1	1
488	Single-cell genomics of co-sorted Nanoarchaeota suggests novel putative host associations and diversification of proteins involved in symbiosis. Microbiome, 2018, 6, 161.	4.9	44
489	Genome-Centered Metagenomics Analysis Reveals the Symbiotic Organisms Possessing Ability to Cross-Feed with Anammox Bacteria in Anammox Consortia. Environmental Science & Technology, 2018, 52, 11285-11296.	4.6	208
490	Metagenomic Insights into the Phylogenetic and Metabolic Diversity of the Prokaryotic Community Dwelling in Hypersaline Soils from the Odiel Saltmarshes (SW Spain). Genes, 2018, 9, 152.	1.0	50
491	Development and characterization of stable anaerobic thermophilic methanogenic microbiomes fermenting switchgrass at decreasing residence times. Biotechnology for Biofuels, 2018, 11, 243.	6.2	37
492	Metagenomic Assembly and Prokaryotic Metagenome-Assembled Genome Sequences from the Northern Gulf of Mexico â€œDead Zoneâ€. Microbiology Resource Announcements, 2018, 7, .	0.3	14

#	Article	IF	Citations
493	Dynamic membrane bioreactor (DMBR) for the treatment of landfill leachate; bioreactor's performance and metagenomic insights into microbial community evolution. Environmental Pollution, 2018, 243, 326-335.	3.7	27
494	Investigating the Composition and Metabolic Potential of Microbial Communities in Chocolate Pots Hot Springs. Frontiers in Microbiology, 2018, 9, 2075.	1.5	19
495	Inhibition of anammox by sludge thermal hydrolysis and metagenomic insights. Bioresource Technology, 2018, 270, 46-54.	4.8	26
496	Genomic Insights Into the Acid Adaptation of Novel Methanotrophs Enriched From Acidic Forest Soils. Frontiers in Microbiology, 2018, 9, 1982.	1.5	23
497	A metagenomic window into the 2-km-deep terrestrial subsurface aquifer revealed multiple pathways of organic matter decomposition. FEMS Microbiology Ecology, 2018, 94, .	1.3	38
498	Draft Genome Sequence of the Cadmium-Resistant Strain JJU2, Belonging to the Family Hapalosiphonaceae of the Cyanobacteria. Microbiology Resource Announcements, 2018, 7, .	0.3	5
499	Genomic Characterization and Copy Number Variation of <i>Bacillus anthracis</i> Plasmids pXO1 and pXO2 in a Historical Collection of 412 Strains. MSystems, 2018, 3, .	1.7	32
500	Bloom of a denitrifying methanotroph, â€˜<i>Candidatus</i> Methylomirabilis limneticaâ€™, in a deep stratified lake. Environmental Microbiology, 2018, 20, 2598-2614.	1.8	87
501	Draft Genome Sequence of a Dictyoglomus sp. from an Enrichment Culture of a New Zealand Geothermal Spring. Genome Announcements, 2018, 6, .	0.8	0
502	Best practices for analysing microbiomes. Nature Reviews Microbiology, 2018, 16, 410-422.	13.6	1,138
503	Taxon-specific aerosolization of bacteria and viruses in an experimental ocean-atmosphere mesocosm. Nature Communications, 2018, 9, 2017.	5.8	103
504	Metagenomic and metatranscriptomic analysis of the microbial community in Swiss-type Maasdam cheese during ripening. International Journal of Food Microbiology, 2018, 281, 10-22.	2.1	63
505	Recovery of genomes from metagenomes via a dereplication, aggregation and scoring strategy. Nature Microbiology, 2018, 3, 836-843.	5.9	906
506	Draft Genome Sequence of a Novel Thermofilum sp. Strain from a New Zealand Hot Spring Enrichment Culture. Genome Announcements, 2018, 6, .	0.8	1
507	Removal of selenate from brine using anaerobic bacteria and zero valent iron. Journal of Environmental Management, 2018, 222, 348-358.	3.8	11
508	Marsarchaeota are an aerobic archaeal lineage abundant in geothermal iron oxide microbial mats. Nature Microbiology, 2018, 3, 732-740.	5.9	53
509	The genome of an endosymbiotic methanogen is very similar to those of its freeâ€living relatives. Environmental Microbiology, 2018, 20, 2538-2551.	1.8	21
510	A closely-related clade of globally distributed bloom-forming cyanobacteria within the Nostocales. Harmful Algae, 2018, 77, 93-107.	2.2	27

#	Article	IF	Citations
511	Temperature modulates Fischerella thermalis ecotypes in Porcelana Hot Spring. Systematic and Applied Microbiology, 2018, 41, 531-543.	1.2	32
512	Genus-wide comparison of Pseudovibrio bacterial genomes reveal diverse adaptations to different marine invertebrate hosts. PLoS ONE, 2018, 13, e0194368.	1.1	50
513	An epizootic of <i>Chlamydia psittaci</i> equine reproductive loss associated with suspected spillover from native Australian parrots. Emerging Microbes and Infections, 2018, 7, 1-13.	3.0	48
514	Genomics of the Uncultivated, Periodontitis-Associated Bacterium <i>Tannerella</i> sp. BU045 (Oral) Tj ETQq1 1 0.784314 rgBT /Overl	1.7	10
515	Hydrocarbon degradation and response of seafloor sediment bacterial community in the northern Gulf of Mexico to light Louisiana sweet crude oil. ISME Journal, 2018, 12, 2532-2543.	4.4	115
516	Integrated methodological approach reveals microbial diversity and functions in aerobic groundwater microcosms adapted to vinyl chloride. FEMS Microbiology Ecology, 2018, 94, .	1.3	11
517	MetaPOAP: presence or absence of metabolic pathways in metagenome-assembled genomes. Bioinformatics, 2018, 34, 4284-4286.	1.8	50
518	Defining endemic cholera at three levels of spatiotemporal resolution within Bangladesh. Nature Genetics, 2018, 50, 951-955.	9.4	37
519	Linking Nitrogen Load to the Structure and Function of Wetland Soil and Rhizosphere Microbial Communities. MSystems, 2018, 3, .	1.7	56
520	Peering into the Genetic Makeup of Natural Microbial Populations Using Metagenomics. Population Genomics, 2018, , 49-75.	0.2	10
521	Galacturonate Metabolism in Anaerobic Chemostat Enrichment Cultures: Combined Fermentation and Acetogenesis by the Dominant sp. nov. â€œCandidatus Galacturonibacter soehngeniiâ€. Applied and Environmental Microbiology, 2018, 84, .	1.4	16
522	Methanotrophy across a natural permafrost thaw environment. ISME Journal, 2018, 12, 2544-2558.	4.4	102
523	Draft Genome Sequence of Mycoplasma arginini Strain NGR_2017. Genome Announcements, 2018, 6, .	0.8	0
524	Complete Genome Sequence of Streptomyces sp. Strain BSE7F, a Bali Mangrove Sediment Actinobacterium with Antimicrobial Activities. Genome Announcements, 2018, 6, .	0.8	4
525	Draft Reference Genome Sequence of Corynebacterium mastitidis 16-1433, Isolated from a Mouse. Genome Announcements, 2018, 6, .	0.8	2
526	Community dynamics and functional characteristics of naphthaleneâ€degrading populations in contaminated surface sediments and hypoxic/anoxic groundwater. Environmental Microbiology, 2018, 20, 3543-3559.	1.8	22
527	Complex Evolutionary History of Translation Elongation Factor 2 and Diphthamide Biosynthesis in Archaea and Parabasalids. Genome Biology and Evolution, 2018, 10, 2380-2393.	1.1	37
528	MARVEL, a Tool for Prediction of Bacteriophage Sequences in Metagenomic Bins. Frontiers in Genetics, 2018, 9, 304.	1.1	133

#	Article	IF	Citations
529	Culture- and metagenomics-enabled analyses of the <i>Methanosphaera</i> genus reveals their monophyletic origin and differentiation according to genome size. ISME Journal, 2018, 12, 2942-2953.	4.4	24
530	Exploring the microbiome of the â€œstarâ€•freshwater diatom <i>Asterionella formosa</i> in a laboratory context. Environmental Microbiology, 2018, 20, 3601-3615.	1.8	6
531	Distinctive characters of Nostoc genomes in cyanolichens. BMC Genomics, 2018, 19, 434.	1.2	30
532	Characterization of Bathyarchaeota genomes assembled from metagenomes of biofilms residing in mesophilic and thermophilic biogas reactors. Biotechnology for Biofuels, 2018, 11, 167.	6.2	38
533	Functional Microbial Features Driving Community Assembly During Seed Germination and Emergence. Frontiers in Plant Science, 2018, 9, 902.	1.7	92
534	Conserved phylogenetic distribution and limited antibiotic resistance of class 1 integrons revealed by assessing the bacterial genome and plasmid collection. Microbiome, 2018, 6, 130.	4.9	83
535	Comparative metatranscriptomics reveals extracellular electron transfer pathways conferring microbial adaptivity to surface redox potential changes. ISME Journal, 2018, 12, 2844-2863.	4.4	68
536	Consensus assessment of the contamination level of publicly available cyanobacterial genomes. PLoS ONE, 2018, 13, e0200323.	1.1	41
537	Microbial Community Structure and Functional Potential Along a Hypersaline Gradient. Frontiers in Microbiology, 2018, 9, 1492.	1.5	41
538	Endosymbiont genomes yield clues of tubeworm success. ISME Journal, 2018, 12, 2785-2795.	4.4	33
539	Genome Reduction in <i>Psychromonas</i> Species within the Gut of an Amphipod from the Oceanâ€™s Deepest Point. MSystems, 2018, 3, .	1.7	21
540	Genomic profiling of four cultivated <i>Candidatus</i> Nitrotoga spp. predicts broad metabolic potential and environmental distribution. ISME Journal, 2018, 12, 2864-2882.	4.4	42
541	Anaerobic degradation of phenanthrene by a sulfateâ€•reducing enrichment culture. Environmental Microbiology, 2018, 20, 3589-3600.	1.8	45
542	Comprehensive Insights Into Composition, Metabolic Potentials, and Interactions Among Archaeal, Bacterial, and Viral Assemblages in Meromictic Lake Shunet in Siberia. Frontiers in Microbiology, 2018, 9, 1763.	1.5	11
543	A Novel Eukaryotic Denitrification Pathway in Foraminifera. Current Biology, 2018, 28, 2536-2543.e5.	1.8	75
544	A metagenomic analysis of the camel rumenâ€™s microbiome identifies the major microbes responsible for lignocellulose degradation and fermentation. Biotechnology for Biofuels, 2018, 11, 216.	6.2	96
545	Metagenomic Characterization of the Human Intestinal Microbiota in Fecal Samples from STEC-Infected Patients. Frontiers in Cellular and Infection Microbiology, 2018, 8, 25.	1.8	47
546	Enterococcus faecalis AHG0090 is a Genetically Tractable Bacterium and Produces a Secreted Peptidic Bioactive that Suppresses Nuclear Factor Kappa B Activation in Human Gut Epithelial Cells. Frontiers in Immunology, 2018, 9, 790.	2.2	15

#	Article	IF	Citations
547	Metagenomic Analysis Shows the Presence of Bacteria Related to Free-Living Forms of Sulfur-Oxidizing Chemolithoautotrophic Symbionts in the Rhizosphere of the Seagrass Zostera marina. Frontiers in Marine Science, 2018, 5, .	1.2	44
548	Labilibaculum manganireducens gen. nov., sp. nov. and Labilibaculum filiforme sp. nov., Novel Bacteroidetes Isolated from Subsurface Sediments of the Baltic Sea. Frontiers in Microbiology, 2017, 8, 2614.	1.5	25
549	Comparative Genomics of Thalassobius Including the Description of Thalassobius activus sp. nov., and Thalassobius autumnalis sp. nov.. Frontiers in Microbiology, 2017, 8, 2645.	1.5	30
550	Environmental Metagenomic Assemblies Reveal Seven New Highly Divergent Chlamydial Lineages and Hallmarks of a Conserved Intracellular Lifestyle. Frontiers in Microbiology, 2018, 9, 79.	1.5	34
551	Cultivation and Genomic Analysis of â€œCandidatus Nitrosocaldus islandicus,â€•an Obligately Thermophilic, Ammonia-Oxidizing Thaumarchaeon from a Hot Spring Biofilm in Graendalur Valley, Iceland. Frontiers in Microbiology, 2018, 9, 193.	1.5	76
552	Recovering Genomics Clusters of Secondary Metabolites from Lakes Using Genome-Resolved Metagenomics. Frontiers in Microbiology, 2018, 9, 251.	1.5	32
553	Evolution of Phototrophy in the Chloroflexi Phylum Driven by Horizontal Gene Transfer. Frontiers in Microbiology, 2018, 9, 260.	1.5	143
554	Physiological and Metagenomic Characterizations of the Synergistic Relationships between Ammonia- and Nitrite-Oxidizing Bacteria in Freshwater Nitrification. Frontiers in Microbiology, 2018, 9, 280.	1.5	15
555	Pan-Genome Analysis Links the Hereditary Variation of Leptospirillum ferriphilum With Its Evolutionary Adaptation. Frontiers in Microbiology, 2018, 9, 577.	1.5	18
556	Metabolic and Evolutionary Insights in the Transformation of Diphenylamine by a Pseudomonas putida Strain Unravelled by Genomic, Proteomic, and Transcription Analysis. Frontiers in Microbiology, 2018, 9, 676.	1.5	4
557	A Large-Scale Comparative Metagenomic Study Reveals the Functional Interactions in Six Bloom-Forming Microcystis-Epibiont Communities. Frontiers in Microbiology, 2018, 9, 746.	1.5	72
558	Comparative Genomics and Mutational Analysis Reveals a Novel XoxF-Utilizing Methylotroph in the Roseobacter Group Isolated From the Marine Environment. Frontiers in Microbiology, 2018, 9, 766.	1.5	13
559	Genome-Wide Comparative Functional Analyses Reveal Adaptations of Salmonella sv. Newport to a Plant Colonization Lifestyle. Frontiers in Microbiology, 2018, 9, 877.	1.5	22
560	Hydrogen-Fueled Microbial Pathways in Biogas Upgrading Systems Revealed by Genome-Centric Metagenomics. Frontiers in Microbiology, 2018, 9, 1079.	1.5	66
561	Comparative Genomics of the Herbivore Gut Symbiont Lactobacillus reuteri Reveals Genetic Diversity and Lifestyle Adaptation. Frontiers in Microbiology, 2018, 9, 1151.	1.5	49
562	Optofluidic Single-Cell Genome Amplification of Sub-micron Bacteria in the Ocean Subsurface. Frontiers in Microbiology, 2018, 9, 1152.	1.5	18
563	In Silico Genome-Wide Analysis Reveals the Potential Links Between Core Genome of Acidithiobacillus thiooxidans and Its Autotrophic Lifestyle. Frontiers in Microbiology, 2018, 9, 1255.	1.5	17
564	Comparative Genomic and Phenotypic Analysis of the Vaginal Probiotic Lactobacillus rhamnosus GR-1. Frontiers in Microbiology, 2018, 9, 1278.	1.5	42

#	Article	IF	Citations
565	Microbial Community Structureâ€"Function Relationships in Yaquina Bay Estuary Reveal Spatially Distinct Carbon and Nitrogen Cycling Capacities. Frontiers in Microbiology, 2018, 9, 1282.	1.5	48
566	Disentangling the drivers of functional complexity at the metagenomic level in Shark Bay microbial mat microbiomes. ISME Journal, 2018, 12, 2619-2639.	4.4	94
567	Metagenomic binning reconstruction coupled with automatic pipeline annotation and giant viruses: A potential source of mistake in annotations. Virus Research, 2018, 255, 36-38.	1.1	5
568	Genomic evidence for the degradation of terrestrial organic matter by pelagic Arctic Ocean Chloroflexi bacteria. Communications Biology, 2018, 1, 90.	2.0	81
569	Ongoing Transposon-Mediated Genome Reduction in the Luminous Bacterial Symbionts of Deep-Sea Ceratioid Anglerfishes. MBio, 2018, 9, .	1.8	51
570	<i>Fusobacterium</i> Genomics Using MinION and Illumina Sequencing Enables Genome Completion and Correction. MSphere, 2018, 3, .	1.3	23
571	Microbial Diversity and Toxin Risk in Tropical Freshwater Reservoirs of Cape Verde. Toxins, 2018, 10, 186.	1.5	8
572	Genome-centric view of carbon processing in thawing permafrost. Nature, 2018, 560, 49-54.	13.7	337
573	Metagenomics reveals functional synergy and novel polysaccharide utilization loci in the <i>Castor canadensis</i> fecal microbiome. ISME Journal, 2018, 12, 2757-2769.	4.4	36
574	Host-linked soil viral ecology along a permafrost thaw gradient. Nature Microbiology, 2018, 3, 870-880.	5.9	372
575	Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome. Cell Host and Microbe, 2018, 24, 133-145.e5.	5.1	822
576	Draft Genome Sequences of Two Basal Members of the Anaerolineae Class of Chloroflexi from a Sulfidic Hot Spring. Genome Announcements, 2018, 6, .	0.8	15
577	Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. Nature Communications, 2018, 9, 2832.	5.8	108
578	Fine metagenomic profile of the Mediterranean stratified and mixed water columns revealed by assembly and recruitment. Microbiome, 2018, 6, 128.	4.9	95
579	Large-scale genomic analysis shows association between homoplastic genetic variation in Mycobacterium tuberculosis genes and meningeal or pulmonary tuberculosis. BMC Genomics, 2018, 19, 122.	1.2	18
580	Lignite coal burning seam in the remote Altai Mountains harbors a hydrogen-driven thermophilic microbial community. Scientific Reports, 2018, 8, 6730.	1.6	19
581	Draft Genome Sequence of a â€œ <i>Candidatus</i> Brocadiaâ€•Bacterium Enriched from Activated Sludge Collected in a Tropical Climate. Genome Announcements, 2018, 6, .	0.8	6
582	Genomic expansion of magnetotactic bacteria reveals an early common origin of magnetotaxis with lineage-specific evolution. ISME Journal, 2018, 12, 1508-1519.	4.4	103

#	Article	IF	Citations
583	Oxygen minimum zone cryptic sulfur cycling sustained by offshore transport of key sulfur oxidizing bacteria. Nature Communications, 2018, 9, 1729.	5.8	93
584	Lignolytic-consortium omics analyses reveal novel genomes and pathways involved in lignin modification and valorization. Biotechnology for Biofuels, 2018, 11, 75.	6.2	65
585	Integrated multi-omic analysis of host-microbiota interactions in acute oak decline. Microbiome, 2018, 6, 21.	4.9	49
586	Genome-resolved metagenomics of sugarcane vinasse bacteria. Biotechnology for Biofuels, 2018, 11, 48.	6.2	20
587	Genome-centric metatranscriptomes and ecological roles of the active microbial populations during cellulosic biomass anaerobic digestion. Biotechnology for Biofuels, 2018, 11, 117.	6.2	29
588	High-quality draft genome of the methanotroph Methylovulum psychrotolerans Str. HV10-M2 isolated from plant material at a high-altitude environment. Standards in Genomic Sciences, 2018, 13, 10.	1.5	5
589	Pseudomonas pharmafabricae sp. nov., Isolated From Pharmaceutical Wastewater. Current Microbiology, 2018, 75, 1119-1125.	1.0	13
590	Genome Sequence of Lysinibacillus sphaericus, a Lignin-Degrading Bacterium Isolated from Municipal Solid Waste Soil. Genome Announcements, 2018, 6, .	0.8	8
591	Metabolic capability and in situ activity of microorganisms in an oil reservoir. Microbiome, 2018, 6, 5.	4.9	70
592	Draft Genome Sequence of Mycobacterium virginiense Strain GF75, Isolated from the Mud of a Swine Farm in Japan. Genome Announcements, 2018, 6, .	0.8	6
593	BMScan: using whole genome similarity to rapidly and accurately identify bacterial meningitis causing species. BMC Infectious Diseases, 2018, 18, 405.	1.3	13
594	Broad Phylogenetic Diversity Associated with Nitrogen Loss through Sulfur Oxidation in a Large Public Marine Aquarium. Applied and Environmental Microbiology, 2018, 84, .	1.4	7
595	Addressing Global Ruminant Agricultural Challenges Through Understanding the Rumen Microbiome: Past, Present, and Future. Frontiers in Microbiology, 2018, 9, 2161.	1.5	255
596	Comparative Genomics and Description of Putative Virulence Factors of Melissococcus plutonius, the Causative Agent of European Foulbrood Disease in Honey Bees. Genes, 2018, 9, 419.	1.0	28
597	Comparative Genomics of Candidatus Methylomirabilis Species and Description of Ca. Methylomirabilis Lanthanidiphila. Frontiers in Microbiology, 2018, 9, 1672.	1.5	67
598	A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. Nature Biotechnology, 2018, 36, 996-1004.	9.4	2,615
599	Salinity-Aided Selection of Progressive Onset Denitrifiers as a Means of Providing Nitrite for Anammox. Environmental Science & Technology, 2018, 52, 10665-10672.	4.6	64
600	Horizontal gene transfer plays a major role in the pathological convergence of Xanthomonas lineages on common bean. BMC Genomics, 2018, 19, 606.	1.2	38

#	Article	IF	Citations
601	ezTree: an automated pipeline for identifying phylogenetic marker genes and inferring evolutionary relationships among uncultivated prokaryotic draft genomes. BMC Genomics, 2018, 19, 921.	1.2	50
602	Novel Autotrophic Organisms Contribute Significantly to the Internal Carbon Cycling Potential of a Boreal Lake. MBio, 2018, 9, .	1.8	18
603	Modeling trophic dependencies and exchanges among insectsâ€™ bacterial symbionts in a host-simulated environment. BMC Genomics, 2018, 19, 402.	1.2	42
604	In silico exploration of Red Sea Bacillus genomes for natural product biosynthetic gene clusters. BMC Genomics, 2018, 19, 382.	1.2	17
605	New Biological Insights Into How Deforestation in Amazonia Affects Soil Microbial Communities Using Metagenomics and Metagenome-Assembled Genomes. Frontiers in Microbiology, 2018, 9, 1635.	1.5	51
606	Viral and metabolic controls on high rates of microbial sulfur and carbon cycling in wetland ecosystems. Microbiome, 2018, 6, 138.	4.9	63
607	Evidence for complete nitrification in enrichment culture of tidal sediments and diversity analysis of clade a comammox Nitrospira in natural environments. Applied Microbiology and Biotechnology, 2018, 102, 9363-9377.	1.7	57
608	Metabolic Capability and Phylogenetic Diversity of Mono Lake during a Bloom of the Eukaryotic Phototroph Picocystis sp. Strain ML. Applied and Environmental Microbiology, 2018, 84, .	1.4	18
609	AMBER: Assessment of Metagenome BinnERs. GigaScience, 2018, 7, .	3.3	72
611	Novel bacterial lineages associated with boreal moss species. Environmental Microbiology, 2018, 20, 2625-2638.	1.8	86
612	Novel prosthecate bacteria from the candidate phylum Acetothermia. ISME Journal, 2018, 12, 2225-2237.	4.4	75
613	Methanogens in the Antarctic Dry Valley permafrost. FEMS Microbiology Ecology, 2018, 94, .	1.3	22
614	Nitrogen-fixing populations of Planctomycetes and Proteobacteria are abundant in surface ocean metagenomes. Nature Microbiology, 2018, 3, 804-813.	5.9	436
615	Draft Genome Sequence of <i>n</i> -Alkane-Utilizing Acinetobacter sp. Strain BS1, Isolated from Ethane Oxidation Culture. Genome Announcements, 2018, 6, .	0.8	0
616	Novel soil bacteria possess diverse genes for secondary metabolite biosynthesis. Nature, 2018, 558, 440-444.	13.7	321
617	Microbial life under ice: Metagenome diversity and <i>in situ</i> activity of Verrucomicrobia in seasonally iceâ€covered Lakes. Environmental Microbiology, 2018, 20, 2568-2584.	1.8	68
618	Metagenomics: A Paradigm Shift in Microbiology. , 2018, , 1-13.		10
619	Genome Rearrangement Shapes Prochlorococcus Ecological Adaptation. Applied and Environmental Microbiology, 2018, 84, .	1.4	17

#	ARTICLE	IF	CITATIONS
620	Asgard archaea do not close the debate about the universal tree of life topology. PLoS Genetics, 2018, 14, e1007215.	1.5	80
621	Collection, Culturing, and Genome Analyses of Tropical Marine Filamentous Benthic Cyanobacteria. Methods in Enzymology, 2018, 604, 3-43.	0.4	10
622	The Functional Potential of the Rhizospheric Microbiome of an Invasive Tree Species, Acacia dealbata. Microbial Ecology, 2019, 77, 191-200.	1.4	46
623	Machine learning meets genome assembly. Briefings in Bioinformatics, 2019, 20, 2116-2129.	3.2	14
624	The importance of designating type material for uncultured taxa. Systematic and Applied Microbiology, 2019, 42, 15-21.	1.2	149
625	Insights into microbial community structure and function from a shallow, simulated CO 2 â€leakage aquifer demonstrate microbial selection and adaptation. Environmental Microbiology Reports, 2019, 11, 338-351.	1.0	14
626	Membrane Lipid Composition of the Moderately Thermophilic Ammonia-Oxidizing Archaeon â€œ <i>Candidatus</i> Nitrosotenuis uzonensisâ€•at Different Growth Temperatures. Applied and Environmental Microbiology, 2019, 85, .	1.4	31
627	Elucidating Syntrophic Butyrate-Degrading Populations in Anaerobic Digesters Using Stable-Isotope-Informed Genome-Resolved Metagenomics. MSystems, 2019, 4, .	1.7	19
628	Complete Genome Sequence of an Uncultured Bacterium of the Candidate Phylum Bipolaricaulota. Microbiology, 2019, 88, 461-468.	0.5	8
629	Phylogenetic, genomic, and biogeographic characterization of a novel and ubiquitous marine invertebrate-associated Rickettsiales parasite, <i>Candidatus</i> Aquarickettsia rohweri, gen. nov., sp. nov. ISME Journal, 2019, 13, 2938-2953.	4.4	82
630	Metabolic Potential of As-yet-uncultured Archaeal Lineages of <i>Candidatus</i> Hydrothermarchaeota Thriving in Deep-sea Metal Sulfide Deposits. Microbes and Environments, 2019, 34, 293-303.	0.7	10
631	Shifts in the Human Gut Microbiota Structure Caused by Quadruple Helicobacter pylori Eradication Therapy. Frontiers in Microbiology, 2019, 10, 1902.	1.5	39
632	Comparative genomic and functional analysis of Akkermansia muciniphila and closely related species. Genes and Genomics, 2019, 41, 1253-1264.	0.5	33
633	Geologic legacy spanning >90â€‰years explains unique Yellowstone hot spring geochemistry and biodiversity. Environmental Microbiology, 2019, 21, 4180-4195.	1.8	17
634	Metagenomic insights into production of zero valent sulfur from dissimilatory sulfate reduction in a methanogenic bioreactor. Bioresource Technology Reports, 2019, 8, 100305.	1.5	6
635	Applications and Considerations of GToTree: A User-Friendly Workflow for Phylogenomics. Evolutionary Bioinformatics, 2019, 15, 117693431986224.	0.6	6
636	Comparative Genomics Reveals Ecological and Evolutionary Insights into Sponge-Associated <i>Thaumarchaeota</i>. MSystems, 2019, 4, .	1.7	59
637	MetaTOR: A Computational Pipeline to Recover High-Quality Metagenomic Bins From Mammalian Gut Proximity-Ligation (meta3C) Libraries. Frontiers in Genetics, 2019, 10, 753.	1.1	22

#	Article	IF	Citations
638	Profiling of Active Microorganisms by Stable Isotope Probingâ€"Metagenomics. Methods in Molecular Biology, 2019, 2046, 151-161.	0.4	3
639	Draft Genome Sequence of Thermodesulfovibrio sp. Strain Kuro-1, a Thermophilic, Lactate-Degrading Anaerobe Isolated from a Thermophilic Anaerobic Digestion Reactor. Microbiology Resource Announcements, 2019, 8, .	0.3	1
640	Compendium of 4,941 rumen metagenome-assembled genomes for rumen microbiome biology and enzyme discovery. Nature Biotechnology, 2019, 37, 953-961.	9.4	353
641	Hybrid metagenomic assembly enables high-resolution analysis of resistance determinants and mobile elements in human microbiomes. Nature Biotechnology, 2019, 37, 937-944.	9.4	216
642	Complete Genome Sequence of Halophilic Deep-Sea Bacterium Halomonas axialensis Strain Althf1. Microbiology Resource Announcements, 2019, 8, .	0.3	4
643	Defining the human gut hostâ€"phage network through single-cell viral tagging. Nature Microbiology, 2019, 4, 2192-2203.	5.9	95
644	Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation. Genome Biology, 2019, 20, 153.	3.8	66
645	Anaerobic Degradation of Non-Methane Alkanes by â€œ <i>Candidatus</i> Methanolipariaâ€•in Hydrocarbon Seeps of the Gulf of Mexico. MBio, 2019, 10, .	1.8	63
646	Time Series Genome-Centric Analysis Unveils Bacterial Response to Operational Disturbance in Activated Sludge. MSystems, 2019, 4, .	1.7	23
647	The class II benzoylâ€coenzyme A reductase complex from the sulfateâ€reducing <i>Desulfosarcina cetonica</i>. Environmental Microbiology, 2019, 21, 4241-4252.	1.8	10
648	The importance of genome sequence quality to microbial comparative genomics. BMC Genomics, 2019, 20, 662.	1.2	35
649	Primer-free FISH probes from metagenomics/metatranscriptomics data permit the study of uncharacterised taxa in complex microbial communities. Npj Biofilms and Microbiomes, 2019, 5, 17.	2.9	11
650	Geomicrobiology of the carbon, nitrogen and sulphur cycles in Powell Lake: a permanently stratified water column containing ancient seawater. Environmental Microbiology, 2019, 21, 3927-3952.	1.8	10
651	Genomic characterization, kinetics, and pathways of sulfamethazine biodegradation by Paenarthrobacter sp. A01. Environment International, 2019, 131, 104961.	4.8	56
652	In marine <i>Bacteroidetes</i> the bulk of glycan degradation during algae blooms is mediated by few clades using a restricted set of genes. ISME Journal, 2019, 13, 2800-2816.	4.4	125
653	Draft Genome Sequence of <i>Desulfosporosinus</i> sp. Strain Sb-LF, Isolated from an Acidic Peatland in Germany. Microbiology Resource Announcements, 2019, 8, .	0.3	8
654	Draft Genome Sequence of Streptococcus anginosus Strain CALM001, Isolated from the Gut of an Elderly Dane. Microbiology Resource Announcements, 2019, 8, .	0.3	5
655	Draft Genome Sequence of Rhodococcus sp. Strain ATCC 49988, a Quinoline-Degrading Bacterium. Microbiology Resource Announcements, 2019, 8, .	0.3	4

#	Article	IF	Citations
656	Complete Genome Sequence of Bacillus mycoides TH26, Isolated from a Permafrost Thaw Gradient. Microbiology Resource Announcements, 2019, 8, .	0.3	5
657	Microbial Community in Hyperalkaline Steel Slag-Fill Emulates Serpentinizing Springs. Diversity, 2019, 11, 103.	0.7	8
658	<i>In situ</i> abundance and carbon fixation activity of distinct anoxygenic phototrophs in the stratified seawater lake Rogoznica. Environmental Microbiology, 2019, 21, 3896-3908.	1.8	10
659	Defending Our Public Biological Databases as a Global Critical Infrastructure. Frontiers in Bioengineering and Biotechnology, 2019, 7, 58.	2.0	13
660	Bacterial and Archaeal Metagenome-Assembled Genome Sequences from Svalbard Permafrost. Microbiology Resource Announcements, 2019, 8, .	0.3	14
661	Genomic Comparison of Lactobacillus helveticus Strains Highlights Probiotic Potential. Frontiers in Microbiology, 2019, 10, 1380.	1.5	50
662	Draft Genome Sequence of Deoxynivalenol-Degrading Actinomycete Nocardioides sp. Strain LS1, Isolated from Wheat Leaves in Japan. Microbiology Resource Announcements, 2019, 8, .	0.3	2
663	Characterization of a thaumarchaeal symbiont that drives incomplete nitrification in the tropical sponge<i>Ianthella basta</i>. Environmental Microbiology, 2019, 21, 3831-3854.	1.8	50
664	Contrasting Winter Versus Summer Microbial Communities and Metabolic Functions in a Permafrost Thaw Lake. Frontiers in Microbiology, 2019, 10, 1656.	1.5	65
665	Evolutionary Implications of Anoxygenic Phototrophy in the Bacterial Phylum Candidatus Eremiobacterota (WPS-2). Frontiers in Microbiology, 2019, 10, 1658.	1.5	88
666	Responses of tundra soil microbial communities to half a decade of experimental warming at two critical depths. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15096-15105.	3.3	83
667	Fulvimarina endophytica sp. nov., a novel endophytic bacterium isolated from bark of Sonneratia caseolaris. Journal of Microbiology, 2019, 57, 655-660.	1.3	6
668	Bioinformatics Tools for Microbial Diversity Analysis. , 2019, , 23-47.		1
669	Genome Sequences of a Plant Beneficial Synthetic Bacterial Community Reveal Genetic Features for Successful Plant Colonization. Frontiers in Microbiology, 2019, 10, 1779.	1.5	36
670	<i>In situ</i> metaâ€omic insights into the community compositions and ecological roles of hadal microbes in the Mariana Trench. Environmental Microbiology, 2019, 21, 4092-4108.	1.8	40
671	Genome evolution and hostâ€microbiome shifts correspond with intraspecific niche divergence within harmful algal bloomâ€forming <i>Microcystis aeruginosa</i>. Molecular Ecology, 2019, 28, 3994-4011.	2.0	29
672	Genomic Evidence for Simultaneous Optimization of Transcription and Translation through Codon Variants in the <i>pmoCAB</i> Operon of Type Ia Methanotrophs. MSystems, 2019, 4, .	1.7	7
673	An Expanded Ribosomal Phylogeny of Cyanobacteria Supports a Deep Placement of Plastids. Frontiers in Microbiology, 2019, 10, 1612.	1.5	49

#	Article	IF	Citations
674	Draft Genome Sequence of Strain LSUCC0112, a Gulf of Mexico Representative of the Oligotrophic Marine <i>Gammaproteobacteria</i>. Microbiology Resource Announcements, 2019, 8, .	0.3	1
675	Genomic Insights of Dyadobacter tibetensis Y620-1 Isolated from Ice Core Reveal Genomic Features for Succession in Glacier Environment. Microorganisms, 2019, 7, 211.	1.6	9
676	Comparison of the sequencing bias of currently available library preparation kits for Illumina sequencing of bacterial genomes and metagenomes. DNA Research, 2019, 26, 391-398.	1.5	88
677	Comparative Genomics of Wild Bee and Flower Isolated Lactobacillus Reveals Potential Adaptation to the Bee Host. Genome Biology and Evolution, 2019, 11, 2151-2161.	1.1	38
678	Alternate succession of aggregate-forming cyanobacterial genera correlated with their attached bacteria by co-pathways. Science of the Total Environment, 2019, 688, 867-879.	3.9	32
679	Core Metabolic Features and Hot Origin of Bathyarchaeota. Engineering, 2019, 5, 498-504.	3.2	42
680	Communal metabolism by <i>Methylococcaceae</i> and <i>Methylophilaceae</i> is driving rapid aerobic methane oxidation in sediments of a shallow seep near Elba, Italy. Environmental Microbiology, 2019, 21, 3780-3795.	1.8	28
681	Differential efficiency of wild type rhizogenic strains for rol gene transformation of plants. Applied Microbiology and Biotechnology, 2019, 103, 6657-6672.	1.7	20
682	Pseudomonas ovata sp. nov., Isolated from the Skin of the Tail of Farmed Murray cod (Maccullochella) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.0	13
683	Probing the geological source and biological fate of hydrogen in Yellowstone hot springs. Environmental Microbiology, 2019, 21, 3816-3830.	1.8	22
684	Direct effects of organic pollutants on the growth and gene expression of the Baltic Sea model bacteriumRheinheimerasp.BAL341. Microbial Biotechnology, 2019, 12, 892-906.	2.0	19
685	Genomics of Aerobic Photoheterotrophs in Wheat Phyllosphere Reveals Divergent Evolutionary Patterns of Photosynthetic Genes in Methylobacterium spp.. Genome Biology and Evolution, 2019, 11, 2895-2908.	1.1	19
686	Communication within East Antarctic Soil Bacteria. Applied and Environmental Microbiology, 2019, 86, .	1.4	11
687	Putative Mixotrophic Nitrifying-Denitrifying Gammaproteobacteria Implicated in Nitrogen Cycling Within the Ammonia/Oxygen Transition Zone of an Oil Sands Pit Lake. Frontiers in Microbiology, 2019, 10, 2435.	1.5	42
688	Segmented Filamentous Bacteria Prevent and Cure Rotavirus Infection. Cell, 2019, 179, 644-658.e13.	13.5	106
689	miComplete: weighted quality evaluation of assembled microbial genomes. Bioinformatics, 2020, 36, 936-937.	1.8	26
690	Genome of a Novel Bacterium â€œCandidatus Jettenia ecosiâ€•Reconstructed From the Metagenome of an Anammox Bioreactor. Frontiers in Microbiology, 2019, 10, 2442.	1.5	30
691	A machine learning-based service for estimating quality of genomes using PATRIC. BMC Bioinformatics, 2019, 20, 486.	1.2	32

#	ARTICLE	IF	CITATIONS
692	Insights into the ecological roles and evolution of methyl-coenzyme M reductase-containing hot spring Archaea. Nature Communications, 2019, 10, 4574.	5.8	90
693	A Bioinformatics Guide to Plant Microbiome Analysis. Frontiers in Plant Science, 2019, 10, 1313.	1.7	54
694	The Prevotella copri Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. Cell Host and Microbe, 2019, 26, 666-679.e7.	5.1	274
695	Genome Assembly of the A-Group Wolbachia in Nasonia oneida Using Linked-Reads Technology. Genome Biology and Evolution, 2019, 11, 3008-3013.	1.1	10
696	Functional diversity enables multiple symbiont strains to coexist in deep-sea mussels. Nature Microbiology, 2019, 4, 2487-2497.	5.9	76
697	Current Status and Potential Applications of Underexplored Prokaryotes. Microorganisms, 2019, 7, 468.	1.6	17
699	MicroScope: an integrated platform for the annotation and exploration of microbial gene functions through genomic, pangenomic and metabolic comparative analysis. Nucleic Acids Research, 2020, 48, D579-D589.	6.5	166
700	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. Nucleic Acids Research, 2020, 48, D606-D612.	6.5	552
701	Analyses of Seven New Genomes of Xanthomonas citri pv. aurantifolii Strains, Causative Agents of Citrus Canker B and C, Show a Reduced Repertoire of Pathogenicity-Related Genes. Frontiers in Microbiology, 2019, 10, 2361.	1.5	14
702	Microbial metabolisms in an abyssal ferromanganese crust from the Takuyo-Daigo Seamount as revealed by metagenomics. PLoS ONE, 2019, 14, e0224888.	1.1	14
703	Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. Science, 2019, 366, 606-612.	6.0	621
704	Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. Genome Biology, 2019, 20, 226.	3.8	47
705	Marine Proteobacteria metabolize glycolate via the Î²-hydroxyaspartate cycle. Nature, 2019, 575, 500-504.	13.7	71
706	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. Cell, 2019, 179, 1068-1083.e21.	13.5	268
707	Distinct Polysaccharide Utilization Profiles of Human Intestinal Prevotella copri Isolates. Cell Host and Microbe, 2019, 26, 680-690.e5.	5.1	115
708	Elucidation of the Genome of Bradyrhizobium sp. Strain USDA 3456, a Historic Agricultural Diazotroph from Cowpea (Vigna unguiculata). Microbiology Resource Announcements, 2019, 8, .	0.3	1
709	Janthinobacterium CG23_2: Comparative Genome Analysis Reveals Enhanced Environmental Sensing and Transcriptional Regulation for Adaptation to Life in an Antarctic Supraglacial Stream. Microorganisms, 2019, 7, 454.	1.6	7
710	Robust taxonomic classification of uncharted microbial sequences and bins with CAT and BAT. Genome Biology, 2019, 20, 217.	3.8	269

#	ARTICLE	IF	CITATIONS
711	New Halonotius Species Provide Genomics-Based Insights Into Cobalamin Synthesis in Haloarchaea. Frontiers in Microbiology, 2019, 10, 1928.	1.5	34
712	Phage-centric ecological interactions in aquatic ecosystems revealed through ultra-deep metagenomics. Microbiome, 2019, 7, 135.	4.9	68
713	Challenges in Clinical Metaproteomics Highlighted by the Analysis of Acute Leukemia Patients with Gut Colonization by Multidrug-Resistant Enterobacteriaceae. Proteomes, 2019, 7, 2.	1.7	71
714	High-throughput DNA sequencing technologies for water and wastewater analysis. Science Progress, 2019, 102, 351-376.	1.0	16
715	Comparative Genomic and Phylogenomic Analyses Clarify Relationships Within and Between Bacillus cereus and Bacillus thuringiensis: Proposal for the Recognition of Two Bacillus thuringiensis Genomovars. Frontiers in Microbiology, 2019, 10, 1978.	1.5	33
716	Comparative Genomic Insights into Secondary Metabolism Biosynthetic Gene Cluster Distributions of Marine Streptomyces. Marine Drugs, 2019, 17, 498.	2.2	31
717	Expansion of <i>Thaumarchaeota</i> habitat range is correlated with horizontal transfer of ATPase operons. ISME Journal, 2019, 13, 3067-3079.	4.4	59
718	Long-read metagenomic exploration of extrachromosomal mobile genetic elements in the human gut. Microbiome, 2019, 7, 119.	4.9	65
719	Top-Down Enrichment Guides in Formation of Synthetic Microbial Consortia for Biomass Degradation. ACS Synthetic Biology, 2019, 8, 2174-2185.	1.9	74
720	Genomic signatures and coâ€occurrence patterns of the ultraâ€small Saccharimonadia (phylum) Tj ETQq1 1 0.784314 rgBT /Overlock	2.0	101
721	Niche differentiation among annually recurrent coastal Marine Group II Euryarchaeota. ISME Journal, 2019, 13, 3024-3036.	4.4	41
722	An archaeal origin of the Woodâ€"Ljungdahl H4MPT branch and the emergence of bacterial methylotrophy. Nature Microbiology, 2019, 4, 2155-2163.	5.9	51
723	Phylogenomics Reveals Clear Cases of Misclassification and Genus-Wide Phylogenetic Markers for Acinetobacter. Genome Biology and Evolution, 2019, 11, 2531-2541.	1.1	60
724	High-Level Abundances of<i>Methanobacteriales</i>and<i>Syntrophobacterales</i>May Help To Prevent Corrosion of Metal Sheet Piles. Applied and Environmental Microbiology, 2019, 85, .	1.4	14
725	Maturation of the infant rhesus macaque gut microbiome and its role in the development of diarrheal disease. Genome Biology, 2019, 20, 173.	3.8	40
726	Genome-centered omics insight into the competition and niche differentiation of Ca. Jettenia and Ca. Brocadia affiliated to anammox bacteria. Applied Microbiology and Biotechnology, 2019, 103, 8191-8202.	1.7	24
727	Space Station conditions are selective but do not alter microbial characteristics relevant to human health. Nature Communications, 2019, 10, 3990.	5.8	79
728	Dietary Energy Level Promotes Rumen Microbial Protein Synthesis by Improving the Energy Productivity of the Ruminal Microbiome. Frontiers in Microbiology, 2019, 10, 847.	1.5	43

#	Article	IF	Citations
729	Potential Interactions between Clade SUP05 Sulfur-Oxidizing Bacteria and Phages in Hydrothermal Vent Sponges. Applied and Environmental Microbiology, 2019, 85, .	1.4	22
730	Draft Genome Sequence of Desulfosporosinus fructosivorans Strain 63.6F T , Isolated from Marine Sediment in the Baltic Sea. Microbiology Resource Announcements, 2019, 8, .	0.3	1
731	Pseudofructophilic Leuconostoc citreum Strain F192-5, Isolated from Satsuma Mandarin Peel. Applied and Environmental Microbiology, 2019, 85, .	1.4	7
732	A library of human gut bacterial isolates paired with longitudinal multiomics data enables mechanistic microbiome research. Nature Medicine, 2019, 25, 1442-1452.	15.2	255
733	Exploring the effects of operational mode and microbial interactions on bacterial community assembly in a one-stage partial-nitritation anammox reactor using integrated multi-omics. Microbiome, 2019, 7, 122.	4.9	65
734	A new family of uncultivated bacteria involved in methanogenesis from the ubiquitous osmolyte glycine betaine in coastal saltmarsh sediments. Microbiome, 2019, 7, 120.	4.9	33
735	Capability for arsenic mobilization in groundwater is distributed across broad phylogenetic lineages. PLoS ONE, 2019, 14, e0221694.	1.1	15
736	Multi-omics reveal various potential antimonate reductases from phylogenetically diverse microorganisms. Applied Microbiology and Biotechnology, 2019, 103, 9119-9129.	1.7	20
737	Horizontally transmitted symbiont populations in deep-sea mussels are genetically isolated. ISME Journal, 2019, 13, 2954-2968.	4.4	42
738	Current and Promising Approaches to Identify Horizontal Gene Transfer Events in Metagenomes. Genome Biology and Evolution, 2019, 11, 2750-2766.	1.1	70
739	Aromatic compounds lead to increased abundance of antibiotic resistance genes in wastewater treatment bioreactors. Water Research, 2019, 166, 115073.	5.3	53
740	Strong Purifying Selection Is Associated with Genome Streamlining in Epipelagic Marinimicrobia. Genome Biology and Evolution, 2019, 11, 2887-2894.	1.1	30
741	Metagenomes from Coastal Marine Sediments Give Insights into the Ecological Role and Cellular Features of <i>Loki</i> - and <i>Thorarchaeota</i>. MBio, 2019, 10, .	1.8	16
742	A shared core microbiome in soda lakes separated by large distances. Nature Communications, 2019, 10, 4230.	5.8	75
743	Metagenomics and metatranscriptomics analyses reveal oxygen detoxification and mixotrophic potentials of an enriched anammox culture in a continuous stirred-tank reactor. Water Research, 2019, 166, 115039.	5.3	57
744	Arsenic mobilization in a high arsenic groundwater revealed by metagenomic and Geochip analyses. Scientific Reports, 2019, 9, 12972.	1.6	23
745	Genomic Insights Into Five Strains of Lactobacillus plantarum With Biotechnological Potential Isolated From chicha, a Traditional Maize-Based Fermented Beverage From Northwestern Argentina. Frontiers in Microbiology, 2019, 10, 2232.	1.5	24
746	Comparative Genomics and Phylogenomic Analysis of the Genus Salinivibrio. Frontiers in Microbiology, 2019, 10, 2104.	1.5	23

#	ARTICLE	IF	CITATIONS
747	Metagenomic Signatures of Gut Infections Caused by Different <i>Escherichia coli</i> Pathotypes. Applied and Environmental Microbiology, 2019, 85, .	1.4	33
748	Novel facultative Methylocella strains are active methane consumers at terrestrial natural gas seeps. Microbiome, 2019, 7, 134.	4.9	19
749	A genomic view of the reef-building coral Porites lutea and its microbial symbionts. Nature Microbiology, 2019, 4, 2090-2100.	5.9	160
750	Gut bacteria responding to dietary change encode sialidases that exhibit preference for red meat-associated carbohydrates. Nature Microbiology, 2019, 4, 2082-2089.	5.9	56
751	Geochemical and Metagenomic Characterization of Jinata Onsen, a Proterozoic-Analog Hot Spring, Reveals Novel Microbial Diversity including Iron-Tolerant Phototrophs and Thermophilic Lithotrophs. Microbes and Environments, 2019, 34, 278-292.	0.7	48
752	First Draft Genome Sequence of a <i>Polymyxa</i> Genus Member, <i>Polymyxa betae,</i> the Protist Vector of Rhizomania. Microbiology Resource Announcements, 2019, 8, .	0.3	5
753	Complete Genome Sequence of Nocardia farcinica W6977 T Obtained by Combining Illumina and PacBio Reads. Microbiology Resource Announcements, 2019, 8, .	0.3	3
754	â€œCandidatus Thermonerobacter thiotrophicus,â€•A Non-phototrophic Member of the Bacteroidetes/Chlorobi With Dissimilatory Sulfur Metabolism in Hot Spring Mat Communities. Frontiers in Microbiology, 2018, 9, 3159.	1.5	57
755	Fueled by methane: deep-sea sponges from asphalt seeps gain their nutrition from methane-oxidizing symbionts. ISME Journal, 2019, 13, 1209-1225.	4.4	68
756	Genomic reconstructions and potential metabolic strategies of generalist and specialist heterotrophic bacteria associated with an estuary<i>Synechococcus</i>culture. FEMS Microbiology Ecology, 2019, 95, .	1.3	26
757	Day and Night: Metabolic Profiles and Evolutionary Relationships of Six Axenic Non-Marine Cyanobacteria. Genome Biology and Evolution, 2019, 11, 270-294.	1.1	35
758	Dark aerobic sulfide oxidation by anoxygenic phototrophs in anoxic waters. Environmental Microbiology, 2019, 21, 1611-1626.	1.8	27
759	Meta-omics based analyses of microbiome involved in biomethanation of rice straw in a thermophilic anaerobic bioreactor under optimized conditions. Bioresource Technology, 2019, 279, 25-33.	4.8	17
760	Anaerobic Degradation of Sulfated Polysaccharides by Two Novel Kiritimatiellales Strains Isolated From Black Sea Sediment. Frontiers in Microbiology, 2019, 10, 253.	1.5	56
761	Mycobacterial metabolic characteristics in a water meter biofilm revealed by metagenomics and metatranscriptomics. Water Research, 2019, 153, 315-323.	5.3	19
762	Marine biofilms constitute a bank of hidden microbial diversity and functional potential. Nature Communications, 2019, 10, 517.	5.8	100
763	Draft Genome Sequence of Acidobacteria Group 1 Acidipila sp. Strain EB88, Isolated from Forest Soil. Microbiology Resource Announcements, 2019, 8, .	0.3	10
764	Comparative analysis reveals the Genomic Islands in Pasteurella multocida population genetics: on Symbiosis and adaptability. BMC Genomics, 2019, 20, 63.	1.2	9

#	ARTICLE	IF	CITATIONS
765	Comparative genomics of 16<i>Microbacterium</i>spp. that tolerate multiple heavy metals and antibiotics. PeerJ, 2019, 6, e6258.	0.9	27
766	Metabolic diversity within the globally abundant Marine Group II Euryarchaea offers insight into ecological patterns. Nature Communications, 2019, 10, 271.	5.8	66
767	Metabolic reconstruction of the genome of candidate <i>Desulfatiglans</i> TRIP_1 and identification of key candidate enzymes for anaerobic phenanthrene degradation. Environmental Microbiology, 2019, 21, 1267-1286.	1.8	31
768	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. Nature Communications, 2019, 10, 463.	5.8	87
769	Biological composition and microbial dynamics of sinking particulate organic matter at abyssal depths in the oligotrophic open ocean. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11824-11832.	3.3	150
770	Modular Assembly of Polysaccharide-Degrading Marine Microbial Communities. Current Biology, 2019, 29, 1528-1535.e6.	1.8	144
771	Life at Home and on the Roam: Genomic Adaptions Reflect the Dual Lifestyle of an Intracellular, Facultative Symbiont. MSystems, 2019, 4, .	1.7	30
772	Draft Genome Sequence from a Putative New Genus and Species in the Family <i>Methanoregulaceae</i> Isolated from the Anoxic Basin of Lake Untersee in East Antarctica. Microbiology Resource Announcements, 2019, 8, .	0.3	3
773	Metagenomic and metatranscriptomic analyses reveal activity and hosts of antibiotic resistance genes in activated sludge. Environment International, 2019, 129, 208-220.	4.8	163
774	New Microbial Lineages Capable of Carbon Fixation and Nutrient Cycling in Deep-Sea Sediments of the Northern South China Sea. Applied and Environmental Microbiology, 2019, 85, .	1.4	36
775	High-Quality Draft Genome Sequences of Rare Nontuberculous Mycobacteria Isolated from Surfaces of a Hospital. Microbiology Resource Announcements, 2019, 8, .	0.3	12
776	Annotated bacterial chromosomes from frame-shift-corrected long-read metagenomic data. Microbiome, 2019, 7, 61.	4.9	69
777	Draft genome sequences of Mycolicibacterium peregrinum isolated from a pig with lymphadenitis and from soil on the same Japanese pig farm. BMC Research Notes, 2019, 12, 341.	0.6	4
778	Draft Genome Sequence of Bacillus subtilis SB-14, an Antimicrobially Active Isolate from Namibian Social Spiders (Stegodyphus dumicola). Microbiology Resource Announcements, 2019, 8, .	0.3	0
779	Draft Genome Sequence of Strain LSUCC0057, a Member of the SAR92 Clade of <i>Gammaproteobacteria</i>. Microbiology Resource Announcements, 2019, 8, .	0.3	1
780	Genome of a Member of the Candidate Archaeal Phylum Verstraetearchaeota from a Subsurface Thermal Aquifer Revealed Pathways of Methyl-Reducing Methanogenesis and Fermentative Metabolism. Microbiology, 2019, 88, 316-323.	0.5	6
781	Metaproteomics: Sample Preparation and Methodological Considerations. Advances in Experimental Medicine and Biology, 2019, 1073, 187-215.	0.8	26
782	Sulfur-Oxidizing Symbionts without Canonical Genes for Autotrophic CO ₂ Fixation. MBio, 2019, 10, .	1.8	29

#	Article	IF	Citations
783	Comparative Genomics of Cyanobacterial Symbionts Reveals Distinct, Specialized Metabolism in Tropical<i>Dysideidae</i>Sponges. MBio, 2019, 10, .	1.8	31
784	Anaerobic hydrocarbon degradation in candidate phylum â€˜Atribacteriaâ€™ (JS1) inferred from genomics. ISME Journal, 2019, 13, 2377-2390.	4.4	63
785	Temporal Analysis of the Microbial Community from the Crystallizer Ponds in Cabo Rojo, Puerto Rico, Using Metagenomics. Genes, 2019, 10, 422.	1.0	15
786	Isolation and characterization of a thermophilic sulfur- and iron-reducing thaumarchaeote from a terrestrial acidic hot spring. ISME Journal, 2019, 13, 2465-2474.	4.4	26
787	Two intracellular and cell type-specific bacterial symbionts in the placozoan Trichoplax H2. Nature Microbiology, 2019, 4, 1465-1474.	5.9	57
788	<i>Methylotetracoccus oryzae</i> Strain C50C1 Is a Novel Type Ib Gammaproteobacterial Methanotroph Adapted to Freshwater Environments. MSphere, 2019, 4, .	1.3	14
789	Linking the resistome and plasmidome to the microbiome. ISME Journal, 2019, 13, 2437-2446.	4.4	183
790	Complete Genome Sequence of the Aerobic Facultative Methanotroph Methylocella tundrae Strain T4. Microbiology Resource Announcements, 2019, 8, .	0.3	5
791	Whole genome sequence of Vibrio cholerae directly from dried spotted filter paper. PLoS Neglected Tropical Diseases, 2019, 13, e0007330.	1.3	7
792	â€œCandidatus Accumulibacter delftensisâ€: A clade IC novel polyphosphate-accumulating organism without denitrifying activity on nitrate. Water Research, 2019, 161, 136-151.	5.3	74
793	Metabolic versatility in a modern lineage of cyanobacteria from terrestrial hot springs. Free Radical Biology and Medicine, 2019, 140, 224-232.	1.3	20
794	Metagenomic analysis exhibited the co-metabolism of polycyclic aromatic hydrocarbons by bacterial community from estuarine sediment. Environment International, 2019, 129, 308-319.	4.8	93
795	Comparative Genomics of Thiohalobacter thiocyanaticus HRh1T and Guyparkeria sp. SCN-R1, Halophilic Chemolithoautotrophic Sulfur-Oxidizing Gammaproteobacteria Capable of Using Thiocyanate as Energy Source. Frontiers in Microbiology, 2019, 10, 898.	1.5	20
796	Genomic analysis of human invasive Salmonella enterica serovar Typhimurium ST313 isolate B3589 from India. Infection, Genetics and Evolution, 2019, 73, 416-424.	1.0	7
797	Genomes from bacteria associated with the canine oral cavity: A test case for automated genome-based taxonomic assignment. PLoS ONE, 2019, 14, e0214354.	1.1	7
798	Integrative Omics Approach for the Community Function Evaluation of Sponge and Coral Microbiomes. , 2019, , 171-179.		0
799	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
800	Whole-Genome Shotgun Sequence of Drug-Resistant Staphylococcus aureus Strain SA9, Isolated from a Slaughterhouse Chicken Carcass in South Africa. Microbiology Resource Announcements, 2019, 8, .	0.3	2

#	ARTICLE	IF	CITATIONS
801	Draft Genome Sequence of a Novel Marine Anaerobic Ammonium-Oxidizing Bacterium, â€œ<i>Candidatus</i> Scalindua sp.â€• Microbiology Resource Announcements, 2019, 8, .	0.3	8
802	Mediterranean grassland soil Câ€“N compound turnover is dependent on rainfall and depth, and is mediated by genomically divergent microorganisms. Nature Microbiology, 2019, 4, 1356-1367.	5.9	170
803	Shotgun Metagenomics Reveals the Benthic Microbial Community Response to Plastic and Bioplastic in a Coastal Marine Environment. Frontiers in Microbiology, 2019, 10, 1252.	1.5	128
804	Uncultured <i>Nitrospina</i>-like species are major nitrite oxidizing bacteria in oxygen minimum zones. ISME Journal, 2019, 13, 2391-2402.	4.4	67
805	Systematic Affiliation and Genome Analysis of Subtercola vilae DB165T with Particular Emphasis on Cold Adaptation of an Isolate from a High-Altitude Cold Volcano Lake. Microorganisms, 2019, 7, 107.	1.6	4
806	PhyloToL: A Taxon/Gene-Rich Phylogenomic Pipeline to Explore Genome Evolution of Diverse Eukaryotes. Molecular Biology and Evolution, 2019, 36, 1831-1842.	3.5	23
807	Ecogenomic characterization of widespread, closely-related SAR11 clades of the freshwater genus â€œCandidatus Fonsibacterâ€•and proposal of Ca. Fonsibacter lacus sp. nov. Systematic and Applied Microbiology, 2019, 42, 495-505.	1.2	33
808	Large-Scale Genomics Reveals the Genetic Characteristics of Seven Species and Importance of Phylogenetic Distance for Estimating Pan-Genome Size. Frontiers in Microbiology, 2019, 10, 834.	1.5	48
809	Genomic Features for Desiccation Tolerance and Sugar Biosynthesis in the Extremophile Gloeocapsopsis sp. UTEX B3054. Frontiers in Microbiology, 2019, 10, 950.	1.5	15
810	Metagenomic recovery of two distinct comammox <i>Nitrospira</i> from the terrestrial subsurface. Environmental Microbiology, 2019, 21, 3627-3637.	1.8	69
811	Draft Genome Sequence of <i>Chlorobium</i> sp. Strain N1, a Marine Fe(II)-Oxidizing Green Sulfur Bacterium. Microbiology Resource Announcements, 2019, 8, .	0.3	7
812	Active subseafloor microbial communities from Mariana back-arc venting fluids share metabolic strategies across different thermal niches and taxa. ISME Journal, 2019, 13, 2264-2279.	4.4	38
813	Ultra-deep, long-read nanopore sequencing of mock microbial community standards. GigaScience, 2019, 8, .	3.3	209
814	Environmental Evidence for and Genomic Insight into the Preference of Iron-Oxidizing Bacteria for More-Corrosion-Resistant Stainless Steel at Higher Salinities. Applied and Environmental Microbiology, 2019, 85, .	1.4	11
815	Antarctic Streptomyces fildesensis So13.3 strain as a promising source for antimicrobials discovery. Scientific Reports, 2019, 9, 7488.	1.6	27
816	Comparative Genomics of the Genus Methanohalophilus, Including a Newly Isolated Strain From Kebrit Deep in the Red Sea. Frontiers in Microbiology, 2019, 10, 839.	1.5	10
817	Microevolution and Adaptive Strategy of Psychrophilic Species Flavobacterium bomense sp. nov. Isolated From Glaciers. Frontiers in Microbiology, 2019, 10, 1069.	1.5	47
818	Differences in resource use lead to coexistence of seed-transmitted microbial populations. Scientific Reports, 2019, 9, 6648.	1.6	17

#	Article	IF	Citations
819	Draft Genome Sequences of the Type Strains of Six Macrococcus Species. Microbiology Resource Announcements, 2019, 8, .	0.3	6
820	The Water Microbiome Through a Pilot Scale Advanced Treatment Facility for Direct Potable Reuse. Frontiers in Microbiology, 2019, 10, 993.	1.5	36
821	Prokaryotic and viral community of the sulfateâ€rich crust from PeÃ±ahueca ephemeral lake, an astrobiology analogue. Environmental Microbiology, 2019, 21, 3577-3600.	1.8	9
822	Draft Genome Sequences of Macrococcus caseolyticus, Macrococcus canis, Macrococcus bohemicus, and Macrococcus goetzii. Microbiology Resource Announcements, 2019, 8, .	0.3	5
823	Marinitoga lauensis sp. nov., a novel deep-sea hydrothermal vent thermophilic anaerobic heterotroph with a prophage. Systematic and Applied Microbiology, 2019, 42, 343-347.	1.2	17
824	Asgard archaea capable of anaerobic hydrocarbon cycling. Nature Communications, 2019, 10, 1822.	5.8	165
825	Uncultured Microbial Phyla Suggest Mechanisms for Multi-Thousand-Year Subsistence in Baltic Sea Sediments. MBio, 2019, 10, .	1.8	45
826	Metabolic potential of uncultured bacteria and archaea associated with petroleum seepage in deep-sea sediments. Nature Communications, 2019, 10, 1816.	5.8	118
827	Closely-related Photobacterium strains comprise the majority of bacteria in the gut of migrating Atlantic cod (Gadus morhua). Microbiome, 2019, 7, 64.	4.9	25
828	Characterization of novel hydrocarbon-degrading Gordonia paraffinivorans and Gordonia sihwensis strains isolated from composting. PLoS ONE, 2019, 14, e0215396.	1.1	19
829	Comparative genomeâ€scale modelling of the pathogenic Flavobacteriaceae species <i>Riemerella anatipestifer</i> in China. Environmental Microbiology, 2019, 21, 2836-2851.	1.8	13
830	â€˜<i>Candidatus</i> Oscillochloris fontisâ€™: a novel mesophilic phototrophic Chloroflexota bacterium belonging to the ubiquitous <i>Oscillochloris</i> genus. FEMS Microbiology Letters, 2019, 366, .	0.7	16
831	Exploring the piezotolerant/piezophilic microbial community and genomic basis of piezotolerance within the deep subsurface Deccan traps. Extremophiles, 2019, 23, 421-433.	0.9	7
832	Ectosymbiotic bacteria at the origin of magnetoreception in a marine protist. Nature Microbiology, 2019, 4, 1088-1095.	5.9	57
833	Red Sea SAR11 and <i>Prochlorococcus</i> Single-Cell Genomes Reflect Globally Distributed Pangenomes. Applied and Environmental Microbiology, 2019, 85, .	1.4	11
834	<i>Candidatus</i> Syntrophosphaera thermopropionivorans: a novel player in syntrophic propionate oxidation during anaerobic digestion. Environmental Microbiology Reports, 2019, 11, 558-570.	1.0	86
835	Metagenome to phenome approach enables isolation and genomics characterization of Kalamiella piersonii gen. nov., sp. nov. from the International Space Station. Applied Microbiology and Biotechnology, 2019, 103, 4483-4497.	1.7	44
836	Genome Features and Secondary Metabolites Biosynthetic Potential of the Class Ktedonobacteria. Frontiers in Microbiology, 2019, 10, 893.	1.5	61

#	Article	IF	Citations
837	Genome-informed Bradyrhizobium taxonomy: where to from here?. Systematic and Applied Microbiology, 2019, 42, 427-439.	1.2	62
838	The Patchy Distribution of Restrictionâ€“Modification System Genes and the Conservation of Orphan Methyltransferases in Halobacteria. Genes, 2019, 10, 233.	1.0	27
839	Genomic Characterization of Candidate Division LCP-89 Reveals an Atypical Cell Wall Structure, Microcompartment Production, and Dual Respiratory and Fermentative Capacities. Applied and Environmental Microbiology, 2019, 85, .	1.4	14
840	High-Quality Draft Genome Sequences of Crenobacter cavernae Strain CAVE-375 and Oxalobacteriaceae sp. Strain CAVE-383, Two Bacteria Isolated from Dripping Water in a Karstic Cave in Portugal. Microbiology Resource Announcements, 2019, 8, .	0.3	0
841	Four Draft Single-Cell Genome Sequences of Novel, Nearly Identical <i>Kiritimatiellaeota</i> Strains Isolated from the Continental Deep Subsurface. Microbiology Resource Announcements, 2019, 8, .	0.3	23
842	An automated Raman-based platform for the sorting of live cells by functional properties. Nature Microbiology, 2019, 4, 1035-1048.	5.9	170
843	Discovery and ecogenomic context of a global Caldiserica-related phylum active in thawing permafrost, Candidatus Cryosericota phylum nov., Ca. Cryosericia class nov., Ca. Cryosericales ord. nov., Ca. Cryosericaceae fam. nov., comprising the four species Cryosericum septentrionale gen. nov. sp. nov., Ca. C. hinesii sp. nov., Ca. C. odellii sp. nov., Ca. C. terrychapinii sp. nov.. Systematic and Applied Microbiology, 2019, 42, 54-66.	1.2	42
844	Microbial abundance, activity and population genomic profiling with mOTUs2. Nature Communications, 2019, 10, 1014.	5.8	298
845	Identification and Characterization of a Dominant Sulfolane-Degrading Rhodoferax sp. via Stable Isotope Probing Combined with Metagenomics. Scientific Reports, 2019, 9, 3121.	1.6	19
846	bin3C: exploiting Hi-C sequencing data to accurately resolve metagenome-assembled genomes. Genome Biology, 2019, 20, 46.	3.8	66
847	Metagenomics sheds light on the metabolic repertoire of oil-biodegrading microbes of the South Atlantic Ocean. Environmental Pollution, 2019, 249, 295-304.	3.7	20
848	Draft Genome Sequences of Seven <i>Chryseobacterium</i> Type Strains. Microbiology Resource Announcements, 2019, 8, .	0.3	8
849	MetaCHIP: community-level horizontal gene transfer identification through the combination of best-match and phylogenetic approaches. Microbiome, 2019, 7, 36.	4.9	69
850	Shotgun Metagenomics of a Water Kefir Fermentation Ecosystem Reveals a Novel Oenococcus Species. Frontiers in Microbiology, 2019, 10, 479.	1.5	80
851	Autometa: automated extraction of microbial genomes from individual shotgun metagenomes. Nucleic Acids Research, 2019, 47, e57-e57.	6.5	69
852	Contrasting Pathways for Anaerobic Methane Oxidation in Gulf of Mexico Cold Seep Sediments. MSystems, 2019, 4, .	1.7	27
853	Wide diversity of methane and short-chain alkane metabolisms in uncultured archaea. Nature Microbiology, 2019, 4, 603-613.	5.9	187
854	Expanding anaerobic alkane metabolism in the domain of Archaea. Nature Microbiology, 2019, 4, 595-602.	5.9	133

#	ARTICLE	IF	CITATIONS
855	Genome-resolved metagenomics of an autotrophic thiocyanate-remediating microbial bioreactor consortium. Water Research, 2019, 158, 106-117.	5.3	11
856	Anaerobic oxidation of ethane by archaea from a marine hydrocarbon seep. Nature, 2019, 568, 108-111.	13.7	149
857	Graph analysis of fragmented long-read bacterial genome assemblies. Bioinformatics, 2019, 35, 4239-4246.	1.8	6
858	Metagenomic reconstructions of gut microbial metabolism in weanling pigs. Microbiome, 2019, 7, 48.	4.9	97
859	Major Traditional Probiotics: Comparative Genomic Analyses and Roles in Gut Microbiome of Eight Cohorts. Frontiers in Microbiology, 2019, 10, 712.	1.5	13
860	Lower Respiratory Tract Microbiome and Resistome of Bovine Respiratory Disease Mortalities. Microbial Ecology, 2019, 78, 446-456.	1.4	46
861	Bacterial fermentation and respiration processes are uncoupled in anoxic permeable sediments. Nature Microbiology, 2019, 4, 1014-1023.	5.9	76
862	A new genomic blueprint of the human gut microbiota. Nature, 2019, 568, 499-504.	13.7	901
863	Genome Sequence of â€œ Candidatus Viridilinea halotoleransâ€•Chok-6, Isolated from a Saline Sulfide-Rich Spring. Microbiology Resource Announcements, 2019, 8, .	0.3	13
864	Gene Expansion and Positive Selection as Bacterial Adaptations to Oligotrophic Conditions. MSphere, 2019, 4, .	1.3	28
865	Bioinformatics applied to biotechnology: A review towards bioenergy research. Biomass and Bioenergy, 2019, 123, 195-224.	2.9	17
866	Proposal of Lysobacter pythonis sp. nov. isolated from royal pythons (Python regius). Systematic and Applied Microbiology, 2019, 42, 326-333.	1.2	10
867	Investigating the Origins of Membrane Phospholipid Biosynthesis Genes Using Outgroup-Free Rooting. Genome Biology and Evolution, 2019, 11, 883-898.	1.1	34
868	Closed Genome Sequence of Bacillus paralicheniformis Strain CBMAI 1303, a Bacterium Applied for Phytopathogen Biocontrol. Microbiology Resource Announcements, 2019, 8, .	0.3	4
869	Genomic Characteristics of Desulfonema ishimotonii Tokyo 01T Implying Horizontal Gene Transfer Among Phylogenetically Dispersed Filamentous Gliding Bacteria. Frontiers in Microbiology, 2019, 10, 227.	1.5	5
870	Metatranscriptomic evidence for classical and RuBisCO-mediated CO2 reduction to methane facilitated by direct interspecies electron transfer in a methanogenic system. Scientific Reports, 2019, 9, 4116.	1.6	30
871	Carbon fixation and energy metabolisms of a subseafloor olivine biofilm. ISME Journal, 2019, 13, 1737-1749.	4.4	39
872	Phylogenomics of an uncultivated, aerobic and thermophilic, photoheterotrophic member of Chlorobia sheds light into the evolution of the phylum Chlorobi. Computational Biology and Chemistry, 2019, 80, 206-216.	1.1	11

#	ARTICLE	IF	CITATIONS
873	Widespread soil bacterium that oxidizes atmospheric methane. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8515-8524.	3.3	149
874	Physiological adaptations to serpentinization in the Samail Ophiolite, Oman. ISME Journal, 2019, 13, 1750-1762.	4.4	61
875	Insights into ecological role of a new deltaproteobacterial order <i>Candidatus</i> Acidulodesulfobacterales by metagenomics and metatranscriptomics. ISME Journal, 2019, 13, 2044-2057.	4.4	112
876	Sequencing the Obligate Intracellular Rhabdochlamydia helvetica within Its Tick Host Ixodes ricinus to Investigate Their Symbiotic Relationship. Genome Biology and Evolution, 2019, 11, 1334-1344.	1.1	21
877	Proliferation of hydrocarbon-degrading microbes at the bottom of the Mariana Trench. Microbiome, 2019, 7, 47.	4.9	128
878	A Physiological and Genomic Comparison of Nitrosomonas Cluster 6a and 7 Ammonia-Oxidizing Bacteria. Microbial Ecology, 2019, 78, 985-994.	1.4	38
879	Multiple Recombination Events Drive the Current Genetic Structure of Xanthomonas perforans in Florida. Frontiers in Microbiology, 2019, 10, 448.	1.5	42
880	New insights from uncultivated genomes of the global human gut microbiome. Nature, 2019, 568, 505-510.	13.7	505
881	â€œ Candidatus Colwellia aromaticivoransâ€•sp. nov., â€œ Candidatus Halocyntiibacter alkanivoransâ€•sp. nov., and â€œ Candidatus Ulvibacter alkanivoransâ€•sp. nov. Genome Sequences. Microbiology Resource Announcements, 2019, 8, .	0.3	21
882	The Distribution of Tryptophan-Dependent Indole-3-Acetic Acid Synthesis Pathways in Bacteria Unraveled by Large-Scale Genomic Analysis. Molecules, 2019, 24, 1411.	1.7	76
883	Highâ€•quality draft genome sequence of <i>Gaiella occulta</i> isolated from a 150 meter deep mineral water borehole and comparison with the genome sequences of other deepâ€•branching lineages of the phylum <i>Actinobacteria</i>. MicrobiologyOpen, 2019, 8, e00840.	1.2	38
884	Impacts of indoor surface finishes on bacterial viability. Indoor Air, 2019, 29, 551-562.	2.0	28
885	Wetland Sediments Host Diverse Microbial Taxa Capable of Cycling Alcohols. Applied and Environmental Microbiology, 2019, 85, .	1.4	10
886	Genomic adaptation to eutrophication of ammoniaâ€•oxidizing archaea in the Pearl River estuary. Environmental Microbiology, 2019, 21, 2320-2332.	1.8	23
887	Casting light on Asgardarchaeota metabolism in a sunlit microoxic niche. Nature Microbiology, 2019, 4, 1129-1137.	5.9	96
888	Nonlabens xiamenensis sp. nov., isolated from coastal seawater. Antonie Van Leeuwenhoek, 2019, 112, 1263-1271.	0.7	11
889	Adaptations of Alteromonas sp. 76-1 to Polysaccharide Degradation: A CAZyme Plasmid for Ulvan Degradation and Two Alginolytic Systems. Frontiers in Microbiology, 2019, 10, 504.	1.5	30
890	Diverse aromatic-degrading bacteria present in a highly enriched autotrophic nitrifying sludge. Science of the Total Environment, 2019, 666, 245-251.	3.9	39

#	Article	IF	Citations
891	Genomic and metatranscriptomic analyses of carbon remineralization in an Antarctic polynya. Microbiome, 2019, 7, 29.	4.9	13
892	Genome-centric metagenomics resolves microbial diversity and prevalent truncated denitrification pathways in a denitrifying PAO-enriched bioprocess. Water Research, 2019, 155, 275-287.	5.3	77
893	Whole-Genome Comparisons Among the Genus Shewanella Reveal the Enrichment of Genes Encoding Ankyrin-Repeats Containing Proteins in Sponge-Associated Bacteria. Frontiers in Microbiology, 2019, 10, 5.	1.5	14
894	Diverse anaerobic methaneâ€•and multiâ€•carbon alkaneâ€•metabolizing archaea coexist and show activity in Guaymas Basin hydrothermal sediment. Environmental Microbiology, 2019, 21, 1344-1355.	1.8	25
895	â€˜Candidatus Viridilinea mediisalinaâ€™, a novel phototrophic Chloroflexi bacterium from a Siberian soda lake. FEMS Microbiology Letters, 2019, 366, .	0.7	17
896	The application of molecular tools to study the drinking water microbiome â€“ Current understanding and future needs. Critical Reviews in Environmental Science and Technology, 2019, 49, 1188-1235.	6.6	38
897	Complete Genome Sequence of Lactobacillus crispatus CO3MRSI1. Microbiology Resource Announcements, 2019, 8, .	0.3	3
898	Genomic comparison of facultatively anaerobic and obligatory aerobic Caldibacillus debilis strains GB1 and Tf helps explain physiological differences. Canadian Journal of Microbiology, 2019, 65, 421-428.	0.8	0
899	Comparative Genomics, Siderophore Production, and Iron Scavenging Potential of Root Zone Soil Bacteria Isolated from â€˜Concordâ€™ Grape Vineyards. Microbial Ecology, 2019, 78, 699-713.	1.4	14
900	Deepâ€•sea hydrothermal vent metagenomeâ€•assembled genomes provide insight into the phylum <i>Nanoarchaeota</i>. Environmental Microbiology Reports, 2019, 11, 262-270.	1.0	15
901	Classification of the inoculant strain of cowpea UFLA03-84 and of other strains from soils of the Amazon region as Bradyrhizobium viridifuturi (symbiovar tropici). Brazilian Journal of Microbiology, 2019, 50, 335-345.	0.8	18
902	Long-Term Transcriptional Activity at Zero Growth of a Cosmopolitan Rare Biosphere Member. MBio, 2019, 10, .	1.8	35
903	Archaea, the tree of life, and cellular evolution in eukaryotes. Science China Earth Sciences, 2019, 62, 489-506.	2.3	5
904	Isolation, characterization, and genome insights into an anaerobic sulfidogenic Tissierella bacterium from Cu-bearing coins. Anaerobe, 2019, 56, 66-77.	1.0	11
905	Carboxydotrophy potential of uncultivated Hydrothermarchaeota from the subseafloor crustal biosphere. ISME Journal, 2019, 13, 1457-1468.	4.4	31
906	SqueezeMeta, A Highly Portable, Fully Automatic Metagenomic Analysis Pipeline. Frontiers in Microbiology, 2018, 9, 3349.	1.5	214
907	Metagenomic and Resistome Analysis of a Full-Scale Municipal Wastewater Treatment Plant in Singapore Containing Membrane Bioreactors. Frontiers in Microbiology, 2019, 10, 172.	1.5	58
908	Genome analysis of a thermophilic exopolysaccharide-producing bacterium - Geobacillus sp. WSUCF1. Scientific Reports, 2019, 9, 1608.	1.6	24

#	ARTICLE	IF	CITATIONS
909	An integrated meta-omics approach reveals substrates involved in synergistic interactions in a bisphenol A (BPA)-degrading microbial community. Microbiome, 2019, 7, 16.	4.9	89
910	Molecular evidence for novel mercury methylating microorganisms in sulfate-impacted lakes. ISME Journal, 2019, 13, 1659-1675.	4.4	64
911	Integrated Omic Analyses Provide Evidence that a â€œ <i>Candidatus</i> Accumulibacter phosphatisâ€• Strain Performs Denitrification under Microaerobic Conditions. MSystems, 2019, 4, .	1.7	44
912	Man-made microbial resistances in built environments. Nature Communications, 2019, 10, 968.	5.8	128
913	Hydrogenotrophic methanogenesis in archaeal phylum Verstraetearchaeota reveals the shared ancestry of all methanogens. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5037-5044.	3.3	187
914	Genome-resolved metagenomics of eukaryotic populations during early colonization of premature infants and in hospital rooms. Microbiome, 2019, 7, 26.	4.9	60
915	Impacts of microbial assemblage and environmental conditions on the distribution of anatoxin-a producing cyanobacteria within a river network. ISME Journal, 2019, 13, 1618-1634.	4.4	60
916	Metagenome-assembled genomes provide new insight into the microbial diversity of two thermal pools in Kamchatka, Russia. Scientific Reports, 2019, 9, 3059.	1.6	63
917	Draft Genome Sequence of Chromatium okenii Isolated from the Stratified Alpine Lake Cadagno. Scientific Reports, 2019, 9, 1936.	1.6	16
918	Genomic blueprints of sponge-prokaryote symbiosis are shared by low abundant and cultivatable Alphaproteobacteria. Scientific Reports, 2019, 9, 1999.	1.6	52
919	Sequence and cultivation study of Muribaculaceae reveals novel species, host preference, and functional potential of this yet undescribed family. Microbiome, 2019, 7, 28.	4.9	481
920	Genome Analysis of the Marine Bacterium Labrenzia sp. Strain 011, a Potential Protective Agent of Mollusks. Data, 2019, 4, 33.	1.2	1
921	Mixing of meteoric and geothermal fluids supports hyperdiverse chemosynthetic hydrothermal communities. Nature Communications, 2019, 10, 681.	5.8	57
922	Anaerobic degradation of hexadecane and phenanthrene coupled to sulfate reduction by enriched consortia from northern Gulf of Mexico seafloor sediment. Scientific Reports, 2019, 9, 1239.	1.6	31
923	Genomics insights into ecotype formation of ammoniaâ€oxidizing archaea in the deep ocean. Environmental Microbiology, 2019, 21, 716-729.	1.8	39
924	Metagenomic Next-Generation Sequencing in Clinical Microbiology. Indian Journal of Medical Microbiology, 2019, 37, 133-140.	0.3	12
925	Draft Genome Sequence of Methanobacterium sp. Strain 34x, Reconstructed from an Enriched Electromethanogenic Biocathode. Microbiology Resource Announcements, 2019, 8, .	0.3	2
926	Draft Genome Sequences of Two Bacterial Strains, <i>Muricauda</i> sp. 72 and NH166, Isolated from the South China Sea and West Pacific Ocean. Microbiology Resource Announcements, 2019, 8, .	0.3	1

#	Article	IF	Citations
927	Draft genome sequences for three unisolated <i>Alnus</i>-infective <i>Frankia</i> Sp+ strains, AgTrS, AiOr and AvVan, the first sequenced <i>Frankia</i> strains able to sporulate <i>in-planta</i>. Journal of Genomics, 2019, 7, 50-55.	0.6	8
928	Trends of Microdiversity Reveal Depth-Dependent Evolutionary Strategies of Viruses in the Mediterranean. MSystems, 2019, 4, .	1.7	26
929	Draft Genomic Sequences of Streptomyces misionensis ACT66 and Streptomyces albidoflavus ACT77, Bacteria with Potential Application for Phytopathogen Biocontrol. Microbiology Resource Announcements, 2019, 8, .	0.3	3
930	Ecological and Genomic Attributes of Novel Bacterial Taxa That Thrive in Subsurface Soil Horizons. MBio, 2019, 10, .	1.8	108
931	Complete Genome Sequence of Sponge-Associated Tenacibaculum mesophilum DSM 13764 ^T. Microbiology Resource Announcements, 2019, 8, .	0.3	2
932	Draft Genome Sequence of Sporolactobacillus inulinus NBRC 111894, Isolated from KÃ´so, a Japanese Sugar-Vegetable Fermented Beverage. Microbiology Resource Announcements, 2019, 8, .	0.3	2
933	Prokaryotic Population Dynamics and Viral Predation in a Marine Succession Experiment Using Metagenomics. Frontiers in Microbiology, 2019, 10, 2926.	1.5	17
934	Reclassification of <i>Bacillus aryabhattai</i> Shivaji <i>etÂal</i>. 2009 as a later heterotypic synonym of <i>Bacillus megaterium</i> de Bary 1884 (Approved Lists 1980). FEMS Microbiology Letters, 2019, 366, .	0.7	11
935	Complete Genome Sequence of Halorubrum ezzemoulense Strain Fb21. Microbiology Resource Announcements, 2019, 8, .	0.3	2
936	Metagenome-Assembled Genome of <i>Halomonas</i> sp. Isolate SL48-SHIP-3 from the Microbial Mat of Salt Lake Number 48 (Novosibirsk Region, Russia). Microbiology Resource Announcements, 2019, 8, .	0.3	1
937	Draft Genome Sequence of a Bombella apis Strain Isolated from Honey Bees. Microbiology Resource Announcements, 2019, 8, .	0.3	8
938	Improved Draft Genome Sequence of <i>Microbacterium</i> sp. Strain LKL04, a Bacterial Endophyte Associated with Switchgrass Plants. Microbiology Resource Announcements, 2019, 8, .	0.3	8
939	The Bacterial Symbionts of Closely Related Hydrothermal Vent Snails With Distinct Geochemical Habitats Show Broad Similarity in Chemoautotrophic Gene Content. Frontiers in Microbiology, 2019, 10, 1818.	1.5	21
940	5. Metagenomics of extreme environments: methods and applications. , 2019, , 93-126.		0
941	6. Practical overview of bioinformatics data mining in environmental genomics. , 2019, , 127-150.		0
942	A Novel Phosphate-Accumulating Bacterium Identified in a Bioreactor for Phosphate Removal from Wastewater. Microbiology, 2019, 88, 751-755.	0.5	6
943	Draft Genome Sequences of Citrobacter freundii and Citrobacter murliniae Strains Isolated from the Feces of Preterm Infants. Microbiology Resource Announcements, 2019, 8, .	0.3	6
944	Whole-Genome Sequence of a Unique <i>Elioraea</i> Species Strain Isolated from a Yellowstone National Park Hot Spring. Microbiology Resource Announcements, 2019, 8, .	0.3	2

#	ARTICLE	IF	CITATIONS
945	Reanalysis of Lactobacillus paracasei Lbs2 Strain and Large-Scale Comparative Genomics Places Many Strains into Their Correct Taxonomic Position. Microorganisms, 2019, 7, 487.	1.6	14
946	<i>Arcobacter peruensis</i> sp. nov., a Chemolithoheterotroph Isolated from Sulfide- and Organic-Rich Coastal Waters off Peru. Applied and Environmental Microbiology, 2019, 85, .	1.4	36
947	Analysing nonsynonymous mutations between two Mycobacterium bovis strains with contrasting pathogenic profiles. Veterinary Microbiology, 2019, 239, 108482.	0.8	5
948	Characteristics of Wetting-Induced Bacteriophage Blooms in Biological Soil Crust. MBio, 2019, 10, .	1.8	56
949	Genome-Resolved Proteomic Stable Isotope Probing of Soil Microbial Communities Using 13CO2 and 13C-Methanol. Frontiers in Microbiology, 2019, 10, 2706.	1.5	23
950	Goethite Reduction by a Neutrophilic Member of the Alphaproteobacterial Genus Telmatospirillum. Frontiers in Microbiology, 2019, 10, 2938.	1.5	25
951	Microbial chemolithotrophy mediates oxidative weathering of granitic bedrock. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26394-26401.	3.3	29
952	Comparison of different technologies for the decipherment of the whole genome sequence of Campylobacter jejuni BfR-CA-14430. Gut Pathogens, 2019, 11, 59.	1.6	7
953	Comprehensive analysis of chromosomal mobile genetic elements in the gut microbiome reveals phylum-level niche-adaptive gene pools. PLoS ONE, 2019, 14, e0223680.	1.1	59
954	Within-species contamination of bacterial whole-genome sequence data has a greater influence on clustering analyses than between-species contamination. Genome Biology, 2019, 20, 286.	3.8	16
955	Pan-genome diversification and recombination in Cronobacter sakazakii, an opportunistic pathogen in neonates, and insights to its xerotolerant lifestyle. BMC Microbiology, 2019, 19, 306.	1.3	12
956	Tal1NXtc01 in Xanthomonas translucens pv. cerealis Contributes to Virulence in Bacterial Leaf Streak of Wheat. Frontiers in Microbiology, 2019, 10, 2040.	1.5	15
957	Evolution of BACON Domain Tandem Repeats in crAssphage and Novel Gut Bacteriophage Lineages. Viruses, 2019, 11, 1085.	1.5	20
958	Draft Genome Sequences of Six Lactobacillus gasseri and Three <i>Lactobacillus paragasseri</i> Strains Isolated from the Female Bladder. Microbiology Resource Announcements, 2019, 8, .	0.3	7
959	Genome analyses of a placozoan rickettsial endosymbiont show a combination of mutualistic and parasitic traits. Scientific Reports, 2019, 9, 17561.	1.6	11
960	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. Nature Communications, 2019, 10, 5477.	5.8	197
961	Genome-Based Metabolic Reconstruction of a Novel Uncultivated Freshwater Magnetotactic coccus â€œCa. Magnetaquicoccus inordinatusâ€•UR-1, and Proposal of a Candidate Family â€œCa. Magnetaquicoccaceaeâ€. Frontiers in Microbiology, 2019, 10, 2290.	1.5	33
962	Obtaining Genome Sequences of Mutualistic Bacteria in Single Microcystis Colonies. International Journal of Molecular Sciences, 2019, 20, 5047.	1.8	5

#	ARTICLE	IF	CITATIONS
963	The Draft Genome of a Hydrogen-producing Cyanobacterium, <i>Arthrospira platensis</i> NIES-46. Journal of Genomics, 2019, 7, 56-59.	0.6	6
964	Intestinal microbiota domination under extreme selective pressures characterized by metagenomic read cloud sequencing and assembly. BMC Bioinformatics, 2019, 20, 585.	1.2	7
965	H2 Metabolism revealed by metagenomic analysis of subglacial sediment from East Antarctica. Journal of Microbiology, 2019, 57, 1095-1104.	1.3	8
966	Comparative genomics reveals a novel genetic organization of the sad cluster in the sulfonamide-degrader â€˜Candidatus Leucobacter sulfamidivoraxâ€™ strain GP. BMC Genomics, 2019, 20, 885.	1.2	13
967	Microbial genomes from non-human primate gut metagenomes expand the primate-associated bacterial tree of life with over 1000 novel species. Genome Biology, 2019, 20, 299.	3.8	58
968	Identification of Novel Putative Bacterial Feruloyl Esterases From Anaerobic Ecosystems by Use of Whole-Genome Shotgun Metagenomics and Genome Binning. Frontiers in Microbiology, 2019, 10, 2673.	1.5	8
969	Stunted microbiota and opportunistic pathogen colonization in caesarean-section birth. Nature, 2019, 574, 117-121.	13.7	617
970	Targeted isolation and cultivation of uncultivated bacteria by reverse genomics. Nature Biotechnology, 2019, 37, 1314-1321.	9.4	231
971	Occurrence and expression of genes encoding methyl-compound production in rumen bacteria. Animal Microbiome, 2019, 1, 15.	1.5	27
972	Comparative Genomics Reveals Metabolic Specificity of Endozoicomonas Isolated from a Marine Sponge and the Genomic Repertoire for Host-Bacteria Symbioses. Microorganisms, 2019, 7, 635.	1.6	13
973	Novel Isoprene-Degrading Proteobacteria From Soil and Leaves Identified by Cultivation and Metagenomics Analysis of Stable Isotope Probing Experiments. Frontiers in Microbiology, 2019, 10, 2700.	1.5	28
975	Charting the Complexity of the Marine Microbiome through Single-Cell Genomics. Cell, 2019, 179, 1623-1635.e11.	13.5	158
976	Light-driven anaerobic microbial oxidation of manganese. Nature, 2019, 576, 311-314.	13.7	90
977	Enrichment of Marinobacter sp. and Halophilic Homoacetogens at the Biocathode of Microbial Electrosynthesis System Inoculated With Red Sea Brine Pool. Frontiers in Microbiology, 2019, 10, 2563.	1.5	24
978	Long-term impact of fecal transplantation in healthy volunteers. BMC Microbiology, 2019, 19, 312.	1.3	55
979	Phylogeny and physiology of candidate phylum BRC1 inferred from the first complete metagenome-assembled genome obtained from deep subsurface aquifer. Systematic and Applied Microbiology, 2019, 42, 67-76.	1.2	38
980	Cryptic CH4 cycling in the sulfateâ€“methane transition of marine sediments apparently mediated by ANME-1 archaea. ISME Journal, 2019, 13, 250-262.	4.4	90
981	Genomic and metabolic features of the Bacillus amyloliquefaciens groupâ€" B. amyloliquefaciens, B. velezensis, and B. siamensisâ€" revealed by pan-genome analysis. Food Microbiology, 2019, 77, 146-157.	2.1	54

#	Article	IF	Citations
982	Relevance of phenotypic information for the taxonomy of not-yet-cultured microorganisms. Systematic and Applied Microbiology, 2019, 42, 22-29.	1.2	34
983	Genomic insights into Candidatus Amarolinea aalborgensis gen. nov., sp. nov., associated with settleability problems in wastewater treatment plants. Systematic and Applied Microbiology, 2019, 42, 77-84.	1.2	58
984	A new symbiotic nanoarchaeote (Candidatus Nanoclepta minutus) and its host (Zestosphaera) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66 2019, 42, 94-106.	1.2	76
985	<i>Deltaproteobacteria</i> (<i>Pelobacter</i>) and <i>Methanococcoides</i> are responsible for choline-dependent methanogenesis in a coastal saltmarsh sediment. ISME Journal, 2019, 13, 277-289.	4.4	27
986	Candidatus Prosiliicoccus vernus, a spring phytoplankton bloom associated member of the Flavobacteriaceae. Systematic and Applied Microbiology, 2019, 42, 41-53.	1.2	39
987	gcMeta: a Global Catalogue of Metagenomics platform to support the archiving, standardization and analysis of microbiome data. Nucleic Acids Research, 2019, 47, D637-D648.	6.5	70
988	Niche Differentiation among Three Closely Related <i>Competibacteraceae</i> Clades at a Full-Scale Activated Sludge Wastewater Treatment Plant and Putative Linkages to Process Performance. Applied and Environmental Microbiology, 2019, 85, .	1.4	9
989	Host Specificity and Spatial Distribution Preference of Three Pseudomonas Isolates. Frontiers in Microbiology, 2018, 9, 3263.	1.5	17
990	Microbial metalâ€sulfide oxidation in inactive hydrothermal vent chimneys suggested by metagenomic and metaproteomic analyses. Environmental Microbiology, 2019, 21, 682-701.	1.8	50
991	Assembling a genome for novel nitrogen-fixing bacteria with capabilities for utilization of aromatic hydrocarbons. Genomics, 2019, 111, 1824-1830.	1.3	22
992	Recovering microbial genomes from metagenomes in hypersaline environments: The Good, the Bad and the Ugly. Systematic and Applied Microbiology, 2019, 42, 30-40.	1.2	29
993	Novel ecological insights and functional roles during anaerobic digestion of saccharides unveiled by genome-centric metagenomics. Water Research, 2019, 151, 271-279.	5.3	83
994	Taxonomic and functional heterogeneity of the gill microbiome in a symbiotic coastal mangrove lucinid species. ISME Journal, 2019, 13, 902-920.	4.4	38
995	Genome reconstruction of a novel carbohydrate digesting bacterium from the chicken caecal microflora. Meta Gene, 2019, 20, 100543.	0.3	11
996	Description of Wenzhouxiangella salilacus sp. nov., a moderate halophilic bacterium isolated from a salt lake in Xinjiang Province, China. Antonie Van Leeuwenhoek, 2019, 112, 847-855.	0.7	5
997	Genomic insights into the metabolism of â€˜<i>Candidatus</i>Defluviicoccus seviouriiâ€™, a member of<i>Defluviicoccus</i>cluster III abundant in industrial activated sludge. FEMS Microbiology Ecology, 2019, 95, .	1.3	17
998	Candidatus Krumholzibacterium zodletonense gen. nov., sp nov, the first representative of the candidate phylum Krumholzibacteriota phyl. nov. recovered from an anoxic sulfidic spring using genome resolved metagenomics. Systematic and Applied Microbiology, 2019, 42, 85-93.	1.2	39
999	Periodic and Spatial Spreading of Alkanes and <i>Alcanivorax</i> Bacteria in Deep Waters of the Mariana Trench. Applied and Environmental Microbiology, 2019, 85, .	1.4	17

#	Article	IF	Citations
1000	The use of next generation sequencing for improving food safety: Translation into practice. Food Microbiology, 2019, 79, 96-115.	2.1	225
1001	MAGpy: a reproducible pipeline for the downstream analysis of metagenome-assembled genomes (MAGs). Bioinformatics, 2019, 35, 2150-2152.	1.8	33
1002	Genome properties in 2019: a new companion database to InterPro for the inference of complete functional attributes. Nucleic Acids Research, 2019, 47, D564-D572.	6.5	27
1003	Selective colonization ability of human fecal microbes in different mouse gut environments. ISME Journal, 2019, 13, 805-823.	4.4	39
1004	The genome of â€˜Candidatus Phytoplasma solaniâ€™ strain SA-1 is highly dynamic and prone to adopting foreign sequences. Systematic and Applied Microbiology, 2019, 42, 117-127.	1.2	53
1005	Pangenomic Approach To Understanding Microbial Adaptations within a Model Built Environment, the International Space Station, Relative to Human Hosts and Soil. MSystems, 2019, 4, .	1.7	34
1006	Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle. Cell, 2019, 176, 649-662.e20.	13.5	1,087
1007	Genomic resolution of bacterial populations in saccharin and cyclamate degradation. Science of the Total Environment, 2019, 658, 357-366.	3.9	10
1008	Structural and Phylogenetic Diversity of Anaerobic Carbon-Monoxide Dehydrogenases. Frontiers in Microbiology, 2018, 9, 3353.	1.5	41
1010	Metagenomic Analysis of Zinc Surfaceâ€“Associated Marine Biofilms. Microbial Ecology, 2019, 77, 406-416.	1.4	25
1011	Genome of the candidate phylum Aminicenantes bacterium from a deep subsurface thermal aquifer revealed its fermentative saccharolytic lifestyle. Extremophiles, 2019, 23, 189-200.	0.9	74
1012	Divergent methyl-coenzyme M reductase genes in a deep-subseafloor Archaeoglobi. ISME Journal, 2019, 13, 1269-1279.	4.4	76
1013	Genomic Advances in Avian Malaria Research. Trends in Parasitology, 2019, 35, 254-266.	1.5	23
1014	Metaepigenomic analysis reveals the unexplored diversity of DNA methylation in an environmental prokaryotic community. Nature Communications, 2019, 10, 159.	5.8	48
1015	Antarctic Relic Microbial Mat Community Revealed by Metagenomics and Metatranscriptomics. Frontiers in Ecology and Evolution, 2019, 7, .	1.1	36
1016	Screening for Fusarium Antagonistic Bacteria From Contrasting Niches Designated the Endophyte Bacillus halotolerans as Plant Warden Against Fusarium. Frontiers in Microbiology, 2018, 9, 3236.	1.5	91
1017	Shaping microbial consortia in coupling glycerol fermentation and carboxylate chain elongation for Co-production of 1,3-propanediol and caproate: Pathways and mechanisms. Water Research, 2019, 148, 281-291.	5.3	30
1018	Elucidating functional microorganisms and metabolic mechanisms in a novel engineered ecosystem integrating C, N, P and S biotransformation by metagenomics. Water Research, 2019, 148, 219-230.	5.3	54

#	Article	IF	Citations
1019	Quantifying the changes in genetic diversity within sequence-discrete bacterial populations across a spatial and temporal riverine gradient. ISME Journal, 2019, 13, 767-779.	4.4	40
1020	Ecological selection for small microbial genomes along a temperate-to-thermal soil gradient. Nature Microbiology, 2019, 4, 55-61.	5.9	42
1021	Novel <i>Caudovirales</i> associated with Marine Group I Thaumarchaeota assembled from metagenomes. Environmental Microbiology, 2019, 21, 1980-1988.	1.8	33
1022	Haloprofundus halophilus sp. nov., isolated from the saline soil of Tarim Basin. Antonie Van Leeuwenhoek, 2019, 112, 553-559.	0.7	12
1023	A phylogenomic and ecological analysis of the globally abundant Marine Group II archaea (<i>Ca</i>.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	4.4	158
1024	Intensive allochthonous inputs along the Ganges River and their effect on microbial community composition and dynamics. Environmental Microbiology, 2019, 21, 182-196.	1.8	40
1025	Cyanate and urea are substrates for nitrification by Thaumarchaeota in the marine environment. Nature Microbiology, 2019, 4, 234-243.	5.9	103
1026	Biogeography of thermophiles and predominance of Thermus scotoductus in domestic water heaters. Extremophiles, 2019, 23, 119-132.	0.9	4
1027	Genomic and transcriptomic insights into the ecology and metabolism of benthic archaeal cosmopolitan, Thermoprofundales (MBG-D archaea). ISME Journal, 2019, 13, 885-901.	4.4	92
1028	Characterizing the microbiome in petroleum reservoir flooded by different water sources. Science of the Total Environment, 2019, 653, 872-885.	3.9	29
1029	Isolation and Identification of Lactic Acid Bacteria from Environmental Samples. Methods in Molecular Biology, 2019, 1887, 3-13.	0.4	11
1030	A full-ocean-depth rated modular lander and pressure-retaining sampler capable of collecting hadal-endemic microbes under in situ conditions. Deep-Sea Research Part I: Oceanographic Research Papers, 2019, 143, 50-57.	0.6	52
1031	From proteins to polysaccharides: lifestyle and genetic evolution of <i>Coprothermobacter proteolyticus</i>. ISME Journal, 2019, 13, 603-617.	4.4	30
1032	Complete genome sequence of Euzebya sp. DY32-46, a marine Actinobacteria isolated from the Pacific Ocean. Marine Genomics, 2019, 44, 65-69.	0.4	8
1033	IMG/M v.5.0: an integrated data management and comparative analysis system for microbial genomes and microbiomes. Nucleic Acids Research, 2019, 47, D666-D677.	6.5	799
1034	Bacterial contributions to delignification and lignocellulose degradation in forest soils with metagenomic and quantitative stable isotope probing. ISME Journal, 2019, 13, 413-429.	4.4	246
1035	Genome analyses of uncultured TG2/ZB3 bacteria in â€˜Margulisbacteriaâ€™ specifically attached to ectosymbiotic spirochetes of protists in the termite gut. ISME Journal, 2019, 13, 455-467.	4.4	55
1036	Pangenomic comparison of globally distributed Poribacteria associated with sponge hosts and marine particles. ISME Journal, 2019, 13, 468-481.	4.4	63

#	ARTICLE	IF	CITATIONS
1037	Metagenomic assembly through the lens of validation: recent advances in assessing and improving the quality of genomes assembled from metagenomes. Briefings in Bioinformatics, 2019, 20, 1140-1150.	3.2	113
1038	A review of methods and databases for metagenomic classification and assembly. Briefings in Bioinformatics, 2019, 20, 1125-1136.	3.2	368
1039	Reconstruction and in silico analysis of new Marinobacter adhaerens t76_800 with potential for long-chain hydrocarbon bioremediation associated with marine environmental lipases. Marine Genomics, 2020, 49, 100685.	0.4	5
1040	New approaches for metagenome assembly with short reads. Briefings in Bioinformatics, 2020, 21, 584-594.	3.2	140
1041	Horizontal acquisition of a patchwork Calvin cycle by symbiotic and free-living Campylobacterota (formerly Epsilonproteobacteria). ISME Journal, 2020, 14, 104-122.	4.4	55
1042	Two pathways for thiosulfate oxidation in the alphaproteobacterial chemolithotroph Paracoccus thiocyanatus SST. Microbiological Research, 2020, 230, 126345.	2.5	25
1043	Methane production in the oxygenated water column of a perennially iceâ€covered Antarctic lake. Limnology and Oceanography, 2020, 65, 143-156.	1.6	14
1044	Microbial genomes retrieved from High Arctic lake sediments encode for adaptation to cold and oligotrophic environments. Limnology and Oceanography, 2020, 65, S233.	1.6	20
1045	Genomic, transcriptomic, and proteomic insights into the symbiosis of deep-sea tubeworm holobionts. ISME Journal, 2020, 14, 135-150.	4.4	41
1046	Genomic and metabolic features of Lactobacillus sakei as revealed by its pan-genome and the metatranscriptome of kimchi fermentation. Food Microbiology, 2020, 86, 103341.	2.1	39
1047	Complex microbial nitrogen-cycling networks in three distinct anammox-inoculated wastewater treatment systems. Water Research, 2020, 168, 115142.	5.3	109
1048	Metagenomic insights into the changes in microbial community and antimicrobial resistance genes associated with different salt content of red pepper (Capsicum annuum L.) sauce. Food Microbiology, 2020, 85, 103295.	2.1	27
1049	Nonâ€cyanobacterial diazotrophs dominate nitrogenâ€fixing communities in permafrost thaw ponds. Limnology and Oceanography, 2020, 65, S180.	1.6	19
1050	Genomic differences within the phylum Marinimicrobia: From waters to sediments in the Mariana Trench. Marine Genomics, 2020, 50, 100699.	0.4	12
1051	Diversity and biogeography of SAR11 bacteria from the Arctic Ocean. ISME Journal, 2020, 14, 79-90.	4.4	35
1052	Timeâ€series metatranscriptomes reveal conserved patterns between phototrophic and heterotrophic microbes in diverse freshwater systems. Limnology and Oceanography, 2020, 65, S101.	1.6	18
1053	Anaerophilus nitritogenes gen. nov., sp. nov., isolated from salt lake sediment in Xinjiang Province, China. Antonie Van Leeuwenhoek, 2020, 113, 417-425.	0.7	1
1054	Evidences of aromatic degradation dominantly via the phenylacetic acid pathway in marine benthic Thermoprofundales. Environmental Microbiology, 2020, 22, 329-342.	1.8	12

#	Article	IF	Citations
1055	Database Mining for Novel Bacterial Î²-Etherases, Glutathione-Dependent Lignin-Degrading Enzymes. Applied and Environmental Microbiology, 2020, 86, .	1.4	13
1056	Long solids retention times and attached growth phase favor prevalence of comammox bacteria in nitrogen removal systems. Water Research, 2020, 169, 115268.	5.3	98
1057	In situ metabolic activities of uncultivated Ferrovum sp. CARN8 evidenced by metatranscriptomic analysis. Research in Microbiology, 2020, 171, 37-43.	1.0	7
1058	Shedding light on biogas: Phototrophic biofilms in anaerobic digesters hold potential for improved biogas production. Systematic and Applied Microbiology, 2020, 43, 126024.	1.2	9
1059	Complete genome and bimodal genomic structure of the amoebal symbiont Neochlamydia strain S13 revealed by ultra-long reads obtained from MinION. Journal of Human Genetics, 2020, 65, 41-48.	1.1	1
1060	100â€yearâ€old enigma solved: identification, genomic characterization and biogeography of the yet uncultured <i>Planctomyces bekefii</i>. Environmental Microbiology, 2020, 22, 198-211.	1.8	25
1061	Computational Framework for High-Quality Production and Large-Scale Evolutionary Analysis of Metagenome Assembled Genomes. Molecular Biology and Evolution, 2020, 37, 593-598.	3.5	11
1062	Discovery of hyperstable carbohydrateâ€active enzymes through metagenomics of extreme environments. FEBS Journal, 2020, 287, 1116-1137.	2.2	32
1063	Stratification of microbiomes during the holomictic period of Lake Fuxian, an alpine monomictic lake. Limnology and Oceanography, 2020, 65, S134.	1.6	25
1064	Microbial abundance, composition, and function in nectar are shaped by flower visitor identity. FEMS Microbiology Ecology, 2020, 96, .	1.3	46
1065	Three marine strains constitute the novel genus and species Crateriforma conspicua in the phylum Planctomycetes. Antonie Van Leeuwenhoek, 2020, 113, 1797-1809.	0.7	35
1066	CAMITAX: Taxon labels for microbial genomes. GigaScience, 2020, 9, .	3.3	6
1067	Pangenomics Analysis Reveals Diversification of Enzyme Families and Niche Specialization in Globally Abundant SAR202 Bacteria. MBio, 2020, 11, .	1.8	39
1068	Description of three bacterial strains belonging to the new genus Novipirellula gen. nov., reclassificiation of Rhodopirellula rosea and Rhodopirellula caenicola and readjustment of the genus threshold of the phylogenetic marker rpoB for Planctomycetaceae. Antonie Van Leeuwenhoek, 2020, 113, 1779-1795.	0.7	56
1069	Tracking microbial evolution in the human gut using Hi-C reveals extensive horizontal gene transfer, persistence and adaptation. Nature Microbiology, 2020, 5, 343-353.	5.9	101
1070	A diverse uncultivated microbial community is responsible for organic matter degradation in the Black Sea sulphidic zone. Environmental Microbiology, 2021, 23, 2709-2728.	1.8	47
1071	Microbial community composition and functional potential in Bothnian Sea sediments is linked to Fe and S dynamics and the quality of organic matter. Limnology and Oceanography, 2020, 65, S113.	1.6	22
1072	Metagenomics reveals microbial community differences lead to differential nitrate production in anammox reactors with differing nitrogen loading rates. Water Research, 2020, 169, 115279.	5.3	62

#	Article	IF	Citations
1073	Linking metagenomics to aquatic microbial ecology and biogeochemical cycles. Limnology and Oceanography, 2020, 65, S2.	1.6	82
1074	Genome analysis of sponge symbiont â€˜<i>Candidatus</i> Halichondribacter symbioticusâ€™ shows genomic adaptation to a hostâ€dependent lifestyle. Environmental Microbiology, 2020, 22, 483-498.	1.8	20
1075	Scalable and cost-effective ribonuclease-based rRNA depletion for transcriptomics. Nucleic Acids Research, 2020, 48, e20-e20.	6.5	42
1076	Novel syntrophic bacteria in full-scale anaerobic digesters revealed by genome-centric metatranscriptomics. ISME Journal, 2020, 14, 906-918.	4.4	117
1077	Alienimonas californiensis gen. nov. sp. nov., a novel Planctomycete isolated from the kelp forest in Monterey Bay. Antonie Van Leeuwenhoek, 2020, 113, 1751-1766.	0.7	40
1078	Bacterial enrichment in highly-selective acetate-fed bioreactors and its application in rapid biofilm formation. Water Research, 2020, 170, 115359.	5.3	5
1079	Comparison of sulfideâ€oxidizing <i>Sulfurimonas</i> strains reveals a new mode of thiosulfate formation in subsurface environments. Environmental Microbiology, 2020, 22, 1784-1800.	1.8	27
1080	Ecogenomics of the SAR11 clade. Environmental Microbiology, 2020, 22, 1748-1763.	1.8	66
1081	Genome Sequences of 72 Bacterial Strains Isolated from Ectocarpus subulatus: A Resource for Algal Microbiology. Genome Biology and Evolution, 2020, 12, 3647-3655.	1.1	30
1082	Degradation of Recalcitrant Polyurethane and Xenobiotic Additives by a Selected Landfill Microbial Community and Its Biodegradative Potential Revealed by Proximity Ligation-Based Metagenomic Analysis. Frontiers in Microbiology, 2019, 10, 2986.	1.5	84
1083	Extremophilic nitrite-oxidizing <i>Chloroflexi</i> from Yellowstone hot springs. ISME Journal, 2020, 14, 364-379.	4.4	93
1084	Investigation of genomic characteristics and carbohydratesâ€™ metabolic activity of Lactococcus lactis subsp. lactis during ripening of a Swiss-type cheese. Food Microbiology, 2020, 87, 103392.	2.1	12
1085	Methane oxidation in anoxic lake water stimulated by nitrate and sulfate addition. Environmental Microbiology, 2020, 22, 766-782.	1.8	66
1086	Novel copper-containing membrane monooxygenases (CuMMOs) encoded by alkane-utilizing <i>Betaproteobacteria</i>. ISME Journal, 2020, 14, 714-726.	4.4	16
1087	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. Nature Microbiology, 2020, 5, 126-140.	5.9	164
1088	Ecological and functional capabilities of an uncultured Kordia sp.. Systematic and Applied Microbiology, 2020, 43, 126045.	1.2	5
1089	Metabolic relationships of uncultured bacteria associated with the microalgae <i>Gambierdiscus</i>. Environmental Microbiology, 2020, 22, 1764-1783.	1.8	28
1090	Zearalenone-induced aberration in the composition of the gut microbiome and function impacts the ovary reserve. Chemosphere, 2020, 244, 125493.	4.2	30

#	ARTICLE	IF	CITATIONS
1091	Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. ISME Journal, 2020, 14, 659-675.	4.4	69
1092	Rare bacteria in seawater are dominant in the bacterial assemblage associated with the Bloom-forming dinoflagellate Noctiluca scintillans. Science of the Total Environment, 2020, 711, 135107.	3.9	16
1093	Bacterial Communities and Functional Genes Stimulated During Anaerobic Arsenite Oxidation and Nitrate Reduction in a Paddy Soil. Environmental Science & Technology, 2020, 54, 2172-2181.	4.6	62
1094	Comparative Genomics Guides Elucidation of Vitamin B₁₂Biosynthesis in Novel Human-Associated<i>Akkermansia</i>Strains. Applied and Environmental Microbiology, 2020, 86, .	1.4	48
1095	Draft Genome Sequence of â€œ Candidatus Phytoplasma pruniâ€•(X-Disease Group, Subgroup 16SrIII-B) Strain ChTDIII from Argentina. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1096	Defining Genomic and Predicted Metabolic Features of the <i>Acetobacterium</i> Genus. MSystems, 2020, 5, .	1.7	11
1097	The new microbiology: cultivating the future of microbiome-directed medicine. American Journal of Physiology - Renal Physiology, 2020, 319, G639-G645.	1.6	5
1098	Comparative Genome Analysis and Phenotypic Characterization of Clostridium gasigenes CGAS001 Isolated From Chilled Vacuum-Packed Lamb Meat. Frontiers in Microbiology, 2020, 11, 2048.	1.5	9
1099	Warming Climate Is Reducing the Diversity of Dominant Microbes in the Largest High Arctic Lake. Frontiers in Microbiology, 2020, 11, 561194.	1.5	13
1100	Reinekea thalattae sp. nov., a New Species of the Genus Reinekea Isolated from Surface Seawater in Sehwa Beach. Current Microbiology, 2020, 77, 4174-4179.	1.0	10
1101	Haloferax profundi sp. nov. and Haloferax marisrubri sp. nov., Isolated from the Discovery Deep Brine-Seawater Interface in the Red Sea. Microorganisms, 2020, 8, 1475.	1.6	1
1102	<i>De Novo</i> Resistance to Arg ₁₀ -Teixobactin Occurs Slowly and Is Costly. Antimicrobial Agents and Chemotherapy, 2020, 65, .	1.4	8
1103	Multispecies Diesel Fuel Biodegradation and Niche Formation Are Ignited by Pioneer Hydrocarbon-Utilizing Proteobacteria in a Soil Bacterial Consortium. Applied and Environmental Microbiology, 2020, 87, .	1.4	20
1104	Assembly of Bacterial Genomes from the Metagenomes of Three Lichen Species. Microbiology Resource Announcements, 2020, 9, .	0.3	3
1105	Reconstruction of Bacterial Metagenome-Assembled Genome Sequences from Alpine Bog Vegetation. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1106	No Assembly Required: Using BTyper3 to Assess the Congruency of a Proposed Taxonomic Framework for the Bacillus cereus Group With Historical Typing Methods. Frontiers in Microbiology, 2020, 11, 580691.	1.5	32
1107	Newly Explored Faecalibacterium Diversity Is Connected to Age, Lifestyle, Geography, and Disease. Current Biology, 2020, 30, 4932-4943.e4.	1.8	72
1108	Deciphering the mobility and bacterial hosts of antibiotic resistance genes under antibiotic selection pressure by metagenomic assembly and binning approaches. Water Research, 2020, 186, 116318.	5.3	160

#	Article	IF	Citations
1109	Genome-Centric Metagenomic Insights into the Impact of Alkaline/Acid and Thermal Sludge Pretreatment on the Microbiome in Digestion Sludge. Applied and Environmental Microbiology, 2020, 86, .	1.4	12
1111	Metabolic Diversity and Evolutionary History of the Archaeal Phylum â€œ <i>Candidatus</i> Micrarchaeotaâ€•Uncovered from a Freshwater Lake Metagenome. Applied and Environmental Microbiology, 2020, 86, .	1.4	22
1112	Discovery of an Abundance of Biosynthetic Gene Clusters in Shark Bay Microbial Mats. Frontiers in Microbiology, 2020, 11, 1950.	1.5	39
1113	Arenibacter lacus sp. nov., Isolated from Chilika Lagoon, India. Current Microbiology, 2020, 77, 4152-4159.	1.0	1
1114	Integration of time-series meta-omics data reveals how microbial ecosystems respond to disturbance. Nature Communications, 2020, 11, 5281.	5.8	57
1115	Ancestral Reconstructions Decipher Major Adaptations of Ammonia-Oxidizing Archaea upon Radiation into Moderate Terrestrial and Marine Environments. MBio, 2020, 11, .	1.8	27
1116	A Multifactorial Approach for Surveillance of Shigella spp. and Entero-Invasive Escherichia coli Is Important for Detecting (Inter)national Clusters. Frontiers in Microbiology, 2020, 11, 564103.	1.5	13
1117	Shotgun metagenomic data of microbiomes on plastic fabrics exposed to harsh tropical environments. Data in Brief, 2020, 32, 106226.	0.5	6
1118	â€˜Candidatus Oscillochloris kuznetsoviiâ€™ a novel mesophilic filamentous anoxygenic phototrophic Chloroflexales bacterium from Arctic coastal environments. FEMS Microbiology Letters, 2020, 367, .	0.7	8
1119	Draft Genome Sequences of Two Phylogenetically Distinct Clostridium gasigenes Strains, CM001 and CM004, Isolated from Chilled Vacuum-Packed Meat. Microbiology Resource Announcements, 2020, 9, .	0.3	2
1120	The intestinal microbiome, weight, and metabolic changes in women treated by adjuvant chemotherapy for breast and gynecological malignancies. BMC Medicine, 2020, 18, 281.	2.3	19
1121	Metagenomic analysis of the dust particles collected from the suction tube and the suction funnel of a dermatological laser smoke evacuator system. Lasers in Medical Science, 2021, 36, 1249-1260.	1.0	1
1122	Evaluation of assembly methods combining long-reads and short-reads to obtain Paenibacillus sp. R4 high-quality complete genome. 3 Biotech, 2020, 10, 480.	1.1	1
1123	Draft genome sequence of â€œCandidatus Afipia apatlaquensisâ€•sp. nov., IBT-C3, a potential strain for decolorization of textile dyes. BMC Research Notes, 2020, 13, 265.	0.6	7
1124	Distinctive gene and protein characteristics of extremely piezophilic Colwellia. BMC Genomics, 2020, 21, 692.	1.2	27
1125	The reductive glycine pathway allows autotrophic growth of Desulfovibrio desulfuricans. Nature Communications, 2020, 11, 5090.	5.8	152
1126	Rational design of a microbial consortium of mucosal sugar utilizers reduces Clostridiodes difficile colonization. Nature Communications, 2020, 11, 5104.	5.8	177
1127	Precise Species Identification and Taxonomy Update for the Genus Kluyvera With Reporting Kluyvera sichuanensis sp. nov.. Frontiers in Microbiology, 2020, 11, 579306.	1.5	13

#	Article	IF	Citations
1128	Metagenomic insights into the diversity of carbohydrate-degrading enzymes in the yak fecal microbial community. BMC Microbiology, 2020, 20, 302.	1.3	24
1129	Methanogens Within a High Salinity Oil Reservoir From the Gulf of Mexico. Frontiers in Microbiology, 2020, 11, 570714.	1.5	5
1130	Metagenomic studies of SAR202 bacteria at the full-ocean depth in the Mariana Trench. Deep-Sea Research Part I: Oceanographic Research Papers, 2020, 165, 103396.	0.6	14
1131	Metagenomic profiling of ammonia- and methane-oxidizing microorganisms in two sequential rapid sand filters. Water Research, 2020, 185, 116288.	5.3	52
1132	Metagenomic characterization of microbial communities on plasticized fabric materials exposed to harsh tropical environments. International Biodeterioration and Biodegradation, 2020, 154, 105061.	1.9	17
1133	Intermittent aeration of landfill simulation bioreactors: Effects on emissions and microbial community. Waste Management, 2020, 117, 146-156.	3.7	22
1134	Tracing the animal sources of surface water contamination with Campylobacter jejuni and Campylobacter coli. Water Research, 2020, 187, 116421.	5.3	34
1135	metaFlye: scalable long-read metagenome assembly using repeat graphs. Nature Methods, 2020, 17, 1103-1110.	9.0	430
1136	Complete Genome of Roseobacter ponti DSM 106830T. Genome Biology and Evolution, 2020, 12, 1013-1018.	1.1	3
1137	Evolutionary Timeline and Genomic Plasticity Underlying the Lifestyle Diversity in <i>Rhizobiales</i>. MSystems, 2020, 5, .	1.7	45
1138	Targeted Cell Sorting Combined With Single Cell Genomics Captures Low Abundant Microbial Dark Matter With Higher Sensitivity Than Metagenomics. Frontiers in Microbiology, 2020, 11, 1377.	1.5	25
1139	Insights into the dynamics between viruses and their hosts in a hot spring microbial mat. ISME Journal, 2020, 14, 2527-2541.	4.4	42
1140	First Complete Genome Sequences of Janthinobacterium lividum EIF1 and EIF2 and Their Comparative Genome Analysis. Genome Biology and Evolution, 2020, 12, 1782-1788.	1.1	15
1141	Novel Syntrophic Isovalerate-Degrading Bacteria and Their Energetic Cooperation with Methanogens in Methanogenic Chemostats. Environmental Science & Technology, 2020, 54, 9618-9628.	4.6	23
1142	Bacterial chemolithoautotrophy via manganese oxidation. Nature, 2020, 583, 453-458.	13.7	152
1143	Metabolome-microbiome signatures in the fermented beverage, Kombucha. International Journal of Food Microbiology, 2020, 333, 108778.	2.1	94
1144	Genomic Blueprint of Glycine Betaine Metabolism in Coral Metaorganisms and Their Contribution to Reef Nitrogen Budgets. IScience, 2020, 23, 101120.	1.9	30
1145	Proposal of Desulfosarcina ovata subsp. sediminis subsp. nov., a novel toluene-degrading sulfate-reducing bacterium isolated from tidal flat sediment of Tokyo Bay. Systematic and Applied Microbiology, 2020, 43, 126109.	1.2	6

#	ARTICLE	IF	CITATIONS
1146	Physiological, chemotaxonomic and genomic characterization of two novel piezotolerant bacteria of the family Marinifilaceae isolated from sulfidic waters of the Black Sea. Systematic and Applied Microbiology, 2020, 43, 126122.	1.2	11
1147	Multi-omic Directed Discovery of Cellulosomes, Polysaccharide Utilization Loci, and Lignocellulases from an Enriched Rumen Anaerobic Consortium. Applied and Environmental Microbiology, 2020, 86, .	1.4	20
1148	Wenzhouxiangella Strain AB-CW3, a Proteolytic Bacterium From Hypersaline Soda Lakes That Preys on Cells of Gram-Positive Bacteria. Frontiers in Microbiology, 2020, 11, 597686.	1.5	15
1149	Disease-associated gut microbiome and metabolome changes in patients with chronic obstructive pulmonary disease. Nature Communications, 2020, 11, 5886.	5.8	194
1150	Emergence of Multidrug Resistant Hypervirulent ST23 Klebsiella pneumoniae: Multidrug Resistant Plasmid Acquisition Drives Evolution. Frontiers in Cellular and Infection Microbiology, 2020, 10, 575289.	1.8	25
1151	Thermogenic hydrocarbon biodegradation by diverse depth-stratified microbial populations at a Scotian Basin cold seep. Nature Communications, 2020, 11, 5825.	5.8	72
1152	Whole-Genome Sequencing and Bioinformatic Analysis of Environmental, Agricultural, and Human Campylobacter jejuni Isolates From East Tennessee. Frontiers in Microbiology, 2020, 11, 571064.	1.5	7
1153	Draft Genome Sequence of <i>Okeania</i> sp. Strain KiyG1, Assembled from Single-Amplified Genomes Collected from Cape Kiyan, Okinawa, Japan. Microbiology Resource Announcements, 2020, 9, .	0.3	0
1154	Gene duplication drives genome expansion in a major lineage of Thaumarchaeota. Nature Communications, 2020, 11, 5494.	5.8	55
1155	Metagenomic analysis revealed the sulfur- and iron- oxidation capabilities of heterotrophic denitrifying sludge. Ecotoxicology, 2021, 30, 1399-1407.	1.1	4
1156	Mercury Methylation Genes Identified across Diverse Anaerobic Microbial Guilds in a Eutrophic Sulfate-Enriched Lake. Environmental Science & Technology, 2020, 54, 15840-15851.	4.6	50
1157	Introducing a â€œcore steel microbiomeâ€•and community functional analysis associated with microbially influenced corrosion. FEMS Microbiology Ecology, 2020, 97, .	1.3	8
1158	Comprehensive prediction of secondary metabolite structure and biological activity from microbial genome sequences. Nature Communications, 2020, 11, 6058.	5.8	174
1159	Unique maternal immune and functional microbial profiles during prenatal stress. Scientific Reports, 2020, 10, 20288.	1.6	26
1160	Microbiota-directed fibre activates both targeted and secondary metabolic shifts in the distal gut. Nature Communications, 2020, 11, 5773.	5.8	55
1161	Reconstructing Genomes of Carbon Monoxide Oxidisers in Volcanic Deposits Including Members of the Class Ktedonobacteria. Microorganisms, 2020, 8, 1880.	1.6	15
1162	Genomic Characterization of a Novel Tenericutes Bacterium from Deep-Sea Holothurian Intestine. Microorganisms, 2020, 8, 1874.	1.6	22
1163	Genome Sequence of the Unusual Purple Photosynthetic Bacterium Phaeovibrio sulfidiphilus, Only Distantly Related to Rhodospirillaceae , Reveals Unique Genes for Respiratory Nitrate Reduction and Glycerol Metabolism. Microbiology Resource Announcements, 2020, 9, .	0.3	1

#	ARTICLE	IF	CITATIONS
1164	High-Quality Draft Genome Sequence of a <i>Rickettsiales</i> Bacterium Found in <i>Acropora tenuis</i> Coral from Okinawa, Japan. Microbiology Resource Announcements, 2020, 9, .	0.3	5
1165	Metagenome-Assembled Genome Sequence of Aphanizomenon flos-aquae Strain Clear-A1, Assembled from an Enrichment Culture. Microbiology Resource Announcements, 2020, 9, .	0.3	0
1166	The Role of the Gut Microbiome in Resisting Norovirus Infection as Revealed by a Human Challenge Study. MBio, 2020, 11, .	1.8	26
1167	Fermented-Food Metagenomics Reveals Substrate-Associated Differences in Taxonomy and Health-Associated and Antibiotic Resistance Determinants. MSystems, 2020, 5, .	1.7	78
1168	A comprehensive investigation of metagenome assembly by linked-read sequencing. Microbiome, 2020, 8, 156.	4.9	12
1169	Taxonomic Novelty and Distinctive Genomic Features of Hot Spring Cyanobacteria. Frontiers in Genetics, 2020, 11, 568223.	1.1	36
1170	Exploring the Influence of Signal Molecules on Marine Biofilms Development. Frontiers in Microbiology, 2020, 11, 571400.	1.5	16
1171	Expanded Phylogenetic Diversity and Metabolic Flexibility of Mercury-Methylating Microorganisms. MSystems, 2020, 5, .	1.7	56
1172	Genome Sequences of Two Microcystis aeruginosa (<i>Chroococcales</i> , <i>Cyanobacteria</i>) Strains from Florida (United States) with Disparate Toxigenic Potentials. Microbiology Resource Announcements, 2020, 9, .	0.3	6
1173	Metagenomic Association Analysis of Gut Symbiont Limosilactobacillus reuteri Without Host-Specific Genome Isolation. Frontiers in Microbiology, 2020, 11, 585622.	1.5	4
1174	Synergistic biodegradation of aromatic-aliphatic copolyester plastic by a marine microbial consortium. Nature Communications, 2020, 11, 5790.	5.8	122
1175	New Frontiers of Anaerobic Hydrocarbon Biodegradation in the Multi-Omics Era. Frontiers in Microbiology, 2020, 11, 590049.	1.5	33
1176	High quality genome assemblies of Mycoplasma bovis using a taxon-specific Bonito basecaller for MinION and Flongle long-read nanopore sequencing. BMC Bioinformatics, 2020, 21, 517.	1.2	32
1177	Anoxygenic photosynthesis and ironâ€"sulfur metabolic potential of <i>Chlorobia</i> populations from seasonally anoxic Boreal Shield lakes. ISME Journal, 2020, 14, 2732-2747.	4.4	22
1178	Inclusion of Oxford Nanopore long reads improves all microbial and viral metagenomeâ€assembled genomes from a complex aquifer system. Environmental Microbiology, 2020, 22, 4000-4013.	1.8	42
1179	Precise Species Identification for <i>Enterobacter</i> : a Genome Sequence-Based Study with Reporting of Two Novel Species, <i>Enterobacter quasiroggenkampii</i> sp. nov. and <i>Enterobacter quasimori</i> sp. nov. MSystems, 2020, 5, .	1.7	95
1180	Unraveling bacteria-mediated degradation of lignin-derived aromatic compounds in a freshwater environment. Science of the Total Environment, 2020, 749, 141236.	3.9	22
1181	Genomic and enzymatic evidence of acetogenesis by anaerobic methanotrophic archaea. Nature Communications, 2020, 11, 3941.	5.8	45

#	ARTICLE	IF	CITATIONS
1182	DRAM for distilling microbial metabolism to automate the curation of microbiome function. Nucleic Acids Research, 2020, 48, 8883-8900.	6.5	410
1183	Bactopia: a Flexible Pipeline for Complete Analysis of Bacterial Genomes. MSystems, 2020, 5, .	1.7	82
1184	Undinarchaeota illuminate DPANN phylogeny and the impact of gene transfer on archaeal evolution. Nature Communications, 2020, 11, 3939.	5.8	102
1185	Comparative Genomics of Microbacterium Species to Reveal Diversity, Potential for Secondary Metabolites and Heavy Metal Resistance. Frontiers in Microbiology, 2020, 11, 1869.	1.5	29
1186	Investigation of the Ecological Roles of Putative Keystone Taxa during Tailing Revegetation. Environmental Science & Technology, 2020, 54, 11258-11270.	4.6	62
1187	A new genomic taxonomy system for the <i>Synechococcus</i> collective. Environmental Microbiology, 2020, 22, 4557-4570.	1.8	32
1188	Virulence as a Side Effect of Interspecies Interaction in <i>Vibrio</i> Coral Pathogens. MBio, 2020, 11, .	1.8	23
1189	Producing polished prokaryotic pangenomes with the Panaroo pipeline. Genome Biology, 2020, 21, 180.	3.8	419
1190	Genome-Wide Identification and Functional Characterization of Î²-Agarases in Vibrio astriarenae Strain HN897. Frontiers in Microbiology, 2020, 11, 1404.	1.5	10
1191	Glacial-interglacial transitions in microbiomes recorded in deep-sea sediments from the western equatorial Atlantic. Science of the Total Environment, 2020, 746, 140904.	3.9	4
1192	AciDB 1.0: a database of acidophilic organisms, their genomic information and associated metadata. Bioinformatics, 2020, 36, 4970-4971.	1.8	9
1193	Comparative Genomics Discloses the Uniqueness and the Biosynthetic Potential of the Marine Cyanobacterium Hyella patelloides. Frontiers in Microbiology, 2020, 11, 1527.	1.5	5
1194	Temporal Shotgun Metagenomics Revealed the Potential Metabolic Capabilities of Specific Microorganisms During Lambic Beer Production. Frontiers in Microbiology, 2020, 11, 1692.	1.5	21
1195	Evaluating metagenomics tools for genome binning with real metagenomic datasets and CAMI datasets. BMC Bioinformatics, 2020, 21, 334.	1.2	53
1196	Prevalence and Implications of Contamination in Public Genomic Resources: A Case Study of 43 Reference Arthropod Assemblies. G3: Genes, Genomes, Genetics, 2020, 10, 721-730.	0.8	25
1197	Genomic Insights of Cryobacterium Isolated From Ice Core Reveal Genome Dynamics for Adaptation in Glacier. Frontiers in Microbiology, 2020, 11, 1530.	1.5	12
1198	High-Quality Draft Genome Sequences of Three Cyanobacteria Isolated from the Limestone Walls of the Old Cathedral of Coimbra, Portugal. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1199	Acquisition and Adaptation of Ultra-small Parasitic Reduced Genome Bacteria to Mammalian Hosts. Cell Reports, 2020, 32, 107939.	2.9	152

#	Article	IF	Citations
1200	Unravelling the diversity of magnetotactic bacteria through analysis of open genomic databases. Scientific Data, 2020, 7, 252.	2.4	32
1201	Globally Abundant â€œ <i>Candidatus</i> Udaeobacterâ€•Benefits from Release of Antibiotics in Soil and Potentially Performs Trace Gas Scavenging. MSphere, 2020, 5, .	1.3	32
1202	Fast start-up of PN/A process in a single-stage packed bed and mechanism of nitrogen removal. Environmental Science and Pollution Research, 2020, 27, 40483-40494.	2.7	10
1203	Anaerobic Degradation of Paraffins by Thermophilic Actinobacteria under Methanogenic Conditions. Environmental Science & Technology, 2020, 54, 10610-10620.	4.6	53
1204	Genome Sequences and Metagenome-Assembled Genome Sequences of Microbial Communities Enriched on Phytoplankton Exometabolites. Microbiology Resource Announcements, 2020, 9, .	0.3	5
1205	Draft Genome Sequences of Micrococcus luteus MFP06 and MFP07, Isolated from the Skin of Healthy Volunteers. Microbiology Resource Announcements, 2020, 9, .	0.3	3
1206	Halomonas plays a central role in the syntrophic community of an alkaline oil reservoir with alkali-surfactant-polymer (ASP) flooding. Science of the Total Environment, 2020, 747, 141333.	3.9	13
1207	Differential prevalence and host-association of antimicrobial resistance traits in disinfected and non-disinfected drinking water systems. Science of the Total Environment, 2020, 749, 141451.	3.9	22
1208	Microbial Metabolic Redundancy Is a Key Mechanism in a Sulfur-Rich Glacial Ecosystem. MSystems, 2020, 5, .	1.7	17
1209	Metabolic acclimation of anammox consortia to decreased temperature. Environment International, 2020, 143, 105915.	4.8	52
1210	Genomic Characteristics and Potential Metabolic Adaptations of Hadal Trench Roseobacter and Alteromonas Bacteria Based on Single-Cell Genomics Analyses. Frontiers in Microbiology, 2020, 11, 1739.	1.5	6
1211	Catabolism and interactions of uncultured organisms shaped by eco-thermodynamics in methanogenic bioprocesses. Microbiome, 2020, 8, 111.	4.9	48
1212	Life in hot acid: a genomeâ€based reassessment of the archaeal order <i>Sulfolobales</i>. Environmental Microbiology, 2021, 23, 3568-3584.	1.8	20
1213	Alterocin, an Antibiofilm Protein Secreted by <i>Pseudoalteromonas</i> sp. Strain 3J6. Applied and Environmental Microbiology, 2020, 86, .	1.4	7
1214	Influence of the polar light cycle on seasonal dynamics of an Antarctic lake microbial community. Microbiome, 2020, 8, 116.	4.9	32
1215	Microbial Life in the Deep Subsurface Aquifer Illuminated by Metagenomics. Frontiers in Microbiology, 2020, 11, 572252.	1.5	48
1216	Description of Erythrobacter mangrovi sp. nov., an aerobic bacterium from rhizosphere soil of mangrove plant (Kandelia candel). Antonie Van Leeuwenhoek, 2020, 113, 1425-1435.	0.7	10
1217	Ecological Structuring of Temperate Bacteriophages in the Inflammatory Bowel Disease-Affected Gut. Microorganisms, 2020, 8, 1663.	1.6	14

#	ARTICLE	IF	CITATIONS
1218	Functional redundancy imparts process stability to acidic Fe(<scp>II</scp>)â€oxidizing microbial reactors. Environmental Microbiology, 2021, 23, 3682-3694.	1.8	6
1219	Antarctic desert soil bacteria exhibit high novel natural product potential, evaluated through longâ€read genome sequencing and comparative genomics. Environmental Microbiology, 2021, 23, 3646-3664.	1.8	18
1220	Draft Genome Sequence of Pseudarthrobacter sp. Strain ATCC 49442 (Formerly Micrococcus luteus), a Pyridine-Degrading Bacterium. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1221	Genome Sequences of Frankineae sp. Strain MT45 and Jatrophihabitans sp. Strain GAS493, Two Actinobacteria Isolated from Forest Soil. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1222	Atribacteria Reproducing over Millions of Years in the Atlantic Abyssal Subseafloor. MBio, 2020, 11, .	1.8	23
1223	Kineococcus vitellinus sp. nov., Kineococcus indalonis sp. nov. and Kineococcus siccus sp. nov., Isolated Nearby the Tabernas Desert (AlmerÃa, Spain). Microorganisms, 2020, 8, 1547.	1.6	15
1224	Co-cultivation of microbial sub-communities in microfluidic droplets facilitates high-resolution genomic dissection of microbial â€˜dark matterâ€™. Integrative Biology (United Kingdom), 2020, 12, 263-274.	0.6	16
1225	Comparative Genomic Analysis Reveals Genetic Mechanisms of the Variety of Pathogenicity, Antibiotic Resistance, and Environmental Adaptation of Providencia Genus. Frontiers in Microbiology, 2020, 11, 572642.	1.5	24
1226	Streamlined and Abundant Bacterioplankton Thrive in Functional Cohorts. MSystems, 2020, 5, .	1.7	8
1227	Genome Characterization of a Novel Wastewater Bacteroides fragilis Bacteriophage (vB_BfrS_23) and its Host GB124. Frontiers in Microbiology, 2020, 11, 583378.	1.5	5
1228	The level of antimicrobial resistance of sewage isolates is higher than that of river isolates in different Escherichia coli lineages. Scientific Reports, 2020, 10, 17880.	1.6	12
1229	Deciphering the Microbial Taxonomy and Functionality of Two Diverse Mangrove Ecosystems and Their Potential Abilities To Produce Bioactive Compounds. MSystems, 2020, 5, .	1.7	23
1230	Streptomyces alkaliterrae sp. nov., isolated from an alkaline soil, and emended descriptions of Streptomyces alkaliphilus, Streptomyces calidiresistens and Streptomyces durbertensis. Systematic and Applied Microbiology, 2020, 43, 126153.	1.2	17
1231	Larger Anammox Granules not only Harbor Higher Species Diversity but also Support More Functional Diversity. Environmental Science & Technology, 2020, 54, 14664-14673.	4.6	34
1232	V^V Reduction by <i>Polaromonas</i> spp. in Vanadium Mine Tailings. Environmental Science & Technology, 2020, 54, 14442-14454.	4.6	47
1233	Expanding magnetic organelle biogenesis in the domain Bacteria. Microbiome, 2020, 8, 152.	4.9	44
1234	Metagenomic and Metatranscriptomic Analyses Revealed Uncultured Bacteroidales Populations as the Dominant Proteolytic Amino Acid Degraders in Anaerobic Digesters. Frontiers in Microbiology, 2020, 11, 593006.	1.5	57
1235	Comparative genomic analysis reveals metabolic diversity of different Paenibacillus groups. Applied Microbiology and Biotechnology, 2020, 104, 10133-10143.	1.7	5

#	Article	IF	Citations
1236	Draft genome of Bugula neritina, a colonial animal packing powerful symbionts and potential medicines. Scientific Data, 2020, 7, 356.	2.4	6
1237	Spirochetes isolated from arthropods constitute a novel genus Entomospira genus novum within the order Spirochaetales. Scientific Reports, 2020, 10, 17053.	1.6	5
1238	Chloramphenicol biodegradation by enriched bacterial consortia and isolated strain Sphingomonas sp. CL5.1: The reconstruction of a novel biodegradation pathway. Water Research, 2020, 187, 116397.	5.3	44
1239	Metagenome-Assembled Genome Sequences from an Anoxygenic Photosynthetic Consortium Involved in Sulfur Cycling. Microbiology Resource Announcements, 2020, 9, .	0.3	0
1240	Targeted isolation based on metagenomeâ€assembled genomes reveals a phylogenetically distinct group of thermophilic spirochetes from deep biosphere. Environmental Microbiology, 2021, 23, 3585-3598.	1.8	23
1241	Comparative genomic analysis of Vibrios yields insights into genes associated with virulence towards C. gigas larvae. BMC Genomics, 2020, 21, 599.	1.2	11
1242	Sulfur and Methane-Oxidizing Microbial Community in a Terrestrial Mud Volcano Revealed by Metagenomics. Microorganisms, 2020, 8, 1333.	1.6	19
1243	Endosymbionts of Metazoans Dwelling in the PACManus Hydrothermal Vent: Diversity and Potential Adaptive Features Revealed by Genome Analysis. Applied and Environmental Microbiology, 2020, 86, .	1.4	6
1244	1200 high-quality metagenome-assembled genomes from the rumen of African cattle and their relevance in the context of sub-optimal feeding. Genome Biology, 2020, 21, 229.	3.8	38
1245	Genome sequence of segmented filamentous bacteria present in the human intestine. Communications Biology, 2020, 3, 485.	2.0	27
1246	PacBio Long Reads Improve Metagenomic Assemblies, Gene Catalogs, and Genome Binning. Frontiers in Genetics, 2020, 11, 516269.	1.1	44
1247	Two hundred and fifty-four metagenome-assembled bacterial genomes from the bank vole gut microbiota. Scientific Data, 2020, 7, 312.	2.4	13
1248	Multi-omic Analysis of the Interaction between Clostridioides difficile Infection and Pediatric Inflammatory Bowel Disease. Cell Host and Microbe, 2020, 28, 422-433.e7.	5.1	45
1249	Warmth Prevents Bone Loss Through the Gut Microbiota. Cell Metabolism, 2020, 32, 575-590.e7.	7.2	88
1250	Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. PLoS ONE, 2020, 15, e0234839.	1.1	8
1251	Genomics Reveals the Metabolic Potential and Functions in the Redistribution of Dissolved Organic Matter in Marine Environments of the Genus Thalassotalea. Microorganisms, 2020, 8, 1412.	1.6	4
1252	Metabolic diversification of anaerobic methanotrophic archaea in a deep-sea cold seep. Marine Life Science and Technology, 2020, 2, 431-441.	1.8	17
1253	Transformation of the recalcitrant pesticide chlordecone by Desulfovibrio sp.86 with a switch from ring-opening dechlorination to reductive sulfidation activity. Scientific Reports, 2020, 10, 13545.	1.6	12

#	ARTICLE	IF	CITATIONS
1254	Genome characteristics of Kordia antarctica IMCC3317T and comparative genome analysis of the genus Kordia. Scientific Reports, 2020, 10, 14715.	1.6	7
1255	Sequencing of five poultry strains elucidates phylogenetic relationships and divergence in virulence genes in Morganella morganii. BMC Genomics, 2020, 21, 579.	1.2	8
1256	High-Quality Draft Genome Sequences of the Uncultured Delta3 Endosymbiont (Deltaproteobacteria) Assembled from Metagenomes of the Gutless Marine Worm Olavius algarvensis. Microbiology Resource Announcements, 2020, 9, .	0.3	3
1257	Discovery of Unusual Cyanobacterial Tryptophan-Containing Anabaenopeptins by MS/MS-Based Molecular Networking. Molecules, 2020, 25, 3786.	1.7	12
1258	Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. PLoS Genetics, 2020, 16, e1008935.	1.5	87
1259	A Shallow Water Ferrous-Hulled Shipwreck Reveals a Distinct Microbial Community. Frontiers in Microbiology, 2020, 11, 1897.	1.5	11
1260	Draft Genome Sequence of Leptospira interrogans Serovar Bataviae Strain D64, Isolated from the Urine of an Asymptomatic Dog in Pathum Thani, Thailand. Microbiology Resource Announcements, 2020, 9, .	0.3	3
1261	A ubiquitous subcuticular bacterial symbiont of a coral predator, the crown-of-thorns starfish, in the Indo-Pacific. Microbiome, 2020, 8, 123.	4.9	10
1262	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. Frontiers in Microbiology, 2020, 11, 1848.	1.5	62
1263	Spartinivicinus ruber gen. nov., sp. nov., a Novel Marine Gammaproteobacterium Producing Heptylprodigiosin and Cycloheptylprodigiosin as Major Red Pigments. Frontiers in Microbiology, 2020, 11, 2056.	1.5	18
1264	Near-Complete Genome Sequences of a <i>Wolbachia</i> Strain Isolated from Diaphorina citri Kuwayama (<i>Hemiptera</i> : <i>Liviidae</i>). Microbiology Resource Announcements, 2020, 9, .	0.3	5
1265	Microbial mats in the Turks and Caicos Islands reveal diversity and evolution of phototrophy in the Chloroflexota order Aggregatilineales. Environmental Microbiomes, 2020, 15, 9.	2.2	15
1266	Two Metagenome-Assembled Genome Sequences of Magnetotactic Bacteria in the Order Magnetococcales. Microbiology Resource Announcements, 2020, 9, .	0.3	5
1267	Identification of a Metagenome-Assembled Genome of an Uncultured <i>Methyloceanibacter</i> sp. Strain Acquired from an Activated Sludge System Used for Landfill Leachate Treatment. Microbiology Resource Announcements, 2020, 9, .	0.3	4
1268	Microbial dark matter filling the niche in hypersaline microbial mats. Microbiome, 2020, 8, 135.	4.9	35
1269	Bacteria are important dimethylsulfoniopropionate producers in marine aphotic and high-pressure environments. Nature Communications, 2020, 11, 4658.	5.8	62
1270	Phylogenomic Analysis Reveals That Arthrobacter mysorens Nand and Rao 1972 (Approved Lists 1980) and Glutamicibacter mysorens Busse 2016 are Later Heterotypic Synonyms of Arthrobacter nicotianae Giovannozzi-Sermanni 1959 (Approved Lists 1980) and Glutamicibacter nicotianae Busse 2016. Current Microbiology, 2020, 77, 3793-3798.	1.0	7
1271	Insights into the Vertical Stratification of Microbial Ecological Roles across the Deepest Seawater Column on Earth. Microorganisms, 2020, 8, 1309.	1.6	18

#	Article	IF	Citations
1272	Draft Genome Sequences of Three <i>Clostridia</i> Isolates Involved in Lactate-Based Chain Elongation. Microbiology Resource Announcements, 2020, 9, .	0.3	8
1273	Binning unassembled short reads based on k-mer abundance covariance using sparse coding. GigaScience, 2020, 9, .	3.3	7
1274	Best Practices for Successfully Writing and Publishing a Genome Announcement in <i>Microbiology Resource Announcements</i>. Microbiology Resource Announcements, 2020, 9, .	0.3	0
1275	Metagenomics: Techniques, Applications, Challenges and Opportunities. , 2020, , .		7
1276	Complete Genome Sequence of Lactobacillus fermentum Strain AGR1485, a Human Oral Isolate. Microbiology Resource Announcements, 2020, 9, .	0.3	2
1277	Metagenomic and Metatranscriptomic Study of Microbial Metal Resistance in an Acidic Pit Lake. Microorganisms, 2020, 8, 1350.	1.6	15
1278	Spatial Metagenomics of Three Geothermal Sites in Pisciarelli Hot Spring Focusing on the Biochemical Resources of the Microbial Consortia. Molecules, 2020, 25, 4023.	1.7	11
1279	Expanded Diversity and Metabolic Versatility of Marine Nitrite-Oxidizing Bacteria Revealed by Cultivation- and Genomics-Based Approaches. Applied and Environmental Microbiology, 2020, 86, .	1.4	38
1280	Estimating the quality of eukaryotic genomes recovered from metagenomic analysis with EukCC. Genome Biology, 2020, 21, 244.	3.8	58
1281	910 metagenome-assembled genomes from the phytobiomes of three urban-farmed leafy Asian greens. Scientific Data, 2020, 7, 278.	2.4	17
1282	A driftâ€barrier model drives the genomic landscape of a structured bacterial population. Molecular Ecology, 2020, 29, 4143-4156.	2.0	3
1283	Abundant Taxa and Favorable Pathways in the Microbiome of Soda-Saline Lakes in Inner Mongolia. Frontiers in Microbiology, 2020, 11, 1740.	1.5	27
1284	Gut microbiome of endangered Tor putitora (Ham.) as a reservoir of antibiotic resistance genes and pathogens associated with fish health. BMC Microbiology, 2020, 20, 249.	1.3	10
1285	Genomic Comparison and Spatial Distribution of Different Synechococcus Phylotypes in the Black Sea. Frontiers in Microbiology, 2020, 11, 1979.	1.5	13
1286	Gammaproteobacteria mediating utilization of methyl-, sulfur- and petroleum organic compounds in deep ocean hydrothermal plumes. ISME Journal, 2020, 14, 3136-3148.	4.4	36
1287	Meta-analysis of cheese microbiomes highlights contributions to multiple aspects of quality. Nature Food, 2020, 1, 500-510.	6.2	60
1288	Termite mounds contain soil-derived methanotroph communities kinetically adapted to elevated methane concentrations. ISME Journal, 2020, 14, 2715-2731.	4.4	21
1289	Use of Newly Designed Primers for Quantification of Complete Ammonia-Oxidizing (Comammox) Bacterial Clades and Strict Nitrite Oxidizers in the Genus <i>Nitrospira</i>. Applied and Environmental Microbiology, 2020, 86, .	1.4	38

#	ARTICLE	IF	CITATIONS
1290	Complete Genome Assembly of a Multidrug-Resistant New Delhi Metallo-Î²-Lactamase 1 (NDM-1)-Producing Escherichia coli Human Isolate from a New Zealand Hospital. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1291	Comparative genomic analysis of Flavobacteriaceae: insights into carbohydrate metabolism, gliding motility and secondary metabolite biosynthesis. BMC Genomics, 2020, 21, 569.	1.2	53
1292	Complete and Circularized Genome Assemblies of the Kroppenstedtia eburnea Genus Type Strain and the Kroppenstedtia pulmonis Species Type Strain with MiSeq and MinION Sequence Data. Microbiology Resource Announcements, 2020, 9, .	0.3	0
1293	Pan-genome analysis and ancestral state reconstruction of class halobacteria: probability of a new super-order. Scientific Reports, 2020, 10, 21205.	1.6	13
1294	Production of the antimicrobial compound tetrabromopyrrole and the Pseudomonas quinolone system precursor, 2-heptyl-4-quinolone, by a novel marine species Pseudoalteromonas galatheae sp. nov.. Scientific Reports, 2020, 10, 21630.	1.6	15
1295	DNA-Stable Isotope Probing Shotgun Metagenomics Reveals the Resilience of Active Microbial Communities to Biochar Amendment in Oxisol Soil. Frontiers in Microbiology, 2020, 11, 587972.	1.5	12
1296	Whole-Genome Sequence of Brevibacillus borstelensis SDM, Isolated from a Sorghum-Adapted Microbial Community. Microbiology Resource Announcements, 2020, 9, .	0.3	10
1297	Draft Genome Sequence of the Carboxydotrophic Alphaproteobacterium Aminobacter carboxidus Type Strain DSM 1086. Microbiology Resource Announcements, 2020, 9, .	0.3	3
1298	Comparative genomics of Klebsiella michiganensis BD177 and related members of Klebsiella sp. reveal the symbiotic relationship with Bactrocera dorsalis. BMC Genetics, 2020, 21, 138.	2.7	5
1299	Metabolic Contributions of an Alphaproteobacterial Endosymbiont in the Apicomplexan Cardiosporidium cionae. Frontiers in Microbiology, 2020, 11, 580719.	1.5	8
1300	Functional Changes of the Community of Microbes With Ni-Dependent Enzyme Genes Accompany Adaptation of the Ruminal Microbiome to Urea-Supplemented Diets. Frontiers in Microbiology, 2020, 11, 596681.	1.5	4
1301	The Weathering Microbiome of an Outcropping Granodiorite. Frontiers in Microbiology, 2020, 11, 601907.	1.5	6
1302	Dichloromethane Degradation Pathway from Unsequenced Hyphomicrobium sp. MC8b Rapidly Explored by Pan-Proteomics. Microorganisms, 2020, 8, 1876.	1.6	6
1303	Genomic and Metabolic Insights into Two Novel Thiothrix Species from Enhanced Biological Phosphorus Removal Systems. Microorganisms, 2020, 8, 2030.	1.6	20
1304	Detection and elimination of a novel non-toxigenic Clostridioides difficile strain from the microbiota of a mouse colony. Gut Microbes, 2020, 12, 1851999.	4.3	4
1305	Metagenomic insights into the metabolism and evolution of a new Thermoplasmata order (<i>Candidatus</i> Gimiplasmatales). Environmental Microbiology, 2021, 23, 3695-3709.	1.8	21
1306	Genome-Resolved Metagenomics and Antibiotic Resistance Genes Analysis in Reclaimed Water Distribution Systems. Water (Switzerland), 2020, 12, 3477.	1.2	7
1307	Functional and genetic markers of niche partitioning among enigmatic members of the human oral microbiome. Genome Biology, 2020, 21, 292.	3.8	132

#	ARTICLE	IF	CITATIONS
1308	Shotgun metagenomic analysis reveals new insights into bacterial community profiles in tempeh. BMC Research Notes, 2020, 13, 562.	0.6	6
1309	Simultaneous Genome Sequencing of Prosthecochloris ethylica and Desulfuromonas acetoxidans within a Syntrophic Mixture Reveals Unique Pili and Protein Interactions. Microorganisms, 2020, 8, 1939.	1.6	7
1310	Genome Sequence of Citrobacter freundii AMC0703, Isolated from the Intestinal Lumen of an 11-Year-Old Organ Donor. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1311	Saccharibacteria as Organic Carbon Sinks in Hydrocarbon-Fueled Communities. Frontiers in Microbiology, 2020, 11, 587782.	1.5	22
1312	Characterization of Metagenome-Assembled Genomes and Carbohydrate-Degrading Genes in the Gut Microbiota of Tibetan Pig. Frontiers in Microbiology, 2020, 11, 595066.	1.5	34
1313	Data on draft genome sequence of Caldanaerobacter sp. strain 1523vc, a thermophilic bacterium, isolated from a hot spring of Uzon Caldera, (Kamchatka, Russia). Data in Brief, 2020, 33, 106336.	0.5	2
1314	A collection of bacterial isolates from the pig intestine reveals functional and taxonomic diversity. Nature Communications, 2020, 11, 6389.	5.8	269
1315	A novel bacterial phylum that participates in carbon and osmolyte cycling in the Challenger Deep sediments. Environmental Microbiology, 2020, 23, 3758-3772.	1.8	4
1316	Evaluation of methods for the reduction of contaminating host reads when performing shotgun metagenomic sequencing of the milk microbiome. Scientific Reports, 2020, 10, 21665.	1.6	33
1317	Dysbiosis in marine aquaculture revealed through microbiome analysis: reverse ecology for environmental sustainability. FEMS Microbiology Ecology, 2020, 96, .	1.3	10
1318	A Klebsiella pneumoniae ST307 outbreak clone from Germany demonstrates features of extensive drug resistance, hypermucoviscosity, and enhanced iron acquisition. Genome Medicine, 2020, 12, 113.	3.6	82
1319	Genome Sequences of Four Strains of Acinetobacter bereziniae Isolated from Human Milk Pumped with a Personal Breast Pump and Hand-Washed Milk Collection Supplies. Microbiology Resource Announcements, 2020, 9, .	0.3	6
1320	Multidrug-resistant enterobacteriaceae in coastal water: an emerging threat. Antimicrobial Resistance and Infection Control, 2020, 9, 169.	1.5	16
1321	Struggle To Survive: the Choir of Target Alteration, Hydrolyzing Enzyme, and Plasmid Expression as a Novel Aztreonam-Avibactam Resistance Mechanism. MSystems, 2020, 5, .	1.7	22
1322	High-quality bacterial genomes of a partial-nitritation/anammox system by an iterative hybrid assembly method. Microbiome, 2020, 8, 155.	4.9	29
1323	Complete Genome and Plasmid Sequences of Salmonella enterica subsp. enterica Serovar Enteritidis PT1, Obtained from the Salmonella Reference Laboratory at Public Health England, Colindale, United Kingdom. Microbiology Resource Announcements, 2020, 9, .	0.3	4
1324	Metagenomic Hi-C of a Healthy Human Fecal Microbiome Transplant Donor. Microbiology Resource Announcements, 2020, 9, .	0.3	9
1325	Phylogenomic Insights into Diversity and Evolution of Nonpathogenic <i>Xanthomonas</i> Strains Associated with Citrus. MSphere, 2020, 5, .	1.3	18

#	Article	IF	Citations
1326	Metagenomic Exploration of the Marine Sponge <i>Mycale hentscheli</i> Uncovers Multiple Polyketide-Producing Bacterial Symbionts. MBio, 2020, 11, .	1.8	43
1327	Complete Genome Sequence of Burkholderia sp. Strain THE68, a Bacterial Symbiont Isolated from Midgut Crypts of the Seed Bug Togo hemipterus. Microbiology Resource Announcements, 2020, 9, .	0.3	3
1328	Metagenome-Assembled Genome Sequences of Five Strains from the <i>Microtus ochrogaster</i> (Prairie Vole) Fecal Microbiome. Microbiology Resource Announcements, 2020, 9, .	0.3	5
1329	A Genomic Toolkit for the Mechanistic Dissection of Intractable Human Gut Bacteria. Cell Host and Microbe, 2020, 27, 1001-1013.e9.	5.1	39
1330	Haloplanus rubicundus sp. nov., an extremely halophilic archaeon isolated from solar salt. Systematic and Applied Microbiology, 2020, 43, 126085.	1.2	6
1331	Diversity, ecology and evolution of Archaea. Nature Microbiology, 2020, 5, 887-900.	5.9	262
1332	Phylogenomic Analyses of Members of the Widespread Marine Heterotrophic Genus Pseudovibrio Suggest Distinct Evolutionary Trajectories and a Novel Genus, Polycladidibacter gen. nov. Applied and Environmental Microbiology, 2020, 86, .	1.4	6
1333	Genomic Evidence for Formate Metabolism by <i>Chloroflexi</i> as the Key to Unlocking Deep Carbon in Lost City Microbial Ecosystems. Applied and Environmental Microbiology, 2020, 86, .	1.4	23
1334	Draft Genome Sequences of Two <i>Paenibacillus</i> Isolates from Goose and Chicken Gastrointestinal Material. Microbiology Resource Announcements, 2020, 9, .	0.3	0
1335	Selective carbon sources influence the end products of microbial nitrate respiration. ISME Journal, 2020, 14, 2034-2045.	4.4	61
1336	Complete Genome Sequence of Lignin-Degrading Streptomyces sp. Strain S6, Isolated from an Oil Palm Plantation in Malaysia. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1337	Genomics of New Ciliate Lineages Provides Insight into the Evolution of Obligate Anaerobiosis. Current Biology, 2020, 30, 2037-2050.e6.	1.8	48
1338	Genome diversification in globally distributed novel marine Proteobacteria is linked to environmental adaptation. ISME Journal, 2020, 14, 2060-2077.	4.4	106
1339	Palantir: a springboard for the analysis of secondary metabolite gene clusters in large-scale genome mining projects. Bioinformatics, 2020, 36, 4345-4347.	1.8	16
1340	Unexpected Abundance and Diversity of Phototrophs in Mats from Morphologically Variable Microbialites in Great Salt Lake, Utah. Applied and Environmental Microbiology, 2020, 86, .	1.4	5
1341	Distinct actions of the fermented beverage kefir on host behaviour, immunity and microbiome gut-brain modules in the mouse. Microbiome, 2020, 8, 67.	4.9	55
1342	A phylogenetically novel cyanobacterium most closely related to <i>Gloeobacter</i>. ISME Journal, 2020, 14, 2142-2152.	4.4	45
1343	Tools for successful proliferation: diverse strategies of nutrient acquisition by a benthic cyanobacterium. ISME Journal, 2020, 14, 2164-2178.	4.4	33

#	Article	IF	Citations
1344	Novel clostridial lineages recovered from metagenomes of a hot oil reservoir. Scientific Reports, 2020, 10, 8048.	1.6	13
1345	MetaSanity: an integrated microbial genome evaluation and annotation pipeline. Bioinformatics, 2020, 36, 4341-4344.	1.8	20
1346	Metabolic diversity and co-occurrence of multiple Ferrovum species at an acid mine drainage site. BMC Microbiology, 2020, 20, 119.	1.3	9
1347	Metabolic strategies of marine subseafloor Chloroflexi inferred from genome reconstructions. Environmental Microbiology, 2020, 22, 3188-3204.	1.8	49
1348	Ecological and genomic analyses of candidate phylum <scp>WPS</scp>â€2 bacteria in an unvegetated soil. Environmental Microbiology, 2020, 22, 3143-3157.	1.8	42
1349	Integrative metagenomic and metabolomic analyses reveal severity-specific signatures of gut microbiota in chronic kidney disease. Theranostics, 2020, 10, 5398-5411.	4.6	77
1350	Interaction between endophytic Proteobacteria strains and Serendipita indica enhances biocontrol activity against fungal pathogens. Plant and Soil, 2020, 451, 277-305.	1.8	27
1351	Metagenome-assembled genomes reveal unique metabolic adaptations of a basal marine Thaumarchaeota lineage. ISME Journal, 2020, 14, 2105-2115.	4.4	54
1352	Strain-resolved microbiome sequencing reveals mobile elements that drive bacterial competition on a clinical timescale. Genome Medicine, 2020, 12, 50.	3.6	43
1353	Parallel reductive genome evolution in <i>Desulfovibrio</i> ectosymbionts independently acquired by <i>Trichonympha</i> protists in the termite gut. ISME Journal, 2020, 14, 2288-2301.	4.4	10
1354	Cultivation-independent and cultivation-dependent metagenomes reveal genetic and enzymatic potential of microbial community involved in the degradation of a complex microbial polymer. Microbiome, 2020, 8, 76.	4.9	59
1355	Novel insights into the Thaumarchaeota in the deepest oceans: their metabolism and potential adaptation mechanisms. Microbiome, 2020, 8, 78.	4.9	47
1356	Illuminating Genetic Mysteries of the Dead Sea Scrolls. Cell, 2020, 181, 1218-1231.e27.	13.5	10
1357	Description of Maribellus sediminis sp. nov., a marine nitrogen-fixing bacterium isolated from sediment of cordgrass and mangrove. Systematic and Applied Microbiology, 2020, 43, 126099.	1.2	15
1358	Integrative omics analysis of the termite gut system adaptation to Miscanthus diet identifies lignocellulose degradation enzymes. Communications Biology, 2020, 3, 275.	2.0	47
1359	Metagenomic and metatranscriptomic insights into the complex nitrogen metabolic pathways in a single-stage bioreactor coupling partial denitrification with anammox. Chemical Engineering Journal, 2020, 398, 125653.	6.6	66
1360	High-Throughput Sequencing Reveals a Potentially Novel Sulfurovum Species Dominating the Microbial Communities of the Seawaterâ€"Sediment Interface of a Deep-Sea Cold Seep in South China Sea. Microorganisms, 2020, 8, 687.	1.6	27
1361	Hybrid Assembly from a Pathogenic Methicillin- and Multidrug-Resistant Staphylococcus pseudintermedius Strain Isolated from a Case of Canine Otitis in Spain. Microbiology Resource Announcements, 2020, 9, .	0.3	7

#	Article	IF	Citations
1362	Activity and Metabolic Versatility of Complete Ammonia Oxidizers in Full-Scale Wastewater Treatment Systems. MBio, 2020, 11, .	1.8	65
1363	Regulatory Noncoding Small RNAs Are Diverse and Abundant in an Extremophilic Microbial Community. MSystems, 2020, 5, .	1.7	14
1364	Draft Genome Sequence of Marinobacter hydrocarbonoclasticus NCT7M, Obtained from the Microbiome of a Marine Copepod. Microbiology Resource Announcements, 2020, 9, .	0.3	0
1365	Culturomicsâ€based genomics sheds light on the ecology of the new haloarchaeal genus <i>Halosegnis</i>. Environmental Microbiology, 2021, 23, 3418-3434.	1.8	25
1366	Draft Genome Sequences of Chlamydiales Bacterium STE3 and Neochlamydia sp. Strain AcF84, Endosymbionts of Acanthamoeba spp. Microbiology Resource Announcements, 2020, 9, .	0.3	3
1367	Genome-centric microbiome analysis reveals solid retention time (SRT)-shaped species interactions and niche differentiation in food waste and sludge co-digesters. Water Research, 2020, 181, 115858.	5.3	37
1368	Large-scale genome-wide analysis links lactic acid bacteria from food with the gut microbiome. Nature Communications, 2020, 11, 2610.	5.8	190
1369	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment. GigaScience, 2020, 9, .	3.3	35
1370	Dental Calculus as a Tool to Study the Evolution of the Mammalian Oral Microbiome. Molecular Biology and Evolution, 2020, 37, 3003-3022.	3.5	28
1371	Draft Genome Assemblies of Two Staphylococcus pseudintermedius Strains Isolated from Canine Skin Biopsy Specimens. Microbiology Resource Announcements, 2020, 9, .	0.3	2
1372	Characterization of Nitrate-Dependent As(III)-Oxidizing Communities in Arsenic-Contaminated Soil and Investigation of Their Metabolic Potentials by the Combination of DNA-Stable Isotope Probing and Metagenomics. Environmental Science & Technology, 2020, 54, 7366-7377.	4.6	82
1373	Antimicrobial Resistance in <i>Salmonella enterica</i> Serovar Paratyphi B Variant Java in Poultry from Europe and Latin America. Emerging Infectious Diseases, 2020, 26, 1164-1173.	2.0	11
1374	Unlocking the Genomic Taxonomy of the Prochlorococcus Collective. Microbial Ecology, 2020, 80, 546-558.	1.4	12
1375	Lactobacilli Have a Niche in the Human Nose. Cell Reports, 2020, 31, 107674.	2.9	75
1376	Cholesterol Metabolism by Uncultured Human Gut Bacteria Influences Host Cholesterol Level. Cell Host and Microbe, 2020, 28, 245-257.e6.	5.1	151
1377	High-Quality Draft Genome Sequence Resources of Eight Xylella fastidiosa Strains Isolated from Citrus, Coffee, Plum, and Hibiscus in South America. Phytopathology, 2020, 110, 1751-1755.	1.1	3
1378	Complete Genome Sequences of Leclercia sp. W6 and W17 Isolated from a Gastric Cancer Patient. Current Microbiology, 2020, 77, 2775-2782.	1.0	1
1379	Description of Paenibacillus yunnanensis sp. nov., Isolated from a Tepid Spring. Current Microbiology, 2020, 77, 3174-3178.	1.0	5

#	ARTICLE	IF	CITATIONS
1380	Comammox <i>Nitrospira</i> within the Yangtze River continuum: community, biogeography, and ecological drivers. ISME Journal, 2020, 14, 2488-2504.	4.4	106
1381	A Novel Microbialite-Associated Phototrophic Chloroflexi Lineage Exhibiting a Quasi-Clonal Pattern along Depth. Genome Biology and Evolution, 2020, 12, 1207-1216.	1.1	11
1382	ATLAS: a Snakemake workflow for assembly, annotation, and genomic binning of metagenome sequence data. BMC Bioinformatics, 2020, 21, 257.	1.2	91
1383	Pontiella desulfatans gen. nov., sp. nov., and Pontiella sulfatireligans sp. nov., Two Marine Anaerobes of the Pontiellaceae fam. nov. Producing Sulfated Glycosaminoglycan-like Exopolymers. Microorganisms, 2020, 8, 920.	1.6	31
1384	Metagenomics and stable isotope probing reveal the complementary contribution of fungal and bacterial communities in the recycling of dead biomass in forest soil. Soil Biology and Biochemistry, 2020, 148, 107875.	4.2	71
1385	Novel keratinolytic enzymes, discovered from a talented and efficient bacterial keratin degrader. Scientific Reports, 2020, 10, 10033.	1.6	16
1386	Comparative Genomics and Metabolomics in the Genus Nocardia. MSystems, 2020, 5, .	1.7	39
1387	Iterative subtractive binning of freshwater chronoseries metagenomes identifies over 400 novel species and their ecologic preferences. Environmental Microbiology, 2020, 22, 3394-3412.	1.8	69
1388	PCR-based screening, isolation, and partial characterization of motile lactobacilli from various animal feces. BMC Microbiology, 2020, 20, 142.	1.3	4
1389	Diversity of isoprene-degrading bacteria in phyllosphere and soil communities from a high isoprene-emitting environment: a Malaysian oil palm plantation. Microbiome, 2020, 8, 81.	4.9	23
1390	Oil leakage induces changes in microbiomes of deep-sea sediments of Campos Basin (Brazil). Science of the Total Environment, 2020, 740, 139556.	3.9	3
1391	Population genomics of Staphylococcus pseudintermedius in companion animals in the United States. Communications Biology, 2020, 3, 282.	2.0	29
1392	Metagenomics as a Tool To Monitor Reclaimed-Water Quality. Applied and Environmental Microbiology, 2020, 86, .	1.4	14
1393	Consistent Metagenome-Derived Metrics Verify and Delineate Bacterial Species Boundaries. MSystems, 2020, 5, .	1.7	135
1394	Thaumarchaea Genome Sequences from a High Arctic Active Layer. Microbiology Resource Announcements, 2020, 9, .	0.3	2
1395	Microbial Nitrogen Metabolism in Chloraminated Drinking Water Reservoirs. MSphere, 2020, 5, .	1.3	28
1396	Complete Genome Sequence Data of Three Xylella fastidiosa subsp. multiplex Strains Isolated from Olive Trees in California, U.S.A.. Phytopathology, 2020, 110, 1759-1762.	1.1	2
1397	A Vibrio cholerae Core Genome Multilocus Sequence Typing Scheme To Facilitate the Epidemiological Study of Cholera. Journal of Bacteriology, 2020, 202, .	1.0	16

#	ARTICLE	IF	CITATIONS
1398	Validating the Cyc2 Neutrophilic Iron Oxidation Pathway Using Meta-omics of <i>Zetaproteobacteria</i> Iron Mats at Marine Hydrothermal Vents. MSystems, 2020, 5, .	1.7	65
1399	The food-gut axis: lactic acid bacteria and their link to food, the gut microbiome and human health. FEMS Microbiology Reviews, 2020, 44, 454-489.	3.9	139
1400	Bacterial Secondary Metabolite Biosynthetic Potential in Soil Varies with Phylum, Depth, and Vegetation Type. MBio, 2020, 11, .	1.8	116
1401	Heterotrophic Thaumarchaea with Small Genomes Are Widespread in the Dark Ocean. MSystems, 2020, 5, .	1.7	50
1402	Genomic and transcriptomic insights into methanogenesis potential of novel methanogens from mangrove sediments. Microbiome, 2020, 8, 94.	4.9	51
1403	Genomic Insights into Two Novel Fe(II)-Oxidizing <i>Zetaproteobacteria</i> Isolates Reveal Lifestyle Adaption to Coastal Marine Sediments. Applied and Environmental Microbiology, 2020, 86, .	1.4	4
1404	Winter warming in Alaska accelerates lignin decomposition contributed by Proteobacteria. Microbiome, 2020, 8, 84.	4.9	47
1405	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. Nature Medicine, 2020, 26, 941-951.	15.2	130
1406	Metagenome Assembly and Metagenome-Assembled Genome Sequences from a Historical Oil Field Located in Wietze, Germany. Microbiology Resource Announcements, 2020, 9, .	0.3	13
1407	Metagenomic- and Cultivation-Based Exploration of Anaerobic Chloroform Biotransformation in Hypersaline Sediments as Natural Source of Chloromethanes. Microorganisms, 2020, 8, 665.	1.6	8
1408	Analysis of 1321 Eubacterium rectale genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. Genome Biology, 2020, 21, 138.	3.8	72
1409	Genomic and Metabolomic Analysis of Antarctic Bacteria Revealed Culture and Elicitation Conditions for the Production of Antimicrobial Compounds. Biomolecules, 2020, 10, 673.	1.8	10
1410	A Modular Metagenomics Pipeline Allowing for the Inclusion of Prior Knowledge Using the Example of Anaerobic Digestion. Microorganisms, 2020, 8, 669.	1.6	1
1411	Metagenomics based approach to reveal the secrets of unculturable microbial diversity from aquatic environment. , 2020, , 537-559.		3
1412	A sister lineage of the Mycobacterium tuberculosis complex discovered in the African Great Lakes region. Nature Communications, 2020, 11, 2917.	5.8	136
1413	High-Quality Draft Genome Sequences of Two Deltaproteobacterial Endosymbionts, Delta1a and Delta1b, from the Uncultured Sva0081 Clade, Assembled from Metagenomes of the Gutless Marine Worm Olavius algarvensis. Microbiology Resource Announcements, 2020, 9, .	0.3	2
1414	Depth-related variability in viral communities in highly stratified sulfidic mine tailings. Microbiome, 2020, 8, 89.	4.9	41
1415	Inoculation With Desulfovibrio sp. Does Not Enhance Chalk Formation in the Pacific Oyster. Frontiers in Marine Science, 2020, 7, .	1.2	3

#	Article	IF	Citations
1416	Impact of Electron Acceptor Availability on Methane-Influenced Microorganisms in an Enrichment Culture Obtained From a Stratified Lake. Frontiers in Microbiology, 2020, 11, 715.	1.5	18
1417	Single-Cell Genomics of Novel Actinobacteria With the Woodâ€“Ljungdahl Pathway Discovered in a Serpentinizing System. Frontiers in Microbiology, 2020, 11, 1031.	1.5	41
1418	Characterization of a Novel Functional Trimeric Catechol 1,2-Dioxygenase From a Pseudomonas stutzeri Isolated From the Gulf of Mexico. Frontiers in Microbiology, 2020, 11, 1100.	1.5	16
1419	Phenomeâ€“Genome Profiling of Single Bacterial Cell by Ramanâ€Activated Gravityâ€Driven Encapsulation and Sequencing. Small, 2020, 16, e2001172.	5.2	33
1420	New bacterial and archaeal lineages discovered in organic rich sediments of a large tropical Bay. Marine Genomics, 2020, 54, 100789.	0.4	22
1421	Draft Genome Sequence of Desulfobacter hydrogenophilus DSM 3380, a Psychrotolerant Sulfate-Reducing Bacterium. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1422	Gut microbiome diversity detected by high-coverage 16S and shotgun sequencing of paired stool and colon sample. Scientific Data, 2020, 7, 92.	2.4	37
1423	Accurate and complete genomes from metagenomes. Genome Research, 2020, 30, 315-333.	2.4	263
1424	Draft Genome Analysis of Christensenella minuta DSM 22607, exhibiting an unusual expansion of transporter homologs of unknown function. Journal of Genomics, 2020, 8, 25-29.	0.6	5
1425	Impact of process temperature and organic loading rate on cellulolytic / hydrolytic biofilm microbiomes during biomethanation of ryegrass silage revealed by genome-centered metagenomics and metatranscriptomics. Environmental Microbiomes, 2020, 15, 7.	2.2	13
1426	Comparative genomics analysis of c-di-GMP metabolism and regulation in Microcystis aeruginosa. BMC Genomics, 2020, 21, 217.	1.2	4
1427	Microbial and Viral Communities and Their Antibiotic Resistance Genes Throughout a Hospital Wastewater Treatment System. Frontiers in Microbiology, 2020, 11, 153.	1.5	65
1428	Phylogenetic Grouping of Human Ocular Escherichia coli Based on Whole-Genome Sequence Analysis. Microorganisms, 2020, 8, 422.	1.6	8
1429	Ecogenomics reveals community interactions in a long-term methanogenic bioreactor and a rapid switch to sulfate-reducing conditions. FEMS Microbiology Ecology, 2020, 96, .	1.3	8
1430	Disinfection exhibits systematic impacts on the drinking water microbiome. Microbiome, 2020, 8, 42.	4.9	48
1431	Comparative genome-centric analysis reveals seasonal variation in the function of coral reef microbiomes. ISME Journal, 2020, 14, 1435-1450.	4.4	40
1432	Novel phosphate-solubilizing bacteria enhance soil phosphorus cycling following ecological restoration of land degraded by mining. ISME Journal, 2020, 14, 1600-1613.	4.4	194
1433	Diverse Asgard archaea including the novel phylum Gerdarchaeota participate in organic matter degradation. Science China Life Sciences, 2020, 63, 886-897.	2.3	61

#	Article	IF	Citations
1434	Mineralâ€hosted biofilm communities in the continental deep subsurface, Deep Mine Microbial Observatory, SD, USA. Geobiology, 2020, 18, 508-522.	1.1	33
1435	Chemolithoautotropic Diazotrophy Dominates the Nitrogen Fixation Process in Mine Tailings. Environmental Science & Technology, 2020, 54, 6082-6093.	4.6	63
1436	Genomic and transcriptomic evidence of light-sensing, porphyrin biosynthesis, Calvin-Benson-Bassham cycle, and urea production in Bathyarchaeota. Microbiome, 2020, 8, 43.	4.9	31
1437	Impact of plants on the diversity and activity of methylotrophs in soil. Microbiome, 2020, 8, 31.	4.9	35
1438	Ecosystem-wide metagenomic binning enables prediction of ecological niches from genomes. Communications Biology, 2020, 3, 119.	2.0	64
1439	Genome repository of oil systems: An interactive and searchable database that expands the catalogued diversity of crude oilâ€associated microbes. Environmental Microbiology, 2020, 22, 2094-2106.	1.8	21
1440	Second-Generation Sequencing with Deep Reinforcement Learning for Lung Infection Detection. Journal of Healthcare Engineering, 2020, 2020, 1-9.	1.1	6
1441	Molecular Mechanisms Underpinning Aggregation in Acidiphilium sp. C61 Isolated from Iron-Rich Pelagic Aggregates. Microorganisms, 2020, 8, 314.	1.6	5
1442	Multi-Omic Profiling of Melophlus Sponges Reveals Diverse Metabolomic and Microbiome Architectures that Are Non-overlapping with Ecological Neighbors. Marine Drugs, 2020, 18, 124.	2.2	21
1443	Genome-based classification of Burkholderia cepacia complex provides new insight into its taxonomic status. Biology Direct, 2020, 15, 6.	1.9	49
1444	A survey of extended-spectrum beta-lactamase-producing Enterobacteriaceae in urban wetlands in southwestern Nigeria as a step towards generating prevalence maps of antimicrobial resistance. PLoS ONE, 2020, 15, e0229451.	1.1	19
1445	An Integrated Metagenome Catalog Reveals New Insights into the Murine Gut Microbiome. Cell Reports, 2020, 30, 2909-2922.e6.	2.9	85
1446	Neotropical termite microbiomes as sources of novel plant cell wall degrading enzymes. Scientific Reports, 2020, 10, 3864.	1.6	28
1447	Long-term serial culture of Piscirickettsia salmonis leads to a genomic and transcriptomic reorganization affecting bacterial virulence. Aquaculture, 2020, 529, 735634.	1.7	7
1448	From bag-of-genes to bag-of-genomes: metabolic modelling of communities in the era of metagenome-assembled genomes. Computational and Structural Biotechnology Journal, 2020, 18, 1722-1734.	1.9	52
1449	Ozone pretreatment of wastewater containing aromatics reduces antibiotic resistance genes in bioreactors: The example of p-aminophenol. Environment International, 2020, 142, 105864.	4.8	17
1450	Draft Genome Sequences of Bacillus glennii V44-8, Bacillus saganii V47-23a, <i>Bacillus</i> sp. Strain V59.32b, <i>Bacillus</i> sp. Strain MER_TA_151, and <i>Paenibacillus</i> sp. Strain MER_111, Isolated from Cleanrooms Where the Viking and Mars Exploration Rover Spacecraft Were Assembled. Microbiology Resource Announcements, 2020, 9, .	0.3	0
1451	What Is Metagenomics Teaching Us, and What Is Missed?. Annual Review of Microbiology, 2020, 74, 117-135.	2.9	54

#	ARTICLE	IF	CITATIONS
1452	Phylogenomics of expanding uncultured environmental Tenericutes provides insights into their pathogenicity and evolutionary relationship with Bacilli. BMC Genomics, 2020, 21, 408.	1.2	65
1453	The rise of diversity in metabolic platforms across the Candidate Phyla Radiation. BMC Biology, 2020, 18, 69.	1.7	54
1454	Draft Genome Sequence of Bifidobacterium pseudocatenulatum Bif4, Isolated from Healthy Infant Feces. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1455	Secondary Metabolism in the Gill Microbiota of Shipworms (Teredinidae) as Revealed by Comparison of Metagenomes and Nearly Complete Symbiont Genomes. MSystems, 2020, 5, .	1.7	15
1456	Draft Genome Sequences of Bacillus subtilis Strains TNC1(2019), TNC3(2019), and TNW1(2019), as Well as Bacillus velezensis Strains TNC2(2019) and TNW2(2019), Isolated from Cabbage Kimchee. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1457	Genome Analysis of a Member of the Uncultured Phylum Riflebacteria Revealed Pathways of Organotrophic Metabolism and Dissimilatory Iron Reduction. Microbiology, 2020, 89, 328-336.	0.5	16
1458	Microbial succession during the transition from active to inactive stages of deep-sea hydrothermal vent sulfide chimneys. Microbiome, 2020, 8, 102.	4.9	62
1459	Deinococcus detaillensis sp. nov., isolated from humus soil in Antarctica. Archives of Microbiology, 2020, 202, 2493-2498.	1.0	8
1460	Diversity, enrichment, and genomic potential of anaerobic methane- and ammonium-oxidizing microorganisms from a brewery wastewater treatment plant. Applied Microbiology and Biotechnology, 2020, 104, 7201-7212.	1.7	9
1461	Terabase-scale metagenome coassembly with MetaHipMer. Scientific Reports, 2020, 10, 10689.	1.6	34
1462	Draft Genome Sequences of Two Strains of Bifidobacterium dentium Isolated from a Crude Fecal Extract Used for Fecal Microbiota Transplantation in the Republic of Korea. Microbiology Resource Announcements, 2020, 9, .	0.3	0
1463	Disproportionation of inorganic sulfur compounds by a novel autotrophic bacterium belonging to Nitrospirota. Systematic and Applied Microbiology, 2020, 43, 126110.	1.2	43
1464	Genomic Characteristics of a Novel Species of Ammonia-Oxidizing Archaea from the Jiulong River Estuary. Applied and Environmental Microbiology, 2020, 86, .	1.4	16
1465	Involvement of NO ₃ ^{âˆ’} in Ecophysiological Regulation of Dissimilatory Nitrate/Nitrite Reduction to Ammonium (DNRA) Is Implied by Physiological Characterization of Soil DNRA Bacteria Isolated via a Colorimetric Screening Method. Applied and Environmental Microbiology, 2020, 86, .	1.4	29
1466	Exploring neighborhoods in large metagenome assembly graphs using spacegraphcats reveals hidden sequence diversity. Genome Biology, 2020, 21, 164.	3.8	32
1467	Genomic insights into evolution of extensive drug resistance in Stenotrophomonas maltophilia complex. Genomics, 2020, 112, 4171-4178.	1.3	14
1468	Lateral Gene Transfer Drives Metabolic Flexibility in the Anaerobic Methane-Oxidizing Archaeal Family <i>Methanoperedenaceae</i>. MBio, 2020, 11, .	1.8	51
1469	Defining Culture Conditions for the Hidden Nitrite-Oxidizing Bacterium Nitrolancea. Frontiers in Microbiology, 2020, 11, 1522.	1.5	30

#	ARTICLE	IF	CITATIONS
1470	Comparative Genome-Centric Analysis of Freshwater and Marine ANAMMOX Cultures Suggests Functional Redundancy in Nitrogen Removal Processes. Frontiers in Microbiology, 2020, 11, 1637.	1.5	37
1471	Advantages and Limits of Metagenomic Assembly and Binning of a Giant Virus. MSystems, 2020, 5, .	1.7	14
1472	A genomic view of trophic and metabolic diversity in clade-specific Lamellodysidea sponge microbiomes. Microbiome, 2020, 8, 97.	4.9	38
1473	Highâ€contiguity genome assembly of the chemosynthetic gammaproteobacterial endosymbiont of the cold seep tubeworm Lamellibrachia barhami. Molecular Ecology Resources, 2020, 20, 1432-1444.	2.2	6
1474	<i>Mycoavidus</i> sp. Strain B2-EB: Comparative Genomics Reveals Minimal Genomic Features Required by a Cultivable <i>Burkholderiaceae</i> -Related Endofungal Bacterium. Applied and Environmental Microbiology, 2020, 86, .	1.4	13
1475	Dominant denitrifying bacteria are important hosts of antibiotic resistance genes in pig farm anoxic-oxic wastewater treatment processes. Environment International, 2020, 143, 105897.	4.8	44
1476	Draft Genome Sequences of Two <i>Clostridium</i> Isolates from the Poultry Gastrointestinal Tract. Microbiology Resource Announcements, 2020, 9, .	0.3	0
1477	Draft Genome Sequences of Two Potentially Novel Bacillus Isolates from Backyard and Commercial Chicken Gastrointestinal Tracts. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1478	Draft Genome Sequences of Spirosoma agri KCTC 52727 and Spirosoma terrae KCTC 52035. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1479	Phylogeographical Analyses and Antibiotic Resistance Genes of <i>Acinetobacter johnsonii</i> Highlight Its Clinical Relevance. MSphere, 2020, 5, .	1.3	13
1480	Integration of culture-dependent and independent methods provides a more coherent picture of the pig gut microbiome. FEMS Microbiology Ecology, 2020, 96, .	1.3	28
1481	Genomics-based epidemiology of bovine Mycoplasma bovis strains in Israel. BMC Genomics, 2020, 21, 70.	1.2	22
1482	Haloglomus irregulare gen. nov., sp. nov., a New Halophilic Archaeon Isolated from a Marine Saltern. Microorganisms, 2020, 8, 206.	1.6	15
1483	Southern Chinese populations harbour non-nucleatum Fusobacteria possessing homologues of the colorectal cancer-associated FadA virulence factor. Gut, 2020, 69, 1998-2007.	6.1	42
1484	Single-Cell Genomics and the Oral Microbiome. Journal of Dental Research, 2020, 99, 613-620.	2.5	18
1485	Complete Circularized Genome Data of Two Spanish strains of <i>Xylella fastidiosa</i> (IVIA5235 and) Tj ETQq1 1 0.784314 rgBT /Ov	1.1	8
1486	New insights from the biogas microbiome by comprehensive genome-resolved metagenomics of nearly 1600 species originating from multiple anaerobic digesters. Biotechnology for Biofuels, 2020, 13, 25.	6.2	136
1487	Microbial community dynamics and coexistence in a sulfide-driven phototrophic bloom. Environmental Microbiomes, 2020, 15, 3.	2.2	16

#	Article	IF	Citations
1488	Minimum influent concentrations of oxytetracycline, streptomycin and spiramycin in selecting antibiotic resistance in biofilm type wastewater treatment systems. Science of the Total Environment, 2020, 720, 137531.	3.9	40
1489	Microbiome of the deep Lake Baikal, a unique oxic bathypelagic habitat. Limnology and Oceanography, 2020, 65, 1471-1488.	1.6	60
1490	â€œCandidatus Galacturonibacter soehngeniiâ€•Shows Acetogenic Catabolism of Galacturonic Acid but Lacks a Canonical Carbon Monoxide Dehydrogenase/Acetyl-CoA Synthase Complex. Frontiers in Microbiology, 2020, 11, 63.	1.5	6
1491	Bradyrhizobium uaiense sp. nov., a new highly efficient cowpea symbiont. Archives of Microbiology, 2020, 202, 1135-1141.	1.0	10
1492	Different Interspecies Electron Transfer Patterns during Mesophilic and Thermophilic Syntrophic Propionate Degradation in Chemostats. Microbial Ecology, 2020, 80, 120-132.	1.4	29
1493	Metabolic potentials of archaeal lineages resolved from metagenomes of deep Costa Rica sediments. ISME Journal, 2020, 14, 1345-1358.	4.4	38
1494	Metabolic dependencies govern microbial syntrophies during methanogenesis in an anaerobic digestion ecosystem. Microbiome, 2020, 8, 22.	4.9	91
1495	A pipeline for targeted metagenomics of environmental bacteria. Microbiome, 2020, 8, 21.	4.9	39
1496	Anaerobic reactor applied to laundry wastewater treatment: Unveiling the microbial community by gene and genome-centric approaches. International Biodeterioration and Biodegradation, 2020, 149, 104916.	1.9	15
1497	DeepMicrobes: taxonomic classification for metagenomics with deep learning. NAR Genomics and Bioinformatics, 2020, 2, lqaa009.	1.5	94
1498	Genome-Centered Metagenomics Analysis Reveals the Microbial Interactions of a Syntrophic Consortium during Methane Generation in a Decentralized Wastewater Treatment System. Applied Sciences (Switzerland), 2020, 10, 135.	1.3	13
1499	A Collection of 13 Archaeal and 46 Bacterial Genomes Reconstructed from Marine Metagenomes Derived from the North Sea. Data, 2020, 5, 15.	1.2	0
1500	Insights into the microbiome of farmed Asian sea bass (Lates calcarifer) with symptoms of tenacibaculosis and description of Tenacibaculum singaporense sp. nov.. Antonie Van Leeuwenhoek, 2020, 113, 737-752.	0.7	28
1501	Polysaccharide niche partitioning of distinct <i>Polaribacter</i> clades during North Sea spring algal blooms. ISME Journal, 2020, 14, 1369-1383.	4.4	50
1502	Comparative genomics: Dominant coral-bacterium <i>Endozoicomonas acroporae</i> metabolizes dimethylsulfoniopropionate (DMSP). ISME Journal, 2020, 14, 1290-1303.	4.4	96
1503	DeepMAsED: evaluating the quality of metagenomic assemblies. Bioinformatics, 2020, 36, 3011-3017.	1.8	27
1504	Genomic insight into the origins and evolution of symbiosis genes in Phaseolus vulgaris microsymbionts. BMC Genomics, 2020, 21, 186.	1.2	24
1505	Nitratireductor mangrovi sp. nov., a Nitrate-Reducing Bacterium Isolated from Mangrove Soil. Current Microbiology, 2020, 77, 1334-1340.	1.0	4

#	ARTICLE	IF	CITATIONS
1506	Data on genome sequencing, assembly, annotation and genomic analysis of Rhodococcus rhodochrous strain SPC17 isolated from Lonar Lake. Data in Brief, 2020, 29, 105336.	0.5	1
1507	Complete, closed bacterial genomes from microbiomes using nanopore sequencing. Nature Biotechnology, 2020, 38, 701-707.	9.4	253
1508	Extensive Genomic Rearrangements along with Distinct Mobilome and TALome are Associated with Extreme Pathotypes of a Rice Pathogen. Genome Biology and Evolution, 2020, 12, 3951-3956.	1.1	2
1509	Active sulfur cycling in the terrestrial deep subsurface. ISME Journal, 2020, 14, 1260-1272.	4.4	72
1510	Machine learning-aided analyses of thousands of draft genomes reveal specific features of activated sludge processes. Microbiome, 2020, 8, 16.	4.9	42
1511	Assembly of hundreds of novel bacterial genomes from the chicken caecum. Genome Biology, 2020, 21, 34.	3.8	112
1512	Giant virus diversity and host interactions through global metagenomics. Nature, 2020, 578, 432-436.	13.7	207
1513	Draft Genome Sequences of Two Phytoplasma Strains Associated with Sugarcane Grassy Shoot (SCGS) and Bermuda Grass White Leaf (BGWL) Diseases. Molecular Plant-Microbe Interactions, 2020, 33, 715-717.	1.4	20
1514	Ecogenomics of the Marine Benthic Filamentous Cyanobacterium Adonisia. Microbial Ecology, 2020, 80, 249-265.	1.4	4
1515	Candidatus Mcinerneyibacterium aminivorans gen. nov., sp. nov., the first representative of the candidate phylum Mcinerneyibacteriota phyl. nov. recovered from a high temperature, high salinity tertiary oil reservoir in north central Oklahoma, USA. Systematic and Applied Microbiology, 2020, 43, 126057.	1.2	23
1516	Microbial composition of Kombucha determined using amplicon sequencing and shotgun metagenomics. Journal of Food Science, 2020, 85, 455-464.	1.5	72
1517	Continuous pre- and post-transplant exposure to a disease-associated gut microbiome promotes hyper-acute graft-versus-host disease in wild-type mice. Gut Microbes, 2020, 11, 754-770.	4.3	17
1518	Antibiotic resistome and microbial community structure during anaerobic co-digestion of food waste, paper and cardboard. FEMS Microbiology Ecology, 2020, 96, .	1.3	25
1519	Characterization of a sponge microbiome using an integrative genome-centric approach. ISME Journal, 2020, 14, 1100-1110.	4.4	98
1520	Host-Specific Evolutionary and Transmission Dynamics Shape the Functional Diversification of Staphylococcus epidermidis in Human Skin. Cell, 2020, 180, 454-470.e18.	13.5	102
1521	Advantages outweigh concerns about using genome sequence as type material for prokaryotic taxonomy. Environmental Microbiology, 2020, 22, 819-822.	1.8	12
1522	Increased replication of dissimilatory nitrate-reducing bacteria leads to decreased anammox bioreactor performance. Microbiome, 2020, 8, 7.	4.9	42
1523	Isolation, Genomic and Metabolomic Characterization of Streptomyces tendae VITAKN with Quorum Sensing Inhibitory Activity from Southern India. Microorganisms, 2020, 8, 121.	1.6	17

#	ARTICLE	IF	CITATIONS
1524	Culture-enriched metagenomic sequencing enables in-depth profiling of the cystic fibrosis lung microbiota. Nature Microbiology, 2020, 5, 379-390.	5.9	57
1525	Single-cell genomics of uncultured bacteria reveals dietary fiber responders in the mouse gut microbiota. Microbiome, 2020, 8, 5.	4.9	100
1526	<i>Thiomicrorhabdus</i> streamers and sulfur cycling in perennial hypersaline cold springs in the Canadian high Arctic. Environmental Microbiology, 2021, 23, 3384-3400.	1.8	17
1527	The Complete Genome of Emcibacter congregatus ZYLT, a Marine Bacterium Encoding a CRISPR-Cas 9 Immune System. Current Microbiology, 2020, 77, 762-768.	1.0	2
1528	In depth metagenomic analysis in contrasting oil wells reveals syntrophic bacterial and archaeal associations for oil biodegradation in petroleum reservoirs. Science of the Total Environment, 2020, 715, 136646.	3.9	28
1529	Diversity and metabolism of <i>Woeseiales</i> bacteria, global members of marine sediment communities. ISME Journal, 2020, 14, 1042-1056.	4.4	51
1530	Parahaliea maris sp. nov., isolated from surface seawater and emended description of the genus Parahaliea. Journal of Microbiology, 2020, 58, 92-98.	1.3	13
1531	Diversity and Host Interactions among Virulent and Temperate Baltic Sea Flavobacterium Phages. Viruses, 2020, 12, 158.	1.5	11
1532	<p>Hybrid Genome Assembly and Annotation of a Pandrug-Resistant Klebsiella pneumoniae Strain Using Nanopore and Illumina Sequencing</p>. Infection and Drug Resistance, 2020, Volume 13, 199-206.	1.1	26
1533	A Novel D-Galacturonate Fermentation Pathway in Lactobacillus suebicus Links Initial Reactions of the Galacturonate-Isomerase Route With the Phosphoketolase Pathway. Frontiers in Microbiology, 2019, 10, 3027.	1.5	14
1534	Pathogenomic Analysis of a Novel Extensively Drug-Resistant Citrobacter freundii Isolate Carrying a blaNDM-1 Carbapenemase in South Africa. Pathogens, 2020, 9, 89.	1.2	10
1535	Genome Sequences of Clinical Isolates of NDM-1-Producing Klebsiella quasipneumoniae subsp. <i>similipneumoniae</i> and KPC-2-Producing Klebsiella quasipneumoniae subsp. <i>quasipneumoniae</i> from Brazil. Microbiology Resource Announcements, 2020, 9, .	0.3	6
1536	The Signal and the Noise: Characteristics of Antisense RNA in Complex Microbial Communities. MSystems, 2020, 5, .	1.7	2
1537	The Pangenome. , 2020, , .		32
1538	Advances in Bioinformatics and Computational Biology. Lecture Notes in Computer Science, 2020, , .	1.0	0
1539	Medium-Chain Fatty Acid Synthesis by â€œ <i>Candidatus</i> Weimeria bifidaâ€•gen. nov., sp. nov., and â€œ <i>Candidatus</i> Pseudoramibacter fermentansâ€•sp. nov. Applied and Environmental Microbiology, 2020, 86, .	1.4	42
1540	Hiding in Plain Sight: The Globally Distributed Bacterial Candidate Phylum PAUC34f. Frontiers in Microbiology, 2020, 11, 376.	1.5	5
1541	Taxogenomics of the Genus Cyclobacterium: Cyclobacterium xiamenense and Cyclobacterium halophilum as Synonyms and Description of Cyclobacterium plantarum sp. nov.. Microorganisms, 2020, 8, 610.	1.6	12

#	Article	IF	Citations
1542	Complete Genome Sequence of â€œ <i>Candidatus</i> Syntrophocurvum alkaliphilumâ€•Strain B(2M), Obtained from the Metagenome of a Salt-Tolerant Alkaliphilic Anaerobic Syntrophic Butyrate-Degrading Consortium. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1543	Extracellular electron transfer-dependent anaerobic oxidation of ammonium by anammox bacteria. Nature Communications, 2020, 11, 2058.	5.8	168
1544	Genome- and Community-Level Interaction Insights into Carbon Utilization and Element Cycling Functions of <i>Hydrothermarchaeota</i> in Hydrothermal Sediment. MSystems, 2020, 5, .	1.7	75
1545	Lysinibacillus cavernae sp. nov., isolated from cave soil. Archives of Microbiology, 2020, 202, 1529-1534.	1.0	7
1546	Streptomyces albicerus sp. nov., a novel actinomycete isolated from the sediments of the Tailan River in Xinjiang, China. Archives of Microbiology, 2020, 202, 1639-1646.	1.0	5
1547	Description of Polystyrenella longa gen. nov., sp. nov., isolated from polystyrene particles incubated in the Baltic Sea. Antonie Van Leeuwenhoek, 2020, 113, 1851-1862.	0.7	14
1548	Lignipirellula cremea gen. nov., sp. nov., a planctomycete isolated from wood particles in a brackish river estuary. Antonie Van Leeuwenhoek, 2020, 113, 1863-1875.	0.7	15
1549	Bacteriophage-mediated extracellular DNA release is important for the structural stability of aerobic granular sludge. Science of the Total Environment, 2020, 726, 138392.	3.9	5
1550	Diversity and evolution of surface polysaccharide synthesis loci in Enterobacteriales. ISME Journal, 2020, 14, 1713-1730.	4.4	40
1551	Dynamic genome evolution and complex virocell metabolism of globally-distributed giant viruses. Nature Communications, 2020, 11, 1710.	5.8	144
1552	The Scaly-foot Snail genome and implications for the origins of biomineralised armour. Nature Communications, 2020, 11, 1657.	5.8	64
1553	Phylogenomics of Rhodocyclales and its distribution in wastewater treatment systems. Scientific Reports, 2020, 10, 3883.	1.6	22
1554	Metagenomic views of microbial dynamics influenced by hydrocarbon seepage in sediments of theÂGulf of Mexico. Scientific Reports, 2020, 10, 5772.	1.6	21
1555	Comparative Whole-Genome Phylogeny of Animal, Environmental, and Human Strains Confirms the Genogroup Organization and Diversity of the Stenotrophomonas maltophilia Complex. Applied and Environmental Microbiology, 2020, 86, .	1.4	21
1556	Draft Genome Sequences of 12 Leuconostoc carnosum Strains Isolated from Cooked Ham Packaged in a Modified Atmosphere and from Fresh Sausages. Microbiology Resource Announcements, 2020, 9, .	0.3	6
1557	â€œ <i>Candidatus</i> Desulfobulbus rimicarensis,â€•an Uncultivated Deltaproteobacterial Epibiont from the Deep-Sea Hydrothermal Vent Shrimp <i>Rimicaris exoculata</i>. Applied and Environmental Microbiology, 2020, 86, .	1.4	24
1558	Comparative Metagenome-Assembled Genome Analysis of â€œCandidatus Lachnocurva vaginaeâ€, Formerly Known as Bacterial Vaginosis-Associated Bacteriumâˆ1 (BVAB1). Frontiers in Cellular and Infection Microbiology, 2020, 10, 117.	1.8	49
1559	Genomic and Phenotypic Analyses of Acinetobacter baumannii Isolates From Three Tertiary Care Hospitals in Thailand. Frontiers in Microbiology, 2020, 11, 548.	1.5	26

#	ARTICLE	IF	CITATIONS
1560	Mechanisms Underlying the Rhizosphere-To-Rhizoplane Enrichment of Cellvibrio Unveiled by Genome-Centric Metagenomics and Metatranscriptomics. Microorganisms, 2020, 8, 583.	1.6	14
1561	Phylogenomic Analysis of Secondary Metabolism in the Toxic Cyanobacterial Genera Anabaena, Dolichospermum and Aphanizomenon. Toxins, 2020, 12, 248.	1.5	34
1562	Decolorization and biodegradation of textile di-azo dye Acid Blue 113 by Pseudomonas stutzeri AK6. 3 Biotech, 2020, 10, 214.	1.1	37
1563	Genome Sequence of a Segmented Filamentous Bacterium Strain That Confers a Rotavirus Resistance Phenotype in Mice. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1564	Whole-Genome Sequencing of Salmonella enterica Serovar Infantis and Kentucky Isolates Obtained from Layer Poultry Farms in Ecuador. Microbiology Resource Announcements, 2020, 9, .	0.3	3
1565	Draft Genome Sequence of Sideroxydans sp. Strain CL21, an Fe(II)-Oxidizing Bacterium. Microbiology Resource Announcements, 2020, 9, .	0.3	9
1566	Draft Genome Sequence of the Novel Coastal Bacterium LSUCC0115 from the MWH-UniPo Clade, Order Burkholderiales , Class Betaproteobacteria. Microbiology Resource Announcements, 2020, 9, .	0.3	0
1567	â€œ <i>Candidatus</i> Ethanoperedens,â€•a Thermophilic Genus of <i>Archaea</i> Mediating the Anaerobic Oxidation of Ethane. MBio, 2020, 11, .	1.8	66
1568	<i>Campylobacter</i> Abundance in Breastfed Infants and Identification of a New Species in the Global Enterics Multicenter Study. MSphere, 2020, 5, .	1.3	34
1569	Natronomonas salsuginis sp. nov., a New Inhabitant of a Marine Solar Saltern. Microorganisms, 2020, 8, 605.	1.6	13
1570	Microbiota Characterization of Agricultural Green Waste-Based Suppressive Composts Using Omics and Classic Approaches. Agriculture (Switzerland), 2020, 10, 61.	1.4	21
1571	Soil bacterial populations are shaped by recombination and gene-specific selection across a grassland meadow. ISME Journal, 2020, 14, 1834-1846.	4.4	43
1572	The phylogenetic landscape and nosocomial spread of the multidrug-resistant opportunist Stenotrophomonas maltophilia. Nature Communications, 2020, 11, 2044.	5.8	76
1573	A complete domain-to-species taxonomy for Bacteria and Archaea. Nature Biotechnology, 2020, 38, 1079-1086.	9.4	883
1574	Draft Genome Sequences of Four <i>Saccharibacter</i> sp. Strains Isolated from Native Bees. Microbiology Resource Announcements, 2020, 9, .	0.3	5
1575	Genome-centric resolution of novel microbial lineages in an excavated Centrosaurus dinosaur fossil bone from the Late Cretaceous of North America. Environmental Microbiomes, 2020, 15, 8.	2.2	8
1576	Efficient Nitrogen-Fixing Bacteria Isolated from Soybean Nodules in the Semi-arid Region of Northeast Brazil are Classified as Bradyrhizobium brasilense (Symbiovar Sojae). Current Microbiology, 2020, 77, 1746-1755.	1.0	6
1577	A novel alphaproteobacterium with a small genome identified from the digestive gland of multiple species of abalone. Environmental Microbiology Reports, 2020, 12, 387-395.	1.0	3

#	ARTICLE	IF	CITATIONS
1578	Pyrene biodegradation and its potential pathway involving Roseobacter clade bacteria. International Biodeterioration and Biodegradation, 2020, 150, 104961.	1.9	28
1579	Alienimonas chondri sp. nov., a novel planctomycete isolated from the biofilm of the red alga Chondrus crispus. Systematic and Applied Microbiology, 2020, 43, 126083.	1.2	17
1580	Why does sulfate inhibit selenate reduction: Molybdenum deprivation from Mo-dependent selenate reductase. Water Research, 2020, 178, 115832.	5.3	16
1581	Draft Genome Sequences of Two Acidophilic, Mesophilic Verrucomicrobial Methanotrophs Contain Only One pmoCAB Operon. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1582	The stepwise assembly of the neonatal virome is modulated by breastfeeding. Nature, 2020, 581, 470-474.	13.7	185
1583	A multiproducer microbiome generates chemical diversity in the marine sponge <i>Mycale hentscheli</i>. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9508-9518.	3.3	71
1584	Metagenome-assembled genome distribution and key functionality highlight importance of aerobic metabolism in Svalbard permafrost. FEMS Microbiology Ecology, 2020, 96, .	1.3	29
1585	Species Identification and Antibiotic Resistance Prediction by Analysis of Whole-Genome Sequence Data by Use of ARESdb: an Analysis of Isolates from the Unyvero Lower Respiratory Tract Infection Trial. Journal of Clinical Microbiology, 2020, 58, .	1.8	46
1586	Draft Genome Sequence of Desulfofundulus thermobenzoicus subsp. thermosyntrophicus DSM 14055, a Moderately Thermophilic Sulfate Reducer. Microbiology Resource Announcements, 2020, 9, .	0.3	7
1587	Draft Genome Sequence of Paenibacillus polymyxa 3A-25AI, a Strain Antagonist to Root Rot Causal Phytopathogens. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1588	Complete Genome Sequence of Akkermansia muciniphila JCM 30893, Isolated from Feces of a Healthy Japanese Male. Microbiology Resource Announcements, 2020, 9, .	0.3	8
1589	Temperature and Nutrient Levels Correspond with Lineage-Specific Microdiversification in the Ubiquitous and Abundant Freshwater Genus <i>Limnohabitans</i>. Applied and Environmental Microbiology, 2020, 86, .	1.4	16
1590	Bacteria from the Genus <i>Arcobacter</i> Are Abundant in Effluent from Wastewater Treatment Plants. Applied and Environmental Microbiology, 2020, 86, .	1.4	65
1591	Metagenomic and Metaproteomic Insights into Photoautotrophic and Heterotrophic Interactions in a <i>Synechococcus</i> Culture. MBio, 2020, 11, .	1.8	45
1592	Complementary Metagenomic Approaches Improve Reconstruction of Microbial Diversity in a Forest Soil. MSystems, 2020, 5, .	1.7	45
1593	Draft Genome Sequence of Desulfovibrio sulfodismutans ThAc01, a Heterotrophic Sulfur-Disproportionating Member of the <i>Desulfobacterota</i>. Microbiology Resource Announcements, 2020, 9, .	0.3	5
1594	Impact of phages on soil bacterial communities and nitrogen availability under different assembly scenarios. Microbiome, 2020, 8, 52.	4.9	82
1595	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. Microbiome, 2020, 8, 51.	4.9	205

#	Article	IF	Citations
1596	Structure and function of the Arctic and Antarctic marine microbiota as revealed by metagenomics. Microbiome, 2020, 8, 47.	4.9	61
1597	Evolution of Predicted Acid Resistance Mechanisms in the Extremely Acidophilic Leptospirillum Genus. Genes, 2020, 11, 389.	1.0	23
1598	Comparative Genomics, Pangenome, and Phylogenomic Analyses of <i>Brenneria</i> spp., and Delineation of <i>Brenneria izadpanahii</i> sp. nov.. Phytopathology, 2021, 111, 78-95.	1.1	11
1599	Next Generation Sequencing Methods: Pushing the Boundaries. , 2021, , 19-46.		0
1600	Underpinning unique genes in Ca. Brocadia sp. and its interspecies association potentials in a partial nitrification/anammox system with low-strength wastewater. Chemical Engineering Journal, 2021, 405, 125904.	6.6	13
1601	Soil Acidobacteria Strain AB23 Resistance to Oxidative Stress Through Production of Carotenoids. Microbial Ecology, 2021, 81, 169-179.	1.4	15
1602	Diversity and functional analysis of Chinese bumblebee gut microbiota reveal the metabolic niche and antibiotic resistance variation of <i>Gilliamella</i>. Insect Science, 2021, 28, 302-314.	1.5	26
1603	Roles of bacteriophages, plasmids and CRISPR immunity in microbial community dynamics revealed using time-series integrated meta-omics. Nature Microbiology, 2021, 6, 123-135.	5.9	47
1604	Genomics and metatranscriptomics of biogeochemical cycling and degradation of lignin-derived aromatic compounds in thermal swamp sediment. ISME Journal, 2021, 15, 879-893.	4.4	34
1605	A genomic catalog of Earthâ€™s microbiomes. Nature Biotechnology, 2021, 39, 499-509.	9.4	457
1606	Phylogeographic Estimation and Simulation of Global Diffusive Dispersal. Systematic Biology, 2021, 70, 340-359.	2.7	4
1607	The genome sequence of the giant phototrophic gammaproteobacterium Thiospirillum jenense gives insight into its physiological properties and phylogenetic relationships. Archives of Microbiology, 2021, 203, 97-105.	1.0	5
1608	Does Intraspecific Variation in rDNA Copy Number Affect Analysis of Microbial Communities?. Trends in Microbiology, 2021, 29, 19-27.	3.5	71
1609	A unified catalog of 204,938 reference genomes from the human gut microbiome. Nature Biotechnology, 2021, 39, 105-114.	9.4	628
1610	Complete genome sequence of Paenibacillus xylanexedens PAMC 22703, a xylan-degrading bacterium. Marine Genomics, 2021, 55, 100788.	0.4	1
1611	Phylogeny resolved, metabolism revealed: functional radiation within a widespread and divergent clade of sponge symbionts. ISME Journal, 2021, 15, 503-519.	4.4	24
1612	Metagenomics reveals the diversity and taxonomy of antibiotic resistance genes in sufu bacterial communities. Food Control, 2021, 121, 107641.	2.8	9
1613	Genome Sequence, Proteome Profile, and Identification of a Multiprotein Reductive Dehalogenase Complex in <i>Dehalogenimonas alkenigignens</i> Strain BRE15M. Journal of Proteome Research, 2021, 20, 613-623.	1.8	9

#	Article	IF	Citations
1614	Acidobacteria are active and abundant members of diverse atmospheric H2-oxidizing communities detected in temperate soils. ISME Journal, 2021, 15, 363-376.	4.4	23
1615	Ecogenomics and metabolic potential of the South Atlantic Ocean microbiome. Science of the Total Environment, 2021, 765, 142758.	3.9	16
1616	Stable nitrogen removal by anammox process after rapid temperature drops: Insights from metagenomics and metaproteomics. Bioresource Technology, 2021, 320, 124231.	4.8	20
1617	Long-run bacteria-phage coexistence dynamics under natural habitat conditions in an environmental biotechnology system. ISME Journal, 2021, 15, 636-648.	4.4	12
1618	Evidence for nonâ€methanogenic metabolisms in globally distributed archaeal clades basal to the <i>Methanomassiliicoccales</i>. Environmental Microbiology, 2021, 23, 340-357.	1.8	19
1619	Genomic Characterization of Emerging Bacterial Uropathogen Neisseria meningitidis, Which Was Misidentified as Neisseria gonorrhoeae by Nucleic Acid Amplification Testing. Journal of Clinical Microbiology, 2021, 59, .	1.8	13
1620	Marine <i>Dadabacteria</i> exhibit genome streamlining and phototrophy-driven niche partitioning. ISME Journal, 2021, 15, 1248-1256.	4.4	39
1621	Genome Resource of <i>Sphingomonas carotinifaciens</i> L9-754^T, an Endophyte Isolated From Leaf Tissues of <i>Jatropha curcas</i>. Plant Disease, 2021, 105, 205-206.	0.7	1
1622	Deep metagenomics examines the oral microbiome during dental caries, revealing novel taxa and co-occurrences with host molecules. Genome Research, 2021, 31, 64-74.	2.4	59
1623	Experimental evidence for longâ€term coexistence of copiotrophic and oligotrophic bacteria in pelagic surface seawater. Environmental Microbiology, 2021, 23, 1162-1173.	1.8	7
1624	Improved high-molecular-weight DNA extraction, nanopore sequencing and metagenomic assembly from the human gut microbiome. Nature Protocols, 2021, 16, 458-471.	5.5	65
1625	Synergistic association between cytochrome bd-encoded Proteiniphilum and reactive oxygen species (ROS)-scavenging methanogens in microaerobic-anaerobic digestion of lignocellulosic biomass. Water Research, 2021, 190, 116721.	5.3	71
1626	Metagenomic analysis reveals a dynamic microbiome with diversified adaptive functions to utilize high lignocellulosic forages in the cattle rumen. ISME Journal, 2021, 15, 1108-1120.	4.4	87
1627	Sources and transmission routes of campylobacteriosis: A combined analysis of genome and exposure data. Journal of Infection, 2021, 82, 216-226.	1.7	42
1628	Time-series transcriptomics from cold, oxic subseafloor crustal fluids reveals a motile, mixotrophic microbial community. ISME Journal, 2021, 15, 1192-1206.	4.4	27
1629	The biogeography of Streptomyces in New Zealand enabled by highâ€throughput sequencing of genusâ€specific rpoB amplicons. Environmental Microbiology, 2021, 23, 1452-1468.	1.8	6
1630	Enrichment and physiological characterization of a novel comammox <i>Nitrospira</i> indicates ammonium inhibition of complete nitrification. ISME Journal, 2021, 15, 1010-1024.	4.4	117
1631	Anomalous Phylogenetic Behavior of Ribosomal Proteins in Metagenome-Assembled Asgard Archaea. Genome Biology and Evolution, 2021, 13, .	1.1	18

#	Article	IF	Citations
1632	The IMG/M data management and analysis system v.6.0: new tools and advanced capabilities. Nucleic Acids Research, 2021, 49, D751-D763.	6.5	332
1633	Muricauda brasiliensis sp. nov., isolated from a mat-forming cyanobacterial culture. Brazilian Journal of Microbiology, 2021, 52, 325-333.	0.8	4
1634	Metagenomic analysis of a keratin-degrading bacterial consortium provides insight into the keratinolytic mechanisms. Science of the Total Environment, 2021, 761, 143281.	3.9	25
1635	Plant resistome profiling in evolutionary old bog vegetation provides new clues to understand emergence of multi-resistance. ISME Journal, 2021, 15, 921-937.	4.4	33
1636	Anaerobic bacterial degradation of protein and lipid macromolecules in subarctic marine sediment. ISME Journal, 2021, 15, 833-847.	4.4	38
1637	Synergistic interactions of Desulfovibrio and Petrimonas for sulfate-reduction coupling polycyclic aromatic hydrocarbon degradation. Journal of Hazardous Materials, 2021, 407, 124385.	6.5	46
1638	Genome sequences of antibiotic-resistant Streptococcus suis strains isolated from human patients and diseased and asymptomatic pigs in Thailand. Infection, Genetics and Evolution, 2021, 87, 104674.	1.0	9
1639	A novel SAR324 bacterium associated with abalone, Haliotis diversicolor. Aquaculture Research, 2021, 52, 1945-1953.	0.9	0
1640	Halovibrio salipaludis sp. nov., Isolated from Saline-Alkaline Soil. Current Microbiology, 2021, 78, 429-434.	1.0	0
1641	Diversification of methanogens into hyperalkaline serpentinizing environments through adaptations to minimize oxidant limitation. ISME Journal, 2021, 15, 1121-1135.	4.4	37
1642	Evolution of gentamicin and arsenite resistance acquisition in Ralstonia pickettii water isolates. Research in Microbiology, 2021, 172, 103790.	1.0	2
1643	Community-led, integrated, reproducible multi-omics with anviâ€™o. Nature Microbiology, 2021, 6, 3-6.	5.9	370
1644	Genomic Insights of â€œCandidatus Nitrosocaldaceaeâ€•Based on Nine New Metagenome-Assembled Genomes, Including â€œCandidatus Nitrosothermusâ€•Gen Nov. and Two New Species of â€œCandidatus Nitrosocaldusâ€•. Frontiers in Microbiology, 2020, 11, 608832.	1.5	13
1645	Genomic Insights Into the Lifestyles of Thaumarchaeota Inside Sponges. Frontiers in Microbiology, 2020, 11, 622824.	1.5	16
1646	Time series metagenomic sampling of the Thermopyles, Greece, geothermal springs reveals stable microbial communities dominated by novel sulfurâ€oxidizing chemoautotrophs. Environmental Microbiology, 2021, 23, 3710-3726.	1.8	10
1647	High temperatures enhance the microbial genetic potential to recycle C and N from necromass in highâ€mountain soils. Global Change Biology, 2021, 27, 1365-1386.	4.2	49
1648	Coevolving Plasmids Drive Gene Flow and Genome Plasticity in Host-Associated Intracellular Bacteria. Current Biology, 2021, 31, 346-357.e3.	1.8	21
1649	Thermogemmata fonticola gen. nov., sp. nov., the first thermophilic planctomycete of the order Gemmatales from a Kamchatka hot spring. Systematic and Applied Microbiology, 2021, 44, 126157.	1.2	22

#	Article	IF	Citations
1650	Highâ€Throughput Metagenomics for Identification of Pathogens in the Clinical Settings. Small Methods, 2021, 5, 2000792.	4.6	96
1651	Pseudidiomarina piscicola sp. nov., isolated from cultured European seabass, Dicenthrarchus labrax. Archives of Microbiology, 2021, 203, 1293-1298.	1.0	7
1652	Electroactive microorganisms in mouse feces. Electrochimica Acta, 2021, 365, 137326.	2.6	8
1653	Genomic and kinetic analysis of novel Nitrospinae enriched by cell sorting. ISME Journal, 2021, 15, 732-745.	4.4	23
1654	gcType: a high-quality type strain genome database for microbial phylogenetic and functional research. Nucleic Acids Research, 2021, 49, D694-D705.	6.5	53
1655	Linking microbial <i>Sphagnum</i> degradation and acetate mineralization in acidic peat bogs: from global insights to a genome-centric case study. ISME Journal, 2021, 15, 293-303.	4.4	14
1656	Bradyrhizobium campsiandrae sp. nov., a nitrogen-fixing bacterial strain isolated from a native leguminous tree from the Amazon adapted to flooded conditions. Archives of Microbiology, 2021, 203, 233-240.	1.0	8
1657	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. ISME Journal, 2021, 15, 421-434.	4.4	46
1658	Bridging the membrane lipid divide: bacteria of the FCB group superphylum have the potential to synthesize archaeal ether lipids. ISME Journal, 2021, 15, 168-182.	4.4	62
1659	Comparative genomics reveals insights into cyanobacterial evolution and habitat adaptation. ISME Journal, 2021, 15, 211-227.	4.4	118
1660	Intracellular amorphous Ca-carbonate and magnetite biomineralization by a magnetotactic bacterium affiliated to the Alphaproteobacteria. ISME Journal, 2021, 15, 1-18.	4.4	52
1661	Current challenges and best-practice protocols for microbiome analysis. Briefings in Bioinformatics, 2021, 22, 178-193.	3.2	268
1662	Metagenomic Assembly: Reconstructing Genomes from Metagenomes. Methods in Molecular Biology, 2021, 2242, 139-152.	0.4	1
1663	Host population diversity as a driver of viral infection cycle in wild populations of green sulfur bacteria with long standing virus-host interactions. ISME Journal, 2021, 15, 1569-1584.	4.4	16
1665	Isoptericola sediminis sp. nov., Isolated from Chilika Lagoon. Current Microbiology, 2021, 78, 848-855.	1.0	1
1666	Isolation, Biochemical and Genomic Characterization of Glyphosate Tolerant Bacteria to Perform Microbe-Assisted Phytoremediation. Frontiers in Microbiology, 2020, 11, 598507.	1.5	12
1667	Metagenome-Assembled Genome Sequences of a Biofilm Derived from Marsberg Copper Mine. Microbiology Resource Announcements, 2021, 10, .	0.3	3
1668	Draft Genome Sequence of the Free-Living, Iridescent Bacterium Tenacibaculum mesophilum Strain ECR. Microbiology Resource Announcements, 2021, 10, .	0.3	0

#	ARTICLE	IF	CITATIONS
1671	Analysis of Genome Sequences of Coagulase-Negative Staphylococci Isolates from South Africa and Nigeria Highlighted Environmentally Driven Heterogeneity. Journal of Genomics, 2021, 9, 26-37.	0.6	0
1672	Comparison of Alginate Utilization Pathways in Culturable Bacteria Isolated From Arctic and Antarctic Marine Environments. Frontiers in Microbiology, 2021, 12, 609393.	1.5	11
1673	Complex History of Aerobic Respiration and Phototrophy in the <i>Chloroflexota</i> Class <i>Anaerolineae</i> Revealed by High-Quality Draft Genome of <i>Ca.</i> Roseilinea mizusawaensis AA3_104. Microbes and Environments, 2021, 36, n/a.	0.7	5
1675	Physiological and genomic analysis of newly-isolated polysaccharide synthesizing cyanobacterium <i>Chroococcus</i> sp. FPU101 and chemical analysis of the exopolysaccharide. Journal of General and Applied Microbiology, 2021, 67, 207-213.	0.4	3
1676	Phanerozoic radiation of ammonia oxidizing bacteria. Scientific Reports, 2021, 11, 2070.	1.6	14
1677	Microbial niche differentiation explains nitrite oxidation in marine oxygen minimum zones. ISME Journal, 2021, 15, 1317-1329.	4.4	28
1678	Engineering Vibrio sp. SP1 for the production of carotenoids directly from brown macroalgae. Computational and Structural Biotechnology Journal, 2021, 19, 1531-1540.	1.9	8
1679	Spirosoma endbachense sp. nov., isolated from a natural salt meadow. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	10
1680	Legionella septentrionalis sp. nov., isolated from aquatic environments in the northern PR China. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	8
1681	Nonlabens ponticola sp. nov., isolated from seawater and reclassification of Nonlabens sediminis as a later heterotypic synonym of Nonlabens tegetincola. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	12
1682	Enrichment and description of novel bacteria performing syntrophic propionate oxidation at high ammonia level. Environmental Microbiology, 2021, 23, 1620-1637.	1.8	21
1683	Mercury methylation by metabolically versatile and cosmopolitan marine bacteria. ISME Journal, 2021, 15, 1810-1825.	4.4	74
1686	Temperature modulates stress response in mainstream anammox reactors. Communications Biology, 2021, 4, 23.	2.0	15
1687	Genome Mining and Characterization of Biosynthetic Gene Clusters in Two Cave Strains of Paenibacillus sp.. Frontiers in Microbiology, 2020, 11, 612483.	1.5	9
1688	Oxford nanopore sequencing in clinical microbiology and infection diagnostics. Briefings in Bioinformatics, 2021, 22, .	3.2	28
1689	Peeling the Layers Away: The Genomic Characterization of Bacillus pumilus 64-1, an Isolate With Antimicrobial Activity From the Marine Sponge Plakina cyanorosea (Porifera, Homoscleromorpha). Frontiers in Microbiology, 2020, 11, 592735.	1.5	9
1690	Genomic and Functional Characterization of Enterococcus faecalis Isolates Recovered From the International Space Station and Their Potential for Pathogenicity. Frontiers in Microbiology, 2020, 11, 515319.	1.5	10
1691	Genomics Insights into Pseudomonas sp. CG01: An Antarctic Cadmium-Resistant Strain Capable of Biosynthesizing CdS Nanoparticles Using Methionine as S-Source. Genes, 2021, 12, 187.	1.0	5

#	Article	IF	Citations
1692	Reconstructing Draft Genomes Using Genome Resolved Metagenomics Reveal Arsenic Metabolizing Genes and Secondary Metabolites in Fresh Water Lake in Eastern India. Bioinformatics and Biology Insights, 2021, 15, 117793222110253.	1.0	2
1694	Genome-resolved metagenomics reveals site-specific diversity of episymbiotic CPR bacteria and DPANN archaea in groundwater ecosystems. Nature Microbiology, 2021, 6, 354-365.	5.9	109
1695	Severe Corrosion of Carbon Steel in Oil Field Produced Water Can Be Linked to Methanogenic Archaea Containing a Special Type of [NiFe] Hydrogenase. Applied and Environmental Microbiology, 2021, 87, .	1.4	29
1696	Draft Genome Sequence of <i>Cytophagales</i> sp. Strain WSM2-2, Isolated from Garden Soil. Microbiology Resource Announcements, 2021, 10, .	0.3	0
1697	Archaea as components of forest microbiome. , 2021, , 357-370.		0
1698	Newly discovered Asgard archaea Hermodarchaeota potentially degrade alkanes and aromatics via alkyl/benzyl-succinate synthase and benzoyl-CoA pathway. ISME Journal, 2021, 15, 1826-1843.	4.4	40
1699	metaGEM: reconstruction of genome scale metabolic models directly from metagenomes. Nucleic Acids Research, 2021, 49, e126-e126.	6.5	50
1700	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. Marine Drugs, 2021, 19, 20.	2.2	19
1701	Rhizosphere Metagenomics: Methods and Challenges. Rhizosphere Biology, 2021, , 1-20.	0.4	0
1703	Genomic adaptation of Pseudomonas strains to acidity and antibiotics in hydrothermal vents at Kolumbo submarine volcano, Greece. Scientific Reports, 2021, 11, 1336.	1.6	9
1705	Improved metagenome binning and assembly using deep variational autoencoders. Nature Biotechnology, 2021, 39, 555-560.	9.4	251
1706	Pareuzebyella sediminis gen. nov., sp. nov., a novel marine bacterium in the family Flavobacteriaceae, isolated from a tidal flat sediment. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	7
1707	Microbial dynamics of elevated carbon flux in the open oceanâ€™s abyss. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	65
1708	Multiple Gene Clusters and Their Role in the Degradation of Chlorophenoxyacetic Acids in <i>Bradyrhizobium</i> sp. RD5-C2 Isolated from Non-Contaminated Soil. Microbes and Environments, 2021, 36, n/a.	0.7	3
1709	Genome Sequence of Bifidobacterium breve INIA P734 (CECT 8178), a Strain Isolated from Human Breast Milk. Microbiology Resource Announcements, 2021, 10, .	0.3	4
1710	The Isolate Caproiciproducens sp. 7D4C2 Produces n-Caproate at Mildly Acidic Conditions From Hexoses: Genome and rBOX Comparison With Related Strains and Chain-Elongating Bacteria. Frontiers in Microbiology, 2020, 11, 594524.	1.5	33
1711	â€œCandidatus Mesenet longicolaâ€: Novel Endosymbionts of Brontispa longissima that Induce Cytoplasmic Incompatibility. Microbial Ecology, 2021, 82, 512-522.	1.4	14
1712	A genomic view of the microbiome of coral reef demosponges. ISME Journal, 2021, 15, 1641-1654.	4.4	67

#	Article	IF	Citations
1713	The <i>Thermosynechococcus</i> Genus: Wide Environmental Distribution, but a Highly Conserved Genomic Core. Microbes and Environments, 2021, 36, n/a.	0.7	5
1714	Draft Genome Sequence and Secondary Metabolite Biosynthetic Potential of the Lysobacter niastensis Type Strain DSM 18481. Microbiology Resource Announcements, 2021, 10, .	0.3	2
1716	NexGen Sequencing Data: Bioinformatic Tools for Visualization and Analysis. , 2021, , 47-90.		0
1717	A comprehensive evaluation of binning methods to recover human gut microbial species from a non-redundant reference gene catalog. NAR Genomics and Bioinformatics, 2021, 3, lqab009.	1.5	5
1718	Genome Recovery, Functional Profiling, and Taxonomic Classification from Metagenomes. Methods in Molecular Biology, 2021, 2242, 153-172.	0.4	2
1719	The microbiome of deep-sea fish reveals new microbial species and a sparsity of antibiotic resistance genes. Gut Microbes, 2021, 13, 1-13.	4.3	19
1720	Persephonella atlantica sp. nov.: How to adapt to physico-chemical gradients in high temperature hydrothermal habitats. Systematic and Applied Microbiology, 2021, 44, 126176.	1.2	7
1721	Identification and Characterization of Mycobacterial Species Using Whole-Genome Sequences. Methods in Molecular Biology, 2021, 2314, 399-457.	0.4	0
1722	Draft Genome Sequence of Terrestrial Streptomyces sp. Strain VITNK9, Isolated from Vellore, Tamil Nadu, India, Exhibiting Antagonistic Activity against Fish Pathogens. Microbiology Resource Announcements, 2021, 10, .	0.3	2
1723	Draft Genome Sequences of Four Commensal Strains of Staphylococcus and Pseudomonas Isolated from Healthy Human Skin. Microbiology Resource Announcements, 2021, 10, .	0.3	2
1724	Metagenome-Assembled Genome Sequences of Raphidiopsis raciborskii and Planktothrix agardhii from a Cyanobacterial Bloom in Kissena Lake, New York, USA. Microbiology Resource Announcements, 2021, 10, .	0.3	1
1725	Properties relevant to atmospheric dispersal of the ice-nucleation active Pseudomonas syringae strain R10.79 isolated from rain water. Aerobiologia, 2021, 37, 225-241.	0.7	2
1726	Complete Genome Sequence of Neonatal Clinical Group B Streptococcal Isolate CJB111. Microbiology Resource Announcements, 2021, 10, .	0.3	10
1727	Pseudomonas cremoris sp. nov., a novel proteolytic species isolated from cream. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	8
1728	Bioinformatics for Human Microbiome. , 2021, , 333-350.		2
1729	Iningainema tapete sp. nov. (Scytonemataceae, Cyanobacteria) from greenhouses in central Florida (USA) produces two types of nodularin with biosynthetic potential for microcystin-LR and anabaenopeptin production. Harmful Algae, 2021, 101, 101969.	2.2	8
1731	Metagenomics Approaches for the Detection and Surveillance of Emerging and Recurrent Plant Pathogens. Microorganisms, 2021, 9, 188.	1.6	55
1732	Leuconostoc falkenbergense sp. nov., isolated from a lactic culture, fermentating string beans and traditional yogurt. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	13

#	ARTICLE	IF	CITATIONS
1733	Complete Annotated Genome Sequence of Limosilactobacillus fermentum AGR1487. Microbiology Resource Announcements, 2021, 10, .	0.3	1
1737	Genomes of Diverse Isolates of Prochlorococcus High-Light-Adapted Clade II in the Western Pacific Ocean. Frontiers in Marine Science, 2021, 7, .	1.2	1
1738	Seasonal Prevalence of Ammonia-Oxidizing Archaea in a Full-Scale Municipal Wastewater Treatment Plant Treating Saline Wastewater Revealed by a 6-Year Time-Series Analysis. Environmental Science & Technology, 2021, 55, 2662-2673.	4.6	11
1739	Direct Conversion of Food Waste Extract into Caproate: Metagenomics Assessment of Chain Elongation Process. Microorganisms, 2021, 9, 327.	1.6	37
1740	Deciphering a Marine Bone-Degrading Microbiome Reveals a Complex Community Effort. MSystems, 2021, 6, .	1.7	10
1741	Expanding our understanding of marine viral diversity through metagenomic analyses of biofilms. Marine Life Science and Technology, 2021, 3, 395-404.	1.8	12
1742	Metagenomics workflow for hybrid assembly, differential coverage binning, metatranscriptomics and pathway analysis (MUFFIN). PLoS Computational Biology, 2021, 17, e1008716.	1.5	18
1743	Complementary Roles of Wood-Inhabiting Fungi and Bacteria Facilitate Deadwood Decomposition. MSystems, 2021, 6, .	1.7	71
1744	Expanded catalog of microbial genes and metagenome-assembled genomes from the pig gut microbiome. Nature Communications, 2021, 12, 1106.	5.8	116
1747	Hologenome analysis reveals dual symbiosis in the deep-sea hydrothermal vent snail Gigantopelta aegis. Nature Communications, 2021, 12, 1165.	5.8	38
1748	Metagenomes and Assembled Genomes from Diarrhea-Affected Cattle (Bos taurus). Microbiology Resource Announcements, 2021, 10, .	0.3	3
1749	An Expanded Gene Catalog of Mouse Gut Metagenomes. MSphere, 2021, 6, .	1.3	13
1750	Metabolic Potential for Reductive Acetogenesis and a Novel Energy-Converting [NiFe] Hydrogenase in Bathyarchaeia From Termite Guts â€“ A Genome-Centric Analysis. Frontiers in Microbiology, 2020, 11, 635786.	1.5	23
1751	Draft Genome Sequence of Flavobacterium sp. Strain PL002, Isolated from Antarctic Porphyra Algae. Microbiology Resource Announcements, 2021, 10, .	0.3	2
1752	Marinobacter caseinilyticus sp. nov., Isolated from Saline Soil. Current Microbiology, 2021, 78, 1045-1052.	1.0	4
1754	MetaHiC phage-bacteria infection network reveals active cycling phages of the healthy human gut. ELife, 2021, 10, .	2.8	57
1755	Phylogenomic analysis of Anabaenopsis elenkinii (Nostocales, Cyanobacteria). International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	3
1757	The Reliability of Metagenome-Assembled Genomes (MAGs) in Representing Natural Populations: Insights from Comparing MAGs against Isolate Genomes Derived from the Same Fecal Sample. Applied and Environmental Microbiology, 2021, 87, .	1.4	82

#	Article	IF	Citations
1758	Interaction dynamics and virusâ€“host range for estuarine actinophages captured by epicPCR. Nature Microbiology, 2021, 6, 630-642.	5.9	29
1759	Tracking Reservoirs of Antimicrobial Resistance Genes in a Complex Microbial Community Using Metagenomic Hi-C: The Case of Bovine Digital Dermatitis. Antibiotics, 2021, 10, 221.	1.5	6
1760	Comparative genomics reveals broad genetic diversity, extensive recombination and nascent ecological adaptation in Micrococcus luteus. BMC Genomics, 2021, 22, 124.	1.2	15
1762	An antimicrobial Staphylococcus sciuri with broad temperature and salt spectrum isolated from the surface of the African social spider, Stegodyphus dumicola. Antonie Van Leeuwenhoek, 2021, 114, 325-335.	0.7	2
1764	Identification and Metabolism of Naturally Prevailing Microorganisms in Zinc and Copper Mineral Processing. Minerals (Basel, Switzerland), 2021, 11, 156.	0.8	10
1765	Characterisation of hydrocarbon degradation, biosurfactant production, and biofilm formation in Serratia sp. Tan611: a new strain isolated from industrially contaminated environment in Algeria. Antonie Van Leeuwenhoek, 2021, 114, 411-424.	0.7	9
1766	Genome Sequence of Streptomyces sp. Strain HB-N217, Isolated from the Marine Sponge Forcepia sp.. Microbiology Resource Announcements, 2021, 10, .	0.3	1
1767	A methylotrophic origin of methanogenesis and early divergence of anaerobic multicarbon alkane metabolism. Science Advances, 2021, 7, .	4.7	24
1768	Distribution of Mixotrophy and Desiccation Survival Mechanisms across Microbial Genomes in an Arid Biological Soil Crust Community. MSystems, 2021, 6, .	1.7	29
1769	Genomic evidence for sulfur intermediates as new biogeochemical hubs in a model aquatic microbial ecosystem. Microbiome, 2021, 9, 46.	4.9	32
1770	Assembly of Bacterial Genome Sequences from Metagenomes of Spacecraft Assembly Cleanrooms. Microbiology Resource Announcements, 2021, 10, .	0.3	1
1771	Gulf of Mexico blue hole harbors high levels of novel microbial lineages. ISME Journal, 2021, 15, 2206-2232.	4.4	13
1772	Acetylene-Fueled Trichloroethene Reductive Dechlorination in a Groundwater Enrichment Culture. MBio, 2021, 12, .	1.8	6
1773	cognac: rapid generation of concatenated gene alignments for phylogenetic inference from large, bacterial whole genome sequencing datasets. BMC Bioinformatics, 2021, 22, 70.	1.2	10
1774	Continental-Scale Gene Flow Prevents Allopatric Divergence of Pelagic Freshwater Bacteria. Genome Biology and Evolution, 2021, 13, .	1.1	50
1775	Production and Excretion of Polyamines To Tolerate High Ammonia, a Case Study on Soil Ammonia-Oxidizing Archaeon â€œ <i>Candidatus</i> Nitrosocosmicus agrestisâ€. MSystems, 2021, 6, .	1.7	15
1776	Depth-discrete metagenomics reveals the roles of microbes in biogeochemical cycling in the tropical freshwater Lake Tanganyika. ISME Journal, 2021, 15, 1971-1986.	4.4	69
1777	Draft Genome Sequence of Antarctic Psychrotroph Streptomyces fildesensis Strain INACH3013, Isolated from King George Island Soil. Microbiology Resource Announcements, 2021, 10, .	0.3	2

#	ARTICLE	IF	CITATIONS
1779	A dataset of four probiotic Bifidobacterium strains genome assemblies. Data in Brief, 2021, 34, 106710.	0.5	5
1780	New Insights Into the Influence of Plant and Microbial Diversity on Denitrification Rates in a Salt Marsh. Wetlands, 2021, 41, 1.	0.7	12
1782	Discovery, Bioactivity Evaluation, Biosynthetic Gene Cluster Identification, and Heterologous Expression of Novel Albofungin Derivatives. Frontiers in Microbiology, 2021, 12, 635268.	1.5	12
1783	The phylogenetic and global distribution of bacterial polyhydroxyalkanoate bioplasticâ€•degrading genes. Environmental Microbiology, 2021, 23, 1717-1731.	1.8	25
1784	Role prediction of Gram-negative species in the resistome of raw cow's milk. International Journal of Food Microbiology, 2021, 340, 109045.	2.1	6
1785	Metagenome Assembly and Metagenome-Assembled Genome Sequences from the Rhizosphere of Maize Plants in Mafikeng, South Africa. Microbiology Resource Announcements, 2021, 10, .	0.3	3
1786	Wide range of metabolic adaptations to the acquisition of the Calvin cycle revealed by comparison of microbial genomes. PLoS Computational Biology, 2021, 17, e1008742.	1.5	13
1787	Myroides fluvii sp. nov., isolated from the Han River, Republic of Korea. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	5
1788	Heminiphilus faecis gen. nov., sp. nov., a member of the family Muribaculaceae, isolated from mouse faeces and emended description of the genus Muribaculum. Antonie Van Leeuwenhoek, 2021, 114, 275-286.	0.7	19
1789	Contribution of horizontal gene transfer to the functionality of microbial biofilm on a macroalgae. ISME Journal, 2021, 15, 807-817.	4.4	28
1790	Bacterial associations in the healthy human gut microbiome across populations. Scientific Reports, 2021, 11, 2828.	1.6	34
1791	A Combined Metagenomics and Metatranscriptomics Approach to Unravel Costa Rican Cocoa Box Fermentation Processes Reveals Yet Unreported Microbial Species and Functionalities. Frontiers in Microbiology, 2021, 12, 641185.	1.5	28
1792	Enrichment of novel <i>Verrucomicrobia</i>, <i>Bacteroidetes</i>, and <i>Krumholzibacteria</i> in an oxygenâ€•limited methaneâ€•and ironâ€•fed bioreactor inoculated with Bothnian Sea sediments. MicrobiologyOpen, 2021, 10, e1175.	1.2	16
1793	Alcanivorax profundimaris sp. nov., a Novel Marine Hydrocarbonoclastic Bacterium Isolated from Seawater and Deep-Sea Sediment. Current Microbiology, 2021, 78, 1053-1060.	1.0	14
1795	Syntrophic Hydrocarbon Degradation in a Decommissioned Off-Shore Subsea Oil Storage Structure. Microorganisms, 2021, 9, 356.	1.6	7
1796	Binnacle: Using Scaffolds to Improve the Contiguity and Quality of Metagenomic Bins. Frontiers in Microbiology, 2021, 12, 638561.	1.5	2
1797	Ferrimonas lipolytica sp. nov., a facultatively anaerobic bacterium isolated from seawater. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
1798	Metagenomic insights into the effect of sulfate on enhanced biological phosphorus removal. Applied Microbiology and Biotechnology, 2021, 105, 2181-2193.	1.7	21

#	ARTICLE	IF	CITATIONS
1799	Genomic and functional analyses of fungal and bacterial consortia that enable lignocellulose breakdown in goat gut microbiomes. Nature Microbiology, 2021, 6, 499-511.	5.9	116
1800	Metagenomic tools in microbial ecology research. Current Opinion in Biotechnology, 2021, 67, 184-191.	3.3	77
1801	Microbial production and consumption of hydrocarbons in the global ocean. Nature Microbiology, 2021, 6, 489-498.	5.9	56
1802	Draft Genome Sequences of 27 Northern Maine Clinical Isolates. Microbiology Resource Announcements, 2021, 10, .	0.3	0
1804	Pseudomonas lopnurensis sp. nov., an endophytic bacterium isolated from Populus euphratica at the ancient Ugan river. Antonie Van Leeuwenhoek, 2021, 114, 399-410.	0.7	2
1805	Draft genome of a novel methanotrophic Methylobacter sp. from the volcanic soils of Pantelleria Island. Antonie Van Leeuwenhoek, 2021, 114, 313-324.	0.7	12
1806	Systematic Detection of Large-Scale Multigene Horizontal Transfer in Prokaryotes. Molecular Biology and Evolution, 2021, 38, 2639-2659.	3.5	10
1807	Roseibium litorale sp. nov., isolated from a tidal flat sediment and proposal for the reclassification of Labrenzia polysiphoniae as Roseibium polysiphoniae comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	15
1808	Bombella favorum sp. nov. and Bombella mellum sp. nov., two novel species isolated from the honeycombs of Apis mellifera. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	19
1809	Limosilactobacillus balticus sp. nov., Limosilactobacillus agrestis sp. nov., Limosilactobacillus albertensis sp. nov., Limosilactobacillus rudii sp. nov. and Limosilactobacillus fastidiosus sp. nov., five novel Limosilactobacillus species isolated from the vertebrate gastrointestinal tract, and proposal of six subspecies of Limosilactobacillus reuteri adapted to the gastrointestinal tract of specific vertebrate hosts. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	60
1810	Novel Microbial Groups Drive Productivity in an Archean Iron Formation. Frontiers in Microbiology, 2021, 12, 627595.	1.5	12
1811	Triclosan Tolerance Is Driven by a Conserved Mechanism in Diverse <i>Pseudomonas</i> Species. Applied and Environmental Microbiology, 2021, 87, .	1.4	8
1813	Bacterial Dimethylsulfoniopropionate Biosynthesis in the East China Sea. Microorganisms, 2021, 9, 657.	1.6	12
1814	Marine sediments harbor diverse archaea and bacteria with the potential for anaerobic hydrocarbon degradation via fumarate addition. FEMS Microbiology Ecology, 2021, 97, .	1.3	13
1815	Two Archaeal Metagenome-Assembled Genomes from El Tatio Provide New Insights into the Crenarchaeota Phylum. Genes, 2021, 12, 391.	1.0	5
1816	Changing expression patterns of TonB-dependent transporters suggest shifts in polysaccharide consumption over the course of a spring phytoplankton bloom. ISME Journal, 2021, 15, 2336-2350.	4.4	42
1819	Legumeâ€“microbiome interactions unlock mineral nutrients in regrowing tropical forests. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	30
1821	Deep-sea microbes as tools to refine the rules of innate immune pattern recognition. Science Immunology, 2021, 6, .	5.6	21

#	Article	IF	Citations
1822	The microbiome of the Black Sea water column analyzed by shotgun and genome centric metagenomics. Environmental Microbiomes, 2021, 16, 5.	2.2	35
1823	Selective enrichment and metagenomic analysis of three novel comammox <i>Nitrospira</i> in a urine-fed membrane bioreactor. ISME Communications, 2021, 1, .	1.7	27
1824	Combined characterization of a new member of Marivita cryptomonadis strain LZ-15-2 isolated from cultivable phycosphere microbiota of highly toxic HAB dinoflagellate Alexandrium catenella LZT09. Brazilian Journal of Microbiology, 2021, 52, 739-748.	0.8	15
1825	Metagenomic Profile of Microbial Communities in a Drinking Water Storage Tank Sediment after Sequential Exposure to Monochloramine, Free Chlorine, and Monochloramine. ACS ES&T Water, 2021, 1, 1283-1294.	2.3	7
1827	Sulfoquinovose is a select nutrient of prominent bacteria and a source of hydrogen sulfide in the human gut. ISME Journal, 2021, 15, 2779-2791.	4.4	30
1828	The diversity and evolution of microbial dissimilatory phosphite oxidation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	17
1829	Composition and potential functions of the dominant microbiota in deep-sea hagfish gut from the South China Sea. Deep-Sea Research Part I: Oceanographic Research Papers, 2021, 169, 103488.	0.6	5
1830	Genetic Basis of Antimicrobial Resistant Gram-Negative Bacteria Isolated From Bloodstream in Brazil. Frontiers in Medicine, 2021, 8, 635206.	1.2	6
1831	Geochemical and metagenomics study of a metal-rich, green-turquoise-coloured stream in the southern Swiss Alps. PLoS ONE, 2021, 16, e0248877.	1.1	0
1832	Isolation, Characterization, and Genomic Investigation of a Phytopathogenic Strain of<i>Stenotrophomonas maltophilia</i>. Phytopathology, 2021, 111, 2088-2099.	1.1	8
1833	The cyanobacterium <i>Prochlorococcus</i> has divergent light-harvesting antennae and may have evolved in a low-oxygen ocean. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	20
1834	Pre-Cambrian roots of novel Antarctic cryptoendolithic bacterial lineages. Microbiome, 2021, 9, 63.	4.9	17
1835	Paenibacillus glycinis sp. nov., an Endophytic Bacterium Isolated from the Nodules of Soybean (Glycine) Tj ETQq0 0 0 rgBT /Overlock 10	1.0	10
1838	Complete and Circularized Bacterial Genome Sequence of Gordonia sp. Strain X0973. Microbiology Resource Announcements, 2021, 10, .	0.3	1
1839	Structural-genetic insight and optimization of protease production from a novel strain of Aeromonas veronii CMF, a gut isolate of Chrysomya megacephala. Archives of Microbiology, 2021, 203, 2961-2977.	1.0	5
1841	Gill microbiome structure and function in the chemosymbiotic coastal lucinid<i>Stewartia floridana</i>. FEMS Microbiology Ecology, 2021, 97, .	1.3	2
1843	Phylogenetic Distribution of Polysaccharide-Degrading Enzymes in Marine Bacteria. Frontiers in Microbiology, 2021, 12, 658620.	1.5	7
1844	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. Water Research, 2021, 191, 116798.	5.3	39

#	Article	IF	Citations
1845	Bacteria responsible for antimonite oxidation in antimony-contaminated soil revealed by DNA-SIP coupled to metagenomics. FEMS Microbiology Ecology, 2021, 97, .	1.3	13
1846	Metabolic Capacity of the Antarctic Cyanobacterium Phormidium pseudopriestleyi That Sustains Oxygenic Photosynthesis in the Presence of Hydrogen Sulfide. Genes, 2021, 12, 426.	1.0	12
1847	Fine-scale metabolic discontinuity in a stratified prokaryote microbiome of a Red Sea deep halocline. ISME Journal, 2021, 15, 2351-2365.	4.4	11
1848	Expanding the repertoire of electron acceptors for the anaerobic oxidation of methane in carbonates in the Atlantic and Pacific Ocean. ISME Journal, 2021, 15, 2523-2536.	4.4	6
1849	Tutorial: assessing metagenomics software with the CAMI benchmarking toolkit. Nature Protocols, 2021, 16, 1785-1801.	5.5	36
1852	<i>Candidatus</i> Eremiobacterota, a metabolically and phylogenetically diverse terrestrial phylum with acid-tolerant adaptations. ISME Journal, 2021, 15, 2692-2707.	4.4	36
1853	Complete genomes derived by directly sequencing freshwater bloom populations emphasize the significance of the genus level ADA clade within the Nostocales. Harmful Algae, 2021, 103, 102005.	2.2	12
1854	Draft Genome Sequences of Nine Environmental Bacterial Isolates Colonizing Plastic. Microbiology Resource Announcements, 2021, 10, .	0.3	2
1855	Persistence of birth mode-dependent effects on gut microbiome composition, immune system stimulation and antimicrobial resistance during the first year of life. ISME Communications, 2021, 1, .	1.7	25
1856	Decoding the interspecies interaction in anammox process with inorganic feeding through metagenomic and metatranscriptomic analysis. Journal of Cleaner Production, 2021, 288, 125691.	4.6	33
1857	Novel cyanotoxin-producing Synechococcus in tropical lakes. Water Research, 2021, 192, 116828.	5.3	21
1858	Characterization of the first cultured free-living representative of <i>Candidatus</i> Izemoplasma uncovers its unique biology. ISME Journal, 2021, 15, 2676-2691.	4.4	32
1859	The Composition and Primary Metabolic Potential of Microbial Communities Inhabiting the Surface Water in the Equatorial Eastern Indian Ocean. Biology, 2021, 10, 248.	1.3	6
1860	Recovery of complete genomes and non-chromosomal replicons from activated sludge enrichment microbial communities with long read metagenome sequencing. Npj Biofilms and Microbiomes, 2021, 7, 23.	2.9	29
1861	Biodiversity of magnetotactic bacteria in the tropical marine environment of Singapore revealed by metagenomic analysis. Environmental Research, 2021, 194, 110714.	3.7	6
1865	Genomic Metrics Applied to Rhizobiales (Hyphomicrobiales): Species Reclassification, Identification of Unauthentic Genomes and False Type Strains. Frontiers in Microbiology, 2021, 12, 614957.	1.5	38
1866	Metagenomic Data Assembly â€“ The Way of Decoding Unknown Microorganisms. Frontiers in Microbiology, 2021, 12, 613791.	1.5	67
1867	Filling the Gaps in the Cyanobacterial Tree of Lifeâ€"Metagenome Analysis of Stigonema ocellatum DSM 106950, Chlorogloea purpurea SAG 13.99 and Gomphosphaeria aponina DSM 107014. Genes, 2021, 12, 389.	1.0	5

#	Article	IF	Citations
1868	Survival of Salmonella Under Heat Stress is Associated with the Presence/Absence of CRISPR Cas Genes and Iron Levels. Current Microbiology, 2021, 78, 1741-1751.	1.0	5
1869	Draft Genome Sequences of <i>Dysgonomonas</i> sp. Strains GY75 and GY617, Isolated from the Hindgut of Reticulitermes flavipes. Microbiology Resource Announcements, 2021, 10, .	0.3	0
1870	Genome Sequence of an <i>Alkaliphilus</i> Species Isolated from Historically Contaminated Sediments of the Gulf of Naples (Mediterranean Sea). Microbiology Resource Announcements, 2021, 10, .	0.3	0
1871	Aestuariibaculum sediminum sp. nov., a marine bacterium isolated from a tidal flat in Zhoushan. Archives of Microbiology, 2021, 203, 2953-2960.	1.0	8
1872	DIAMOND+MEGAN: Fast and Easy Taxonomic and Functional Analysis of Short and Long Microbiome Sequences. Current Protocols, 2021, 1, e59.	1.3	55
1873	Predicted Input of Uncultured Fungal Symbionts to a Lichen Symbiosis from Metagenome-Assembled Genomes. Genome Biology and Evolution, 2021, 13, .	1.1	19
1876	Homopolish: a method for the removal of systematic errors in nanopore sequencing by homologous polishing. Genome Biology, 2021, 22, 95.	3.8	79
1879	Revealing taxon-specific heavy metal-resistance mechanisms in denitrifying phosphorus removal sludge using genome-centric metaproteomics. Microbiome, 2021, 9, 67.	4.9	34
1880	Connecting structure to function with the recovery of over 1000 high-quality metagenome-assembled genomes from activated sludge using long-read sequencing. Nature Communications, 2021, 12, 2009.	5.8	177
1881	First Description of the Composition and the Functional Capabilities of the Skin Microbial Community Accompanying Severe Scabies Infestation in Humans. Microorganisms, 2021, 9, 907.	1.6	2
1882	Evolution of Sequence Type 4821 Clonal Complex Hyperinvasive and Quinolone-Resistant Meningococci. Emerging Infectious Diseases, 2021, 27, 1110-1122.	2.0	7
1883	Whole-Genome Sequencing and <i>De Novo</i> Assembly of 61 Staphylococcus pseudintermedius Isolates from Healthy Dogs and Dogs with Pyoderma. Microbiology Resource Announcements, 2021, 10, .	0.3	2
1886	Unraveling the Metabolic Potential of Asgardarchaeota in a Sediment from the Mediterranean Hydrocarbon-Contaminated Water Basin Mar Piccolo (Taranto, Italy). Microorganisms, 2021, 9, 859.	1.6	5
1888	Asgard archaea in the haima cold seep: Spatial distribution and genomic insights. Deep-Sea Research Part I: Oceanographic Research Papers, 2021, 170, 103489.	0.6	11
1889	Hybrid Genome Assembly for Predicting Functional Potential of a Novel Streptomyces Strain as Plant Biomass Valorisation Agent. Indian Journal of Microbiology, 2021, 61, 283-290.	1.5	2
1891	Antarctic Rahnella inusitata: A Producer of Cold-Stable Î²-Galactosidase Enzymes. International Journal of Molecular Sciences, 2021, 22, 4144.	1.8	8
1892	Vertical Transmission at the Pathogen-Symbiont Interface: Serratia symbiotica and Aphids. MBio, 2021, 12, .	1.8	19
1893	Reductive evolution and unique predatory mode in the CPR bacterium Vampirococcus lugosii. Nature Communications, 2021, 12, 2454.	5.8	64

#	Article	IF	Citations
1894	Description of Candidatus Mesopelagibacter carboxydoxydans and Candidatus Anoxipelagibacter denitrificans: Nitrate-reducing SAR11 genera that dominate mesopelagic and anoxic marine zones. Systematic and Applied Microbiology, 2021, 44, 126185.	1.2	14
1895	Complete and Draft Genome Sequences of the Cruciferous Pathogens Pseudomonas cannabina pv. alisalensis and Pseudomonas syringae pv. maculicola. Microbiology Resource Announcements, 2021, 10, .	0.3	1
1896	Two Metagenome-Assembled Genomes of Hydrogen-Dependent <i>Methanomassiliicoccales</i> Methanogens from the Zoige Wetland of the Tibetan Plateau. Microbiology Resource Announcements, 2021, 10, .	0.3	0
1897	Thiocyanate and Organic Carbon Inputs Drive Convergent Selection for Specific Autotrophic Afipia and Thiobacillus Strains Within Complex Microbiomes. Frontiers in Microbiology, 2021, 12, 643368.	1.5	10
1898	Draft genome sequence of a nontypeable Haemophilus influenzae strain used in the study of human respiratory infection. BMC Research Notes, 2021, 14, 123.	0.6	0
1900	Thermococcus bergensis sp. nov., a Novel Hyperthermophilic Starch-Degrading Archaeon. Biology, 2021, 10, 387.	1.3	0
1901	Elevated rates of horizontal gene transfer in the industrialized human microbiome. Cell, 2021, 184, 2053-2067.e18.	13.5	167
1902	Evaluation of the Microba Community Profiler for Taxonomic Profiling of Metagenomic Datasets From the Human Gut Microbiome. Frontiers in Microbiology, 2021, 12, 643682.	1.5	25
1903	Evolutionary stasis of a deep subsurface microbial lineage. ISME Journal, 2021, 15, 2830-2842.	4.4	23
1904	Pontixanthobacter rizhaonensis sp. nov., a marine bacterium isolated from surface seawater of the Yellow Sea, and proposal of Pseudopontixanthobacter gen. nov., Pseudopontixanthobacter confluentis comb. nov. and Pseudopontixanthobacter sediminis comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	15
1905	Longitudinal Profiling of the Macaque Vaginal Microbiome Reveals Similarities to Diverse Human Vaginal Communities. MSystems, 2021, 6, .	1.7	15
1906	Strain-Resolved Dynamics of the Lung Microbiome in Patients with Cystic Fibrosis. MBio, 2021, 12, .	1.8	13
1907	Functional genome-centric view of the CO-driven anaerobic microbiome. ISME Journal, 2021, 15, 2906-2919.	4.4	14
1908	Genomic features underlying the evolutionary transitions of <i>Apibacter</i> to honey bee gut symbionts. Insect Science, 2022, 29, 259-275.	1.5	13
1909	Simultaneous nitrate and sulfate dependent anaerobic oxidation of methane linking carbon, nitrogen and sulfur cycles. Water Research, 2021, 194, 116928.	5.3	43
1910	Recovering prokaryotic genomes from host-associated, short-read shotgun metagenomic sequencing data. Nature Protocols, 2021, 16, 2520-2541.	5.5	25
1911	Shotgun metagenomics reveals distinct functional diversity and metabolic capabilities between 12â€Š000-year-old permafrost and active layers on Muot da Barba Peider (Swiss Alps). Microbial Genomics, 2021, 7, .	1.0	7
1914	Drift of the Subgingival Periodontal Microbiome during Chronic Periodontitis in Type 2 Diabetes Mellitus Patients. Pathogens, 2021, 10, 504.	1.2	16

#	ARTICLE	IF	CITATIONS
1915	A total of 219 metagenome-assembled genomes of microorganisms from Icelandic marine waters. PeerJ, 2021, 9, e11112.	0.9	11
1916	Genomic analysis reveals the potential for hydrocarbon degradation of Rhodopirellula sp. MGV isolated from a polluted Brazilian mangrove. Brazilian Journal of Microbiology, 2021, 52, 1397-1404.	0.8	7
1917	Reacquisition of light-harvesting genes in a marine cyanobacterium confers a broader solar niche. Current Biology, 2021, 31, 1539-1546.e4.	1.8	7
1918	Inhella proteolytica sp. nov. and Inhella gelatinilytica sp. nov., two novel species of the genus Inhella isolated from aquaculture water. Archives of Microbiology, 2021, 203, 3191-3200.	1.0	12
1919	Litoribacterium kuwaitense gen. nov., sp. nov., isolated from a Kuwait tidal flat. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	8
1920	Seafloor Incubation Experiment with Deep-Sea Hydrothermal Vent Fluid Reveals Effect of Pressure and Lag Time on Autotrophic Microbial Communities. Applied and Environmental Microbiology, 2021, 87, .	1.4	12
1921	Genomes of Gut Bacteria from <i>Nasonia</i> Wasps Shed Light on Phylosymbiosis and Microbe-Assisted Hybrid Breakdown. MSystems, 2021, 6, .	1.7	9
1922	Draft Genome Sequences of Three Strains of Acidithiobacillus spp. Isolated from Acidic Cold Springs in a Freshwater Wetland. Microbiology Resource Announcements, 2021, 10, .	0.3	0
1923	Comparative genomics of the ADA clade within the Nostocales. Harmful Algae, 2021, 104, 102037.	2.2	11
1924	Cysteiniphilum marinum sp. nov., isolated from coastal seawater. Antonie Van Leeuwenhoek, 2021, 114, 1079-1089.	0.7	11
1925	Genomes of Thaumarchaeota from deep sea sediments reveal specific adaptations of three independently evolved lineages. ISME Journal, 2021, 15, 2792-2808.	4.4	27
1927	Cometabolic Vinyl Chloride Degradation at Acidic pH Catalyzed by Acidophilic Methanotrophs Isolated from Alpine Peat Bogs. Environmental Science & Technology, 2021, 55, 5959-5969.	4.6	14
1928	Expanded diversity of Asgard archaea and their relationships with eukaryotes. Nature, 2021, 593, 553-557.	13.7	161
1930	Supervised extraction of near-complete genomes from metagenomic samples: A new service in PATRIC. PLoS ONE, 2021, 16, e0250092.	1.1	7
1931	Phylogenomic Insights into Distribution and Adaptation of Bdellovibrionota in Marine Waters. Microorganisms, 2021, 9, 757.	1.6	14
1932	Functional genomics of a Spiroplasma associated with the carmine cochineals Dactylopius coccus and Dactylopius opuntiae. BMC Genomics, 2021, 22, 240.	1.2	7
1933	Patterns of Microbiome Variation Among Infrapopulations of Permanent Bloodsucking Parasites. Frontiers in Microbiology, 2021, 12, 642543.	1.5	6
1934	Insights on the Evolutionary Genomics of the Blautia Genus: Potential New Species and Genetic Content Among Lineages. Frontiers in Microbiology, 2021, 12, 660920.	1.5	33

#	Article	IF	Citations
1936	Algae Biofilm Reduces Microbe-Derived Dissolved Organic Nitrogen Discharges: Performance and Mechanisms. Environmental Science & Technology, 2021, 55, 6227-6238.	4.6	42
1937	Metagenome-Assembled Genome Sequences of Novel Prokaryotic Species from the Mercury-Contaminated East Fork Poplar Creek, Oak Ridge, Tennessee, USA. Microbiology Resource Announcements, 2021, 10, .	0.3	2
1938	Alterinioella nitratireducens gen. nov., sp. nov., Isolated from Seawater in the West Pacific Ocean. Current Microbiology, 2021, 78, 2455-2463.	1.0	9
1939	Free-Living, Psychrotrophic Bacteria of the Genus <i>Psychrobacter</i> Are Descendants of Pathobionts. MSystems, 2021, 6, .	1.7	23
1940	Genomic Insight of Alicyclobacillus mali FL18 Isolated From an Arsenic-Rich Hot Spring. Frontiers in Microbiology, 2021, 12, 639697.	1.5	17
1941	Comparative genomics and physiological investigation supported safety, cold adaptation, efficient hydrolytic and plant growth-promoting potential of psychrotrophic Glutamicibacter arilaitensis LJH19, isolated from night-soil compost. BMC Genomics, 2021, 22, 307.	1.2	17
1942	Dissulfurispira thermophila gen. nov., sp. nov., a thermophilic chemolithoautotroph growing by sulfur disproportionation, and proposal of novel taxa in the phylum Nitrospirota to reclassify the genus Thermodesulfovibrio. Systematic and Applied Microbiology, 2021, 44, 126184.	1.2	48
1943	Draconibacterium halophilum sp. nov., A Halophilic Bacterium Isolated from Marine Sediment. Current Microbiology, 2021, 78, 2440-2446.	1.0	0
1944	Microbiome assembly for sulfonamide subsistence and the transfer of genetic determinants. ISME Journal, 2021, 15, 2817-2829.	4.4	10
1945	Complete Genome Sequence of Bacillus safensis Strain 3A, a Heavy Metal-Resistant Bacterium Isolated from Contaminated Estuarine Sediment in Brazil. Microbiology Resource Announcements, 2021, 10, .	0.3	1
1946	Metabolic capabilities mute positive response to direct and indirect impacts of warming throughout the soil profile. Nature Communications, 2021, 12, 2089.	5.8	36
1948	â€œ <i>Sifarchaeota</i> ,â€•a Novel Asgard Phylum from Costa Rican Sediment Capable of Polysaccharide Degradation and Anaerobic Methylotrophy. Applied and Environmental Microbiology, 2021, 87, .	1.4	24
1949	Niche-specific adaptation of Lactobacillus helveticus strains isolated from malt whisky and dairy fermentations. Microbial Genomics, 2021, 7, .	1.0	5
1950	Common Presence of Phototrophic<i>Gemmatimonadota</i>in Temperate Freshwater Lakes. MSystems, 2021, 6, .	1.7	20
1951	Permianibacter fluminis sp. nov., isolated from a freshwater stream. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	4
1952	Decrypting bacterial polyphenol metabolism in an anoxic wetland soil. Nature Communications, 2021, 12, 2466.	5.8	45
1953	Disentangling Microbial Syntrophic Mechanisms for Hexavalent Chromium Reduction in Autotrophic Biosystems. Environmental Science & Technology, 2021, 55, 6340-6351.	4.6	35
1954	A comprehensive metagenomics framework to characterize organisms relevant for planetary protection. Microbiome, 2021, 9, 82.	4.9	15

#	Article	IF	Citations
1957	Case-Control Microbiome Study of Chronic Otitis Media with Effusion in Children Points at Streptococcus salivarius as a Pathobiont-Inhibiting Species. MSystems, 2021, 6, .	1.7	17
1958	Metagenomic Insights into the Metabolic and Ecological Functions of Abundant Deep-Sea Hydrothermal Vent DPANN Archaea. Applied and Environmental Microbiology, 2021, 87, .	1.4	7
1959	Aminipila terrae sp. nov., a strictly anaerobic bacterium isolated from river sediment. Archives of Microbiology, 2021, 203, 3163-3169.	1.0	9
1960	Complete Genome Sequence of Geobacter sp. Strain SVR, an Antimonate-Reducing Bacterium Isolated from Antimony-Rich Mine Soil. Microbiology Resource Announcements, 2021, 10, .	0.3	1
1961	Casting Light on the Adaptation Mechanisms and Evolutionary History of the Widespread Sumerlaeota. MBio, 2021, 12, .	1.8	12
1962	Genome-Based Targeted Sequencing as a Reproducible Microbial Community Profiling Assay. MSphere, 2021, 6, .	1.3	4
1963	Metaproteogenomic Profiling of Chemosynthetic Microbial Biofilms Reveals Metabolic Flexibility During Colonization of a Shallow-Water Gas Vent. Frontiers in Microbiology, 2021, 12, 638300.	1.5	14
1964	Complete Genome Sequence of Anaerostipes caccae Strain L1-92 ^T , a Butyrate-Producing Bacterium Isolated from Human Feces. Microbiology Resource Announcements, 2021, 10, .	0.3	6
1965	Draft Genome Sequence and Polyhydroxyalkanoate Biosynthetic Potential of Jeongeupia naejangsanensis Type Strain DSM 24253. Microbiology Resource Announcements, 2021, 10, .	0.3	1
1966	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. PeerJ, 2021, 9, e10941.	0.9	79
1968	Biotransformation of Doxorubicin Promotes Resilience in Simplified Intestinal Microbial Communities. MSphere, 2021, 6, e0006821.	1.3	9
1969	Prophage Genomics and Ecology in the Family Rhodobacteraceae. Microorganisms, 2021, 9, 1115.	1.6	22
1970	A highâ€quality carabid genome assembly provides insights into beetle genome evolution and cold adaptation. Molecular Ecology Resources, 2021, 21, 2145-2165.	2.2	13
1971	Genome-Resolved Metagenomics of a Photosynthetic Bioreactor Performing Biological Nutrient Removal. Microbiology Resource Announcements, 2021, 10, .	0.3	9
1972	Phylogenomic analysis and characterization of carbon monoxide utilization genes in the family Phyllobacteriaceae with reclassification of Aminobacter carboxidus (Meyer et al. 1993, HÃ¶rdt et al.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Microbiology, 2021, 44, 126199.	1.2	8
1973	A method for achieving complete microbial genomes and improving bins from metagenomics data. PLoS Computational Biology, 2021, 17, e1008972.	1.5	22
1974	Microbiome Analysis Reveals Diversity and Function of <i>Mollicutes</i> Associated with the Eastern Oyster, <i>Crassostrea virginica</i>. MSphere, 2021, 6, .	1.3	21
1975	Diversity and distribution of viruses inhabiting the deepest ocean on Earth. ISME Journal, 2021, 15, 3094-3110.	4.4	55

#	Article	IF	Citations
1976	Bremerella alba sp. nov., a novel planctomycete isolated from the surface of the macroalga Fucus spiralis. Systematic and Applied Microbiology, 2021, 44, 126189.	1.2	14
1977	Microbial Hotspots in Lithic Microhabitats Inferred from DNA Fractionation and Metagenomics in the Atacama Desert. Microorganisms, 2021, 9, 1038.	1.6	19
1978	Gut microbiome diversity and composition is associated with hypertension in women. Journal of Hypertension, 2021, 39, 1810-1816.	0.3	22
1979	Genome Sequence of Streptomyces cavourensis BUU135, Isolated from Soil from a Tropical Fruit Farm in Thailand. Microbiology Resource Announcements, 2021, 10, .	0.3	0
1980	Metagenomes, Metatranscriptomes, and Metagenome-Assembled Genomes from Chesapeake and Delaware Bay (USA) Water Samples. Microbiology Resource Announcements, 2021, 10, e0026221.	0.3	6
1981	Ecotoxicological effects of erythromycin on a multispecies biofilm model, revealed by metagenomic and metabolomic approaches. Environmental Pollution, 2021, 276, 116737.	3.7	16
1983	Evolutionary origin and ecological implication of a unique <i>nif</i> island in free-living <i>Bradyrhizobium</i> lineages. ISME Journal, 2021, 15, 3195-3206.	4.4	27
1985	A rooted phylogeny resolves early bacterial evolution. Science, 2021, 372, .	6.0	128
1986	Integrated omics analyses reveal differential gene expression and potential for cooperation between denitrifying polyphosphate and glycogen accumulating organisms. Environmental Microbiology, 2021, 23, 3274-3293.	1.8	17
1987	Massilia horti sp. nov. and Noviherbaspirillum arenae sp. nov., two novel soil bacteria of the Oxalobacteraceae. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	12
1988	Genome Reduction and Secondary Metabolism of the Marine Sponge-Associated Cyanobacterium Leptothoe. Marine Drugs, 2021, 19, 298.	2.2	4
1989	Genome-resolved metagenomics reveals role of iron metabolism in drought-induced rhizosphere microbiome dynamics. Nature Communications, 2021, 12, 3209.	5.8	93
1990	Recovering Individual Genomes from Metagenomes Using MaxBin 2.0. Current Protocols, 2021, 1, e128.	1.3	6
1991	Tamock: simulation of habitat-specific benchmark data in metagenomics. BMC Bioinformatics, 2021, 22, 227.	1.2	1
1992	Acinetobacter pollinis sp. nov., Acinetobacter baretiae sp. nov. and Acinetobacter rathckeae sp. nov., isolated from floral nectar and honey bees. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	31
1993	Metagenomic Characterization of Soil Microbial Communities in the Luquillo Experimental Forest (Puerto Rico) and Implications for Nitrogen Cycling. Applied and Environmental Microbiology, 2021, 87, e0054621.	1.4	8
1994	Metagenome Assembled Genome of a Novel Verrucomicrobial Methanotroph From Pantelleria Island. Frontiers in Microbiology, 2021, 12, 666929.	1.5	13
1995	Endozoicomonadaceae symbiont in gills of <i>Acesta</i> clam encodes genes for essential nutrients and polysaccharide degradation. FEMS Microbiology Ecology, 2021, 97, .	1.3	7

#	ARTICLE	IF	CITATIONS
1996	Wheat-based food form has a greater effect than amylose content on fermentation outcomes and microbial community shifts in an in vitro fermentation model. Food Hydrocolloids, 2021, 114, 106560.	5.6	10
1997	Microbial iron and carbon metabolism as revealed by taxonomy-specific functional diversity in the Southern Ocean. ISME Journal, 2021, 15, 2933-2946.	4.4	9
1998	Diet, habitat environment and lifestyle conversion affect the gut microbiomes of giant pandas. Science of the Total Environment, 2021, 770, 145316.	3.9	27
2000	Genome-resolved metagenomics suggests a mutualistic relationship between Mycoplasma and salmonid hosts. Communications Biology, 2021, 4, 579.	2.0	55
2001	One-Cell Metabolic Phenotyping and Sequencing of Soil Microbiome by Raman-Activated Gravity-Driven Encapsulation (RAGE). MSystems, 2021, 6, e0018121.	1.7	21
2002	Genomeâ€informed approach to identify genetic determinants of Flavobacterium psychrophilum phage susceptibility. Environmental Microbiology, 2021, 23, 4185-4199.	1.8	8
2003	Microbial Ecological Mechanism for Long-Term Production of High Concentrations of <i>n</i> -Caproate via Lactate-Driven Chain Elongation. Applied and Environmental Microbiology, 2021, 87, .	1.4	20
2004	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. Communications Biology, 2021, 4, 604.	2.0	107
2005	Metabolic flexibility allows bacterial habitat generalists to become dominant in a frequently disturbed ecosystem. ISME Journal, 2021, 15, 2986-3004.	4.4	89
2007	Interâ€domain horizontal gene transfer of nickelâ€binding superoxide dismutase. Geobiology, 2021, 19, 450-459.	1.1	11
2008	<i>Desulfovibrio diazotrophicus</i> sp. nov., a sulfateâ€reducing bacterium from the human gut capable of nitrogen fixation. Environmental Microbiology, 2021, 23, 3164-3181.	1.8	26
2009	Probiotic consumption relieved human stress and anxiety symptoms possibly via modulating the neuroactive potential of the gut microbiota. Neurobiology of Stress, 2021, 14, 100294.	1.9	70
2011	Reconstruction of ancient microbial genomes from the human gut. Nature, 2021, 594, 234-239.	13.7	139
2012	Bacteria responsible for nitrate-dependent antimonite oxidation in antimony-contaminated paddy soil revealed by the combination of DNA-SIP and metagenomics. Soil Biology and Biochemistry, 2021, 156, 108194.	4.2	25
2013	Genome Investigation of Urinary <i>Gardnerella</i> Strains and Their Relationship to Isolates of the Vaginal Microbiota. MSphere, 2021, 6, .	1.3	7
2014	An Integrative Bioinformatic Analysis for Keratinase Detection in Marine-Derived Streptomyces. Marine Drugs, 2021, 19, 286.	2.2	2
2015	Indicator species drive the key ecological functions of microbiota in a river impacted by acid mine drainage generated by rare earth elements mining in South China. Environmental Microbiology, 2022, 24, 919-937.	1.8	18
2017	Unraveling a Lignocellulose-Decomposing Bacterial Consortium from Soil Associated with Dry Sugarcane Straw by Genomic-Centered Metagenomics. Microorganisms, 2021, 9, 995.	1.6	17

#	Article	IF	Citations
2018	Genomic reconstruction of fossil and living microorganisms in ancient Siberian permafrost. Microbiome, 2021, 9, 110.	4.9	17
2019	The Eastern Nebraska Salt Marsh Microbiome Is Well Adapted to an Alkaline and Extreme Saline Environment. Life, 2021, 11, 446.	1.1	5
2023	Unification of functional annotation descriptions using text mining. Biological Chemistry, 2021, 402, 983-990.	1.2	6
2024	Long-read metagenomics retrieves complete single-contig bacterial genomes from canine feces. BMC Genomics, 2021, 22, 330.	1.2	41
2025	Antibiotic-Resistant Enterobacteriaceae in Wastewater of Abattoirs. Antibiotics, 2021, 10, 568.	1.5	26
2026	Enlightening the taxonomy darkness of human gut microbiomes with a cultured biobank. Microbiome, 2021, 9, 119.	4.9	479
2027	Living in a Puddle of Mud: Isolation and Characterization of Two Novel Caulobacteraceae Strains Brevundimonas pondensis sp. nov. and Brevundimonas goettingensis sp. nov.. Applied Microbiology, 2021, 1, 38-59.	0.7	20
2028	Early-Life Immune System Maturation in Chickens Using a Synthetic Community of Cultured Gut Bacteria. MSystems, 2021, 6, .	1.7	68
2029	ToRQuEMaDA: tool for retrieving queried Eubacteria, metadata and dereplicating assemblies. PeerJ, 2021, 9, e11348.	0.9	5
2030	A Machine Learning Approach to Study Glycosidase Activities from Bifidobacterium. Microorganisms, 2021, 9, 1034.	1.6	5
2031	Responses of cyanobacterial aggregate microbial communities to algal blooms. Water Research, 2021, 196, 117014.	5.3	31
2032	Variation of Metagenome From Feedstock to Digestate in Full-Scale Biogas Plants. Frontiers in Microbiology, 2021, 12, 660225.	1.5	7
2033	Ecology and molecular targets of hypermutation in the global microbiome. Nature Communications, 2021, 12, 3076.	5.8	35
2035	Complete Genome Sequence of Adlercreutzia equolifaciens subsp. celatus DSM 18785. Microbiology Resource Announcements, 2021, 10, .	0.3	5
2036	Complete Genome Sequences of Curtobacterium , Pantoea , Erwinia , and Two Pseudomonas sp. Strains, Isolated from Apple Flower Stigmas from Connecticut, USA. Microbiology Resource Announcements, 2021, 10, .	0.3	2
2037	Genomic Analysis of the Yet-Uncultured Binatota Reveals Broad Methylotrophic, Alkane-Degradation, and Pigment Production Capacities. MBio, 2021, 12, .	1.8	13
2039	Comprehensive dataset of shotgun metagenomes from oxygen stratified freshwater lakes and ponds. Scientific Data, 2021, 8, 131.	2.4	48
2040	Qipengyuania soli sp. nov., Isolated from Mangrove Soil. Current Microbiology, 2021, 78, 2806-2814.	1.0	11

#	ARTICLE	IF	CITATIONS
2041	Inhibition of a nutritional endosymbiont by glyphosate abolishes mutualistic benefit on cuticle synthesis in Oryzaephilus surinamensis. Communications Biology, 2021, 4, 554.	2.0	21
2042	Sweet spheres: succession and <scp>CAZyme</scp> expression of marine bacterial communities colonizing a mix of alginate and pectin particles. Environmental Microbiology, 2021, 23, 3130-3148.	1.8	17
2043	Chemosynthetic and photosynthetic bacteria contribute differentially to primary production across a steep desert aridity gradient. ISME Journal, 2021, 15, 3339-3356.	4.4	48
2044	Novel taxa of Acidobacteriota implicated in seafloor sulfur cycling. ISME Journal, 2021, 15, 3159-3180.	4.4	54
2045	Microbial Taxonomy Run Amok. Trends in Microbiology, 2021, 29, 394-404.	3.5	38
2046	Genomics, Exometabolomics, and Metabolic Probing Reveal Conserved Proteolytic Metabolism of Thermoflexus hugenholtzii and Three Candidate Species From China and Japan. Frontiers in Microbiology, 2021, 12, 632731.	1.5	8
2048	Potential syntrophic relationship between coral-associated Prosthecochloris and its companion sulfate-reducing bacterium unveiled by genomic analysis. Microbial Genomics, 2021, 7, .	1.0	5
2050	Expanded Genomic Sampling Refines Current Understanding of the Distribution and Evolution of Sulfur Metabolisms in the Desulfobulbales. Frontiers in Microbiology, 2021, 12, 666052.	1.5	15
2051	Metagenome and analysis of metabolic potential of the microbial community in pit mud used for Chinese strong-flavor liquor production. Food Research International, 2021, 143, 110294.	2.9	33
2053	Distinct microbial community along the chronic oil pollution continuum of the Persian Gulf converge with oil spill accidents. Scientific Reports, 2021, 11, 11316.	1.6	24
2054	Anaerobic Sulfur Oxidation Underlies Adaptation of a Chemosynthetic Symbiont to Oxic-Anoxic Interfaces. MSystems, 2021, 6, e0118620.	1.7	10
2055	Complete Genome Sequence of Lentilactobacillus parabuchneri Strain KEM. Microbiology Resource Announcements, 2021, 10, .	0.3	6
2056	Metagenome-Assembled Genomes Isolated from a Human Fecal Diarrhea Sample. Microbiology Resource Announcements, 2021, 10, .	0.3	0
2057	Prevotella diversity, niches and interactions with the human host. Nature Reviews Microbiology, 2021, 19, 585-599.	13.6	248
2059	UBCG2: Up-to-date bacterial core genes and pipeline for phylogenomic analysis. Journal of Microbiology, 2021, 59, 609-615.	1.3	83
2060	Comparative genomic analysis of the genus Novosphingobium and the description of two novel species Novosphingobium aerophilum sp. nov. and Novosphingobium jiangmenense sp. nov. Systematic and Applied Microbiology, 2021, 44, 126202.	1.2	31
2061	Insight into the function and evolution of the Woodâ€"Ljungdahl pathway in <i>Actinobacteria</i>. ISME Journal, 2021, 15, 3005-3018.	4.4	55
2062	Automated analysis of genomic sequences facilitates high-throughput and comprehensive description of bacteria. ISME Communications, 2021, 1, .	1.7	228

#	ARTICLE	IF	CITATIONS
2063	Characterization and description of Faecalibacterium butyricigenerans sp. nov. and F. longum sp. nov., isolated from human faeces. Scientific Reports, 2021, 11, 11340.	1.6	42
2064	Evaluation of acidogenesis productsâ€™ effect on biogas production performed with metagenomics and isotopic approaches. Biotechnology for Biofuels, 2021, 14, 125.	6.2	23
2065	Novel strain-level resolution of Crohnâ€™s disease mucosa-associated microbiota via an ex vivo combination of microbe culture and metagenomic sequencing. ISME Journal, 2021, 15, 3326-3338.	4.4	11
2066	Gut Microbiome Changes with Acute Diarrheal Disease in Urban Versus Rural Settings in Northern Ecuador. American Journal of Tropical Medicine and Hygiene, 2021, 104, 2275-2285.	0.6	7
2067	Specific metagenomic asset drives the spontaneous fermentation of Italian sausages. Food Research International, 2021, 144, 110379.	2.9	13
2068	Integrated Multi-omics Investigations Reveal the Key Role of Synergistic Microbial Networks in Removing Plasticizer Di-(2-Ethylhexyl) Phthalate from Estuarine Sediments. MSystems, 2021, 6, e0035821.	1.7	18
2069	Mobile Gene Sequence Evolution within Individual Human Gut Microbiomes Is Better Explained by Gene-Specific Than Host-Specific Selective Pressures. Genome Biology and Evolution, 2021, 13, .	1.1	8
2074	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
2075	Ecophysiology of the Cosmopolitan OM252 Bacterioplankton (<i>Gammaproteobacteria</i>). MSystems, 2021, 6, e0027621.	1.7	5
2077	Proposal for reunification of the genus Raoultella with the genus Klebsiella and reclassification of Raoultella electrica as Klebsiella electrica comb. nov.. Research in Microbiology, 2021, 172, 103851.	1.0	24
2078	Metagenome-assembled genome (MAG) of <i>Oceancaulis alexandrii</i> NP7 isolated from Mediterranean Sea polluted marine sediments and its bioremediation potential. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	6
2079	Comparative genomic analysis of Mycoplasma anatis strains. Genes and Genomics, 2021, 43, 1327-1337.	0.5	2
2080	Inferring trophic conditions in managed aquifer recharge systems from metagenomic data. Science of the Total Environment, 2021, 772, 145512.	3.9	2
2081	Salimicrobium humidisoli sp. nov., Isolated from Salineâ€"Alkaline Soil. Current Microbiology, 2021, 78, 3292-3298.	1.0	1
2082	Roseobacters in a Sea of Poly- and Paraphyly: Whole Genome-Based Taxonomy of the Family Rhodobacteraceae and the Proposal for the Split of the â€œRoseobacter Cladeâ€•Into a Novel Family, Roseobacteraceae fam. nov.. Frontiers in Microbiology, 2021, 12, 683109.	1.5	263
2083	Degradation of biological macromolecules supports uncultured microbial populations in Guaymas Basin hydrothermal sediments. ISME Journal, 2021, 15, 3480-3497.	4.4	22
2084	Linking genomic and physiological characteristics of psychrophilic Arthrobacter to metagenomic data to explain global environmental distribution. Microbiome, 2021, 9, 136.	4.9	9
2085	Growth-promoting effect of alginate on Faecalibacterium prausnitzii through cross-feeding with Bacteroides. Food Research International, 2021, 144, 110326.	2.9	32

#	ARTICLE	IF	CITATIONS
2089	Freshwater <i>Chlorobia</i> Exhibit Metabolic Specialization among Cosmopolitan and Endemic Populations. MSystems, 2021, 6, .	1.7	8
2090	Genomic adaptations enabling Acidithiobacillus distribution across wide-ranging hot spring temperatures and pHs. Microbiome, 2021, 9, 135.	4.9	22
2091	Metabolic potentials of members of the class <i>Acidobacteriia</i> in metalâ€contaminated soils revealed by metagenomic analysis. Environmental Microbiology, 2022, 24, 803-818.	1.8	29
2092	Ecogenomics of Groundwater Phages Suggests Niche Differentiation Linked to Specific Environmental Tolerance. MSystems, 2021, 6, e0053721.	1.7	8
2093	Pangenomics reveals alternative environmental lifestyles among chlamydiae. Nature Communications, 2021, 12, 4021.	5.8	29
2094	Bacterioplankton respond with similar transcriptional activity to allochthonous dissolved organic matter in coastal and offshore Lake Michigan. Limnology and Oceanography, 2021, 66, 3162-3175.	1.6	2
2095	Assessing Biosynthetic Gene Cluster Diversity of Specialized Metabolites in the Conserved Gut Symbionts of Herbivorous Turtle Ants. Frontiers in Microbiology, 2021, 12, 678100.	1.5	10
2096	Hymenobacter caeli sp. nov., an airborne bacterium isolated from King George Island, Antarctica. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	10
2097	Description of Acinetobacter kanungonis sp. nov., based on phylogenomic analysis. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	14
2098	Genomic Aromatic Compound Degradation Potential of Novel Paraburkholderia Species: Paraburkholderia domus sp. nov., Paraburkholderia haematera sp. nov. and Paraburkholderia nemoris sp. nov.. International Journal of Molecular Sciences, 2021, 22, 7003.	1.8	22
2099	Challenges, Strategies, and Perspectives for Reference-Independent Longitudinal Multi-Omic Microbiome Studies. Frontiers in Genetics, 2021, 12, 666244.	1.1	8
2100	DOE JGI Metagenome Workflow. MSystems, 2021, 6, .	1.7	56
2101	Evolutionary, genomic, and biogeographic characterization of two novel xenobiotics-degrading strains affiliated with Dechloromonas. Heliyon, 2021, 7, e07181.	1.4	12
2102	Patterns of transmission and horizontal gene transfer in the Dioscorea sansibarensis leaf symbiosis revealed by whole-genome sequencing. Current Biology, 2021, 31, 2666-2673.e4.	1.8	6
2103	Mechanisms driving genome reduction of a novel Roseobacter lineage. ISME Journal, 2021, 15, 3576-3586.	4.4	12
2104	Genomic analysis of extra-intestinal Campylobacter jejuni and Campylobacter coli isolated from commercial chickens. Veterinary Microbiology, 2021, 259, 109161.	0.8	6
2106	Complete Genome Sequences of Two <i>Rhodococcus</i> sp. Strains with Large and Linear Chromosomes, Isolated from Apple Rhizosphere. Microbiology Resource Announcements, 2021, 10, e0015921.	0.3	4
2107	Influence of Taxonomic and Functional Content of Microbial Communities on the Quality of Fermented Cocoa Pulp-Bean Mass. Applied and Environmental Microbiology, 2021, 87, e0042521.	1.4	9

#	Article	IF	Citations
2108	Low Global Diversity of Candidatus Microthrix, a Troublesome Filamentous Organism in Full-Scale WWTPs. Frontiers in Microbiology, 2021, 12, 690251.	1.5	18
2110	A Novel Freshwater to Marine Evolutionary Transition Revealed within <i>Methylophilaceae</i> Bacteria from the Arctic Ocean. MBio, 2021, 12, e0130621.	1.8	15
2111	Exploring Viral Diversity in a Gypsum Karst Lake Ecosystem Using Targeted Single-Cell Genomics. Genes, 2021, 12, 886.	1.0	6
2112	Genomic Characterization of mcr-1.1-Producing Escherichia coli Recovered From Human Infections in SÃ£o Paulo, Brazil. Frontiers in Microbiology, 2021, 12, 663414.	1.5	7
2114	Correlation of Key Physiological Properties of <i>Methanosarcina</i> Isolates with Environment of Origin. Applied and Environmental Microbiology, 2021, 87, e0073121.	1.4	26
2115	Comparative Genomic Insights Into the Taxonomic Classification, Diversity, and Secondary Metabolic Potentials of Kitasatospora, a Genus Closely Related to Streptomyces. Frontiers in Microbiology, 2021, 12, 683814.	1.5	11
2116	<i>Maribellus comscasis</i> sp. nov., a novel deepâ€sea <i>Bacteroidetes</i> bacterium, possessing a prominent capability of degrading cellulose. Environmental Microbiology, 2021, 23, 4561-4575.	1.8	14
2117	<scp>¹³C</scp>â€chloromethane incubations provide evidence for novel bacterial chloromethane degraders in a living tree fern. Environmental Microbiology, 2021, 23, 4450-4465.	1.8	5
2118	A standardized archaeal taxonomy for the Genome Taxonomy Database. Nature Microbiology, 2021, 6, 946-959.	5.9	198
2119	Selective enrichment of comammox from activated sludge using antibiotics. Water Research, 2021, 197, 117087.	5.3	31
2120	Ecological Divergence Within the Enterobacterial Genus Sodalis: From Insect Symbionts to Inhabitants of Decomposing Deadwood. Frontiers in Microbiology, 2021, 12, 668644.	1.5	11
2121	Genomic and Phenotypic Characterization of Chloracidobacterium Isolates Provides Evidence for Multiple Species. Frontiers in Microbiology, 2021, 12, 704168.	1.5	3
2122	Persistence and resistance: survival mechanisms of <i>Candidatus</i> Dormibacterota from nutrientâ€poor Antarctic soils. Environmental Microbiology, 2021, 23, 4276-4294.	1.8	7
2123	Protein Family Content Uncovers Lineage Relationships and Bacterial Pathway Maintenance Mechanisms in DPANN Archaea. Frontiers in Microbiology, 2021, 12, 660052.	1.5	20
2125	Precise Species Identification for Acinetobacter: a Genome-Based Study with Description of Two Novel Acinetobacter Species. MSystems, 2021, 6, e0023721.	1.7	13
2126	Insights into rumen microbial biosynthetic gene cluster diversity through genome-resolved metagenomics. Communications Biology, 2021, 4, 818.	2.0	20
2127	Phylogenomic Reconstruction and Metabolic Potential of the Genus Aminobacter. Microorganisms, 2021, 9, 1332.	1.6	7
2130	GRINS: Genetic elements that recode assembly-line polyketide synthases and accelerate their diversification. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	13

#	ARTICLE	IF	CITATIONS
2131	Diversity and metagenome analysis of a hydrocarbon-degrading bacterial consortium from asphalt lakes located in Wietze, Germany. AMB Express, 2021, 11, 89.	1.4	22
2132	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
2133	Brachybacterium subflavum sp. nov., a novel actinobacterium isolated from the foregut of grass carp. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	7
2134	The infant gut resistome associates withÂE. coli, environmental exposures, gut microbiome maturity, and asthma-associated bacterial composition. Cell Host and Microbe, 2021, 29, 975-987.e4.	5.1	64
2135	A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.	13.5	164
2136	An integrated gene catalog and over 10,000 metagenome-assembled genomes from the gastrointestinal microbiome of ruminants. Microbiome, 2021, 9, 137.	4.9	110
2137	Caloric restriction disrupts the microbiota and colonization resistance. Nature, 2021, 595, 272-277.	13.7	109
2138	Spinal Cord Injury Changes the Structure and Functional Potential of Gut Bacterial and Viral Communities. MSystems, 2021, 6, .	1.7	28
2139	Benchmarking DNA Extraction Methods for Phylogenomic Analysis of Sub-Antarctic Rhodococcus and Williamsia Species. Microorganisms, 2021, 9, 1253.	1.6	7
2140	Substrate-dependent competition and cooperation relationships between <i>Geobacter</i> and <i>Dehalococcoides</i> for their organohalide respiration. ISME Communications, 2021, 1, .	1.7	27
2141	Genome Analysis of a Verrucomicrobial Endosymbiont With a Tiny Genome Discovered in an Antarctic Lake. Frontiers in Microbiology, 2021, 12, 674758.	1.5	18
2142	Whole-Genome Sequencing and Machine Learning Analysis of Staphylococcus aureus from Multiple Heterogeneous Sources in China Reveals Common Genetic Traits of Antimicrobial Resistance. MSystems, 2021, 6, e0118520.	1.7	17
2143	Genomic characterization of three novel Desulfobacterota classes expand the metabolic and phylogenetic diversity of the phylum. Environmental Microbiology, 2021, 23, 4326-4343.	1.8	65
2146	Novel clades of soil biphenyl degraders revealed by integrating isotope probing, multi-omics, and single-cell analyses. ISME Journal, 2021, 15, 3508-3521.	4.4	14
2147	Genomic epidemiology of methicillin-resistant and -susceptible Staphylococcus aureus from bloodstream infections. BMC Infectious Diseases, 2021, 21, 589.	1.3	13
2148	A microbial eukaryote with a unique combination of purple bacteria and green algae as endosymbionts. Science Advances, 2021, 7, .	4.7	21
2149	Recoding of stop codons expands the metabolic potential of two novel Asgardarchaeota lineages. ISME Communications, 2021, 1, .	1.7	23
2150	Draft Genome Sequences of <i>Acidithrix</i> sp. Strain C25 and <i>Acidocella</i> sp. Strain C78, Acidophiles Isolated from Iron-Rich Pelagic Aggregates (Iron Snow). Microbiology Resource Announcements, 2021, 10, e0010221.	0.3	0

#	ARTICLE	IF	CITATIONS
2152	Salinimonas marina sp. nov. Isolated from Jeju Island Marine Sediment. Current Microbiology, 2021, 78, 3321-3327.	1.0	0
2153	Growth faltering regardless of chronic diarrhea is associated with mucosal immune dysfunction and microbial dysbiosis in the gut lumen. Mucosal Immunology, 2021, 14, 1113-1126.	2.7	20
2154	An investigation into the optimal granular sludge size for simultaneous nitrogen and phosphate removal. Water Research, 2021, 198, 117119.	5.3	28
2155	Methane-dependent selenate reduction by a bacterial consortium. ISME Journal, 2021, 15, 3683-3692.	4.4	17
2156	Stable high-density and maternally inherited Wolbachia infections in Anopheles moucheti and Anopheles demeilloni mosquitoes. Current Biology, 2021, 31, 2310-2320.e5.	1.8	49
2157	Genomic insights into diverse bacterial taxa that degrade extracellular DNA in marine sediments. Nature Microbiology, 2021, 6, 885-898.	5.9	29
2158	Microbial metagenome-assembled genomes of the Fram Strait from short and long read sequencing platforms. PeerJ, 2021, 9, e11721.	0.9	14
2159	The reduced genome of a heritable symbiont from an ectoparasitic feather feeding louse. Bmc Ecology and Evolution, 2021, 21, 108.	0.7	7
2160	Genome analysis of Pseudomonas sp. OF001 and Rubrivivax sp. A210 suggests multicopper oxidases catalyze manganese oxidation required for cylindrospermopsin transformation. BMC Genomics, 2021, 22, 464.	1.2	1
2161	GUNC: detection of chimerism and contamination in prokaryotic genomes. Genome Biology, 2021, 22, 178.	3.8	94
2162	Helarchaeota and co-occurring sulfate-reducing bacteria in subseafloor sediments from the Costa Rica Margin. ISME Communications, 2021, 1, .	1.7	16
2163	Phylogeny and Evolutionary History of Respiratory Complex I Proteins in Melainabacteria. Genes, 2021, 12, 929.	1.0	1
2164	High-Quality Draft Genome Sequence of Pantanalinema sp. GBBB05, a Cyanobacterium From Cerrado Biome. Frontiers in Ecology and Evolution, 2021, 9, .	1.1	1
2165	Comparative metagenomic analysis of the vaginal microbiome in healthy women. Synthetic and Systems Biotechnology, 2021, 6, 77-84.	1.8	11
2166	MiMiC: a bioinformatic approach for generation of synthetic communities from metagenomes. Microbial Biotechnology, 2021, 14, 1757-1770.	2.0	12
2167	Diverse Viruses Carrying Genes for Microbial Extremotolerance in the Atacama Desert Hyperarid Soil. MSystems, 2021, 6, .	1.7	27
2168	Muriiphilus fusiformis gen. nov., sp. nov., a novel non-marine bacterium belonging to the Roseobacter group, and reclassification of Maritimibacter lacisalsi (Zhong et al. 2015) as Muriicola lacisalsi gen. nov., comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	14
2169	Diversity and Adaptations of Escherichia coli Strains: Exploring the Intestinal Community in Crohnâ€™s Disease Patients and Healthy Individuals. Microorganisms, 2021, 9, 1299.	1.6	6

#	ARTICLE	IF	CITATIONS
2170	Disentangling the syntrophic electron transfer mechanisms of Candidatus geobacter eutrophica through electrochemical stimulation and machine learning. Scientific Reports, 2021, 11, 15140.	1.6	8
2172	Marinomonas vulgaris sp. nov., a marine bacterium isolated from seawater in a coastal intertidal zone of Zhoushan island. Archives of Microbiology, 2021, 203, 5133-5139.	1.0	9
2173	Towards omics-based predictions of planktonic functional composition from environmental data. Nature Communications, 2021, 12, 4361.	5.8	16
2175	Hi-C deconvolution of a textile dyeâ€“related microbiome reveals novel taxonomic landscapes and links phenotypic potential to individual genomes. International Microbiology, 2022, 25, 99-110.	1.1	4
2176	HumGut: a comprehensive human gut prokaryotic genomes collection filtered by metagenome data. Microbiome, 2021, 9, 165.	4.9	38
2177	RaFAH: Host prediction for viruses of Bacteria and Archaea based on protein content. Patterns, 2021, 2, 100274.	3.1	53
2178	Host preference and invasiveness of commensal bacteria in the Lotus and Arabidopsis root microbiota. Nature Microbiology, 2021, 6, 1150-1162.	5.9	89
2179	Bacteria associated with wood tissues of Escaâ€diseased grapevines: functional diversity and synergy with <i>Fomitiporia mediterranea</i> to degrade wood components. Environmental Microbiology, 2021, 23, 6104-6121.	1.8	19
2180	Sphingomonas sabuli sp. nov., a carotenoid-producing bacterium isolated from beach sand. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	17
2181	Cultureâ€enriched community profiling improves resolution of the vertebrate gut microbiota. Molecular Ecology Resources, 2022, 22, 122-136.	2.2	12
2182	Identification and Genomic Characterization of Two Previously Unknown Magnetotactic Nitrospirae. Frontiers in Microbiology, 2021, 12, 690052.	1.5	7
2183	A methylotrophic origin of methanogenesis and early divergence of anaerobic multicarbon alkane metabolism. Science Advances, 2021, 7, .	4.7	33
2184	Genome Mining and Comparative Genome Analysis Revealed Niche-Specific Genome Expansion in Antibacterial Bacillus pumilus Strain SF-4. Genes, 2021, 12, 1060.	1.0	11
2185	Energy efficiency and biological interactions define the core microbiome of deep oligotrophic groundwater. Nature Communications, 2021, 12, 4253.	5.8	22
2187	Complete Genome Sequence of the Ammonia-Oxidizing Bacterium <i>Nitrosospira</i> sp. Strain NRS527, Isolated from the Rhizoplane of Paddy Rice. Microbiology Resource Announcements, 2021, 10, e0042021.	0.3	1
2188	Complete Genome Sequence of Atopobiaceae Bacterium Strain P1, Isolated from Mouse Feces. Microbiology Resource Announcements, 2021, 10, e0062721.	0.3	1
2189	Chryseobacterium pennae sp. nov., isolated from poultry feather waste. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
2190	Physiological and genomic features of Henriciella with the description of Henriciella mobilis sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6

#	ARTICLE	IF	CITATIONS
2191	Chitinilyticum piscinae sp. nov., isolated from aquaculture water. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
2192	Description of Novosphingopyxis iocasae sp. nov., isolated from deep sea sediment from the Mariana Trench, and emended description of the genus Novosphingopyxis. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
2193	Hemicellulosic biomass conversion by Moroccan hot spring Bacillus paralicheniformis CCMM B940 evidenced by glycoside hydrolase activities and whole genome sequencing. 3 Biotech, 2021, 11, 379.	1.1	4
2194	Functional diversity of microbial communities in inactive seafloor sulfide deposits. FEMS Microbiology Ecology, 2021, 97, .	1.3	16
2195	Pathogenic and Indigenous Denitrifying Bacteria are Transcriptionally Active and Key Multi-Antibiotic-Resistant Players in Wastewater Treatment Plants. Environmental Science & Technology, 2021, 55, 10862-10874.	4.6	60
2196	Characterization of Spacesuit Associated Microbial Communities and Their Implications for NASA Missions. Frontiers in Microbiology, 2021, 12, 608478.	1.5	5
2197	Root Endophytes and Ginkgo biloba Are Likely to Share and Compensate Secondary Metabolic Processes, and Potentially Exchange Genetic Information by LTR-RTs. Frontiers in Plant Science, 2021, 12, 704985.	1.7	12
2198	Physicochemical Properties of Extracellular Polymeric Substances Produced by Three Bacterial Isolates From Biofouled Reverse Osmosis Membranes. Frontiers in Microbiology, 2021, 12, 668761.	1.5	19
2199	Strainberry: automated strain separation in low-complexity metagenomes using long reads. Nature Communications, 2021, 12, 4485.	5.8	25
2200	Sandaracinobacteroides hominis gen. nov., sp. nov., isolated from human skin. Archives of Microbiology, 2021, 203, 5067-5074.	1.0	12
2201	Antifungal potential against Sclerotinia sclerotiorum (Lib.) de Bary and plant growth promoting abilities of Bacillus isolates from canola (Brassica napus L.) roots. Microbiological Research, 2021, 248, 126754.	2.5	21
2202	Genomic Expansions in the Human Gut Microbiome. Genome Biology and Evolution, 2021, 13, .	1.1	1
2203	Apilactobacillus nanyangensis sp. nov., Secundilactobacillus hailunensis sp. nov., Secundilactobacillus yichangensis sp. nov., Levilactobacillus andaensis sp. nov., Levilactobacillus wangkuiensis sp. nov., Levilactobacillus lanxiensis sp. nov., Lacticaseibacillus mingshuiensis sp. nov. and Lacticaseibacillus suilingensis sp. nov., isolated from traditional Chinese pickle and the gut of honeybee (Apis mellifera). International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	39
2204	Mesorhizobium microcysteis sp. nov., isolated from a culture of Microcystis aeruginosa. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	8
2205	Nocardioides malaquae sp. nov., a novel actinobacterium isolated from sewage sludge of a fisheries processing factory. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	5
2206	Ancient saltern metagenomics: tracking changes in microbes and their viruses from the underground to the surface. Environmental Microbiology, 2021, 23, 3477-3498.	1.8	6
2208	Complete Genome Sequence of a Third- and Fourth-Generation Cephalosporin-Resistant Comamonas kerstersii Isolate. Microbiology Resource Announcements, 2021, 10, e0039121.	0.3	4
2209	Whole-Genome Sequences of Mycobacterium abscessus subsp. <i>massiliense</i> Isolates from Brazil. Microbiology Resource Announcements, 2021, 10, e0036121.	0.3	1

#	ARTICLE	IF	CITATIONS
2210	Metagenome-Assembled Genomes Contribute to Unraveling of the Microbiome of Cocoa Fermentation. Applied and Environmental Microbiology, 2021, 87, e0058421.	1.4	11
2211	Genome Sequence Resource of <i>Bacillus</i> sp. RRD69, a Beneficial Bacterial Endophyte Isolated from Switchgrass Plants. Molecular Plant-Microbe Interactions, 2021, 34, 1320-1323.	1.4	4
2212	Draft Genome Sequences of Two Bacteria from the <i>Roseobacter</i> Group. Microbiology Resource Announcements, 2021, 10, e0039021.	0.3	2
2213	Sulfate differentially stimulates but is not respired by diverse anaerobic methanotrophic archaea. ISME Journal, 2022, 16, 168-177.	4.4	21
2214	Interstrain Variability of Human Vaginal Lactobacillus crispatus for Metabolism of Biogenic Amines and Antimicrobial Activity against Urogenital Pathogens. Molecules, 2021, 26, 4538.	1.7	8
2216	â€œCandidatus Chlorobium masyuteum,â€• a Novel Photoferrotrophic Green Sulfur Bacterium Enriched From a Ferruginous Meromictic Lake. Frontiers in Microbiology, 2021, 12, 695260.	1.5	8
2217	Metagenome-Assembled Genome Sequences from Different Wastewater Treatment Stages in Germany. Microbiology Resource Announcements, 2021, 10, e0050421.	0.3	6
2218	The Evolutionary Origins of Extreme Halophilic Archaeal Lineages. Genome Biology and Evolution, 2021, 13, .	1.1	20
2219	Rhodococcus comparative genomics reveals a phylogenomic-dependent non-ribosomal peptide synthetase distribution: insights into biosynthetic gene cluster connection to an orphan metabolite. Microbial Genomics, 2021, 7, .	1.0	10
2221	Deep-Sea Carbonates Are a Reservoir of Fossil Microbes Previously Inhabiting Cold Seeps. Frontiers in Marine Science, 2021, 8, .	1.2	1
2223	Circulating Levels of the Short-Chain Fatty Acid Acetate Mediate the Effect of the Gut Microbiome on Visceral Fat. Frontiers in Microbiology, 2021, 12, 711359.	1.5	86
2224	Complete Genome Sequences of Two <i>Lysobacter</i> Strains, Isolated from Seawater (<i>Lysobacter) Tj ETQq1 1 0.784314 rgBT /Ov Announcements, 2021, 10, e0033721.	0.3	0
2225	Global biogeography of chemosynthetic symbionts reveals both localized and globally distributed symbiont groups. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	15
2226	Absence of Host-Specific Genes in Canine and Human Staphylococcus pseudintermedius as Inferred from Comparative Genomics. Antibiotics, 2021, 10, 854.	1.5	8
2227	Revealing the full biosphere structure and versatile metabolic functions in the deepest ocean sediment of the Challenger Deep. Genome Biology, 2021, 22, 207.	3.8	27
2228	309 metagenome assembled microbial genomes from deep sediment samples in the Gulfs of Kathiawar Peninsula. Scientific Data, 2021, 8, 194.	2.4	6
2229	Salipiger mangrovisoli sp. nov., isolated from mangrove soil and the proposal for the reclassification of Paraphaeobacter pallidus as Salipiger pallidus comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	15
2230	Physiological and Genomic Characterization of a Hyperthermophilic Archaeon Archaeoglobus neptunius sp. nov. Isolated From a Deep-Sea Hydrothermal Vent Warrants the Reclassification of the Genus Archaeoglobus. Frontiers in Microbiology, 2021, 12, 679245.	1.5	13

#	ARTICLE	IF	CITATIONS
2231	Pseudoroseicyclus tamaricis sp. nov., isolated from seashore sediment of a Tamarix chinensis forest and emended descriptions of the genus Pseudoroseicyclus Park et al. 2016. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
2232	Belnapia mucosa sp. nov. and Belnapia arida sp. nov., isolated from desert biocrust. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	7
2234	The rates of global bacterial and archaeal dispersal. ISME Journal, 2022, 16, 159-167.	4.4	38
2236	The link between broiler flock heterogeneity and cecal microbiome composition. Animal Microbiome, 2021, 3, 54.	1.5	18
2238	Draft Metagenomes of Endolithic Cyanobacteria and Cohabitants from Hyper-Arid Deserts. Microbiology Resource Announcements, 2021, 10, e0020621.	0.3	7
2239	Microbial metabolism and adaptations in <i>Atribacteria</i>â€dominated methane hydrate sediments. Environmental Microbiology, 2021, 23, 4646-4660.	1.8	20
2241	Arenibaculum pallidiluteum gen. nov., sp. nov., a novel bacterium in the family Azospirillaceae, isolated from desert soil, and reclassification of Skermanella xinjiangensis to a new genus Deserticella as Deserticella xinjiangensis comb. nov., and transfer of the genera Indioceanicola and Oleisolibacter from the family Rhodospirillaceae to the family Azospirillaceae. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	22
2242	Flavobacterium solisilvae sp. nov. and Flavobacterium silvaticum sp. nov., isolated from forest soil. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	8
2245	Improving Phylogenies Based on Average Nucleotide Identity, Incorporating Saturation Correction and Nonparametric Bootstrap Support. Systematic Biology, 2022, 71, 396-409.	2.7	14
2246	Illuminating the Virosphere Through Global Metagenomics. Annual Review of Biomedical Data Science, 2021, 4, 369-391.	2.8	17
2247	Comparative Genomics Revealing Insights into Niche Separation of the Genus Methylophilus. Microorganisms, 2021, 9, 1577.	1.6	0
2248	Diazotrophic Cyanobacteria are Associated With a Low Nitrate Resupply to Surface Waters in Lake Tanganyika. Frontiers in Environmental Science, 2021, 9, .	1.5	8
2249	Dispersal strategies shape persistence and evolution of human gut bacteria. Cell Host and Microbe, 2021, 29, 1167-1176.e9.	5.1	66
2250	Improved draft reference genome for the Glassy-winged Sharpshooter (<i>Homalodisca) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.8	9
2251	Ammonia-oxidizing archaea possess a wide range of cellular ammonia affinities. ISME Journal, 2022, 16, 272-283.	4.4	96
2252	Large-scale protein level comparison of Deltaproteobacteria reveals cohesive metabolic groups. ISME Journal, 2022, 16, 307-320.	4.4	71
2254	Vertical Stratification of Dissolved Organic Matter Linked to Distinct Microbial Communities in Subtropic Estuarine Sediments. Frontiers in Microbiology, 2021, 12, 697860.	1.5	12
2257	Draft Genome Sequence of Rhodococcus erythropolis VKPM Ac-1659, a Putative Oil-Degrading Strain Isolated from Polluted Soil in Siberia. Microbiology Resource Announcements, 2021, 10, e0053521.	0.3	1

#	ARTICLE	IF	CITATIONS
2258	Five Metagenome-Assembled Genomes of the Rare Phylum CSSED10-310 from Zodletone Spring (Oklahoma, USA). Microbiology Resource Announcements, 2021, 10, e0041421.	0.3	0
2259	EasyBin: Metagenomics Binning Services for Non-Specialists. , 2021, , .		1
2260	Microbial dynamics in biogas digesters treating lipid-rich substrates via genome-centric metagenomics. Science of the Total Environment, 2021, 778, 146296.	3.9	17
2261	An Exploratory Study for the Association of Gut Microbiome with Efficacy of Immune Checkpoint Inhibitor in Patients with Hepatocellular Carcinoma. Journal of Hepatocellular Carcinoma, 2021, Volume 8, 809-822.	1.8	17
2262	Microbial drivers of methane emissions from unrestored industrial salt ponds. ISME Journal, 2022, 16, 284-295.	4.4	24
2264	Metabolic potential and survival strategies of microbial communities across extreme temperature gradients on Deception Island volcano, Antarctica. Environmental Microbiology, 2021, 23, 4054-4073.	1.8	7
2265	Genomic diversity and ecology of human-associated Akkermansia species in the gut microbiome revealed by extensive metagenomic assembly. Genome Biology, 2021, 22, 209.	3.8	65
2266	Algoriphagus pacificus sp. nov. and Algoriphagus oliviformis sp. nov., isolated from a mariculture fishpond. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	7
2267	Euzebya pacifica sp. nov., a novel member of the class Nitriliruptoria. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	9
2268	Facklamia lactis sp. nov., isolated from raw milk. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	10
2269	Lactobacillus corticis sp. nov., isolated from hardwood bark. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	9
2270	Reticulibacter mediterranei gen. nov., sp. nov., within the new family Reticulibacteraceae fam. nov., and Ktedonospora formicarum gen. nov., sp. nov., Ktedonobacter robiniae sp. nov., Dictyobacter formicarum sp. nov. and Dictyobacter arantiisoli sp. nov., belonging to the class Ktedonobacteria. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	35
2271	BUSCO Update: Novel and Streamlined Workflows along with Broader and Deeper Phylogenetic Coverage for Scoring of Eukaryotic, Prokaryotic, and Viral Genomes. Molecular Biology and Evolution, 2021, 38, 4647-4654.	3.5	1,968
2272	Salvaging high-quality genomes of microbial species from a meromictic lake using a hybrid sequencing approach. Communications Biology, 2021, 4, 996.	2.0	12
2274	Hypervirulent Klebsiella pneumoniae Sequence Type 420 with a Chromosomally Inserted Virulence Plasmid. International Journal of Molecular Sciences, 2021, 22, 9196.	1.8	18
2275	Horizontal Gene Transfer Is the Main Driver of Antimicrobial Resistance in Broiler Chicks Infected with Salmonella enterica Serovar Heidelberg. MSystems, 2021, 6, e0072921.	1.7	8
2276	Complete genome sequencing and comparative genome analysis of the extremely halophilic archaea, <i>Haloterrigena daqingensis</i>. Biotechnology and Applied Biochemistry, 2022, 69, 1482-1488.	1.4	3
2277	Patterns of Gene Content and Co-occurrence Constrain the Evolutionary Path toward Animal Association in Candidate Phyla Radiation Bacteria. MBio, 2021, 12, e0052121.	1.8	30

#	Article	IF	Citations
2278	Purple sulfur bacteria fix N2 via molybdenum-nitrogenase in a low molybdenum Proterozoic ocean analogue. Nature Communications, 2021, 12, 4774.	5.8	24
2279	Expanding Asgard members in the domain of Archaea sheds new light on the origin of eukaryotes. Science China Life Sciences, 2022, 65, 818-829.	2.3	18
2280	Biogeochemical Gradients in a Serpentinizationâ€Influenced Aquifer: Implications for Gas Exchange Between the Subsurface and Atmosphere. Journal of Geophysical Research G: Biogeosciences, 2021, 126, e2020JG006209.	1.3	10
2281	Physiology of the Nitrite-Oxidizing Bacterium Candidatus Nitrotoga sp. CP45 Enriched From a Colorado River. Frontiers in Microbiology, 2021, 12, 709371.	1.5	4
2282	Aurantimonas marina sp. nov., isolated from deep-sea sediment. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	5
2283	Genome-based reclassification of Caldicellulosiruptor lactoaceticus and Caldicellulosiruptor kristjanssonii as later heterotypic synonyms of Caldicellulosiruptor acetigenus. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	11
2284	Genome-Resolved Meta-Analysis of the Microbiome in Oil Reservoirs Worldwide. Microorganisms, 2021, 9, 1812.	1.6	10
2285	Trends in Freeâ€access Genomic Data Accelerate Advances in Cyanobacteria Taxonomy. Journal of Phycology, 2021, 57, 1392-1402.	1.0	13
2286	Metabolic Differentiation of Co-occurring Accumulibacter Clades Revealed through Genome-Resolved Metatranscriptomics. MSystems, 2021, 6, e0047421.	1.7	15
2291	Metagenomic Insights Into Ecosystem Function in the Microbial Mats of a Large Hypersaline Coastal Lagoon System. Frontiers in Marine Science, 2021, 8, .	1.2	2
2293	Genome Evolution in Bacteria Isolated from Million-Year-Old Subseafloor Sediment. MBio, 2021, 12, e0115021.	1.8	9
2294	Taxogenomic and Metabolic Insights into Marinobacterium ramblicola sp. nov., a New Slightly Halophilic Bacterium Isolated from Rambla Salada, Murcia. Microorganisms, 2021, 9, 1654.	1.6	12
2295	Human reference gut microbiome catalog including newly assembled genomes from under-represented Asian metagenomes. Genome Medicine, 2021, 13, 134.	3.6	47
2296	Metagenomic insights into the effects of submerged plants on functional potential of microbial communities in wetland sediments. Marine Life Science and Technology, 2021, 3, 405-415.	1.8	19
2297	Methane-derived carbon flows into hostâ€"virus networks at different trophic levels in soil. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	38
2298	Distinctive Mobile Genetic Elements Observed in the Clonal Expansion of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> in India. Microbial Drug Resistance, 2021, 27, 1096-1104.	0.9	14
2299	Mesonia hitae sp. nov., isolated from the seawater of the South Atlantic Ocean. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	5
2300	Shewanella cyperi sp. nov., a facultative anaerobic bacterium isolated from mangrove sediment. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	8

#	Article	IF	Citations
2301	Proposal of Lactococcus garvieae subsp. bovis Varsha and Nampoothiri 2016 as a later heterotypic synonym of Lactococcus formosensis Chen et al. 2014 and Lactococcus formosensis subsp. bovis comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	11
2302	Draft Genome Sequence of Stenotrophomonas maltophilia Strain PE591, a Polyethylene-Degrading Bacterium Isolated from Savanna Soil. Microbiology Resource Announcements, 2021, 10, e0049021.	0.3	4
2305	Genome erosion and evidence for an intracellular niche â€" exploring the biology of mycoplasmas in Atlantic salmon. Aquaculture, 2021, 541, 736772.	1.7	27
2306	Post-weaning shifts in microbiome composition and metabolism revealed by over 25â€Š000 pig gut metagenome-assembled genomes. Microbial Genomics, 2021, 7, .	1.0	9
2307	Comparative Genome Analysis Provides Molecular Evidence for Reclassification of the Photosynthetic Bacterium Rhodobacter sphaeroides EBL0706 as a Strain of Luteovulum azotoformans. Microorganisms, 2021, 9, 1754.	1.6	3
2308	Petrobactin, a siderophore produced by <i>Alteromonas</i>, mediates community iron acquisition in the global ocean. ISME Journal, 2022, 16, 358-369.	4.4	30
2309	A general approach to explore prokaryotic protein glycosylation reveals the unique surface layer modulation of an anammox bacterium. ISME Journal, 2022, 16, 346-357.	4.4	8
2311	Marixanthomonas spongiae sp. nov., isolated from marine sponge. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
2312	Enhanced Recovery of Microbial Genes and Genomes From a Marine Water Column Using Long-Read Metagenomics. Frontiers in Microbiology, 2021, 12, 708782.	1.5	17
2313	Pathways of Iron and Sulfur Acquisition, Cofactor Assembly, Destination, and Storage in Diverse Archaeal Methanogens and Alkanotrophs. Journal of Bacteriology, 2021, 203, e0011721.	1.0	15
2314	Genome- and community-level interaction insights into the ecological role of archaea in rare earth element mine drainage in South China. Water Research, 2021, 201, 117331.	5.3	18
2316	Draft Genomic Sequences of Bacillus amyloliquefaciens CBMAI 1301 and Bacillus subtilis CBMAI 1302, Strains with Potential for the Biocontrol of Phytopathogens. Microbiology Resource Announcements, 2021, 10, e0032121.	0.3	0
2317	Complete Genome Sequence of <i>Gelria</i> sp. Strain Kuro-4, a Thermophilic Anaerobe Isolated from a Thermophilic Anaerobic Digestion Reactor Treating Poly(<scp>L</scp> -Lactic Acid). Microbiology Resource Announcements, 2021, 10, e0054421.	0.3	0
2318	Genomic Analysis of Family UBA6911 (Group 18 <i>Acidobacteria</i>) Expands the Metabolic Capacities of the Phylum and Highlights Adaptations to Terrestrial Habitats. Applied and Environmental Microbiology, 2021, 87, e0094721.	1.4	7
2319	Genomic Variation Influences Methanothermococcus Fitness in Marine Hydrothermal Systems. Frontiers in Microbiology, 2021, 12, 714920.	1.5	3
2321	Complete Genome Resources for <i>Xylella fastidiosa</i> Strains AlmaEM3 and BB08-1 Reveal Prophage-Associated Structural Variation Among Blueberry-Infecting Strains. Phytopathology, 2022, 112, 732-736.	1.1	4
2322	Revealing the community and metabolic potential of active methanotrophs by targeted metagenomics in the Zoige wetland of the Tibetan Plateau. Environmental Microbiology, 2021, 23, 6520-6535.	1.8	8
2323	Accessory Genomic Epidemiology of Cocirculating Acinetobacter baumannii Clones. MSystems, 2021, 6, e0062621.	1.7	15

#	ARTICLE	IF	CITATIONS
2325	High-quality draft genome sequence data of six Lactiplantibacillus plantarum subsp. argentoratensis strains isolated from various Greek wheat sourdoughs. Data in Brief, 2021, 37, 107172.	0.5	4
2327	Rethinking water treatment targets: Bacteria regrowth under unprovable conditions. Water Research, 2021, 201, 117374.	5.3	17
2330	Genome-Resolved Metagenomic Analyses Reveal the Presence of a Putative Bacterial Endosymbiont in an Avian Nasal Mite (Rhinonyssidae; Mesostigmata). Microorganisms, 2021, 9, 1734.	1.6	1
2331	North Sea spring bloom-associated Gammaproteobacteria fill diverse heterotrophic niches. Environmental Microbiomes, 2021, 16, 15.	2.2	32
2332	Carbapenem-resistant bacteria over a wastewater treatment process: Carbapenem-resistant Enterobacteriaceae in untreated wastewater and intrinsically-resistant bacteria in final effluent. Science of the Total Environment, 2021, 782, 146892.	3.9	18
2334	Comparative Genomic Analyses of Flavobacterium psychrophilum Isolates Reveals New Putative Genetic Determinants of Virulence Traits. Microorganisms, 2021, 9, 1658.	1.6	5
2335	Reconstruction of Metagenome-Assembled Genomes from Aquaria. Microbiology Resource Announcements, 2021, 10, e0055721.	0.3	1
2337	Draft Genome Sequence of <i>Desulfurobacterium</i> sp. Strain AV08, a Thermophilic Chemolithoautotroph Isolated from a Deep-Sea Hydrothermal Vent. Microbiology Resource Announcements, 2021, 10, e0061521.	0.3	1
2338	Bog ecosystems as a playground for plantâ€“microbe coevolution: bryophytes and vascular plants harbour functionally adapted bacteria. Microbiome, 2021, 9, 170.	4.9	28
2339	Lentzea tibetensis sp. nov., a novel Actinobacterium with antimicrobial activity isolated from soil of the Qinghaiâ€“Tibet Plateau. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	8
2340	Serpentinimonas gen. nov., Serpentinimonas raichei sp. nov., Serpentinimonas barnesii sp. nov. and Serpentinimonas maccroryi sp. nov., hyperalkaliphilic and facultative autotrophic bacteria isolated from terrestrial serpentinizing springs. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	20
2341	Longitudinal study on the effects of growth-promoting and therapeutic antibiotics on the dynamics of chicken cloacal and litter microbiomes and resistomes. Microbiome, 2021, 9, 178.	4.9	30
2344	Metagenome-assembled genome of a Chitinophaga sp. and its potential in plant biomass degradation, as well of affiliated Pandoraea and Labrys species. World Journal of Microbiology and Biotechnology, 2021, 37, 162.	1.7	7
2345	Metabolic Features of Ganjang (a Korean Traditional Soy Sauce) Fermentation Revealed by Genome-Centered Metatranscriptomics. MSystems, 2021, 6, e0044121.	1.7	17
2346	A Combination of Metagenomic and Cultivation Approaches Reveals Hypermutator Phenotypes within Vibrio cholerae-Infected Patients. MSystems, 2021, 6, e0088921.	1.7	8
2347	Deciphering Symbiotic Interactions of â€œ <i>Candidatus</i> Aenigmarchaeotaâ€•with Inferred Horizontal Gene Transfers and Co-occurrence Networks. MSystems, 2021, 6, e0060621.	1.7	11
2348	Veronia nyctiphanis gen. nov., sp. nov., Isolated from the Stomach of the Euphausiid Nyctiphanes simplex (Hansen, 1911) in the Gulf of California, and Reclassification of Enterovibrio pacificus as Veronia pacifica comb. nov.. Current Microbiology, 2021, 78, 3782-3790.	1.0	16
2350	The coral symbiont <i>Candidatus</i> Aquarickettsia is variably abundant in threatened Caribbean acroporids and transmitted horizontally. ISME Journal, 2022, 16, 400-411.	4.4	21

#	Article	IF	Citations
2351	A mouse model displays host and bacterial strain differences in <i>Aerococcus urinae</i> urinary tract infection. Biology Open, 2021, 10, .	0.6	6
2352	â€˜Candidatus Chloroploca mongolicaâ€™ sp. nov. a new mesophilic filamentous anoxygenic phototrophic bacterium. FEMS Microbiology Letters, 2021, 368, .	0.7	2
2353	Identification of Reductive Dehalogenases That Mediate Complete Debromination of Penta- and Tetrabrominated Diphenyl Ethers in <i>Dehalococcoides</i> spp.. Applied and Environmental Microbiology, 2021, 87, e0060221.	1.4	19
2354	Genome-Resolved Metagenomics of the Chicken Gut Microbiome. Frontiers in Microbiology, 2021, 12, 726923.	1.5	30
2355	Metagenomes Binning Using Proximity-Ligation Data. Methods in Molecular Biology, 2022, 2301, 163-181.	0.4	3
2356	Complete and Circularized Genome Sequences of Three Xanthomonas Strains Pathogenic on Soybean and Alfalfa. Microbiology Resource Announcements, 2021, 10, e0053721.	0.3	1
2358	Bowmanella yangjiangensis sp. nov. and Amphritea pacifica sp. nov., isolated from mariculture fishponds in China. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	11
2359	Psychrosphaera ytuae sp. nov., isolated from the deep-sea cold seep sediment of South China Sea. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	7
2360	Zobellia roscoffensis sp. nov. and Zobellia nedashkovskayae sp. nov., two flavobacteria from the epiphytic microbiota of the brown alga Ascophyllum nodosum, and emended description of the genus Zobellia. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	18
2361	Comparative Genomics of <i>Exiguobacterium</i> Reveals What Makes a Cosmopolitan Bacterium. MSystems, 2021, 6, e0038321.	1.7	13
2362	Comparative Genomics Provides Insights into the Genetic Diversity and Evolution of the DPANN Superphylum. MSystems, 2021, 6, e0060221.	1.7	9
2363	Metagenomes, metatranscriptomes and microbiomes of naturally decomposing deadwood. Scientific Data, 2021, 8, 198.	2.4	6
2364	Draft <i>De Novo</i> Genome Assembly of Acinetobacter pittii Strain VKPM B-3780, a Prospective Multifunctional Bioremediation Agent. Microbiology Resource Announcements, 2021, 10, e0055421.	0.3	0
2365	The worm affair: fidelity and environmental adaptation in symbiont species that coâ€occur in vestimentiferan tubeworms. Environmental Microbiology Reports, 2021, 13, 744-752.	1.0	3
2366	Large-scale quality assessment of prokaryotic genomes with metashot/prok-quality. F1000Research, 2021, 10, 822.	0.8	6
2367	Paenarthrobacter sp. GOM3 Is a Novel Marine Species With Monoaromatic Degradation Relevance. Frontiers in Microbiology, 2021, 12, 713702.	1.5	8
2368	Isoprene-degrading bacteria associated with the phyllosphere of Salix fragilis, a high isoprene-emitting willow of the Northern Hemisphere. Environmental Microbiomes, 2021, 16, 17.	2.2	6
2369	Metapangenomics reveals depth-dependent shifts in metabolic potential for the ubiquitous marine bacterial SAR324 lineage. Microbiome, 2021, 9, 172.	4.9	25

#	Article	IF	Citations
2370	Complete and Circularized Genome Sequences of 17 <i>Xanthomonas</i> Strains Responsible for Common Bacterial Blight of Bean. Microbiology Resource Announcements, 2021, 10, e0037121.	0.3	1
2371	Collinsella acetigenes sp. nov., an Anaerobic Actinobacterium Isolated from Human Feces, and Emended Description of the Genus Collinsella and Collinsella aerofaciens. Current Microbiology, 2021, 78, 3667-3673.	1.0	7
2372	Comparative Genomics Reveals Thermal Adaptation and a High Metabolic Diversity in â€œ <i>Candidatus</i> Bathyarchaeiaâ€. MSystems, 2021, 6, e0025221.	1.7	20
2373	New approaches for archaeal genome-guided cultivation. Science China Earth Sciences, 2021, 64, 1658-1673.	2.3	7
2374	Host adaptation in gut Firmicutes is associated with sporulation loss and altered transmission cycle. Genome Biology, 2021, 22, 204.	3.8	25
2375	Taxonomic profiling of skin microbiome and correlation with clinical skin parameters in healthy Koreans. Scientific Reports, 2021, 11, 16269.	1.6	20
2376	Metagenome-Assembled Genomes of Novel Taxa from an Acid Mine Drainage Environment. Applied and Environmental Microbiology, 2021, 87, e0077221.	1.4	9
2377	Complete Genome Sequence of Lactobacillus helveticus JCM 1004, an Aminopeptidase-Producing Lactic Acid Bacterium. Microbiology Resource Announcements, 2021, 10, e0064121.	0.3	1
2378	Pararhodonellum marinum gen. nov., sp. nov., isolated from deep-sea sediment. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
2379	Dynamic Surveillance of Mosquitoes and Their Viromes in Wuhan During 2020. Zoonoses, 2021, 1, .	0.5	8
2380	Differences in chlorine and peracetic acid disinfection kinetics of Enterococcus faecalis and Escherichia fergusonii and their susceptible strains based on gene expressions and genomics. Water Research, 2021, 203, 117480.	5.3	9
2382	Metagenomic insights into the bacteria responsible for producing biogenic amines in sufu. Food Microbiology, 2021, 98, 103762.	2.1	17
2383	Living to the High Extreme: Unraveling the Composition, Structure, and Functional Insights of Bacterial Communities Thriving in the Arsenic-Rich Salar de Huasco Altiplanic Ecosystem. Microbiology Spectrum, 2021, 9, e0044421.	1.2	16
2384	Microbiome degrading linear alkylbenzene sulfonate in activated sludge. Journal of Hazardous Materials, 2021, 418, 126365.	6.5	9
2385	Acesulfame aerobic biodegradation by enriched consortia and Chelatococcus spp.: Kinetics, transformation products, and genomic characterization. Water Research, 2021, 202, 117454.	5.3	21
2386	Genome Sequencing and Functional Characterization of Xanthomonas cucurbitae, the Causal Agent of Bacterial Spot Disease of Cucurbits. Phytopathology, 2021, 111, PHYTO-06-20-022.	1.1	2
2387	Whole Genome Sequence-Based Identification of Clostridium estertheticum Complex Strains Supports the Need for Taxonomic Reclassification Within the Species Clostridium estertheticum. Frontiers in Microbiology, 2021, 12, 727022.	1.5	10
2388	Re-examining the association of AmpC variants with Enterobacter species in the context of updated taxonomy. Antimicrobial Agents and Chemotherapy, 2021, 65, e0159621.	1.4	6

#	Article	IF	Citations
2389	Methylomonas albis sp. nov. and Methylomonas fluvii sp. nov.: Two cold-adapted methanotrophs from the river Elbe and emended description of the species Methylovulum psychrotolerans. Systematic and Applied Microbiology, 2021, 44, 126248.	1.2	18
2390	Draft Genome Sequence of the Anoxygenic Phototrophic Bacterium <i>Rhodomicrobium</i> sp. Strain Az07, Isolated from a Brackish Canal. Microbiology Resource Announcements, 2021, 10, e0058521.	0.3	0
2391	Genomes of Novel <i>Myxococcota</i> Reveal Severely Curtailed Machineries for Predation and Cellular Differentiation. Applied and Environmental Microbiology, 2021, 87, e0170621.	1.4	28
2392	Pilot-scale biomethanation in a trickle bed reactor: Process performance and microbiome functional reconstruction. Energy Conversion and Management, 2021, 244, 114491.	4.4	39
2393	Viruses and Their Interactions With Bacteria and Archaea of Hypersaline Great Salt Lake. Frontiers in Microbiology, 2021, 12, 701414.	1.5	11
2394	Draft Genome Sequence of the Phototropic Cyanobacterium <i>Rivularia</i> sp. Strain IAM M-261. Microbiology Resource Announcements, 2021, 10, e0079021.	0.3	3
2395	Metagenome Assembly and Metagenome-Assembled Genome of â€œ <i>Candidatus</i> Aramenus sulfurataquaeâ€•from Thermal Sediments from the Los Azufres Volcanic Complex. Microbiology Resource Announcements, 2021, 10, e0037921.	0.3	3
2396	Metagenomic analysis of ancient dental calculus reveals unexplored diversity of oral archaeal Methanobrevibacter. Microbiome, 2021, 9, 197.	4.9	18
2398	Draft Genome Sequence of <i>Salegentibacter</i> sp. Strain BDJ18, a Plankton-Associated Bacterium in the Northeast Atlantic Ocean. Microbiology Resource Announcements, 2021, 10, e0062821.	0.3	0
2399	Draft Genome Sequences of Heat Shock-Tolerant Microbes Isolated from a Spacecraft Assembly Facility. Microbiology Resource Announcements, 2021, 10, e0065321.	0.3	1
2400	Whole genome sequencing reveals great diversity of Vibrio spp in prawns at retail. Microbial Genomics, 2021, 7, .	1.0	7
2402	Microorganisms of Two Thermal Pools on Kunashir Island, Russia. Biology, 2021, 10, 924.	1.3	3
2403	Over 50,000 Metagenomically Assembled Draft Genomes for the Human Oral Microbiome Reveal New Taxa. Genomics, Proteomics and Bioinformatics, 2022, 20, 246-259.	3.0	38
2404	Comparative genomic analysis reveals metabolic flexibility of Woesearchaeota. Nature Communications, 2021, 12, 5281.	5.8	25
2405	Whole genome sequences reveal the <i>Xanthomonas perforans</i> population is shaped by the tomato production system. ISME Journal, 2022, 16, 591-601.	4.4	6
2406	Draft Genome Sequences of Three Shewanella sp. Strains Isolated from Urban Freshwaters in the Ohio River Valley, USA. Microbiology Resource Announcements, 2021, 10, e0074221.	0.3	0
2407	Comparative Genomics Provides Insight into the Function of Broad-Host Range Sponge Symbionts. MBio, 2021, 12, e0157721.	1.8	5
2408	Nesterenkonia ebinurensis sp. nov., a Novel Actinobacterium Isolated From Populus euphratica. Current Microbiology, 2021, 78, 3804-3810.	1.0	3

#	Article	IF	Citations
2410	Whole Genome Sequencing Based Taxonomic Classification, and Comparative Genomic Analysis of Potentially Human Pathogenic Enterobacter spp. Isolated from Chlorinated Wastewater in the North West Province, South Africa. Microorganisms, 2021, 9, 1928.	1.6	3
2411	Deciphering microbial mechanisms underlying soil organic carbon storage in a wheat-maize rotation system. Science of the Total Environment, 2021, 788, 147798.	3.9	23
2412	Frigoriflavimonas asaccharolytica gen. nov., sp. nov., a novel psychrophilic esterase and protease producing bacterium isolated from Antarctica. Antonie Van Leeuwenhoek, 2021, 114, 1991-2002.	0.7	7
2413	Understanding Responses of Soil Microbiome to the Nitrogen and Phosphorus Addition in Metasequoia glyptostroboides Plantations of Different Ages. Microbial Ecology, 2022, 84, 565-579.	1.4	5
2414	Nocardioides baculatus sp. nov., a novel actinomycete isolated from the rhizosphere of Tagetes patula. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
2415	Analysis of Draft Genome Resources of Thirty-Three Canadian Strains of <i>Pseudomonas syringae</i> pv. <i>tomato</i> Isolated Between 1992 and 2008 Reveals Achromobactin Virulence Cluster that Is Absent in the Reference Strain DC3000. Phytopathology, 2022, 112, 968-972.	1.1	1
2416	Metagenomic insights into nitrogen and phosphorus cycling at the soil aggregate scale driven by organic material amendments. Science of the Total Environment, 2021, 785, 147329.	3.9	56
2417	Characterization of Bifidobacterium apousia sp. nov., Bifidobacterium choladohabitans sp. nov., and Bifidobacterium polysaccharolyticum sp. nov., three novel species of the genus Bifidobacterium from honey bee gut. Systematic and Applied Microbiology, 2021, 44, 126247.	1.2	23
2418	The Hidden Genomic Diversity, Specialized Metabolite Capacity, and Revised Taxonomy of Burkholderia Sensu Lato. Frontiers in Microbiology, 2021, 12, 726847.	1.5	16
2420	Metagenomic Analysis Reveals Microbial Interactions at the Biocathode of a Bioelectrochemical System Capable of Simultaneous Trichloroethylene and Cr(VI) Reduction. Frontiers in Microbiology, 2021, 12, 747670.	1.5	5
2421	Genomic characterization of Enterobacter xiangfangensis STP-3: Application to real time petroleum oil sludge bioremediation. Microbiological Research, 2021, 253, 126882.	2.5	8
2422	Potential of Variovorax paradoxus isolate BFB1_13 for bioremediation of BTEX contaminated sites. AMB Express, 2021, 11, 126.	1.4	15
2423	Exploring syntenic conservation across genomes for phylogenetic studies of organisms subjected to horizontal gene transfers: A case study with Cyanobacteria and cyanolichens. Molecular Phylogenetics and Evolution, 2021, 162, 107100.	1.2	8
2424	Effects of laboratory domestication on the rodent gut microbiome. ISME Communications, 2021, 1, .	1.7	21
2425	Microbial characterisation and Cold-Adapted Predicted Protein (CAPP) database construction from the active layer of Greenland's permafrost. FEMS Microbiology Ecology, 2021, 97, .	1.3	2
2426	Genome-resolved metagenome and metatranscriptome analyses of thermophilic composting reveal key bacterial players and their metabolic interactions. BMC Genomics, 2021, 22, 652.	1.2	16
2427	Rejection of the reclassification of Leuconostoc gasicomitatum as Leuconostoc gelidum subsp. gasicomitatum based on whole genome analysis. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	7
2428	Whatâ€™s under the Christmas Tree? A Soil Sulfur Amendment Lowers Soil pH and Alters Fir Tree Rhizosphere Bacterial and Eukaryotic Communities, Their Interactions, and Functional Traits. Microbiology Spectrum, 2021, 9, e0016621.	1.2	6

#	Article	IF	Citations
2429	Streptomyces poriferorum sp. nov., a novel marine sponge-derived Actinobacteria species expressing anti-MRSA activity. Systematic and Applied Microbiology, 2021, 44, 126244.	1.2	10
2430	Extensive Horizontal Gene Transfer within and between Species of Coagulase-Negative <i>Staphylococcus</i>. Genome Biology and Evolution, 2021, 13, .	1.1	14
2432	Diversity and Metabolic Potential of the Terrestrial Mud Volcano Microbial Community with a High Abundance of Archaea Mediating the Anaerobic Oxidation of Methane. Life, 2021, 11, 953.	1.1	16
2433	Comparative Genomic Analysis of Bifidobacterium bifidum Strains Isolated from Different Niches. Genes, 2021, 12, 1504.	1.0	6
2435	Sixteen Genome Sequences of Denitrifying Bacteria Assembled from Enriched Cultures of Anaerobic Pig Manure Digestate. Microbiology Resource Announcements, 2021, 10, e0078221.	0.3	1
2436	Occurrence of the Colistin Resistance Gene <i>mcr-1</i> and Additional Antibiotic Resistance Genes in ESBL/AmpC-Producing Escherichia coli from Poultry in Lebanon: A Nationwide Survey. Microbiology Spectrum, 2021, 9, e0002521.	1.2	17
2437	Phyllobacterium calauticae sp. nov. isolated from a microaerophilic veil transversed by cable bacteria in freshwater sediment. Antonie Van Leeuwenhoek, 2021, 114, 1877-1887.	0.7	8
2439	Diesel and Crude Oil Biodegradation by Cold-Adapted Microbial Communities in the Labrador Sea. Applied and Environmental Microbiology, 2021, 87, e0080021.	1.4	28
2440	Ramlibacter terrae sp. nov. and Ramlibacter montanisoli sp. nov., Isolated from Soil. Journal of Microbiology and Biotechnology, 2021, 31, 1210-1217.	0.9	10
2441	MetaPlatanus: a metagenome assembler that combines long-range sequence links and species-specific features. Nucleic Acids Research, 2021, 49, e130-e130.	6.5	6
2442	Genome Evolution of Filamentous Cyanobacterium Nostoc Species: From Facultative Symbiosis to Free Living. Microorganisms, 2021, 9, 2015.	1.6	4
2444	Aberrant gut-microbiota-immune-brain axis development in premature neonates with brain damage. Cell Host and Microbe, 2021, 29, 1558-1572.e6.	5.1	80
2445	Spread of Carbapenem-Resistant Klebsiella pneumoniae in an Intensive Care Unit: A Whole-Genome Sequence-Based Prospective Observational Study. Microbiology Spectrum, 2021, 9, e0005821.	1.2	12
2446	Sedimentation rate and organic matter dynamics shape microbiomes across a continental margin. Biogeosciences, 2021, 18, 5203-5222.	1.3	8
2447	Reconstituting the genus Mycobacterium. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	34
2448	Identification of Faecalibacterium prausnitzii strains for gut microbiome-based intervention in Alzheimerâ€™s-type dementia. Cell Reports Medicine, 2021, 2, 100398.	3.3	42
2449	Stimulation of Nicotiana tabacum L. In Vitro Shoot Growth by Endophytic Bacillus cereus Group Bacteria. Microorganisms, 2021, 9, 1893.	1.6	4
2450	Struo2: efficient metagenome profiling database construction for ever-expanding microbial genome datasets. PeerJ, 2021, 9, e12198.	0.9	24

#	ARTICLE	IF	CITATIONS
2451	Pontivivens ytuae sp. nov., isolated from deep sea sediment of the Mariana Trench. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	5
2453	Draft Genome Sequence of Pseudoalteromonas sp. Strain JC3. Microbiology Resource Announcements, 2021, 10, e0021221.	0.3	0
2454	Comparative genomic analysis of <i>Methanimicrococcus blatticola</i> provides insights into host adaptation in archaea and the evolution of methanogenesis. ISME Communications, 2021, 1, .	1.7	17
2456	Genomic Insights into the Ecological Role and Evolution of a Novel <i>Thermoplasmata</i> Order, â€œ <i>Candidatus</i> Sysuiplasmatalesâ€• Applied and Environmental Microbiology, 2021, 87, e0106521.	1.4	3
2457	Ecological Dichotomies Arise in Microbial Communities Due to Mixing of Deep Hydrothermal Waters and Atmospheric Gas in a Circumneutral Hot Spring. Applied and Environmental Microbiology, 2021, 87, e0159821.	1.4	6
2459	Methyloradius palustris gen. nov., sp. nov., a methanol-oxidizing bacterium isolated from snow. Archives of Microbiology, 2021, 203, 5715-5721.	1.0	7
2460	Early-Life Microbial Restitution Reduces Colitis Risk Promoted by Antibiotic-Induced Gut Dysbiosis in Interleukin 10â€“/â€“ Mice. Gastroenterology, 2021, 161, 940-952.e15.	0.6	20
2461	Aerobactin Seems To Be a Promising Marker Compared With Unstable RmpA2 for the Identification of Hypervirulent Carbapenem-Resistant Klebsiella pneumoniae: In Silico and In Vitro Evidence. Frontiers in Cellular and Infection Microbiology, 2021, 11, 709681.	1.8	30
2462	Metagenome-Assembled Genome Sequences Obtained from a Reactivated Kombucha Microbial Community Exposed to a Mars-Like Environment outside the International Space Station. Microbiology Resource Announcements, 2021, 10, e0054921.	0.3	4
2464	Diversity and Metabolic Potentials of As(III)-Oxidizing Bacteria in Activated Sludge. Applied and Environmental Microbiology, 2021, 87, e0176921.	1.4	21
2465	Horizontal gene transfer-mediated bacterial strain variation affects host fitness in Drosophila. BMC Biology, 2021, 19, 187.	1.7	4
2466	First report from Bangladesh on genetic diversity of multidrug-resistant Pasteurella multocida type B:2 in fowl cholera. Veterinary World, 2021, 14, 2527-2542.	0.7	7
2467	Hydrodynamic disturbance controls microbial community assembly and biogeochemical processes in coastal sediments. ISME Journal, 2022, 16, 750-763.	4.4	38
2469	Feeding the Microbes: A Strategy to Control Verticillium Wilt. Agronomy, 2021, 11, 1946.	1.3	3
2470	Accessing the Subsurface Biosphere Within Rocks Undergoing Active Lowâ€Temperature Serpentinization in the Samail Ophiolite (Oman Drilling Project). Journal of Geophysical Research G: Biogeosciences, 2021, 126, e2021JG006315.	1.3	27
2471	Genome-Based Taxonomic Rearrangement of the Order Geobacterales Including the Description of Geomonas azotofigens sp. nov. and Geomonas diazotrophica sp. nov.. Frontiers in Microbiology, 2021, 12, 737531.	1.5	59
2472	Activity and structure of methanogenic microbial communities in sediments of cascade hydropower reservoirs, Southwest China. Science of the Total Environment, 2021, 786, 147515.	3.9	7
2473	Mechanistic insights into the success of xenobiotic degraders resolved from metagenomes of microbial enrichment cultures. Journal of Hazardous Materials, 2021, 418, 126384.	6.5	10

#	Article	IF	Citations
2474	GTDB: an ongoing census of bacterial and archaeal diversity through a phylogenetically consistent, rank normalizedÂand complete genome-based taxonomy. Nucleic Acids Research, 2022, 50, D785-D794.	6.5	662
2475	Viability-Resolved Metagenomics Reveals Antagonistic Colonization Dynamics of Staphylococcus epidermidis Strains on Preterm Infant Skin. MSphere, 2021, 6, e0053821.	1.3	5
2476	Arms race in a cell: genomic, transcriptomic, and proteomic insights into intracellular phageâ€“bacteria interplay in deep-sea snail holobionts. Microbiome, 2021, 9, 182.	4.9	7
2477	Desulfovibrio feeding Methanobacterium with electrons in conductive methanogenic aggregates from coastal zones. Water Research, 2021, 202, 117490.	5.3	70
2480	Iron-Fueled Life in the Continental Subsurface: Deep Mine Microbial Observatory, South Dakota, USA. Applied and Environmental Microbiology, 2021, 87, e0083221.	1.4	10
2481	Chryseobacterium potabilaquae sp. nov., Chryseobacterium aquaeductus sp. nov. and Chryseobacterium fistulae sp. nov., from drinking water systems. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	12
2483	Eikenella glucosivorans sp. nov., isolated from a human throat swab, and emendation of the genus Eikenella to include saccharolytic species. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	8
2484	VicPred: A Vibrio cholerae Genotype Prediction Tool. Frontiers in Microbiology, 2021, 12, 691895.	1.5	12
2485	Eight Metagenome-Assembled Genomes Provide Evidence for Microbial Adaptation in 20,000- to 1,000,000-Year-Old Siberian Permafrost. Applied and Environmental Microbiology, 2021, 87, e0097221.	1.4	13
2486	<i>Verrucomicrobiota</i> are specialist consumers of sulfated methyl pentoses during diatom blooms. ISME Journal, 2022, 16, 630-641.	4.4	62
2487	Flavobacterium tagetis sp. nov., a novel urea-hydrolysing bacterium isolated from the roots of Tagetes patula. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	10
2488	Metagenome-Assembled Genome Sequences Recovered from Epilithic River Biofilm in the Tama River, Japan. Microbiology Resource Announcements, 2021, 10, e0066421.	0.3	1
2490	A novel thermostable prokaryotic fucoidan active sulfatase PsFucS1 with an unusual quaternary hexameric structure. Scientific Reports, 2021, 11, 19523.	1.6	8
2491	Three Draft Single-Cell Genome Sequences of Novel SAR324 Strains Isolated from the Abyssopelagic Southern Ocean. Microbiology Resource Announcements, 2021, 10, e0075921.	0.3	0
2492	Draft Genome Sequence of Streptococcus salivarius AGIRA0003, Isolated from Functional Gastrointestinal Disorder Duodenal Tissue. Microbiology Resource Announcements, 2021, 10, e0075821.	0.3	2
2493	Prospects for multi-omics in the microbial ecology of water engineering. Water Research, 2021, 205, 117608.	5.3	26
2494	Soil bacteria, genes, and metabolites stimulated during sulfur cycling and cadmium mobilization under sodium sulfate stress. Environmental Research, 2021, 201, 111599.	3.7	29
2495	Metagenomic insights into the effect of thermal hydrolysis pre-treatment on microbial community of an anaerobic digestion system. Science of the Total Environment, 2021, 791, 148096.	3.9	31

#	ARTICLE	IF	CITATIONS
2496	Kefir ameliorates specific microbiota-gut-brain axis impairments in a mouse model relevant to autism spectrum disorder. Brain, Behavior, and Immunity, 2021, 97, 119-134.	2.0	19
2497	The widespread IS200/IS605 transposon family encodes diverse programmable RNA-guided endonucleases. Science, 2021, 374, 57-65.	6.0	152
2498	Variations of antibiotic resistome in swine wastewater during full-scale anaerobic digestion treatment. Environment International, 2021, 155, 106694.	4.8	48
2499	Genomic and phenotypic comparison of two Salmonella Typhimurium strains responsible for consecutive salmonellosis outbreaks in New Zealand. International Journal of Medical Microbiology, 2021, 311, 151534.	1.5	2
2500	Genomic adaptation and metabolic hierarchy: Microbial community response to oxygen stress in community derived from sludge treating refinery wastewater. Journal of Cleaner Production, 2021, 320, 128808.	4.6	6
2501	Strain-level multiomics analysis reveals significant variation in cheeses from different regions. LWT - Food Science and Technology, 2021, 151, 112043.	2.5	17
2502	Description and functional testing of four species of the novel phototrophic genus Chioneia gen. nov., isolated from different East Antarctic environments. Systematic and Applied Microbiology, 2021, 44, 126250.	1.2	26
2503	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.. Systematic and Applied Microbiology, 2021, 44, 126251.	1.2	46
2504	Response of microbial nitrogen transformation processes to antibiotic stress in a drinking water reservoir. Science of the Total Environment, 2021, 797, 149119.	3.9	27
2505	Genomic and in silico protein structural analyses provide insights into marine polysaccharide-degrading enzymes in the sponge-derived Pseudoalteromonas sp. PA2MD11. International Journal of Biological Macromolecules, 2021, 191, 973-995.	3.6	1
2506	Nonribosomal peptide synthetases and nonribosomal cyanopeptides synthesis in Microcystis: A comparative genomics study. Algal Research, 2021, 59, 102432.	2.4	3
2507	Current production by non-methanotrophic bacteria enriched from an anaerobic methane-oxidizing microbial community. Biofilm, 2021, 3, 100054.	1.5	8
2508	Draft genome sequence of a multidrug-resistant novel candidate Pseudomonas sp. NCCP-436T isolated from faeces of a bovine host in Pakistan. Journal of Global Antimicrobial Resistance, 2021, 27, 91-94.	0.9	7
2509	Distinct metabolic strategies of the dominant heterotrophic bacterial groups associated with marine Synechococcus. Science of the Total Environment, 2021, 798, 149208.	3.9	10
2510	Bioplastic accumulates antibiotic and metal resistance genes in coastal marine sediments. Environmental Pollution, 2021, 291, 118161.	3.7	20
2511	Enhanced survival of multi-species biofilms under stress is promoted by low-abundant but antimicrobial-resistant keystone species. Journal of Hazardous Materials, 2022, 422, 126836.	6.5	17
2512	Survival strategy of comammox bacteria in a wastewater nutrient removal system with sludge fermentation liquid as additional carbon source. Science of the Total Environment, 2022, 802, 149862.	3.9	13
2513	Functional filtering and random processes affect the assembly of microbial communities of snow algae blooms at Maritime Antarctic. Science of the Total Environment, 2022, 805, 150305.	3.9	11

#	ARTICLE	IF	CITATIONS
2514	Metagenomic and metabolic analyses of poly-extreme microbiome from an active crater volcano lake. Environmental Research, 2022, 203, 111862.	3.7	9
2518	'Candidatus Phytoplasma sacchariâ€™, a novel taxon - associated with Sugarcane Grassy Shoot (SCGS) disease. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	29
2519	Toothbrush microbiomes feature a meeting ground for human oral and environmental microbiota. Microbiome, 2021, 9, 32.	4.9	9
2520	Comparative metagenomic discovery of the dynamic cellulose-degrading process from a synergistic cellulolytic microbiota. Cellulose, 2021, 28, 2105-2123.	2.4	8
2521	Microdiversity of <i>Enterococcus faecalis</i> isolates in cases of infective endocarditis: selection of non-synonymous mutations and large deletions is associated with phenotypic modifications. Emerging Microbes and Infections, 2021, 10, 929-938.	3.0	9
2522	Fly-over phylogeny across invertebrate to vertebrate: The giant panda and insects share a highly similar gut microbiota. Computational and Structural Biotechnology Journal, 2021, 19, 4676-4683.	1.9	7
2523	Cometabolism of the Superphylum Patescibacteria with Anammox Bacteria in a Long-Term Freshwater Anammox Column Reactor. Water (Switzerland), 2021, 13, 208.	1.2	51
2524	The Functional Evolution of Termite Gut Microbiota. SSRN Electronic Journal, 0, , .	0.4	0
2525	Comparative genomics analyses indicate differential methylated amine utilization trait within members of the genus <i>Gemmobacter</i>. Environmental Microbiology Reports, 2021, 13, 195-208.	1.0	8
2526	A microbial gene catalog of anaerobic digestion from full-scale biogas plants. GigaScience, 2021, 10, .	3.3	23
2527	Accurate Annotation of Microbial Metagenomic Genes and Identification of Core Sets. Methods in Molecular Biology, 2021, 2242, 115-138.	0.4	0
2529	Bioactivity Screening and Gene-Trait Matching across Marine Sponge-Associated Bacteria. Marine Drugs, 2021, 19, 75.	2.2	12
2531	Draft Genome Sequences of <i>Dysgonomonas</i> sp. Strains BGC7 and HGC4, Isolated from the Hindgut of a Lower Termite. Microbiology Resource Announcements, 2021, 10, .	0.3	4
2532	Draft Genome Sequences of Idiomarina abyssalis Strain KJE, Marinobacter salarius Strain NP2017, and Marinobacter salarius Strain AT3901, Isolated from Deep-Sea Sediment near the Western Flank of the Mid-Atlantic Ridge. Microbiology Resource Announcements, 2021, 10, .	0.3	1
2533	Intestinal Î±1-2-Fucosylation Contributes to Obesity and Steatohepatitis in Mice. Cellular and Molecular Gastroenterology and Hepatology, 2021, 12, 293-320.	2.3	14
2534	The Taxonomy of Bacteria in the Genomic Era. , 2021, , 289-309.		2
2535	Antibiotic-driven intestinal dysbiosis in pediatric short bowel syndrome is associated with persistently altered microbiome functions and gut-derived bloodstream infections. Gut Microbes, 2021, 13, 1940792.	4.3	15
2536	Clostridium fessum sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	10

#	Article	IF	Citations
2537	Gluconacetobacter dulcium sp. nov., a novel Gluconacetobacter species from sugar-rich environments. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	5
2538	Genome sequence analysis of the beneficial Bacillus subtilis PTA-271 isolated from a Vitis vinifera (cv.) Tj ETQq1 1 0.784314 rgBT /Overl 16, 3.	2.2	20
2539	Microbiome connections with host metabolism and habitual diet from 1,098 deeply phenotyped individuals. Nature Medicine, 2021, 27, 321-332.	15.2	477
2540	Trace gas oxidizers are widespread and active members of soil microbial communities. Nature Microbiology, 2021, 6, 246-256.	5.9	97
2541	Aerobic Hydrocarbon-Degrading Gammaproteobacteria: Oleiphilaceae and Relatives. , 2019, , 153-166.		1
2542	Meta-Pangenome: At the Crossroad of Pangenomics and Metagenomics. , 2020, , 205-218.		7
2543	Metagenomic Analysis of Low-Temperature Environments. , 2017, , 389-421.		4
2544	Natronorubrum halophilum sp. nov. isolated from two inland salt lakes. Journal of Microbiology, 2020, 58, 105-112.	1.3	20
2545	Effect of ammonia on the active microbiome and metagenome from stable full-scale digesters. Bioresource Technology, 2018, 250, 513-522.	4.8	56
2546	Genome recovery and metatranscriptomic confirmation of functional acetate-oxidizing bacteria from enriched anaerobic biogas digesters. Environmental Pollution, 2020, 265, 114843.	3.7	42
2547	Comparative metagenomics and characterization of antimicrobial resistance genes in pasteurized and homemade fermented Arabian laban. Food Research International, 2020, 137, 109639.	2.9	11
2548	Candidatus Abditibacter, a novel genus within the Cryomorphaceae, thriving in the North Sea. Systematic and Applied Microbiology, 2020, 43, 126088.	1.2	21
2549	Will a Non-antibiotic Metalloid Enhance the Spread of Antibiotic Resistance Genes: The Selenate Story. Environmental Science & Technology, 2021, 55, 1004-1014.	4.6	42
2550	Discovery and quantification of anaerobic nitrogen metabolisms among oxygenated tropical Cuban stony corals. ISME Journal, 2021, 15, 1222-1235.	4.4	22
2551	Aerobic and anaerobic iron oxidizers together drive denitrification and carbon cycling at marine iron-rich hydrothermal vents. ISME Journal, 2021, 15, 1271-1286.	4.4	46
2552	Anaerobic methane oxidation coupled to manganese reduction by members of the <i>Methanoperedenaceae</i>. ISME Journal, 2020, 14, 1030-1041.	4.4	203
2553	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. Nature Biotechnology, 2019, 37, 179-185.	9.4	402
2554	A human gut bacterial genome and culture collection for improved metagenomic analyses. Nature Biotechnology, 2019, 37, 186-192.	9.4	420

#	Article	IF	Citations
2555	Soil microbiomes mediate degradation of vinyl ester-based polymer composites. Communications Materials, 2020, 1, .	2.9	25
2556	Single cell genomes of Prochlorococcus, Synechococcus, and sympatric microbes from diverse marine environments. Scientific Data, 2018, 5, 180154.	2.4	81
2557	Complete genome sequencing of Comamonas kerstersii 8943, a causative agent for peritonitis. Scientific Data, 2018, 5, 180222.	2.4	12
2558	Complex subsurface hydrothermal fluid mixing at a submarine arc volcano supports distinct and highly diverse microbial communities. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32627-32638.	3.3	36
2559	Vertical stratification patterns of methanotrophs and their genetic controllers in water columns of oxygen-stratified boreal lakes. FEMS Microbiology Ecology, 2021, 97, .	1.3	29
2560	Phylogenomics insights into order and families of Lysobacterales. Access Microbiology, 2019, 1, e000015.	0.2	22
2561	Complete genome dynamics of a dominant-lineage strain of Xanthomonas oryzae pv. oryzae harbouring a novel plasmid encoding a type IV secretion system. Access Microbiology, 2019, 1, e000063.	0.2	13
2562	â€˜Candidatus Tenderia electrophaga', an uncultivated electroautotroph from a biocathode enrichment. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 2178-2185.	0.8	54
2563	Haloprofundus marisrubri gen. nov., sp. nov., an extremely halophilic archaeon isolated from a brineâ€“seawater interface. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 9-16.	0.8	21
2564	ContEst16S: an algorithm that identifies contaminated prokaryotic genomes using 16S RNA gene sequences. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2053-2057.	0.8	377
2565	Enterococcus crotali sp. nov., isolated from faecal material of a timber rattlesnake. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1984-1989.	0.8	11
2566	Henriciella pelagia sp. nov., isolated from seawater. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3020-3025.	0.8	22
2567	Vibrio palustris sp. nov. and Vibrio spartinae sp. nov., two novel members of the Gazogenes clade, isolated from salt-marsh plants (Arthrocnemum macrostachyum and Spartina maritima). International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3506-3512.	0.8	20
2568	Ponticoccus marisrubri sp. nov., a moderately halophilic marine bacterium of the family Rhodobacteraceae. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4358-4364.	0.8	7
2569	Rejection of reclassification of Lactobacillus kimchii and Lactobacillus bobalius as later subjective synonyms of Lactobacillus paralimentarius using comparative genomics. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4515-4517.	0.8	7
2570	Ruegeria profundi sp. nov. and Ruegeria marisrubri sp. nov., isolated from the brineâ€“seawater interface at Erba Deep in the Red Sea. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4624-4631.	0.8	17
2571	Actibacterium pelagium sp. nov., a novel alphaproteobacterium, and emended description of the genus Actibacterium. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 5080-5086.	0.8	18
2572	Proposed minimal standards for the use of genome data for the taxonomy of prokaryotes. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 461-466.	0.8	2,359

#	Article	IF	Citations
2573	Pseudooceanicola lipolyticus sp. nov., a marine alphaproteobacterium, reclassification of Oceanicola flagellatus as Pseudooceanicola flagellatus comb. nov. and emended description of the genus Pseudooceanicola. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 409-415.	0.8	31
2574	Raineya orbicola gen. nov., sp. nov. a slightly thermophilic bacterium of the phylum Bacteroidetes and the description of Raineyaceae fam. nov.. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 982-989.	0.8	19
2575	Halomonas endophytica sp. nov., isolated from liquid in the stems of Populus euphratica. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1633-1638.	0.8	20
2576	Lysobacter silvestris sp. nov., isolated from alpine forest soil, and reclassification of Luteimonas tolerans as Lysobacter tolerans comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1571-1577.	0.8	20
2577	Thioclava electrotropha sp. nov., a versatile electrode and sulfur-oxidizing bacterium from marine sediments. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1652-1658.	0.8	23
2578	Gracilimonas amylolytica sp. nov., isolated from deep-sea sediment. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1713-1718.	0.8	8
2579	Rhodohalobacter barkolensis sp. nov., isolated from a saline lake and emended description of the genus Rhodohalobacter. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1949-1954.	0.8	14
2580	Marinicaulis flavus gen. nov., sp. nov., a novel stalked bacterium of the family Parvularculaceae. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2061-2067.	0.8	11
2581	Solimicrobium silvestre gen. nov., sp. nov., isolated from alpine forest soil. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2491-2498.	0.8	11
2582	Ruegeria denitrificans sp. nov., a marine bacterium in the family Rhodobacteraceae with the potential ability for cyanophycin synthesis. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2515-2522.	0.8	37
2583	Emcibacter congregatus sp. nov., isolated from sediment cultured in situ. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2846-2850.	0.8	7
2584	Marinobacter fuscus sp. nov., a marine bacterium of Gammaproteobacteria isolated from surface seawater. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3156-3162.	0.8	12
2585	Chryseobacterium aurantiacum sp. nov., isolated from a freshwater pond used for Murray cod (Maccullochella peelii peelii) culture. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3397-3403.	0.8	8
2586	Chryseolinea flava sp. nov., a new species of Chryseolinea isolated from soil. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3518-3522.	0.8	11
2587	Hyphobacterium indicum sp. nov., isolated from deep seawater, and emended description of the genus Hyphobacterium. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3760-3765.	0.8	11
2588	Alcanivorax indicus sp. nov., isolated from seawater. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3785-3789.	0.8	13
2589	Paracoccus salipaludis sp. nov., isolated from salineâ€"alkaline soil. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3812-3817.	0.8	11
2590	Halomonas litopenaei sp. nov., a moderately halophilic, exopolysaccharide-producing bacterium isolated from a shrimp hatchery. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3914-3921.	0.8	10

#	Article	IF	Citations
2591	Bacillus safensis subsp. osmophilus subsp. nov., isolated from condensed milk, and description of Bacillus safensis subsp. safensis subsp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 189-195.	0.8	12
2592	Paracandidimonas caeni sp. nov., isolated from sludge. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3332-3337.	0.8	10
2593	Erythrobacter zhengii sp. nov., a bacterium isolated from deep-sea sediment. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 241-248.	0.8	18
2594	Pseudomonas mangrovi sp. nov., isolated from mangrove soil. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 377-383.	0.8	14
2595	Description of Paracoccus endophyticus sp. nov., isolated from Gastrodia elata Blume. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 261-265.	0.8	14
2596	Marinimicrobium alkaliphilum sp. nov., an alkaliphilic bacterium isolated from soil and emended description of the genus Marinimicrobium. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 481-485.	0.8	10
2597	Meridianimarinicoccus roseus gen. nov., sp. nov., a novel genus of the family Rhodobacteraceae isolated from seawater. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 504-510.	0.8	12
2598	Lactobacillus salitolerans sp. nov., a novel lactic acid bacterium isolated from spent mushroom substrates. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 964-969.	0.8	14
2599	Halorussus litoreus sp. nov., isolated from the salted brown alga Laminaria. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 767-772.	0.8	13
2600	Algihabitans albus gen. nov., sp. nov., isolated from a culture of the green alga Ulva prolifera. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 828-832.	0.8	10
2601	Botryobacter ruber gen. nov., sp. nov., a novel member of the family Hymenobacteraceae. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 821-827.	0.8	9
2602	Transfer of Meiothermus chliarophilus (Tenreiro et al.1995) Nobre et al. 1996, Meiothermus roseus Ming et al. 2016, Meiothermus terrae Yu et al. 2014 and Meiothermus timidus Pires et al. 2005, to Calidithermus gen. nov., as Calidithermus chliarophilus comb. nov., Calidithermus roseus comb. nov., Calidithermus terrae comb. nov. and Calidithermus timidus comb. nov., respectively, and emended description of the genus Meiothermus. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1060-1068.	0.8	28
2603	Aggregatilinea lenta gen. nov., sp. nov., a slow-growing, facultatively anaerobic bacterium isolated from subseafloor sediment, and proposal of the new order Aggregatilineales ord. nov. within the class Anaerolineae of the phylum Chloroflexi. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1185-1194.	0.8	32
2604	Frateuria defendens sp. nov., bacterium isolated from the yellows grapevineâ€™s disease vector Hyalesthes obsoletus. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1281-1287.	0.8	11
2605	Genome-based reclassification of Weissella jogaejeotgali as a later heterotypic synonym of Weissella thailandensis. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3672-3675.	0.8	10
2606	Alkalilacustris brevis gen. nov., sp. nov., isolated from a soda lake. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1669-1675.	0.8	8
2607	Altererythrobacter aerophilus sp. nov., isolated from deep-sea water of the north-west Pacific. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1689-1695.	0.8	16
2608	Magnetospirillum kuznetsovii sp. nov., a novel magnetotactic bacterium isolated from a lake in the Moscow region. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1953-1959.	0.8	17

#	Article	IF	Citations
2609	Oceaniradius stylonematis gen. nov., sp. nov., isolated from a red alga, Stylonema cornu-cervi. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1967-1973.	0.8	16
2610	Faecalibacillus intestinalis gen. nov., sp. nov. and Faecalibacillus faecis sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2120-2128.	0.8	18
2611	Olsenella faecalis sp. nov., an anaerobic actinobacterium isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2323-2328.	0.8	15
2612	Shewanella psychromarinicola sp. nov., a psychrophilic bacterium isolated from pelagic sediment of the Ross Sea (Antarctica), and reclassification of Shewanella arctica Kim et al. 2012 as a later heterotypic synonym of Shewanella frigidimarina Bowman et al. 1997. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2415-2423.	0.8	13
2613	Streptomyces rhizosphaericola sp. nov., an actinobacterium isolated from the wheat rhizosphere. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2431-2439.	0.8	10
2614	Tabrizicola sediminis sp. nov., one aerobic anoxygenic photoheterotrophic bacteria from sediment of saline lake. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2565-2570.	0.8	18
2615	Shimia thalassica sp. nov., and reclassification of Pseudopelagicola gijangensis as Shimia gijangensis comb. nov., and Thalassobius activus as Cognatishimia activa comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3405-3413.	0.8	19
2616	Halostella limicola sp. nov., isolated from saline soil sampled at the Tarim Basin. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3299-3304.	0.8	13
2617	Schaedlerella arabinosiphila gen. nov., sp. nov., a D-arabinose-utilizing bacterium isolated from faeces of C57BL/6J mice that is a close relative of Clostridium species ASF 502. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3616-3622.	0.8	12
2618	Facilibium subflavum gen. nov., sp. nov. and Cysteiniphilum halobium sp. nov., new members of the family Fastidiosibacteraceae isolated from coastal seawater. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3757-3764.	0.8	14
2619	Prevotella brunnea sp. nov., isolated from a wound of a patient. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3933-3938.	0.8	7
2620	Pseudidiomarina gelatinasegens sp. nov., isolated from surface sediment of the Terra Nova Bay, Antarctica. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 708-714.	0.8	9
2621	Pelagicola marinus sp. nov. isolated from deep-sea water. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3961-3966.	0.8	8
2622	Mabikibacter ruber Choi et al. 2017 is a later heterotypic synonym of Notoacmeibacter marinus Huang et al. 2017. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 439-441.	0.8	5
2623	Sulfurimonas crateris sp. nov., a facultative anaerobic sulfur-oxidizing chemolithoautotrophic bacterium isolated from a terrestrial mud volcano. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 487-492.	0.8	22
2624	Aquabacterium pictum sp. nov., the first aerobic bacteriochlorophyll a-containing fresh water bacterium in the genus Aquabacterium of the class Betaproteobacteria. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 596-603.	0.8	15
2625	Pseudomonas saxonica sp. nov., isolated from raw milk and skimmed milk concentrate. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 935-943.	0.8	10
2626	Ktedonosporobacter rubrisoli gen. nov., sp. nov., a novel representative of the class Ktedonobacteria, isolated from red soil, and proposal of Ktedonosporobacteraceae fam. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1015-1025.	0.8	18

#	ARTICLE	IF	CITATIONS
2627	Genome analysis-based reclassification of Enterobacter tabaci Duan et al. 2016 as a later heterotypic synonym of Enterobacter mori Zhu et al. 2011. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1055-1058.	0.8	6
2628	Ferrovibrio terrae sp. nov., isolated from soil. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1042-1047.	0.8	6
2629	Thalassocella blandensis gen. nov., sp. nov., a novel member of the family Cellvibrionaceae. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1231-1239.	0.8	19
2630	Brevilactibacter flavus gen. nov., sp. nov., a novel bacterium of the family Propionibacteriaceae isolated from raw milk and dairy products and reclassification of Propioniciclava sinopodophylli as Brevilactibacter sinopodophylli comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2186-2193.	0.8	25
2631	Update on the classification of higher ranks in the phylum Actinobacteria. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1331-1355.	0.8	255
2632	Comparative genome sequence analysis of several species in the genus Tepidimonas and the description of a novel species Tepidimonas charontis sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1596-1604.	0.8	8
2633	Sphingorhabdus soli sp. nov., isolated from Arctic soil. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1610-1616.	0.8	8
2634	Salinigranum halophilum sp. nov., isolated from marine solar salterns. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1648-1655.	0.8	11
2635	Dictyobacter vulcani sp. nov., belonging to the class Ktedonobacteria, isolated from soil of the Mt Zao volcano. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1805-1813.	0.8	10
2636	Sphingomonas solaris sp. nov., isolated from a solar panel in Boston, Massachusetts. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1814-1821.	0.8	12
2637	Natrialba swarupiae sp. nov., a halophilic archaeon isolated from a hypersaline lake in India. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1876-1881.	0.8	16
2638	Halostella pelagica sp. nov. and Halostella litorea sp. nov., isolated from salted brown alga Laminaria. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1969-1976.	0.8	26
2639	Description of Paenibacillus tepidiphilus sp. nov., isolated from a tepid spring. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1977-1981.	0.8	39
2640	Acetobacter oryzoeni sp. nov., isolated from Korean rice wine vinegar. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2026-2033.	0.8	17
2641	Calorimonas adulescens 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
2642	Pseudomonas haemolytica sp. nov., isolated from raw milk and skimmed milk concentrate. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2339-2347.	0.8	15
2643	Reclassification of Clostridium diolis Biebl and SprÃ¶er 2003 as a later heterotypic synonym of Clostridium beijerinckii Donker 1926 (Approved Lists 1980) emend. Keis et al. 2001. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2463-2466.	0.8	12
2644	Lactobacillus hegangensis sp. nov., Lactobacillus suibinensis sp. nov., Lactobacillus daqingensis sp. nov., Lactobacillus yichunensis sp. nov., Lactobacillus mulanensis sp. nov., Lactobacillus achengensis sp. nov., Lactobacillus wuchangensis sp. nov., Lactobacillus gannanensis sp. nov., Lactobacillus binensis sp. nov. and Lactobacillus angrenensis sp. nov., isolated from Chinese traditional pickle and yogurt. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2467-2484.	0.8	42

#	Article	IF	Citations
2645	Weissella sagaensis sp. nov., isolated from traditional Chinese yogurt. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2485-2492.	0.8	22
2646	Vitreimonas flagellata gen. nov., sp. nov., a novel member of the family Hyphomonadaceae isolated from an activated sludge sample. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2632-2639.	0.8	10
2647	Janthinobacterium violaceinigrum sp. nov., Janthinobacterium aquaticum sp. nov. and Janthinobacterium rivuli sp. nov., isolated from a subtropical stream in China. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2719-2725.	0.8	30
2648	Lactobacillus buchneri subsp. silagei subsp. nov., isolated from rice grain silage. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3111-3116.	0.8	17
2649	Genome-based reclassification of Paenibacillus jamilae Aguilera et al. 2001 as a later heterotypic synonym of Paenibacillus polymyxa (Prazmowski 1880) Ash et al. 1994. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3134-3138.	0.8	10
2650	Proposal of Lactobacillus kosoi Chiou et al. 2018 as a later heterotypic synonym of Lactobacillus micheneri McFrederick et al. 2018, elevation of Lactobacillus plantarum subsp. argentoratensis to the species level as Lactobacillus argentoratensis sp. nov., and Lactobacillus zhaodongensis sp. nov., isolated from traditional Chinese pickle and the intestinal tract of a honey bee (Apis mellifera). International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3123-3133.	0.8	30
2651	Sphingorhabdus lacus sp. nov. and Sphingorhabdus profundilacus sp. nov., isolated from freshwater environments. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3202-3209.	0.8	10
2652	Nocardiopsis deserti sp. nov., isolated from a high altitude Atacama Desert soil. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3210-3218.	0.8	15
2653	Francisella salimarina sp. nov., isolated from coastal seawater. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3264-3272.	0.8	12
2654	Pseudomonas neustonica sp. nov., isolated from the sea surface microlayer of the Ross Sea (Antarctica). International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3832-3838.	0.8	19
2655	Ningiella ruwaisensis gen. nov., sp. nov., a member of the family Alteromonadaceae isolated from marine water of the Arabian Gulf. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4130-4138.	0.8	22
2656	Serratia inhibens sp. nov., a new antifungal species isolated from potato (Solanum tuberosum). International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4204-4211.	0.8	12
2657	Genomic-based taxonomic classification of the family Erythrobacteraceae. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4470-4495.	0.8	319
2658	Mesonia oceanica sp. nov., isolated from oceans during the Tara oceans expedition, with a preference for mesopelagic waters. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4329-4338.	0.8	11
2659	Halovulum marinum sp. nov., isolated from deep-sea water of the Indian Ocean, and emended description of the genus Halovulum. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4523-4530.	0.8	7
2660	Sandaracinobacter neustonicus sp. nov., isolated from the sea surface microlayer in the Southwestern Pacific Ocean, and emended description of the genus Sandaracinobacter. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4698-4703.	0.8	15
2661	Muribaculum gordoncarteri sp. nov., an anaerobic bacterium from the faeces of C57BL/6J mice. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4725-4729.	0.8	19
2662	Hymenobacter ginkgonis sp. nov., isolated from bark of Ginkgo biloba. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4760-4766.	0.8	9

#	Article	IF	Citations
2663	Craterilacuibacter sinensis gen. nov. sp. nov., isolated from a crater lake in China. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4831-4837.	0.8	9
2664	Hymenobacter artigasi sp. nov., isolated from air sampling in maritime Antarctica. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4935-4941.	0.8	14
2665	Caldichromatium japonicum gen. nov., sp. nov., a novel thermophilic phototrophic purple sulphur bacterium of the Chromatiaceae isolated from Nakabusa hot springs, Japan. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5701-5710.	0.8	17
2666	Lewinella aurantiaca sp. nov., a carotenoid pigment-producing bacterium isolated from surface seawater. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6180-6187.	0.8	28
2667	Genome-based reclassification of Azospirillum brasilense Sp245 as the type strain of Azospirillum baldaniorum sp. nov. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6203-6212.	0.8	58
2668	Muricauda maritima sp. nov., Muricauda aequoris sp. nov. and Muricauda oceanensis sp. nov., three marine bacteria isolated from seawater. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6240-6250.	0.8	21
2669	Psychroflexus aurantiacus sp. nov., isolated from soil in the Yellow River Delta wetlands. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6284-6293.	0.8	7
2670	Pseudodesulfovibrio mercurii sp. nov., a mercury-methylating bacterium isolated from sediment. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	13
2671	Elevation of Lactococcus lactis subsp. cremoris to the species level as Lactococcus cremoris sp. nov. and transfer of Lactococcus lactis subsp. tructae to Lactococcus cremoris as Lactococcus cremoris subsp. tructae comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	43
2672	Muricauda sediminis sp. nov., isolated from western Pacific Ocean sediment. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	10
2673	A complete high-quality MinION nanopore assembly of an extensively drug-resistant Mycobacterium tuberculosis Beijing lineage strain identifies novel variation in repetitive PE/PPE gene regions. Microbial Genomics, 2018, 4, .	1.0	35
2674	Taxonogenomics reveal multiple novel genomospecies associated with clinical isolates of Stenotrophomonas maltophilia. Microbial Genomics, 2018, 4, .	1.0	24
2675	Metagenomic assembly of new (sub)polar Cyanobacteria and their associated microbiome from non-axenic cultures. Microbial Genomics, 2018, 4, .	1.0	23
2676	Comparative genome analysis of Lactobacillus mudanjiangensis, an understudied member of the Lactobacillus plantarum group. Microbial Genomics, 2019, 5, .	1.0	9
2677	Loss of microbial diversity and pathogen domination of the gut microbiota in critically ill patients. Microbial Genomics, 2019, 5, .	1.0	59
2678	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. Microbial Genomics, 2019, 5, .	1.0	171
2679	Complete hybrid genome assembly of clinical multidrug-resistant Bacteroides fragilis isolates enables comprehensive identification of antimicrobial-resistance genes and plasmids. Microbial Genomics, 2019, 5, .	1.0	16
2680	O-antigen biosynthesis gene clusters of Escherichia albertii: their diversity and similarity to Escherichia coli gene clusters and the development of an O-genotyping method. Microbial Genomics, 2019, 5, .	1.0	27

#	Article	IF	Citations
2681	Differential dynamics and impacts of prophages and plasmids on the pangenome and virulence factor repertoires of Shiga toxin-producing Escherichia coli O145:H28. Microbial Genomics, 2020, 6, .	1.0	28
2682	Preterm infants harbour diverse Klebsiella populations, including atypical species that encode and produce an array of antimicrobial resistance- and virulence-associated factors. Microbial Genomics, 2020, 6, .	1.0	35
2683	Genomic sequence analysis of Dissulfurirhabdus thermomarina SH388 and proposed reassignment to Dissulfurirhabdaceae fam. nov.. Microbial Genomics, 2020, 6, .	1.0	2
2684	Comparative genomics of the genus Roseburia reveals divergent biosynthetic pathways that may influence colonic competition among species. Microbial Genomics, 2020, 6, .	1.0	21
2685	Metagenomic approaches in microbial ecology: an update on whole-genome and marker gene sequencing analyses. Microbial Genomics, 2020, 6, .	1.0	69
2686	Genomic diversity of Escherichia coli isolates from non-human primates in the Gambia. Microbial Genomics, 2020, 6, .	1.0	12
2687	Molecular mechanism of sulfur chemolithotrophy in the betaproteobacterium Pusillimonas ginsengisoli SBSA. Microbiology (United Kingdom), 2020, 166, 386-397.	0.7	10
2918	Genome Sequence of Serratia fonticola Strain S14, Isolated from the Mosquito Aedes triseriatus. Microbiology Resource Announcements, 2020, 9, .	0.3	1
2919	Metagenome-Assembled Genome Sequence of Sulfuricurvum sp. Strain IAE1, Isolated from a 4-Chlorophenol-Degrading Consortium. Microbiology Resource Announcements, 2019, 8, .	0.3	6
2920	Draft Genome Sequence of Raoultella ornithinolytica P079F W, Isolated from the Feces of a Preterm Infant. Microbiology Resource Announcements, 2019, 8, .	0.3	2
2921	Complete Genome Sequence of <i>Paenibacillus</i> sp. Strain E222, a Bacterial Symbiont of an <i>EpichloÃ«</i> Fungal Endophyte of Ryegrass. Microbiology Resource Announcements, 2020, 9, .	0.3	6
2922	Coastal Ocean Metagenomes and Curated Metagenome-Assembled Genomes from Marsh Landing, Sapelo Island (Georgia, USA). Microbiology Resource Announcements, 2019, 8, .	0.3	4
2923	Draft Genome Sequences of 11 Lactobacillus jensenii Strains Isolated from the Female Bladder. Microbiology Resource Announcements, 2019, 8, .	0.3	6
2924	Genome Sequence of <i>Mariprofundus</i> sp. Strain EBB-1, a Novel Marine Autotroph Isolated from an Iron-Sulfur Mineral. Microbiology Resource Announcements, 2019, 8, .	0.3	2
2925	Whole-Genome Sequence Analysis of Multidrug-Resistant Enterobacter hormaechei Isolated from Imported Retail Shrimp. Microbiology Resource Announcements, 2020, 9, .	0.3	4
2926	Complete Genome Sequence of Salmonella enterica subsp. <i>enterica</i> Serovar Kottbus Strain Kharkiv, Isolated from a Commercial Pork Production Facility in Ukraine. Microbiology Resource Announcements, 2020, 9, .	0.3	12
2927	Metagenome-Assembled Genome of USCÎ± AHI, a Potential High-Affinity Methanotroph from Axel Heiberg Island, Canadian High Arctic. Microbiology Resource Announcements, 2019, 8, .	0.3	8
2928	Draft Genome Sequences of Fructobacillus fructosus DPC 7238 and Leuconostoc mesenteroides DPC 7261, Mannitol-Producing Organisms Isolated from Fructose-Rich Honeybee-Resident Flowers on an Irish Farm. Microbiology Resource Announcements, 2020, 9, .	0.3	9

#	Article	IF	Citations
2929	Draft Genome Sequence of Acidianus ambivalens DSM 3772, an Aerobic Thermoacidophilic Sulfur Disproportionator. Microbiology Resource Announcements, 2020, 9, .	0.3	6
2930	Damage Repair versus Aging in an Individual-Based Model of Biofilms. MSystems, 2020, 5, .	1.7	5
2931	Theoretical and Simulation-Based Investigation of the Relationship between Sequencing Effort, Microbial Community Richness, and Diversity in Binning Metagenome-Assembled Genomes. MSystems, 2019, 4, .	1.7	5
2932	Discovery of Euryhaline Phycoerythrobilin-Containing Synechococcus and Its Mechanisms for Adaptation to Estuarine Environments. MSystems, 2020, 5, .	1.7	4
2933	Genomes of the â€œ <i>Candidatus</i> Actinomarinalesâ€•Order: Highly Streamlined Marine Epipelagic Actinobacteria. MSystems, 2020, 5, .	1.7	24
2934	Genome-wide association studies of Shigella spp. and Enteroinvasive Escherichia coli isolates demonstrate an absence of genetic markers for prediction of disease severity. BMC Genomics, 2020, 21, 138.	1.2	11
2935	Model-based and phylogenetically adjusted quantification of metabolic interaction between microbial species. PLoS Computational Biology, 2020, 16, e1007951.	1.5	11
2936	Asgard archaea are the closest prokaryotic relatives of eukaryotes. PLoS Genetics, 2018, 14, e1007080.	1.5	114
2937	Physiological and genomic features of a novel violacein-producing bacterium isolated from surface seawater. PLoS ONE, 2017, 12, e0179997.	1.1	21
2938	Arsenic exposure and intestinal microbiota in children from Sirajdikhan, Bangladesh. PLoS ONE, 2017, 12, e0188487.	1.1	41
2939	Gammaproteobacterial methanotrophs dominate methanotrophy in aerobic and anaerobic layers of boreal lake waters. Aquatic Microbial Ecology, 2018, 81, 257-276.	0.9	72
2940	Characterization of Burkholderia cepacia Complex Core Genome and the Underlying Recombination and Positive Selection. Frontiers in Genetics, 2020, 11, 506.	1.1	12
2941	Genomic Characterization of a Novel Gut Symbiont From the Hadal Snailfish. Frontiers in Microbiology, 2019, 10, 2978.	1.5	29
2942	Anti-Inflammatory, Antioxidant, and Wound-Healing Properties of Cyanobacteria from Thermal Mud of Balaruc-Les-Bains, France: A Multi-Approach Study. Biomolecules, 2021, 11, 28.	1.8	20
2943	Pan-Genome-Based Analysis as a Framework for Demarcating Two Closely Related Methanotroph Genera Methylocystis and Methylosinus. Microorganisms, 2020, 8, 768.	1.6	15
2944	Genomics and metagenomics technologies to recover ribosomal DNA and single-copy genes from old fruit-body and ectomycorrhiza specimens. MycoKeys, 0, 13, 1-20.	0.8	21
2945	Microfluidic-based mini-metagenomics enables discovery of novel microbial lineages from complex environmental samples. ELife, 2017, 6, .	2.8	69
2946	Emergence of trait variability through the lens of nitrogen assimilation in Prochlorococcus. ELife, 2019, 8, .	2.8	57

#	Article	IF	Citations
2947	Diverse deep-sea anglerfishes share a genetically reduced luminous symbiont that is acquired from the environment. ELife, 2019, 8, .	2.8	23
2948	Metage2Metabo, microbiota-scale metabolic complementarity for the identification of key species. ELife, 2020, 9, .	2.8	44
2949	Biases in genome reconstruction from metagenomic data. PeerJ, 2020, 8, e10119.	0.9	32
2950	MetaBAT, an efficient tool for accurately reconstructing single genomes from complex microbial communities. PeerJ, 2015, 3, e1165.	0.9	1,546
2951	Comparative genomics of non-pseudomonal bacterial species colonising paediatric cystic fibrosis patients. PeerJ, 2015, 3, e1223.	0.9	35
2952	Identifying contamination with advanced visualization and analysis practices: metagenomic approaches for eukaryotic genome assemblies. PeerJ, 2016, 4, e1839.	0.9	91
2953	Validation of picogram- and femtogram-input DNA libraries for microscale metagenomics. PeerJ, 2016, 4, e2486.	0.9	64
2954	Metagenomic identification of active methanogens and methanotrophs in serpentinite springs of the Voltri Massif, Italy. PeerJ, 2017, 5, e2945.	0.9	91
2955	Genomic comparisons of a bacterial lineage that inhabits both marine and terrestrial deep subsurface systems. PeerJ, 2017, 5, e3134.	0.9	50
2956	Short reads from honey bee (<i>Apis</i> sp.) sequencing projects reflect microbial associate diversity. PeerJ, 2017, 5, e3529.	0.9	13
2957	290 metagenome-assembled genomes from the Mediterranean Sea: a resource for marine microbiology. PeerJ, 2017, 5, e3558.	0.9	71
2958	Challenging a bioinformatic toolâ€™s ability to detect microbial contaminants using<i>in silico</i>whole genome sequencing data. PeerJ, 2017, 5, e3729.	0.9	8
2959	Benchmarking viromics: an <i>in silico</i> evaluation of metagenome-enabled estimates of viral community composition and diversity. PeerJ, 2017, 5, e3817.	0.9	235
2960	Gene and genome-centric analyses of koala and wombat fecal microbiomes point to metabolic specialization for digestion. PeerJ, 2017, 5, e4075.	0.9	24
2961	Metabolic marker gene mining provides insight in global<i>mcrA</i>diversity and, coupled with targeted genome reconstruction, sheds further light on metabolic potential of the<i>Methanomassiliicoccales</i>. PeerJ, 2018, 6, e5614.	0.9	34
2962	Phylogenomics picks out the par excellence markers for species phylogeny in the genus <i>Staphylococcus</i>. PeerJ, 2018, 6, e5839.	0.9	9
2963	Improved genome of<i>Agrobacterium radiobacter</i>type strain provides new taxonomic insight into<i>Agrobacterium</i>genomospecies 4. PeerJ, 2019, 7, e6366.	0.9	3
2964	Assessing alignment-based taxonomic classification of ancient microbial DNA. PeerJ, 2019, 7, e6594.	0.9	23

#	ARTICLE	IF	CITATIONS
2965	Optimizing <i>de novo</i> genome assembly from PCR-amplified metagenomes. PeerJ, 2019, 7, e6902.	0.9	28
2966	ConFindr: rapid detection of intraspecies and cross-species contamination in bacterial whole-genome sequence data. PeerJ, 2019, 7, e6995.	0.9	78
2967	MetaBAT 2: an adaptive binning algorithm for robust and efficient genome reconstruction from metagenome assemblies. PeerJ, 2019, 7, e7359.	0.9	1,704
2968	First genomic insights into members of a candidate bacterial phylum responsible for wastewater bulking. PeerJ, 2015, 3, e740.	0.9	157
2969	Whole genome sequencing of a novel, dichloromethane-fermenting<i>Peptococcaceae</i>from an enrichment culture. PeerJ, 2019, 7, e7775.	0.9	14
2970	Phylogenomic analysis of 589 metagenome-assembled genomes encompassing all major prokaryotic lineages from the gut of higher termites. PeerJ, 2020, 8, e8614.	0.9	43
2971	Probabilistic model based on circular statistics for quantifying coverage depth dynamics originating from DNA replication. PeerJ, 2020, 8, e8722.	0.9	4
2972	Evaluating Eucalyptus leaf colonization by Brasilonema octagenarum (Cyanobacteria,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 46	0.9	2
2973	Back from the dead; the curious tale of the predatory cyanobacterium<i>Vampirovibrio chlorellavorus</i>. PeerJ, 2015, 3, e968.	0.9	104
2974	Optimised biomolecular extraction for metagenomic analysis of microbial biofilms from high-mountain streams. PeerJ, 2020, 8, e9973.	0.9	18
2975	Draft Genome Sequences and Genomic Analysis for Pigment Production in Bacteria Isolated from Blue Discolored Soymilk and Tofu. Journal of Genomics, 2021, 9, 55-67.	0.6	2
2976	Metagenomic Analysis of the Microbial Community in the Underground Coal Fire Area (Kemerovo) Tj ETQq1 1 0.784314 rgBT /Overlock Aquificae, and Firmicutes. Microbiology, 2021, 90, 578-587.	0.5	5
2977	Functions predict horizontal gene transfer and the emergence of antibiotic resistance. Science Advances, 2021, 7, eabj5056.	4.7	44
2981	Phylogenomic Analysis Substantiates the gyrB Gene as a Powerful Molecular Marker to Efficiently Differentiate the Most Closely Related Genera Myxococcus, Corallococcus, and Pyxidicoccus. Frontiers in Microbiology, 2021, 12, 763359.	1.5	8
2982	Recovery of strain-resolved genomes from human microbiome through an integration framework of single-cell genomics and metagenomics. Microbiome, 2021, 9, 202.	4.9	23
2984	Complete Genome Sequence of the Marine-Derived Bacterium Streptomyces sp. Strain GMY02. Microbiology Resource Announcements, 2021, 10, e0068121.	0.3	1
2985	Pangenomic and functional investigations for dormancy and biodegradation features of an organic pollutant-degrading bacterium Rhodococcus biphenylivorans TG9. Science of the Total Environment, 2022, 809, 151141.	3.9	10
2986	Active virus-host interactions at sub-freezing temperatures in Arctic peat soil. Microbiome, 2021, 9, 208.	4.9	52

#	ARTICLE	IF	CITATIONS
2987	Bacteria-Oil Microaggregates Are an Important Mechanism for Hydrocarbon Degradation in the Marine Water Column. MSystems, 2021, 6, e0110521.	1.7	5
2988	Microbial population genomes from the Amazon River reveal possible modulation of the organic matter degradation process in tropical freshwaters. Molecular Ecology, 2022, 31, 206-219.	2.0	2
2990	Genomic Characterization of Endemic and Ecdemic Non-typhoidal Salmonella enterica Lineages Circulating Among Animals and Animal Products in South Africa. Frontiers in Microbiology, 2021, 12, 748611.	1.5	10
2991	Genome features and antibiotic resistance of Pseudomonas aeruginosa strains isolated in patients with cystic fibrosis in the Russian Federation. Klinichescheskaya Laboratornaya Diagnostika, 2021, 66, 629-634.	0.2	2
2992	High quality genome resource of mango bacterial black spot pathogen Xanthomonas citri pv. mangiferaeindicae GXG07 isolated from Guangxi, China. Plant Disease, 2021, , .	0.7	1
2993	Comprehensive Comparative Genomics and Phenotyping of Methylobacterium Species. Frontiers in Microbiology, 2021, 12, 740610.	1.5	20
2994	Diverse sediment microbiota shape methane emission temperature sensitivity in Arctic lakes. Nature Communications, 2021, 12, 5815.	5.8	15
2995	Genome sequencing of the NIES Cyanobacteria collection with a focus on the heterocyst-forming clade. DNA Research, 2021, 28, .	1.5	12
2997	Microbial chemolithotrophic oxidation of pyrite in a subsurface shale weathering environment: Geologic considerations and potential mechanisms. Geobiology, 2022, 20, 271-291.	1.1	4
2998	Annotating unknown species of urban microorganisms on a global scale unveils novel functional diversity and local environment association. Environmental Research, 2022, 207, 112183.	3.7	7
2999	Metagenomic Sequencing Reveals that High-Grain Feeding Alters the Composition and Metabolism of Cecal Microbiota and Induces Cecal Mucosal Injury in Sheep. MSystems, 2021, 6, e0091521.	1.7	13
3000	Citrobacter amalonaticus Inhibits the Growth of Citrobacter rodentium in the Gut Lumen. MBio, 2021, 12, e0241021.	1.8	9
3001	Metagenomic and Metatranscriptomic Characterization of a Microbial Community That Catalyzes Both Energy-Generating and Energy-Storing Electrode Reactions. Applied and Environmental Microbiology, 2021, 87, e0167621.	1.4	10
3002	Functional attractors in microbial community assembly. Cell Systems, 2022, 13, 29-42.e7.	2.9	59
3003	Sphingosinicella flava sp. nov., indole acetic acid producing bacteria isolated from maize field soil. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
3006	Luteimonas deserti sp. nov., a novel strain isolated from desert soil. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	7
3008	Pontibacter cellulosilyticus sp. nov., a carboxymethyl cellulose-hydrolysing bacterium isolated from coastal water. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	8
3009	Zobellia barbeyronii sp. nov., a New Member of the Family Flavobacteriaceae, Isolated from Seaweed, and Emended Description of the Species Z. amurskyensis, Z. laminariae, Z. russellii and Z. uliginosa. Diversity, 2021, 13, 520.	0.7	28

#	Article	IF	Citations
3010	Successional dynamics and alternative stable states in a saline activated sludge microbial community over 9Âyears. Microbiome, 2021, 9, 199.	4.9	33
3012	Methanogenesis and Salt Tolerance Genes of a Novel Halophilic Methanosarcinaceae Metagenome-Assembled Genome from a Former Solar Saltern. Genes, 2021, 12, 1609.	1.0	10
3013	Contamination in Reference Sequence Databases: Time for Divide-and-Rule Tactics. Frontiers in Microbiology, 2021, 12, 755101.	1.5	25
3014	Comparative Genome Analysis of the Genus Thiothrix Involving Three Novel Species, Thiothrix subterranea sp. nov. Ku-5, Thiothrix litoralis sp. nov. AS and â€œCandidatus Thiothrix anitrataâ€•sp. nov. A52, Revealed the Conservation of the Pathways of Dissimilatory Sulfur Metabolism and Variations in the Genetic Inventory for Nitrogen Metabolism and Autotrophic Carbon Fixation. Frontiers in Microbiology, 2021, 12, 760289.	1.5	22
3015	Exploring the Meta-regulon of the CRP/FNR Family of Global Transcriptional Regulators in a Partial-Nitritation Anammox Microbiome. MSystems, 2021, 6, e0090621.	1.7	3
3016	Comparative Genomics of Mycobacterium avium Complex Reveals Signatures of Environment-Specific Adaptation and Community Acquisition. MSystems, 2021, 6, e0119421.	1.7	7
3017	Genome Streamlining, Plasticity, and Metabolic Versatility Distinguish Co-occurring Toxic and Nontoxic Cyanobacterial Strains of <i>Microcoleus</i>. MBio, 2021, 12, e0223521.	1.8	11
3018	Draft genome and description of Waterburya agarophytonicola gen. nov. sp. nov. (Pleurocapsales,) Tj ETQq1 1 0.784314 rgBT /Overlo	0.7	5
3019	Undibacterium baiyunense sp. nov., Undibacterium curvum sp. nov., Undibacterium fentianense sp. nov., Undibacterium flavidum sp. nov., Undibacterium griseum sp. nov., Undibacterium hunanense sp. nov., Undibacterium luofuense sp. nov., Undibacterium nitidum sp. nov., Undibacterium rivi sp. nov., Undibacterium rugosum sp. nov. and Undibacterium umbellatum sp. nov., isolated from streams in China. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	34
3020	Unveiling metabolic characteristics of an uncultured Gammaproteobacterium responsible for <i>in situ</i>â€‰<scp>PAH</scp> biodegradation in petroleum polluted soil. Environmental Microbiology, 2021, 23, 7093-7104.	1.8	4
3021	Trichococcus shcherbakoviae subsp. psychrophilus subsp. nov., a psychrotolerant facultative anaerobe isolated from a cold spring. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	8
3023	Genome-Wide Association Study Reveals Genetic Markers for Antimicrobial Resistance in Mycoplasma bovis. Microbiology Spectrum, 2021, 9, e0026221.	1.2	21
3024	Western and non-western gut microbiomes reveal new roles of Prevotella in carbohydrate metabolism and mouthâ€“gut axis. Npj Biofilms and Microbiomes, 2021, 7, 77.	2.9	28
3026	Biological Mitigation of Antibiotic Resistance Gene Dissemination by Antioxidant-Producing Microorganisms in Activated Sludge Systems. Environmental Science & Technology, 2021, 55, 15831-15842.	4.6	24
3027	Genomic and transcriptomic dissection of Theionarchaea in marine ecosystem. Science China Life Sciences, 2021, , 1.	2.3	2
3028	Music of metagenomicsâ€”a review of its applications, analysis pipeline, and associated tools. Functional and Integrative Genomics, 2022, 22, 3-26.	1.4	3
3029	Phylogenomics of SAR116 Clade Reveals Two Subclades with Different Evolutionary Trajectories and an Important Role in the Ocean Sulfur Cycle. MSystems, 2021, 6, e0094421.	1.7	12
3030	The Bioinformatics Virtual Coordination Network: An Open-Source and Interactive Learning Environment. Frontiers in Education, 2021, 6, .	1.2	2

#	Article	IF	Citations
3032	Heterotrophic bacterial diazotrophs are more abundant than their cyanobacterial counterparts in metagenomes covering most of the sunlit ocean. ISME Journal, 2022, 16, 927-936.	4.4	41
3034	The Predatory Myxobacterium Citreicoccus inhibens gen. nov. sp. nov. Showed Antifungal Activity and Bacteriolytic Property against Phytopathogens. Microorganisms, 2021, 9, 2137.	1.6	18
3035	Monitoring the Microevolution of Salmonella enterica in Healthy Dairy Cattle Populations at the Individual Farm Level Using Whole-Genome Sequencing. Frontiers in Microbiology, 2021, 12, 763669.	1.5	10
3036	Biogeographical distributions of nitrogenâ€cycling functional genes in a subtropical estuary. Functional Ecology, 2022, 36, 187-201.	1.7	23
3037	Metagenome-Assembled Genomes from Monte Cristo Cave (Diamantina, Brazil) Reveal Prokaryotic Lineages As Functional Models for Life on Mars. Astrobiology, 2021, , .	1.5	4
3038	WGA-LP: a pipeline for whole genome assembly of contaminated reads. Bioinformatics, 2022, 38, 846-848.	1.8	1
3041	Phytoplankton exudates and lysates support distinct microbial consortia with specialized metabolic and ecophysiological traits. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	37
3044	Wood-Ljungdahl pathway utilisation during in situ H2 biomethanation. Science of the Total Environment, 2022, 806, 151254.	3.9	11
3045	Charting the complexity of the activated sludge microbiome through a hybrid sequencing strategy. Microbiome, 2021, 9, 205.	4.9	29
3046	Microbial ecology of sulfur cycling near the sulfateâ€"methane transition of deepâ€sea cold seep sediments. Environmental Microbiology, 2021, 23, 6844-6858.	1.8	31
3047	Adjunctive Probiotics Alleviates Asthmatic Symptoms via Modulating the Gut Microbiome and Serum Metabolome. Microbiology Spectrum, 2021, 9, e0085921.	1.2	63
3048	Shedding Light on Microbial â€œDark Matterâ€: Insights Into Novel Cloacimonadota and Omnitrophota From an Antarctic Lake. Frontiers in Microbiology, 2021, 12, 741077.	1.5	20
3049	Pontibacter flavimaris sp. nov., of the family Hymenobacteraceae, isolated from marine sediment. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	4
3050	Luteirhabdus pelagi gen. nov., sp. nov., a novel member of the family Flavobacteriaceae, isolated from the West Pacific Ocean. Archives of Microbiology, 2021, 203, 6021-6031.	1.0	6
3051	Antimicrobial resistance and virulence in Helicobacter pylori: Genomic insights. Genomics, 2021, 113, 3951-3966.	1.3	11
3052	Deep phylo-taxono genomics reveals Xylella as a variant lineage of plant associated Xanthomonas and supports their taxonomic reunification along with Stenotrophomonas and Pseudoxanthomonas. Genomics, 2021, 113, 3989-4003.	1.3	17
3053	Activities and metabolic versatility of distinct anammox bacteria in a full-scale wastewater treatment system. Water Research, 2021, 206, 117763.	5.3	42
3054	A case study on the distribution of the environmental resistome in Korean shrimp farms. Ecotoxicology and Environmental Safety, 2021, 227, 112858.	2.9	7

#	ARTICLE	IF	CITATIONS
3055	Genome-resolved metagenomics reveals how soil bacterial communities respond to elevated H2 availability. Soil Biology and Biochemistry, 2021, 163, 108464.	4.2	12
3056	Shedding light on the functional role of the Ignavibacteria in Italian rice field soil: A meta-genomic/transcriptomic analysis. Soil Biology and Biochemistry, 2021, 163, 108444.	4.2	12
3071	Streptococcus azizii sp. nov., isolated from naÃ¯ve weanling mice. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 5032-5037.	0.8	5
3087	Amylibacter lutimaris sp. nov., isolated from sea-tidal flat sediment. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2088-2092.	0.8	5
3103	Aerobic Hydrocarbon-Degrading Gammaproteobacteria: Oleiphilaceae and Relatives. , 2019, , 1-14.		0
3108	Alginatibacterium sediminis gen. nov., sp. nov., a novel marine gammaproteobacterium isolated from coastal sediment. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 511-516.	0.8	8
3120	Stenotrophobium rhamnosiphilum gen. nov., sp. nov., isolated from a glacier, proposal of Steroidobacteraceae fam. nov. in Nevskiales and emended description of the family Nevskiaceae. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1404-1410.	0.8	26
3124	Marortus luteolus gen. nov., sp. nov., isolated from surface seawater of the East Sea in China. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1490-1495.	0.8	8
3125	Tsuneonella suprasediminis sp. nov., isolated from the Pacific Ocean. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	16
3126	Grimontia sedimenti sp. nov., isolated from benthic sediments near coral reefs south of Kuwait. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	8
3129	Idiomarina mangrovi sp. nov., isolated from rhizosphere soil of a mangrove Avicennia marina forest. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1662-1668.	0.8	10
3132	Spirosoma utsteinense sp. nov. isolated from Antarctic ice-free soils from the Utsteinen region, East Antarctica. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	6
3133	Arenibacter amylolyticus sp. nov., an amylase-producing bacterium of the family Flavobacteriaceae isolated from marine water in India. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	5
3134	Characterization of novel Gluconobacter species from fruits and fermented food products: Gluconobacter cadivus sp. nov., Gluconobacter vitians sp. nov. and Gluconobacter potus sp. nov. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	20
3135	Proposal of Enterococcus xinjiangensis Ren et al. 2020 as a later heterotypic synonym of Enterococcus lactis Morandi et al. 2012. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	7
3142	Draft Genome Sequences of Four Lactococcus lactis Strains Isolated from Diverse Niches, Including Dairy Products, Grass, and Green Peas. Microbiology Resource Announcements, 2019, 8, .	0.3	1
3143	Genome Sequence of a Novel Enterococcus faecalis Sequence Type 922 Strain Isolated from a Door Handle in the Intensive Care Unit of a District Hospital in Durban, South Africa. Microbiology Resource Announcements, 2019, 8, .	0.3	2
3146	Whole-Genome Sequence of the Ammonia-Oxidizing Bacterium Nitrosomonas stercoris Type Strain KYUHI-S, Isolated from Composted Cattle Manure. Microbiology Resource Announcements, 2019, 8, .	0.3	1

#	Article	IF	Citations
3152	Revealing the Draft Genome Sequence of <i>Bradyrhizobium</i> sp. Strain USDA 3458, an Effective Symbiotic Diazotroph Isolated from Cowpea (<i>Vigna unguiculata</i>) Genotype IT82E-16. Microbiology Resource Announcements, 2019, 8, .	0.3	1
3157	Draft Genome Sequence of <i>Brevibacillus</i> sp. Strain LEMMJ03, Isolated from an Antarctic Volcano. Microbiology Resource Announcements, 2019, 8, .	0.3	0
3159	Draft Genome Sequences of Three Filamentous Cyanobacterial Strains, Dolichospermum planctonicum NIES-80, Planktothrix agardhii NIES-905, and Sphaerospermopsis reniformis NIES-1949. Microbiology Resource Announcements, 2019, 8, .	0.3	0
3161	Draft Genome Sequence of Geobacillus sp. Strain LEMMJ02, a Thermophile Isolated from Deception Island, an Active Volcano in Antarctica. Microbiology Resource Announcements, 2019, 8, .	0.3	1
3162	Pleionea sediminis sp. nov., isolated from coastal sediment and emendation of the description of the genus Pleionea. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3524-3528.	0.8	8
3168	Pleomorphovibrio marinus gen. nov., sp. nov., isolated from deep-sea sediment. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3723-3727.	0.8	7
3170	OBSOLETE: NexGen Sequencing Data: Bioinformatic Tools for Visualization and Analysis. , 2020, , .		0
3171	Lumen and mucosa-associated<i>Lactobacillus rhamnosus</i>from the intestinal tract of organ donors. Gut Microbiome, 2020, 1, .	0.8	1
3181	Draft Genome Sequences of Four Microcystis aeruginosa Strains (NIES-3787, NIES-3804, NIES-3806, and) Tj ETQq0 0 0 rgBT /Overlock 1	0.3	1
3184	Exilibacterium tricleocarpae gen. nov., sp. nov., a marine bacterium from coralline algae Tricleocarpa sp.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3427-3432.	0.8	10
3187	Pusillimonas maritima sp. nov., isolated from surface seawater. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3483-3490.	0.8	23
3191	Marinobacter changyiensis, sp. nov., isolated from offshore sediment. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3004-3011.	0.8	7
3192	Draft Genome Sequence of Blautia luti DSM 14534 ^T , Isolated from Human Stool. Microbiology Resource Announcements, 2020, 9, .	0.3	1
3200	Sunxiuqinia indica sp. nov., isolated from deep sea. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4186-4192.	0.8	7
3201	Prevotella vespertina sp. nov., isolated from an abscess of a hospital patient. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4576-4582.	0.8	9
3205	Draft Genome Sequence of 2-Methylpyridine-, 2-Ethylpyridine-, and 2-Hydroxypyridine-Degrading Arthrobacter sp. Strain ATCC 49987. Microbiology Resource Announcements, 2020, 9, .	0.3	0
3206	Isachenkonia alkalipeptolytica gen. nov. sp. nov., a new anaerobic, alkaliphilic proteolytic bacterium capable of reducing Fe(III) and sulfur. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4730-4738.	0.8	10
3210	Draft Genome Sequence of a New <i>Methanobacterium</i> Strain Potentially Resistant to Bile Salts, Isolated from Deer Feces. Microbiology Resource Announcements, 2020, 9, .	0.3	0

#	ARTICLE	IF	CITATIONS
3211	High-Quality Draft Single-Cell Genome Sequences of Two <i>Gammaproteobacteria</i> Strains Sampled from Soil in a Strawberry Farm. Microbiology Resource Announcements, 2020, 9, .	0.3	2
3218	MinION sequencing from sea ice cryoconites leads to de novo genome reconstruction from metagenomes. Scientific Reports, 2021, 11, 21041.	1.6	9
3219	Establishment of a Publicly Available Core Genome Multilocus Sequence Typing Scheme for Clostridium perfringens. Microbiology Spectrum, 2021, 9, e0053321.	1.2	5
3220	Genome-centric metagenomics reveals insights into the evolution and metabolism of a new free-living group in Rhizobiales. BMC Microbiology, 2021, 21, 294.	1.3	5
3221	Patterns in the Microbial Community of Salt-Tolerant Plants and the Functional Genes Associated with Salt Stress Alleviation. Microbiology Spectrum, 2021, 9, e0076721.	1.2	27
3222	Artificial intelligence reveals roles of gut microbiota in driving human colorectal cancer evolution. Artificial Intelligence in Cancer, 2021, 2, 69-78.	1.1	1
3223	Prokaryotic Genome Annotation. Methods in Molecular Biology, 2022, 2349, 193-214.	0.4	2
3225	Metagenomic Investigation of a Low Diversity, High Salinity Offshore Oil Reservoir. Microorganisms, 2021, 9, 2266.	1.6	7
3226	Contiguous Genome Sequence of Frankia sp. Strain ArI3, Isolated from Root Nodules of Alnus rubra Bong. Microbiology Resource Announcements, 2021, 10, e0080021.	0.3	0
3227	Complete Genome Analysis of Undecylprodigiosin Pigment Biosynthesizing Marine Streptomyces Species Displaying Potential Bioactive Applications. Microorganisms, 2021, 9, 2249.	1.6	5
3228	ORPER: A Workflow for Constrained SSU rRNA Phylogenies. Genes, 2021, 12, 1741.	1.0	2
3231	Characterization of Komagataeibacter Isolate Reveals New Prospects in Waste Stream Valorization for Bacterial Cellulose Production. Microorganisms, 2021, 9, 2230.	1.6	2
3232	Metagenomic Analysis of Biocide-Treated Neotropical Oil Reservoir Water Unveils Microdiversity of Thermophile Tepidiphilus. Frontiers in Microbiology, 2021, 12, 741555.	1.5	4
3233	Top-Down Enrichment Strategy to Co-cultivate Lactic Acid and Lignocellulolytic Bacteria From the Megathyrsus maximus Phyllosphere. Frontiers in Microbiology, 2021, 12, 744075.	1.5	8
3234	Pseudomonas xionganensis sp. nov., isolated from Baiyangdian Lake in Xiong'an New Area. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6052-6059.	0.8	5
3235	Complete Genome Sequence of Marinobacterium sp. Strain LSUCC0821, Isolated from the Coastal Gulf of Mexico. Microbiology Resource Announcements, 2020, 9, .	0.3	1
3236	Draft Genome Sequence of a Filamentous Anoxygenic Phototrophic Bacterium, â€œ <i>Candidatus</i> Roseilinea sp. Strain NK_OTU-006,â€•Recovered from Metagenomic Data of a Hot Spring Microbial Mat. Microbiology Resource Announcements, 2020, 9, .	0.3	2
3239	Traditional Human Populations and Nonhuman Primates Show Parallel Gut Microbiome Adaptations to Analogous Ecological Conditions. MSystems, 2020, 5, .	1.7	13

#	Article	IF	Citations
3240	Metagenome-Assembled Genome Sequence of Dolichospermum circinale Strain Clear-D4, Assembled from a Harmful Cyanobacterial Bloom Enrichment Culture. Microbiology Resource Announcements, 2020, 9, .	0.3	2
3241	Expansion of the â€œSodium Worldâ€•through Evolutionary Time and Taxonomic Space. Biochemistry (Moscow), 2020, 85, 1518-1542.	0.7	4
3244	Metagenome-Assembled Genome Sequence of <i>Vulcanococcus</i> sp. Strain Clear-D1, Assembled from a Cyanobacterial Enrichment Culture. Microbiology Resource Announcements, 2020, 9, .	0.3	0
3246	Draft Genome Sequence of a Terrestrial Planctomycete, <i>Singulisphaera</i> sp. Strain GP187, Isolated from Forest Soil. Microbiology Resource Announcements, 2020, 9, .	0.3	2
3247	Draft Genome Sequence of Lactobacillus rhamnosus NCB 441, Isolated from Egyptian White Domiati Cheese. Microbiology Resource Announcements, 2020, 9, .	0.3	0
3248	New Insights into the Ecology and Physiology of Methanomassiliicoccales from Terrestrial and Aquatic Environments. Microorganisms, 2021, 9, 30.	1.6	23
3251	Metagenome-Assembled Genome Sequence of Rhodobacteraceae Bacterium Strain Clear-D3, Assembled from a Dolichospermum Consortium from Clear Lake, California. Microbiology Resource Announcements, 2020, 9, .	0.3	1
3253	ÐÐºÑÐ¿Ð°Ð½ÑÐ¸Ñ•Â«ÐÐ°Ñ‚Ñ€Ð¸ÐµÐ²Ð¾Ð³Ð¾ Ð¼Ð¸Ñ€Ð°Â» ÑÐºÐ²Ð¾Ð·ÑŒ ÑÐ²Ð¾Ð»ÑŽÑ†Ð¸Ð¾Ð½Ð½Ð¾Ðµ Ð²Ñ€ÐµÐ¼Ñ		
3254	Metagenome-Assembled Genome Sequence of Kapabacteriales Bacterium Strain Clear-D13, Assembled from a Harmful Algal Bloom Enrichment Culture. Microbiology Resource Announcements, 2020, 9, .	0.3	2
3255	Draft Genome Sequence of a Novel Methylobacterium brachiatum Strain Isolated from Human Skin. Microbiology Resource Announcements, 2020, 9, .	0.3	0
3256	Evaluating Selective Pressures Driving Clades Differentiation of the <i>Faecalibacterium prausnitzii</i> Complex. SSRN Electronic Journal, 0, , .	0.4	0
3257	Comparative genomics and proposal of Streptomyces radicis sp. nov., an endophytic actinomycete from roots of plants in Thailand. Microbiological Research, 2022, 254, 126889.	2.5	2
3258	Extracellular hydrolytic potential drives microbiome shifts during anaerobic co-digestion of sewage sludge and food waste. Bioresource Technology, 2022, 343, 126102.	4.8	13
3259	Carbon sources driven supernatant micro-particles differentiate in submerged anaerobic membrane bioreactors (AnMBRs). Chemical Engineering Journal, 2022, 430, 133020.	6.6	10
3260	Towards understanding microbial degradation of chloroquine in large saltwater systems. Science of the Total Environment, 2022, 807, 150532.	3.9	4
3261	Nocardioides guangzhouensis sp. nov., an actinobacterium isolated from soil. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 112-119.	0.8	8
3263	Mini-review: Advances of metagenomics research for lake microbiomes. Hupo Kexue/Journal of Lake Sciences, 2020, 32, 271-280.	0.3	0
3264	Computational Metagenomics: State-of-the-Art, Facts and Artifacts. , 2020, , 199-227.		0

#	ARTICLE	IF	CITATIONS
3268	On Clustering Validation in Metagenomics Sequence Binning. Lecture Notes in Computer Science, 2020, , 3-15.	1.0	0
3269	<i>Candidatus</i> Anthektikosiphon siderophilum OHK22, a New Member of the Chloroflexi Family Herpetosiphonaceae from Oku-okuhachikurou Onsen. Microbes and Environments, 2020, 35, n/a.	0.7	12
3270	Maribacter algicola sp. nov., isolated from a marine red alga, Porphyridium marinum, and transfer of Maripseudobacter aurantiacus Chen et al. 2017 to the genus Maribacter as Maribacter aurantiacus comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 797-804.	0.8	15
3276	Dyadobacter flavalbus sp. nov., isolated from lake sediment. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1064-1070.	0.8	11
3277	Flavicella sediminum sp. nov., isolated from marine sediment. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 868-873.	0.8	4
3278	Hydrogeniiclostidium mannosilyticum gen. nov., sp. nov. isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1210-1216.	0.8	14
3280	Single-cell genomics of environmental bacteria-Development of microfluidic droplet-based whole genome sequencing method and its application to environmental samples. Japanese Journal of Lactic Acid Bacteria, 2020, 31, 17-24.	0.1	0
3281	Nesterenkonia muleiensis sp. nov., a novel actinobacterium isolated from sap of Populus euphratica. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1888-1894.	0.8	5
3285	Vulcaniibacterium gelatinicum sp. nov., a moderately thermophilic bacterium isolated from a hot spring. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1571-1577.	0.8	5
3288	Formosa sediminum sp. nov., a starch-degrading bacterium isolated from marine sediment. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2008-2015.	0.8	4
3290	Metagenomic sequencing of clinical samples reveals a single widespread clone of Lawsonia intracellularis responsible for porcine proliferative enteropathy. Microbial Genomics, 2020, 6, .	1.0	2
3291	Genome Sequence of the Fish Brain Bacterium Clostridium tarantellae. Microbiology Resource Announcements, 2020, 9, .	0.3	0
3292	Antarcticibacterium arcticum sp. nov., a bacterium isolated from marine sediment of the Canadian Beaufort Sea. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2912-2917.	0.8	4
3296	Nitrogeniibacter aestuarii sp. nov., a Novel Nitrogen-Fixing Bacterium Affiliated to the Family Zoogloeaceae and Phylogeny of the Family Zoogloeaceae Revisited. Frontiers in Microbiology, 2021, 12, 755908.	1.5	40
3297	Genomic Insights Into the Archaea Inhabiting an Australian Radioactive Legacy Site. Frontiers in Microbiology, 2021, 12, 732575.	1.5	5
3298	Unveiling the occurrence, hosts and mobility potential of antibiotic resistance genes in the deep ocean. Science of the Total Environment, 2022, 816, 151539.	3.9	14
3299	Complete Genome Sequence of Bacillus velezensis GMEKP1, Isolated from a Natural Bamboo Hive of Stingless Bees. Microbiology Resource Announcements, 2021, 10, e0065921.	0.3	0
3300	Genomic Insights Into New Species of the Genus Halomicroarcula Reveals Potential for New Osmoadaptative Strategies in Halophilic Archaea. Frontiers in Microbiology, 2021, 12, 751746.	1.5	18

#	ARTICLE	IF	CITATIONS
3301	Enhanced primary treatment for net energy production from sewage â€“ The genetic clarification of substrate-acetate-methane pathway in anaerobic digestion. Chemical Engineering Journal, 2022, 431, 133416.	6.6	28
3303	Down in the pond: Isolation and characterization of a new Serratia marcescens strain (LVF3) from the surface water near frogâ€™s lettuce (Groenlandia densa). PLoS ONE, 2021, 16, e0259673.	1.1	8
3305	Cultivation of a vampire: â€˜<i>Candidatus</i> Absconditicoccus praedatorâ€™. Environmental Microbiology, 2022, 24, 30-49.	1.8	30
3307	Evaluating <i>de Novo</i> Assembly and Binning Strategies for Time Series Drinking Water Metagenomes. Microbiology Spectrum, 2021, 9, e0143421.	1.2	16
3308	Multiple energy sources and metabolic strategies sustain microbial diversity in Antarctic desert soils. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	68
3310	Desulfomarina profundi gen. nov., sp. nov., a novel mesophilic, hydrogen-oxidizing, sulphate-reducing chemolithoautotroph isolated from a deep-sea hydrothermal vent chimney. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	11
3311	Metagenome-assembled genomes: concepts, analogies, and challenges. Biophysical Reviews, 2021, 13, 905-909.	1.5	17
3312	Draft Genome Sequence of <i>Schaalia odontolytica</i> Strain ORNL0103, a Basibiont of â€œ <i>Candidatus</i> Saccharibacteriaâ€•HMT352. Microbiology Resource Announcements, 2021, 10, e0079321.	0.3	2
3313	Draft Genome Sequences of the Ferric Iron-Reducing Geobacter sp. Strains AOG1 and AOG2, Isolated from Enrichment Cultures on Crystalline Iron(III) Oxides. Microbiology Resource Announcements, 2021, 10, e0091321.	0.3	0
3314	Draft Genome Sequence of the Bacterium Delftia acidovorans Strain D4B, Isolated from Soil. Microbiology Resource Announcements, 2021, 10, e0063521.	0.3	3
3315	Terrestrial-type nitrogen-fixing symbiosis between seagrass and a marine bacterium. Nature, 2021, 600, 105-109.	13.7	48
3316	Proteome and strain analysis of cyanobacterium Candidatus â€œPhormidium alkaliphilumâ€•reveals traits for success in biotechnology. IScience, 2021, 24, 103405.	1.9	13
3317	Metagenome-Assembled Genomes recovered from the datasets of a high-altitude Himalayan hot spring Khirganga, Himachal Pradesh, India. Data in Brief, 2021, 39, 107551.	0.5	3
3319	Halomonas salipaludis sp. nov., isolated from a saline-alkali wetland soil. Archives of Microbiology, 2021, 203, 6033-6039.	1.0	2
3320	Clostridium zeae sp. nov., isolated from corn silage. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
3321	Genomic analysis of a rare recurrent Listeria monocytogenes prosthetic joint infection indicates a protected niche within biofilm on prosthetic materials. Scientific Reports, 2021, 11, 21864.	1.6	7
3323	The rumen microbiome inhibits methane formation through dietary choline supplementation. Scientific Reports, 2021, 11, 21761.	1.6	3
3324	Bakta: rapid and standardized annotation of bacterial genomes via alignment-free sequence identification. Microbial Genomics, 2021, 7, .	1.0	168

#	Article	IF	Citations
3325	Universal activity-based labeling method for ammonia- and alkane-oxidizing bacteria. ISME Journal, 2022, 16, 958-971.	4.4	12
3326	Evidence for Long-Term Anthropogenic Pollution: The Hadal Trench as a Depository and Indicator for Dissemination of Antibiotic Resistance Genes. Environmental Science & Technology, 2021, 55, 15136-15148.	4.6	41
3327	Strain-level analysis reveals the vertical microbial transmission during the life cycle of bumblebee. Microbiome, 2021, 9, 216.	4.9	26
3329	Polaribacter septentrionalilitoris sp. nov., isolated from the biofilm of a stone from the North Sea. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4305-4314.	0.8	7
3336	Nitrincola iocasae sp. nov., a bacterium isolated from sediment collected at a cold seep field in the South China Sea. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4897-4902.	0.8	7
3337	Isolation and sequence-based characterization of a koala symbiont: <i>Lonepinella koalarum</i>. PeerJ, 2020, 8, e10177.	0.9	5
3343	Draft Genome Sequence of Escherichia coli Strain Tj, Isolated from the Varzob River in Tajikistan. Microbiology Resource Announcements, 2020, 9, .	0.3	1
3344	Ketobacter nezhaii sp. nov., a marine bacterium isolated from coastal sediment. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4960-4965.	0.8	5
3345	Brevibacterium rongguiense sp. nov., isolated from freshwater sediment. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5205-5210.	0.8	7
3346	Paucihalobacter ruber gen. nov., sp. nov., isolated from a haloalkaline lake sediment sample. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5373-5381.	0.8	7
3347	Proposal of Bifidobacterium saeculare Biavati et al. 1992 as a later heterotypic synonym of Bifidobacterium gallinarum Watabe et al. 1983 and Bifidobacterium gallinarum subsp. saeculare subsp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5964-5968.	0.8	10
3348	Agromyces kandeliae sp. nov., isolated from rhizosphere soil of Kandelia candel in a mangrove. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5861-5867.	0.8	5
3352	DATMA: Distributed AuTomatic Metagenomic Assembly and annotation framework. PeerJ, 2020, 8, e9762.	0.9	2
3364	Draft Whole-Genome Sequence of the Alkane-Synthesizing Polar Cyanobacterium Pseudanabaena biceps Strain O-153. Microbiology Resource Announcements, 2020, 9, .	0.3	0
3365	Genome Sequence of Eubacterium callanderi AMC0717, Isolated from the Colonic Mucosa of an 11-Year-Old Organ Donor. Microbiology Resource Announcements, 2020, 9, .	0.3	0
3366	Feces Metagenomes and Metagenome-Assembled Genome Sequences from Two Separate Dogs (Canis) Tj ETQq1 1 0.784314 rgBT /Ove	0.3	2
3367	Draft Genome Sequences of Four Bacterial Species as Part of an Experiential Microbiology Project at SUNY Geneseo. Microbiology Resource Announcements, 2020, 9, .	0.3	0
3368	Draft Genome Sequence of the Toxic Freshwater Microcystis aeruginosa Strain PMC 728.11 (Cyanobacteria, Chroococcales). Microbiology Resource Announcements, 2020, 9, .	0.3	5

#	ARTICLE	IF	CITATIONS
3369	Complete Genome Sequence of Microbacterium sp. Strain Nx66, Isolated from Waters Contaminated with Petrochemicals in El Saf-Saf Valley, Algeria. Microbiology Resource Announcements, 2020, 9, .	0.3	1
3370	Draft Genome Sequence of Halomonas titanicae Strain TAT1, a Hydrocarbon-Oxidizing Halophilic Bacterium Isolated from a Petroleum Reservoir in Russia. Microbiology Resource Announcements, 2020, 9, .	0.3	3
3371	Investigating hospital Mycobacterium chelonae infection using whole genome sequencing and hybrid assembly. PLoS ONE, 2020, 15, e0236533.	1.1	5
3373	Molecular characterization and improved diagnostics of strains isolated over the last two decades at a German tertiary care center. EXCLI Journal, 2021, 20, 851-862.	0.5	1
3374	Taxonomic and functional characterization of the rumen microbiome of Japanese Black cattle revealed by 16S rRNA gene amplicon and metagenome shotgun sequencing. FEMS Microbiology Ecology, 2021, 97, .	1.3	9
3375	Genome-resolved metagenomics provides insights into the functional complexity of microbial mats in Blue Holes, Shark Bay. FEMS Microbiology Ecology, 2022, 98, .	1.3	10
3376	Metagenomics: the boon for microbial world knowledge and current challenges. , 2022, , 159-175.		4
3377	Genomic diversity and distribution of Mesorhizobium nodulating chickpea (Cicer arietinum L.) from low pH soils of Ethiopia. Systematic and Applied Microbiology, 2022, 45, 126279.	1.2	6
3378	Metagenomics approach for Polymyxa betae genome assembly enables comparative analysis towards deciphering the intracellular parasitic lifestyle of the plasmodiophorids. Genomics, 2022, 114, 9-22.	1.3	4
3379	Culture Enrichment Combined With Long-Read Sequencing Facilitates Genomic Understanding of Hadal Sediment Microbes. Frontiers in Marine Science, 2021, 8, .	1.2	5
3380	A machine learning-based typing scheme refinement for Listeria monocytogenes core genome multilocus sequence typing with high discriminatory power for common source outbreak tracking. PLoS ONE, 2021, 16, e0260293.	1.1	0
3381	Genome Sequence of Lacticaseibacillus rhamnosus Strain NCDC610, Isolated from a Traditional Cereal-Based Fermented Milk Product (Raabadi). Microbiology Resource Announcements, 2021, 10, e0067221.	0.3	1
3382	Genome In Silico and In Vitro Analysis of the Probiotic Properties of a Bacterial Endophyte, Bacillus Paranthracis Strain MHSD3. Frontiers in Genetics, 2021, 12, 672149.	1.1	14
3383	RFPlasmid: predicting plasmid sequences from short-read assembly data using machine learning. Microbial Genomics, 2021, 7, .	1.0	31
3384	PangenomeNet: a pan-genome-based network reveals functional modules on antimicrobial resistome for Escherichia coli strains. BMC Bioinformatics, 2021, 22, 548.	1.2	7
3385	Ancient DNA diffuses from human bones to cave stones. IScience, 2021, 24, 103397.	1.9	5
3387	Circadian dynamics of the teleost skin immune-microbiome interface. Microbiome, 2021, 9, 222.	4.9	20
3388	Complete Genome Sequences of Four Soil-Derived Isolates for Studying Synthetic Bacterial Community Assembly. Microbiology Resource Announcements, 2021, 10, e0084821.	0.3	6

#	Article	IF	Citations
3389	Transcriptional responses of <i>Trichodesmium</i> to natural inverse gradients of Fe and P availability. ISME Journal, 2022, 16, 1055-1064.	4.4	18
3390	Metagenomics Analysis to Investigate the Microbial Communities and Their Functional Profile During Cyanobacterial Blooms in Lake Varese. Microbial Ecology, 2022, 83, 850-868.	1.4	15
3391	Genomic features of Mycobacterium avium subsp. hominissuis isolated from pigs inÂJapan. GigaByte, 0, 2021, 1-12.	0.0	3
3392	The highly diverse Antarctic Peninsula soil microbiota as a source of novel resistance genes. Science of the Total Environment, 2022, 810, 152003.	3.9	18
3393	Unveiling Ecological and Genetic Novelty within Lytic and Lysogenic Viral Communities of Hot Spring Phototrophic Microbial Mats. Microbiology Spectrum, 2021, , e0069421.	1.2	4
3394	Exploring bacterial diversity via a curated and searchable snapshot of archived DNA sequences. PLoS Biology, 2021, 19, e3001421.	2.6	60
3395	Transcriptomic evidence for versatile metabolic activities of mercury cycling microorganisms in brackish microbial mats. Npj Biofilms and Microbiomes, 2021, 7, 83.	2.9	25
3396	Halobacillus fulvus sp. nov., a moderately halophilic bacterium isolated from shrimp paste (Ka-pi) in Thailand. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
3397	Microbacterium paulum sp. nov., isolated from microfiltered milk. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	10
3398	Current understanding and perspectives in anaerobic digestion based on genome-resolved metagenomic approaches. Bioresource Technology, 2022, 344, 126350.	4.8	23
3399	Complete Genome Sequencing of a Novel<i>Gloeobacter</i>Species from a Waterfall Cave in Mexico. Genome Biology and Evolution, 2021, 13, .	1.1	9
3400	Microbial traits determine soil C emission in response to fresh carbon inputs in forests across biomes. Global Change Biology, 2022, 28, 1516-1528.	4.2	37
3401	Whole genome sequencing and <i>de novo</i> assembly of <i>Staphylococcus pseudintermedius</i>: a pangenome approach to unravelling pathogenesis of canine pyoderma. Veterinary Dermatology, 2021, 32, 654-663.	0.4	7
3402	A high-quality fungal genome assembly resolved from a sample accidentally contaminated by multiple taxa. BioTechniques, 2022, 72, 39-50.	0.8	4
3403	Devosia rhizoryzae sp. nov., and Devosia oryziradicis sp. nov., novel plant growth promoting members of the genus Devosia, isolated from the rhizosphere of rice plants. Journal of Microbiology, 2022, 60, 1-10.	1.3	33
3405	Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. Nature Microbiology, 2021, 6, 1561-1574.	5.9	57
3406	A primer and discussion on DNA-based microbiome data and related bioinformatics analyses. , 0, 1, .		6
3407	Commensal Bifidobacterium Strains Enhance the Efficacy of Neo-Epitope Based Cancer Vaccines. Vaccines, 2021, 9, 1356.	2.1	10

#	Article	IF	Citations
3408	Pan-genome analysis identifies intersecting roles for Pseudomonas specialized metabolites in potato pathogen inhibition. ELife, 2021, 10, .	2.8	25
3411	A review of the resistome within the digestive tract of livestock. Journal of Animal Science and Biotechnology, 2021, 12, 121.	2.1	17
3413	Undervalued Pseudo- <i>nifH</i> Sequences in Public Databases Distort Metagenomic Insights into Biological Nitrogen Fixers. MSphere, 2021, 6, e0078521.	1.3	17
3414	Leave no stone unturned: individually adapted xerotolerant Thaumarchaeota sheltered below the boulders of the Atacama Desert hyperarid core. Microbiome, 2021, 9, 234.	4.9	18
3415	Microbial Community Dynamics during Biodegradation of Crude Oil and Its Response to Biostimulation in Svalbard Seawater at Low Temperature. Microorganisms, 2021, 9, 2425.	1.6	13
3416	Genome-centric metagenomics provides new insights into the microbial community and metabolic potential of landfill leachate microbiota. Science of the Total Environment, 2022, 816, 151635.	3.9	7
3417	Metagenome-assembled genomes and gene catalog from the chicken gut microbiome aid in deciphering antibiotic resistomes. Communications Biology, 2021, 4, 1305.	2.0	49
3418	Pangenome inventory of Burkholderia sensu lato, Burkholderia sensu stricto, and the Burkholderia cepacia complex reveals the uniqueness of Burkholderia catarinensis. Genomics, 2022, 114, 398-408.	1.3	13
3419	Complete Genome Sequence of <i>Halomonas</i> sp. Strain FeN2, a Novel Cathode-Oxidizing Bacterium Isolated from Catalina Harbor Sediments. Microbiology Resource Announcements, 2021, 10, e0086221.	0.3	0
3420	Novel Insights into Dimethylsulfoniopropionate Catabolism by Cultivable Bacteria in the Arctic Kongsfjorden. Applied and Environmental Microbiology, 2021, , AEM0180621.	1.4	3
3421	Comparative Genomic and Pan-Genomic Characterization of Staphylococcus epidermidis From Different Sources Unveils the Molecular Basis and Potential Biomarkers of Pathogenic Strains. Frontiers in Microbiology, 2021, 12, 770191.	1.5	4
3425	The ATCC Genome Portal: Microbial Genome Reference Standards with Data Provenance. Microbiology Resource Announcements, 2021, 10, e0081821.	0.3	10
3426	Complete Genome Sequence of Leptospira kobayashii Strain E30, Isolated from Soil in Japan. Microbiology Resource Announcements, 2021, 10, e0090721.	0.3	1
3427	Translation stalling proline motifs are enriched in slow-growing, thermophilic, and multicellular bacteria. ISME Journal, 2022, 16, 1065-1073.	4.4	2
3428	Minnesota peat viromes reveal terrestrial and aquatic niche partitioning for local and global viral populations. Microbiome, 2021, 9, 233.	4.9	53
3429	Metagenomic analysis reveals microbiome and resistome in the seawater and sediments of Kongsfjorden (Svalbard, High Arctic). Science of the Total Environment, 2022, 809, 151937.	3.9	16
3430	Multispecies Populations of Methanotrophic <i>Methyloprofundus</i> and Cultivation of a Likely Dominant Species from the Iheya North Deep-Sea Hydrothermal Field. Applied and Environmental Microbiology, 2022, 88, AEM0075821.	1.4	12
3431	Antimicrobial Resistance in <i>Enterococcus</i> Spp. Isolated from a Beef Processing Plant and Retail Ground Beef. Microbiology Spectrum, 2021, 9, e0198021.	1.2	10

#	Article	IF	Citations
3433	Sphingobacterium micropteri sp. nov. and Sphingobacterium litopenaei sp. nov., isolated from aquaculture water. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	12
3434	<i>Muribaculaceae</i> Genomes Assembled from Metagenomes Suggest Genetic Drivers of Differential Response to Acarbose Treatment in Mice. MSphere, 2021, 6, e0085121.	1.3	53
3435	Microbial Technologies Employed for Biodegradation of Neonicotinoids in the Agroecosystem. Frontiers in Microbiology, 2021, 12, 759439.	1.5	15
3437	Genome Sequence of Pseudomonas sp. Strain LAP_36, A Rhizosphere Bacterium Isolated from King George Island, Antarctica. Microbiology Resource Announcements, 2021, 10, e0073121.	0.3	0
3438	Complete Genome Sequence of a Thin-Sheath Mutant of the Phototropic Cyanobacterium Calothrix sp. Strain PCC 7716. Microbiology Resource Announcements, 2021, 10, e0094721.	0.3	0
3439	Isolation, Whole-Genome Sequencing, and Annotation of Three Unclassified Antibiotic-Producing Bacteria, Enterobacter sp. Strain RIT 637, Pseudomonas sp. Strain RIT 778, and Deinococcus sp. Strain RIT 780. Microbiology Resource Announcements, 2021, 10, e0086321.	0.3	1
3441	ECTyper: in silico Escherichia coli serotype and species prediction from raw and assembled whole-genome sequence data. Microbial Genomics, 2021, 7, .	1.0	27
3442	Discovery of an Antarctic Ascidian-Associated Uncultivated <i>Verrucomicrobia</i> with Antimelanoma Palmerolide Biosynthetic Potential. MSphere, 2021, 6, e0075921.	1.3	7
3443	Draft Genome Sequence of <i>Schnuerera</i> sp. Strain xch1, Isolated from the Tibetan Plateau. Microbiology Resource Announcements, 2021, 10, e0099321.	0.3	0
3444	Draft Genome Sequences of Cefepime-Resistant and -Susceptible Escherichia coli Strains and Imipenem-Resistant and -Susceptible Pseudomonas aeruginosa Strains. Microbiology Resource Announcements, 2021, 10, e0074921.	0.3	0
3445	Ancient Metabolisms of a Thermophilic Subseafloor Bacterium. Frontiers in Microbiology, 2021, 12, 764631.	1.5	1
3446	A review of computational tools for generating metagenome-assembled genomes from metagenomic sequencing data. Computational and Structural Biotechnology Journal, 2021, 19, 6301-6314.	1.9	80
3447	16S rRNA gene sequences of Candidatus Methylumidiphilus (Methylococcales), a putative methanotrophic genus in lakes and ponds. Aquatic Microbial Ecology, 2022, 88, 25-30.	0.9	0
3448	Intestinal microbial communities and <i>Holdemanella</i> isolated from HIV+/â^' men who have sex with men increase frequencies of lamina propria CCR5⁺ CD4⁺ T cells. Gut Microbes, 2021, 13, 1997292.	4.3	8
3449	Evolutionary Ecology of Natural Comammox <i>Nitrospira</i> Populations. MSystems, 2022, 7, e0113921.	1.7	14
3450	A Genomic Perspective Across Earthâ€™s Microbiomes Reveals That Genome Size in Archaea and Bacteria Is Linked to Ecosystem Type and Trophic Strategy. Frontiers in Microbiology, 2021, 12, 761869.	1.5	29
3451	Structure and Function of Rhizosphere Soil and Root Endophytic Microbial Communities Associated With Root Rot of Panax notoginseng. Frontiers in Plant Science, 2021, 12, 752683.	1.7	13
3452	Identification of Putative Î²-Galactosidase Genes in the Genome of <i>Lactobacillus helveticus</i> OSU-PECh-4A. Microbiology Resource Announcements, 2022, 11, e0076621.	0.3	2

#	Article	IF	Citations
3453	Genome-Resolved Metagenomics Reveals Distinct Phosphorus Acquisition Strategies between Soil Microbiomes. MSystems, 2022, 7, e0110721.	1.7	64
3454	Metagenomic features of traditional fermented milk products. LWT - Food Science and Technology, 2022, 155, 112945.	2.5	24
3455	The anammox coupled partial-denitrification process in an integrated granular sludge and fixed-biofilm reactor developed for mainstream wastewater treatment: Performance and community structure. Water Research, 2022, 210, 117964.	5.3	52
3456	Metagenomics combined with comprehensive validation as a public health risk assessment tool for urban and agricultural run-off. Water Research, 2022, 209, 117941.	5.3	9
3457	Unveil the role of dissolved and sedimentary metal(loid)s on bacterial communities and metal resistance genes (MRGs) in an urban river of the Qinghai-Tibet Plateau. Water Research, 2022, 211, 118050.	5.3	22
3459	Evidence for Microbial Sulfur Cycling in an Extremely High Ph Marine-Like Terrestrial Serpentinizing System: Ney Springs. SSRN Electronic Journal, 0, , .	0.4	0
3460	Parvimonas parva sp. nov., derived from a human genito-urinary lesion. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	5
3461	Draft Genome Sequence of Bryobacteraceae Strain F-183. Microbiology Resource Announcements, 2022, 11, e0045321.	0.3	1
3462	Investigation of fiber utilization in the rumen of dairy cows based on metagenome-assembled genomes and single-cell RNA sequencing. Microbiome, 2022, 10, 11.	4.9	24
3464	The Mouse Gastrointestinal Bacteria Catalogue enables translation between the mouse and human gut microbiotas via functional mapping. Cell Host and Microbe, 2022, 30, 124-138.e8.	5.1	59
3467	The promiscuous and highly mobile resistome of Acinetobacter baumannii. Microbial Genomics, 2022, 8, .	1.0	18
3469	Assembly of 97 Novel Bacterial Genomes in the Microbial Community Affiliated with Polyvinyl Alcohol in Soil of Northern China. BioMed Research International, 2022, 2022, 1-14.	0.9	1
3470	Comparative Genomic Analyses of the Genus Nesterenkonia Unravels the Genomic Adaptation to Polar Extreme Environments. Microorganisms, 2022, 10, 233.	1.6	10
3471	Flavobacterium proteolyticum sp. nov., isolated from aquaculture water. Archives of Microbiology, 2022, 204, 146.	1.0	4
3472	Secreted Toxins From Staphylococcus aureus Strains Isolated From Keratinocyte Skin Cancers Mediate Pro-tumorigenic Inflammatory Responses in the Skin. Frontiers in Microbiology, 2021, 12, 789042.	1.5	14
3473	Rare transmission of commensal and pathogenic bacteria in the gut microbiome of hospitalized adults. Nature Communications, 2022, 13, 586.	5.8	21
3474	Diet leaves a genetic signature in a keystone member of the gut microbiota. Cell Host and Microbe, 2022, 30, 183-199.e10.	5.1	43
3475	Streptomyces apricus sp. nov., isolated from soil. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	4

#	Article	IF	Citations
3476	Sphingomonas arenae sp. nov., isolated from desert soil. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	11
3477	Novel insights into the role of the mobilome in ecological diversification and success of Staphylococcus haemolyticus as an opportunistic pathogen. Microbial Genomics, 2022, 8, .	1.0	1
3478	Distribution, organization and expression of genes concerned with anaerobic lactate utilization in human intestinal bacteria. Microbial Genomics, 2022, 8, .	1.0	10
3479	GAL08, an Uncultivated Group of Acidobacteria, Is a Dominant Bacterial Clade in a Neutral Hot Spring. Frontiers in Microbiology, 2021, 12, 787651.	1.5	1
3480	Unique high Arctic methane metabolizing community revealed through in situ 13CH4-DNA-SIP enrichment in concert with genome binning. Scientific Reports, 2022, 12, 1160.	1.6	9
3481	Distribution and Evolutionary History of Sialic Acid Catabolism in the Phylum <i>Actinobacteria</i>. Microbiology Spectrum, 2022, 10, e0238021.	1.2	4
3482	Microbial colonization and persistence in deep fractured shales is guided by metabolic exchanges and viral predation. Microbiome, 2022, 10, 5.	4.9	9
3483	Soils and sediments host Thermoplasmata archaea encoding novel copper membrane monooxygenases (CuMMOs). ISME Journal, 2022, 16, 1348-1362.	4.4	17
3484	Description of Aureibaculum luteum sp. nov. and Aureibaculum flavum sp. nov. isolated from Antarctic intertidal sediments. Antonie Van Leeuwenhoek, 2022, 115, 391.	0.7	1
3485	Degradation of Sugarcane Bagasse by Cockroach Consortium Bacteria. Bioenergy Research, 2022, 15, 1144-1156.	2.2	3
3486	Bacterial Metabolic Potential and Micro-Eukaryotes Enriched in Stony Coral Tissue Loss Disease Lesions. Frontiers in Marine Science, 2022, 8, .	1.2	15
3487	Sulfate-dependant microbially induced corrosion of mild steel in the deep sea: a 10-year microbiome study. Microbiome, 2022, 10, 4.	4.9	16
3488	Whole Genome Resources of 17 <i>Curtobacterium flaccumfaciens</i> Strains Including Pathotypes of <i>C.Âflaccumfaciens</i> pv. <i>betae</i>, <i>C. flaccumfaciens</i> pv. <i>oortii</i>, and <i>C. flaccumfaciens</i> pv. <i>poinsettiae</i>. Molecular Plant-Microbe Interactions, 2022, 35, 352-356.	1.4	6
3489	Shared features and reciprocal complementation of the Chlamydomonas and Arabidopsis microbiota. Nature Communications, 2022, 13, 406.	5.8	28
3490	Diverse DNA modification in marine prokaryotic and viral communities. Nucleic Acids Research, 2022, 50, 1531-1550.	6.5	9
3491	Genome-resolved evidence for functionally redundant communities and novel nitrogen fixers in the deyin-1 hydrothermal field, Mid-Atlantic Ridge. Microbiome, 2022, 10, 8.	4.9	5
3492	Draft Genome Sequence of Leifsonia poae Strain BS71, Isolated from a Drought Microcosm. Microbiology Resource Announcements, 2022, 11, e0095121.	0.3	1
3493	Considerations for constructing a protein sequence database for metaproteomics. Computational and Structural Biotechnology Journal, 2022, 20, 937-952.	1.9	22

#	ARTICLE	IF	CITATIONS
3494	Enrichment of gut microbiome strains for cultivation-free genome sequencing using droplet microfluidics. Cell Reports Methods, 2022, 2, 100137.	1.4	14
3495	Changes in chemical composition, structural and functional microbiome during alfalfa (Medicago) Tj ETQq1 1 0.784314 rgBT /Overlock	2.1	13
3496	De Novo Assembly and Annotation of the Vaginal Metatranscriptome Associated with Bacterial Vaginosis. International Journal of Molecular Sciences, 2022, 23, 1621.	1.8	4
3497	<i>Dehalococcoides</i>-Containing Enrichment Cultures Transform Two Chlorinated Organophosphate Esters. Environmental Science & Technology, 2022, 56, 1951-1962.	4.6	12
3499	Characterization of a Novel Hot-Spring Cyanobacterium Leptodesmis sichuanensis sp. Nov. and Genomic Insights of Molecular Adaptations Into Its Habitat. Frontiers in Microbiology, 2021, 12, 739625.	1.5	9
3501	Genome diversity of domesticated Acinetobacter baumannii ATCC 19606T strains. Microbial Genomics, 2022, 8, .	1.0	7
3502	Complete de novo assembly of Wolbachia endosymbiont of Diaphorina citri Kuwayama (Hemiptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.6	14
3503	Specific Denitrifying and Dissimilatory Nitrate Reduction to Ammonium Bacteria Assisted the Recovery of Anammox Community From Nitrite Inhibition. Frontiers in Microbiology, 2021, 12, 781156.	1.5	10
3504	Draft Genome Sequences of Saccharopolyspora sp. Strains and Streptomyces sp. Strains, Isolated from Social Wasps (Vespidae; Polistinae: Epiponini). Microbiology Resource Announcements, 2022, 11, e0093521.	0.3	1
3505	Draft Genome Sequences of Three Identified Rhizobacteria Associated with Maize Rhizosphere. Microbiology Resource Announcements, 2022, 11, e0097021.	0.3	0
3506	Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. PLoS Biology, 2022, 20, e3001508.	2.6	62
3507	Polysaccharide utilization loci in Bacteroides determine population fitness and community-level interactions. Cell Host and Microbe, 2022, 30, 200-215.e12.	5.1	40
3508	Whole-Genome Resources and Species-Level Taxonomic Validation of 89 Plant-Pathogenic <i>Xanthomonas</i> Strains Isolated from Various Host Plants. Plant Disease, 2022, 106, 1558-1565.	0.7	4
3509	The Probiotic Identity Card: A Novel â€œProbiogenomicsâ€•Approach to Investigate Probiotic Supplements. Frontiers in Microbiology, 2021, 12, 790881.	1.5	11
3510	Hybrid, ultra-deep metagenomic sequencing enables genomic and functional characterization of low-abundance species in the human gut microbiome. Gut Microbes, 2022, 14, 2021790.	4.3	27
3511	Aggregatimonas sangjinii gen. nov., sp. nov., a novel silver nanoparticle synthesizing bacterium belonging to the family Flavobacteriaceae. Antonie Van Leeuwenhoek, 2022, 115, 325-335.	0.7	1
3512	In Silico Characterisation of Putative Prophages in Lactobacillaceae Used in Probiotics for Vaginal Health. Microorganisms, 2022, 10, 214.	1.6	5
3513	Intake of Bifidobacterium lactis Probio-M8 fermented milk protects against alcoholic liver disease. Journal of Dairy Science, 2022, 105, 2908-2921.	1.4	11

#	ARTICLE	IF	CITATIONS
3514	Draft Genome Sequence of Isolate POC01, a Novel Anaerobic Member of the Oscillospiraceae Family, Isolated from Human Feces. Microbiology Resource Announcements, 2022, 11, e0113421.	0.3	0
3515	Phylogenetically and functionally diverse microorganisms reside under the Ross Ice Shelf. Nature Communications, 2022, 13, 117.	5.8	17
3516	Genomic analyses of Staphylococcus aureus isolated from yaks in Ganzi Tibetan Autonomous Prefecture, China. Journal of Antimicrobial Chemotherapy, 2022, , .	1.3	1
3517	Methylphosphonate Degradation and Salt-Tolerance Genes of Two Novel Halophilic Marivita Metagenome-Assembled Genomes from Unrestored Solar Salterns. Genes, 2022, 13, 148.	1.0	4
3518	A Metagenomics Investigation of Intergenerational Effects of Non-nutritive Sweeteners on Gut Microbiome. Frontiers in Nutrition, 2021, 8, 795848.	1.6	13
3519	Genomic Analysis of ESBL-Producing E. coli in Wildlife from North-Eastern Germany. Antibiotics, 2022, 11, 123.	1.5	15
3521	Comparative Genomics of Bacteroides fragilis Group Isolates Reveals Species-Dependent Resistance Mechanisms and Validates Clinical Tools for Resistance Prediction. MBio, 2022, 13, e0360321.	1.8	17
3522	Long-Term Cultivation and Meta-Omics Reveal Methylotrophic Methanogenesis in Hydrocarbon-Impacted Habitats. Engineering, 2023, 24, 264-275.	3.2	1
3523	Unique mobile elements and scalable gene flow at the prokaryoteâ€“eukaryote boundary revealed by circularized Asgard archaea genomes. Nature Microbiology, 2022, 7, 200-212.	5.9	29
3524	Microbacterium sulfonylureivorans sp. nov., isolated from sulfonylurea herbicides degrading consortium. Archives of Microbiology, 2022, 204, 136.	1.0	6
3525	Draft Genome Sequence of Bifidobacterium adolescentis 4-2, Isolated from Healthy Human Feces. Microbiology Resource Announcements, 2022, 11, e0084621.	0.3	1
3526	Multilocus sequence based identification and adaptational strategies of Pseudomonas sp. from the supraglacial site of Sikkim Himalaya. PLoS ONE, 2022, 17, e0261178.	1.1	7
3527	Genomic Investigation of Two Acinetobacter baumannii Outbreaks in a Veterinary Intensive Care Unit in The Netherlands. Pathogens, 2022, 11, 123.	1.2	7
3528	Definition of the Metagenomic Profile of Ocean Water Samples From the Gulf of Mexico Based on Comparison With Reference Samples From Sites Worldwide. Frontiers in Microbiology, 2021, 12, 781497.	1.5	3
3529	<i>Serratia</i> spp. Are Responsible for Nitrogen Fixation Fueled by As(III) Oxidation, a Novel Biogeochemical Process Identified in Mine Tailings. Environmental Science & Technology, 2022, 56, 2033-2043.	4.6	46
3532	Site-and-branch-heterogeneous analyses of an expanded dataset favour mitochondria as sister to known Alphaproteobacteria. Nature Ecology and Evolution, 2022, 6, 253-262.	3.4	48
3533	Oceanic Crustal Fluid Single Cell Genomics Complements Metagenomic and Metatranscriptomic Surveys With Orders of Magnitude Less Sample Volume. Frontiers in Microbiology, 2021, 12, 738231.	1.5	1
3535	Natronococcus pandeyae sp. nov., a Novel Haloarchaeon from Sambhar Salt Lake. Current Microbiology, 2022, 79, 51.	1.0	1

#	Article	IF	Citations
3536	Selective Isolation of Eggerthella lenta from Human Faeces and Characterisation of the Species Prophage Diversity. Microorganisms, 2022, 10, 195.	1.6	9
3537	Proximity ligation strategy for the genomic reconstruction of microbial communities associated with the ectoparasite Caligus rogercresseyi. Scientific Reports, 2022, 12, 783.	1.6	3
3538	Archaeal and Bacterial Metagenome-Assembled Genome Sequences Derived from Pig Feces. Microbiology Resource Announcements, 2022, 11, e0114221.	0.3	6
3539	Third generation cephalosporin-resistant Klebsiella pneumoniae thriving in patients and in wastewater: what do they have in common?. BMC Genomics, 2022, 23, 72.	1.2	12
3540	Metagenomic insights into the environmental adaptation and metabolism of <i>Candidatus</i> Haloplasmatales, one archaeal order thriving in saline lakes. Environmental Microbiology, 2022, 24, 2239-2258.	1.8	9
3541	Paenibacillus albicereus sp. nov. and Niallia alba sp. nov., isolated from digestive syrup. Archives of Microbiology, 2022, 204, 127.	1.0	3
3543	Complete Genome Sequence of Curtobacterium sp. Strain TXMA1, Isolated from a Grapevine in Texas, USA. Microbiology Resource Announcements, 2022, 11, e0096821.	0.3	0
3544	Genome-Resolved Metagenomic Insights into Massive Seasonal Ammonia-Oxidizing Archaea Blooms in San Francisco Bay. MSystems, 2022, 7, e0127021.	1.7	11
3545	Comparative Genomics of Borderline Oxacillin-Resistant Staphylococcus aureus Detected during a Pseudo-outbreak of Methicillin-Resistant S. aureus in a Neonatal Intensive Care Unit. MBio, 2022, 13, e0319621.	1.8	7
3546	Complete Genome Sequence and Benzophenone-3 Mineralisation Potential of Rhodococcus sp. USK10, A Bacterium Isolated from Riverbank Sediment. Applied Microbiology, 2022, 2, 104-112.	0.7	2
3547	Genomic insights into versatile lifestyle of three new bacterial candidate phyla. Science China Life Sciences, 2022, 65, 1547-1562.	2.3	8
3548	Genomic evidence of functional diversity in DPANN archaea, from oxic species to anoxic vampiristic consortia. ISME Communications, 2022, 2, .	1.7	15
3549	FtsZ-mediated fission of a cuboid bacterial symbiont. IScience, 2022, 25, 103552.	1.9	2
3550	Complete Genome Sequences of Hydrogenotrophic Denitrifiers. Microbiology Resource Announcements, 2022, 11, e0102021.	0.3	0
3551	Fulvivirga lutea sp. nov., a marine bacterium isolated from seawater. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	8
3552	MetaCRS: unsupervised clustering of contigs with the recursive strategy of reducing metagenomic datasetâ€™s complexity. BMC Bioinformatics, 2021, 22, 315.	1.2	1
3553	Functional convergence of Yunnan snub-nosed monkey and bamboo-eating panda gut microbiomes revealing the driving by dietary flexibility on mammal gut microbiome. Computational and Structural Biotechnology Journal, 2022, 20, 685-699.	1.9	13
3554	Niche differentiation of sulfur-oxidizing bacteria (SUP05) in submarine hydrothermal plumes. ISME Journal, 2022, 16, 1479-1490.	4.4	11

#	ARTICLE	IF	CITATIONS
3556	Panoramic Insights into Microevolution and Macroevolution of A Prevotella copri-containing Lineage in Primate Guts. Genomics, Proteomics and Bioinformatics, 2022, 20, 334-349.	3.0	3
3557	Gut microbiome of the largest living rodent harbors unprecedented enzymatic systems to degrade plant polysaccharides. Nature Communications, 2022, 13, 629.	5.8	26
3558	Genotypic and phenotypic characterization of hydrogenotrophic denitrifiers. Environmental Microbiology, 2022, 24, 1887-1901.	1.8	7
3559	Response and resilience of anammox consortia to nutrient starvation. Microbiome, 2022, 10, 23.	4.9	16
3560	Metagenomics indicate that public health risk may be higher from flooding following dry versus rainy periods. Environmental Microbiology Reports, 2022, , .	1.0	2
3561	Changes in the skin microbiome associated with squamous cell carcinoma in transplant recipients. ISME Communications, 2022, 2, .	1.7	6
3562	New Insight Into the Interspecies Shift of Anammox Bacteria Ca. â€œBrocadiaâ€•and Ca. â€œJetteniaâ€•in Reactors Fed With Formate and Folate. Frontiers in Microbiology, 2021, 12, 802201.	1.5	13
3563	A computational learning paradigm to targeted discovery of biocatalysts from metagenomic data: A case study of lipase identification. Biotechnology and Bioengineering, 2022, 119, 1115-1128.	1.7	13
3564	Arthrobacter sunyaminii sp. nov. and Arthrobacter jiangjiafuii sp. nov., new members in the genus Arthrobacter. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	11
3566	Assessment of Hydrocarbon Degradation Potential in Microbial Communities in Arctic Sea Ice. Microorganisms, 2022, 10, 328.	1.6	13
3567	Simultaneous Single-Cell Genome and Transcriptome Sequencing of Termite Hindgut Protists Reveals Metabolic and Evolutionary Traits of Their Endosymbionts. MSphere, 2022, 7, e0002122.	1.3	1
3568	Identification of the rhizosphere microbes that actively consume plant-derived carbon. Soil Biology and Biochemistry, 2022, 166, 108577.	4.2	14
3569	Complete genome sequence of Kordiimonas pumila N18T sheds light on biogeochemical roles of the genus Kordiimonas. Marine Genomics, 2022, 62, 100930.	0.4	3
3570	Molecular dissemination of emerging antibiotic, biocide, and metal co-resistomes in the Himalayan hot springs. Journal of Environmental Management, 2022, 307, 114569.	3.8	8
3571	Reconstructing polyaromatic hydrocarbons degrading pathways in the enriched bacterial consortium and their biosurfactants characterization. Journal of Environmental Chemical Engineering, 2022, 10, 107219.	3.3	12
3572	Efficient biodegradation of tetrabromobisphenol A by the novel strain Enterobacter sp. T2 with good environmental adaptation: Kinetics, pathways and genomic characteristics. Journal of Hazardous Materials, 2022, 429, 128335.	6.5	16
3573	Metagenomic assemblage genomes analyses reveal the polysaccharides hydrolyzing potential of marine group II euryarchaea. Environmental Research, 2022, 209, 112865.	3.7	6
3574	Comparative genomic analysis of 455 Lactiplantibacillus plantarum isolates: Habitat-specific genomes shaped by frequent recombination. Food Microbiology, 2022, 104, 103989.	2.1	17

#	ARTICLE	IF	CITATIONS
3575	Diplocloster agilis gen. nov., sp. nov. and Diplocloster modestus sp. nov., two novel anaerobic fermentative members of Lachnospiraceae isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	10
3576	Spongiibacter pelagi sp. nov., a marine gammaproteobacterium isolated from coastal seawater. Antonie Van Leeuwenhoek, 2022, 115, 487.	0.7	6
3577	Physiological and Genomic Characterization of Actinotalea subterranea sp. nov. from Oil-Degrading Methanogenic Enrichment and Reclassification of the Family Actinotaleaceae. Microorganisms, 2022, 10, 378.	1.6	6
3578	Mesobacterium pallidum gen. nov., sp. nov., Heliomarina baculiformis gen. nov., sp. nov. and Oricola indica sp. nov., three novel Alphaproteobacteria members isolated from deep-sea water in the southwest Indian ridge. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	23
3579	Phyllosphere-associated microbiota in built environment: Do they have the potential to antagonize human pathogens?. Journal of Advanced Research, 2023, 43, 109-121.	4.4	9
3580	Complete Genome Sequence of Bacillus sp. Strain NC3, Isolated from Trichonephila Spider Ground Extract. Microbiology Resource Announcements, 2022, , e0111021.	0.3	2
3581	Complete Genome Sequences of Three Phocaeicola vulgatus Strains Isolated from a Healthy Japanese Individual. Microbiology Resource Announcements, 2022, 11, e0112421.	0.3	4
3582	The microbiome of the buffalo digestive tract. Nature Communications, 2022, 13, 823.	5.8	30
3583	Draft Metagenome-Assembled Genomes from Methane-Rich Echo Lake, Montana. Microbiology Resource Announcements, 2022, , e0111221.	0.3	1
3584	Giant sponge grounds of Central Arctic seamounts are associated with extinct seep life. Nature Communications, 2022, 13, 638.	5.8	22
3585	Accessory Genome Dynamics of Local and Global Staphylococcus pseudintermedius Populations. Frontiers in Microbiology, 2022, 13, 798175.	1.5	7
3586	Ecological Interactions of Cyanobacteria and Heterotrophs Enhances the Robustness of Cyanobacterial Consortium for Carbon Sequestration. Frontiers in Microbiology, 2022, 13, 780346.	1.5	14
3587	Genome Analysis and Description of Three Novel Diazotrophs Geomonas Species Isolated From Paddy Soils. Frontiers in Microbiology, 2021, 12, 801462.	1.5	26
3589	Physiology of anammox adaptation to low temperatures and promising biomarkers: A review. Bioresource Technology, 2022, 349, 126847.	4.8	25
3590	Draft genome sequence of Psychrobacter nivimaris LAMA 639 and its biotechnological potential. Data in Brief, 2022, 41, 107927.	0.5	2
3591	Draft Genome Sequence of a Methanogenic Archaeon from West Spitsbergen Permafrost. Microbiology Resource Announcements, 2022, , e0093821.	0.3	1
3592	Lactobacillus huangpiensis sp. nov. and Lactobacillus laiwuensis sp. nov., isolated from the gut of honeybee (Apis mellifera). International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	11
3594	Hi-C Metagenomics in the ICU: Exploring Clinically Relevant Features of Gut Microbiome in Chronically Critically Ill Patients. Frontiers in Microbiology, 2021, 12, 770323.	1.5	12

#	ARTICLE	IF	CITATIONS
3596	Identification of Bacterial Populations and Functional Mechanisms Potentially Involved in Biochar-Facilitated Antagonism of the Soilborne Pathogen<i>Fusarium oxysporum</i>. Phytobiomes Journal, 2022, 6, 139-150.	1.4	5
3597	Massilia soli sp. nov., isolated from soil. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	16
3598	Single-cell genomics for resolution of conserved bacterial genes and mobile genetic elements of the human intestinal microbiota using flow cytometry. Gut Microbes, 2022, 14, 2029673.	4.3	5
3602	An amidase and a novel phenol hydroxylase catalyze the degradation of the antibacterial agent triclocarban by Rhodococcus rhodochrous. Journal of Hazardous Materials, 2022, 430, 128444.	6.5	11
3603	Metagenomic analysis further extends the role of Chloroflexi in fundamental biogeochemical cycles. Environmental Research, 2022, 209, 112888.	3.7	38
3604	A catalogue of 1,167 genomes from the human gut archaeome. Nature Microbiology, 2022, 7, 48-61.	5.9	72
3605	Towards the biogeography of prokaryotic genes. Nature, 2022, 601, 252-256.	13.7	85
3606	Non-syntrophic methanogenic hydrocarbon degradation by an archaeal species. Nature, 2022, 601, 257-262.	13.7	83
3607	Fast and accurate metagenotyping of the human gut microbiome with GT-Pro. Nature Biotechnology, 2022, 40, 507-516.	9.4	18
3608	Maternal inheritance of the koala gut microbiome and its compositional and functional maturation during juvenile development. Environmental Microbiology, 2022, 24, 475-493.	1.8	12
3609	Crossâ€linkage between bacterial taxonomy and gene functions: a study of metagenomeâ€assembled genomes of gut microbiota in adult nonâ€alcoholic fatty liver disease. Alimentary Pharmacology and Therapeutics, 2021, 53, 722-732.	1.9	7
3610	New Insights into Lincomycin Biodegradation by Conexibacter Sp. Ld01: Genomics Characterization, Biodegradation Kinetics and Pathways. SSRN Electronic Journal, 0, , .	0.4	0
3612	Amplicon-based and metagenomic approaches provide insights into toxigenic potential in understudied Atlantic Canadian lakes. Facets, 2022, 7, 194-214.	1.1	3
3613	Proteogenomics Identification of Tbbpa Degraders in Anaerobic Bioreactor. SSRN Electronic Journal, 0, , .	0.4	0
3614	Desulfovulcanus ferrireducens gen. nov., sp. nov., a thermophilic autotrophic iron and sulfate-reducing bacterium from subseafloor basalt that grows on akaganÃ©ite and lepidocrocite minerals. Extremophiles, 2022, 26, 13.	0.9	2
3615	HiCBin: binning metagenomic contigs and recovering metagenome-assembled genomes using Hi-C contact maps. Genome Biology, 2022, 23, 63.	3.8	20
3616	Insights Into the Cultivable Bacterial Fraction of Sediments From the Red Sea Mangroves and Physiological, Chemotaxonomic, and Genomic Characterization of Mangrovibacillus cuniculi gen. nov., sp. nov., a Novel Member of the Bacillaceae Family. Frontiers in Microbiology, 2022, 13, 777986.	1.5	8
3617	Shewanella jiangmenensis sp. nov., isolated from aquaculture water. Archives of Microbiology, 2022, 204, 198.	1.0	7

#	ARTICLE	IF	CITATIONS
3618	Unraveling Nitrogen, Sulfur, and Carbon Metabolic Pathways and Microbial Community Transcriptional Responses to Substrate Deprivation and Toxicity Stresses in a Bioreactor Mimicking Anoxic Brackish Coastal Sediment Conditions. Frontiers in Microbiology, 2022, 13, 798906.	1.5	2
3619	Catabolic protein degradation in marine sediments confined to distinct archaea. ISME Journal, 2022, 16, 1617-1626.	4.4	12
3620	Mining Marine Metagenomes Revealed a Quorum-Quenching Lactonase with Improved Biochemical Properties That Inhibits the Food Spoilage Bacterium Pseudomonas fluorescens. Applied and Environmental Microbiology, 2022, 88, AEM0168021.	1.4	3
3621	A holistic genome dataset of bacteria, archaea and viruses of the Pearl River estuary. Scientific Data, 2022, 9, 49.	2.4	12
3622	Niche partitioning of the ubiquitous and ecologically relevant NS5 marine group. ISME Journal, 2022, 16, 1570-1582.	4.4	11
3624	Closed Genome Sequences of Providencia alcalifaciens Isolates from Dogs. Microbiology Resource Announcements, 2022, 11, e0095521.	0.3	1
3626	A Bacterial Genome and Culture Collection of Gut Microbial in Weanling Piglet. Microbiology Spectrum, 2022, 10, e0241721.	1.2	3
3627	Short- and long-read metagenomics of urban and rural South African gut microbiomes reveal a transitional composition and undescribed taxa. Nature Communications, 2022, 13, 926.	5.8	26
3629	Host ecology regulates interspecies recombination in bacteria of the genus Campylobacter. ELife, 2022, 11, .	2.8	17
3630	The novel genus, â€˜<i>Candidatus</i> Phosphoribacterâ€™, 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
3631	Halobaculum rubrum sp. nov., an extremely halophilic archaeon isolated from a salt lake. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	7
3632	Contamination detection in genomic data: more is not enough. Genome Biology, 2022, 23, 60.	3.8	37
3633	Newly Isolated Paenibacillus monticola sp. nov., a Novel Plant Growth-Promoting Rhizobacteria Strain From High-Altitude Spruce Forests in the Qilian Mountains, China. Frontiers in Microbiology, 2022, 13, 833313.	1.5	9
3634	Microbial Biomass, Composition, and Functions Are Responsible for the Differential Removal of Trace Organic Chemicals in Biofiltration Systems: A Batch Study. Frontiers in Water, 2022, 4, .	1.0	4
3635	Metabolic Diversity and Aero-Tolerance in Anammox Bacteria from Geochemically Distinct Aquifers. MSystems, 2022, 7, e0125521.	1.7	13
3636	New Report: Genome Mining Untaps the Antibiotics Biosynthetic Gene Cluster of Pseudoalteromonas xiamenensis STKMTI.2 from a Mangrove Soil Sediment. Marine Biotechnology, 2022, 24, 190-202.	1.1	2
3637	Flemish soils contain rhizobia partners for Northwestern Europeâ€•adapted soybean cultivars. Environmental Microbiology, 2022, 24, 3334-3354.	1.8	6
3638	Microbial Community Structure and Functional Potential of Deep-Sea Sediments on Low Activity Hydrothermal Area in the Central Indian Ridge. Frontiers in Marine Science, 2022, 9, .	1.2	6

#	ARTICLE	IF	CITATIONS
3639	Complete Genome Sequence of â€œ <i>Candidatus</i> Hydrogeosomobacter endosymbioticus,â€•an Intracellular Bacterial Symbiont of the Anaerobic Ciliate Scuticociliate GW7. Microbiology Resource Announcements, 2022, 11, e0115021.	0.3	1
3640	Genetic and phenotypic characteristics of Clostridium (Clostridioides) difficile from canine, bovine, and pediatric populations. Anaerobe, 2022, , 102539.	1.0	4
3641	BugSplit enables genome-resolved metagenomics through highly accurate taxonomic binning of metagenomic assemblies. Communications Biology, 2022, 5, 151.	2.0	7
3642	Cultivation and metabolic insights of an uncultured clade, Bacteroidetes <scp>VC2</scp>.1 Bac22 (<i>Candidatus</i> Sulfidibacteriales ord. nov.), from deepâ€•sea hydrothermal vents. Environmental Microbiology, 2022, 24, 2484-2501.	1.8	7
3643	Complete Genome Sequence of <i>Luteitalea</i> sp. Strain TBR-22. Microbiology Resource Announcements, 2022, 11, e0045521.	0.3	1
3644	Unamplified, Long-Read Metagenomic Sequencing Approach to Close Endosymbiont Genomes of Low-Biomass Insect Populations. Microorganisms, 2022, 10, 513.	1.6	6
3645	Active anaerobic methane oxidation and sulfur disproportionation in the deep terrestrial subsurface. ISME Journal, 2022, 16, 1583-1593.	4.4	16
3646	Complete Genome Sequence of Stenotrophomonas maltophilia 1800, a New Bacterial Strain with Potential for Bioremediation of Oil-Contaminated Environments. Microbiology Resource Announcements, 2022, 11, e0111621.	0.3	0
3648	A Descriptive Analysis of Urinary ESBL-Producing-Escherichia coli in Cerdanya Hospital. Microorganisms, 2022, 10, 488.	1.6	5
3649	Diversity of Pseudomonas aeruginosa Temperate Phages. MSphere, 2022, 7, e0101521.	1.3	16
3650	Pufferfish (Tetraodon cutcutia) Sampled from a Freshwater River Serves as an Intermediate Reservoir of a Sucrose Nonfermenting Variant of Vibrio cholerae PS-4. Microbiology Spectrum, 2022, 10, e0122121.	1.2	5
3651	Comparative Genomic Analysis Reveals Preserved Features in Organohalide-Respiring <i>Sulfurospirillum</i> Strains. MSphere, 2022, 7, e0093121.	1.3	3
3652	Genome binning of viral entities from bulk metagenomics data. Nature Communications, 2022, 13, 965.	5.8	41
3655	Characterization and Demonstration of Mock Communities as Control Reagents for Accurate Human Microbiome Community Measurements. Microbiology Spectrum, 2022, 10, e0191521.	1.2	17
3656	Disentangle genus microdiversity within a complex microbial community by using a multiâ€•distance longâ€•read binning method: example of <i>Candidatus</i> Accumulibacter. Environmental Microbiology, 2022, 24, 2136-2156.	1.8	4
3657	Genome-based reclassification of the genus Meiothermus along with the proposal of a new genus Allomeiothermus gen. nov. Antonie Van Leeuwenhoek, 2022, 115, 645.	0.7	12
3658	Genomic and Functional Variation of the Chlorophyll d-Producing Cyanobacterium Acaryochloris marina. Microorganisms, 2022, 10, 569.	1.6	3
3659	Draft Genome Sequences of a <i>Bifidobacterium</i> Strain and a <i>Bacteroides</i> Strain Isolated from a Human Stool Sample. Microbiology Resource Announcements, 2022, , e0001122.	0.3	0

#	ARTICLE	IF	CITATIONS
3660	Sagittula salina sp. nov., isolated from marine waste. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	4
3661	Genomic and antigenic diversity of colonizing Klebsiella pneumoniae isolates mirrors that of invasive isolates in Blantyre, Malawi. Microbial Genomics, 2022, 8, .	1.0	5
3662	Pan-Genome Analysis of Delftia tsuruhatensis Reveals Important Traits Concerning the Genetic Diversity, Pathogenicity, and Biotechnological Properties of the Species. Microbiology Spectrum, 2022, 10, e0207221.	1.2	13
3663	Unraveling the Genotypic and Phenotypic Diversity of the Psychrophilic Clostridium estertheticum Complex, a Meat Spoilage Agent. Frontiers in Microbiology, 2022, 13, 856810.	1.5	4
3667	Pan-Genomic and Transcriptomic Analyses of Marine Pseudoalteromonas agarivorans Hao 2018 Revealed Its Genomic and Metabolic Features. Marine Drugs, 2022, 20, 248.	2.2	0
3668	Comparative Genome Analysis of the Photosynthetic Betaproteobacteria of the Genus Rhodocyclus: Heterogeneity within Strains Assigned to Rhodocyclus tenuis and Description of Rhodocyclus gracilis sp. nov. as a New Species. Microorganisms, 2022, 10, 649.	1.6	11
3669	Some like it cold: the cellular organization and physiological limits of coldâ€tolerant nitriteâ€oxidizing <i>Nitrotoga</i>. Environmental Microbiology, 2022, 24, 2059-2077.	1.8	9
3670	Shared antibiotic resistance and virulence genes in Staphylococcus aureus from diverse animal hosts. Scientific Reports, 2022, 12, 4413.	1.6	23
3671	Machine learning-assisted identification of bioindicators predicts medium-chain carboxylate production performance of an anaerobic mixed culture. Microbiome, 2022, 10, 48.	4.9	14
3672	Genome Sequence of <i>Synechococcus</i> sp. Strain LA31, Isolated from a Temperate Estuary. Microbiology Resource Announcements, 2022, 11, e0077521.	0.3	3
3673	Multikingdom interactions govern the microbiome in subterranean cultural heritage sites. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2121141119.	3.3	7
3674	Whole-Genome Sequencing and <i>De Novo</i> Assembly of 67 Staphylococcus pseudintermedius Strains Isolated from the Skin of Healthy Dogs. Microbiology Resource Announcements, 2022, 11, e0003922.	0.3	4
3675	Nitratireductor rhodophyticola sp. nov., isolated from marine red algae. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	10
3676	Discovery of the nonâ€cosmopolitan lineages in <i>Candidatus</i> Thermoprofundales. Environmental Microbiology, 2022, 24, 3063-3080.	1.8	3
3678	Long-Term Cellulose Enrichment Selects for Highly Cellulolytic Consortia and Competition for Public Goods. MSystems, 2022, 7, e0151921.	1.7	5
3679	Comamonas fluminis sp. nov., isolated from the Han River, Republic of Korea. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	8
3682	Metagenome-Assembled Genomes from a Microbiome Converting Xylose to Medium-Chain Carboxylic Acids. Microbiology Resource Announcements, 2022, 11, e0115121.	0.3	2
3683	Mycetocola spongiae sp. nov., isolated from deep-sea sponge Cacospongia mycofijiensis. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	10

#	ARTICLE	IF	CITATIONS
3684	Flavobacterium ammonificans sp. nov. and Flavobacterium ammoniigenes sp. nov., ammonifying bacteria isolated from surface river water. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	12
3685	Metagenomic Insights into Chicken Gut Antibiotic Resistomes and Microbiomes. Microbiology Spectrum, 2022, , e0190721.	1.2	10
3686	Comammox<i>Nitrospira</i>bacteria outnumber canonical nitrifiers irrespective of electron donor mode and availability in biofiltration systems. FEMS Microbiology Ecology, 2022, 98, .	1.3	10
3688	Meta-analysis of the Ralstonia solanacearum species complex (RSSC) based on comparative evolutionary genomics and reverse ecology. Microbial Genomics, 2022, 8, .	1.0	18
3690	Characterization of the First Cultured Representative of â€œ <i>Candidatus</i> Thermofonsiaâ€•Clade 2 within <i>Chloroflexi</i> Reveals Its Phototrophic Lifestyle. MBio, 2022, 13, e0028722.	1.8	8
3691	Global population structure of the Serratia marcescens complex and identification of hospital-adapted lineages in the complex. Microbial Genomics, 2022, 8, .	1.0	8
3692	Genome Sequences of Marichromatium gracile HOL-1 and Its Purple Photosynthetic Coisolate, <i>Afifella</i> sp. H1R. Microbiology Resource Announcements, 2022, , e0003322.	0.3	1
3693	A Large-Scale Genome-Based Survey of Acidophilic Bacteria Suggests That Genome Streamlining Is an Adaption for Life at Low pH. Frontiers in Microbiology, 2022, 13, 803241.	1.5	12
3694	Functional and Phylogenetic Characterization of Bacteria in Bovine Rumen Using Fractionation of Ruminal Fluid. Frontiers in Microbiology, 2022, 13, 813002.	1.5	8
3695	Finding the right fit: evaluation of short-read and long-read sequencing approaches to maximize the utility of clinical microbiome data. Microbial Genomics, 2022, 8, .	1.0	15
3696	Horizontal transmission enables flexible associations with locally adapted symbiont strains in deep-sea hydrothermal vent symbioses. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2115608119.	3.3	20
3697	Landscape of mobile genetic elements and their antibiotic resistance cargo in prokaryotic genomes. Nucleic Acids Research, 2022, 50, 3155-3168.	6.5	34
3698	Microbiomes in the Challenger Deep slope and bottom-axis sediments. Nature Communications, 2022, 13, 1515.	5.8	31
3700	SprayNPray: user-friendly taxonomic profiling of genome and metagenome contigs. BMC Genomics, 2022, 23, 202.	1.2	4
3701	MetaDecoder: a novel method for clustering metagenomic contigs. Microbiome, 2022, 10, 46.	4.9	13
3702	TAL effectors and the predicted host targets of pomegranate bacterial blight pathogen Xanthomonas citri pv. punicae. Current Genetics, 2022, , 1.	0.8	3
3703	The Genome Sequence of Brucella intermedia DF13, a 2,4-Dichlorophenoxyacetic Acid-Degrading Soil Bacterium Isolated in Brazil. Microbiology Resource Announcements, 2022, , e0110521.	0.3	0
3706	Identification of key microorganisms in facultative stabilization ponds from dairy industries, using metagenomics. PeerJ, 2022, 10, e12772.	0.9	3

#	Article	IF	Citations
3707	Habitatâ€adapted microbial communities mediate <i>Sphagnum</i> peatmoss resilience to warming. New Phytologist, 2022, 234, 2111-2125.	3.5	18
3708	The Genome of Enterobacter hormaechei Strain MG02, a 2,4-Dichlorophenoxyacetic Acid-Degrading Bacterium Isolated from Brazilian Soil. Microbiology Resource Announcements, 2022, 11, e0110421.	0.3	0
3709	Draft Genome Sequence of Plesiomonas shigelloides Strain PI-19, Isolated from the Intestine of Pufferfish (Tetraodon cutcutia). Microbiology Resource Announcements, 2022, 11, e0125221.	0.3	0
3710	Alkaliphilus flagellatus sp. nov., Butyricicoccus intestinisimiae sp. nov., Clostridium mobile sp. nov., Clostridium simiarum sp. nov., Dysosmobacter acutus sp. nov., Paenibacillus brevis sp. nov., Peptoniphilus ovalis sp. nov. and Tissierella simiarum sp. nov., isolated from monkey faeces. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	34
3711	The microbiome and resistome of apple fruits alter in the post-harvest period. Environmental Microbiomes, 2022, 17, 10.	2.2	11
3712	Stimulated Organic Carbon Cycling and Microbial Community Shift Driven by a Simulated Cold-Seep Eruption. MBio, 2022, 13, e0008722.	1.8	5
3713	Comparative Genomics on Cultivated and Uncultivated Freshwater and Marine â€œ<i>Candidatus</i>Manganitrophaceaeâ€• Species Implies Their Worldwide Reach in Manganese Chemolithoautotrophy. MBio, 2022, 13, e0342121.	1.8	4
3714	Production of Epoxyketone Peptide-Based Proteasome Inhibitors by Streptomyces sp. BRA-346: Regulation and Biosynthesis. Frontiers in Microbiology, 2022, 13, 786008.	1.5	0
3715	Complete Genome Sequence of Halopseudomonas aestusnigri Strain GOM5, Isolated from Asphalt Marine Sediments of the Gulf of Mexico. Microbiology Resource Announcements, 2022, , e0122221.	0.3	2
3716	A Glyphosate-Based Herbicide Cross-Selects for Antibiotic Resistance Genes in Bacterioplankton Communities. MSystems, 2022, 7, e0148221.	1.7	12
3718	A Comparative Analysis of Weizmannia coagulans Genomes Unravels the Genetic Potential for Biotechnological Applications. International Journal of Molecular Sciences, 2022, 23, 3135.	1.8	11
3719	The role of organic matter and microbial community controlling nitrate reduction under elevated ferrous iron concentrations in boreal lake sediments. Hydrobiologia, 0, , 1.	1.0	4
3720	Strain-level profiling of viable microbial community by selective single-cell genome sequencing. Scientific Reports, 2022, 12, 4443.	1.6	11
3721	Accurate prediction of metagenome-assembled genome completeness by MAGISTA, a random forest model built on alignment-free intra-bin statistics. Environmental Microbiomes, 2022, 17, 9.	2.2	3
3722	Deciphering Genomes: Genetic Signatures of Plant-Associated Micromonospora. Frontiers in Plant Science, 2022, 13, 872356.	1.7	3
3723	Phosphonate production by marine microbes: Exploring new sources and potential function. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2113386119.	3.3	31
3724	Meta-omics-aided isolation of an elusive anaerobic arsenic-methylating soil bacterium. ISME Journal, 2022, 16, 1740-1749.	4.4	16
3725	Comparative analysis of Streptococcus suis genomes identifies novel candidate virulence-associated genes in North American isolates. Veterinary Research, 2022, 53, 23.	1.1	11

#	Article	IF	Citations
3726	Comprehensive mouse microbiota genome catalog reveals major difference to its human counterpart. PLoS Computational Biology, 2022, 18, e1009947.	1.5	36
3727	Halomonas antri sp. nov., a carotenoid-producing bacterium isolated from surface seawater. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	12
3728	Thiosulfatihalobacter marinus gen. nov. sp. nov., a novel member of the family Roseobacteraceae, isolated from the West Pacific Ocean. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	7
3729	Leclercia pneumoniae sp. nov., a bacterium isolated from clinical specimen in Leipzig, Germany. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	7
3732	Complete and Draft Genome Sequences of 48 Staphylococcus aureus Isolates Obtained from Atopic Dermatitis Patients and Healthy Controls. Microbiology Resource Announcements, 2022, , e0007222.	0.3	0
3733	Abundant and persistent sulfurâ€oxidizing microbial populations are responsive to hypoxia in the Chesapeake Bay. Environmental Microbiology, 2022, 24, 2315-2332.	1.8	10
3734	Metabolism of the Genus Guyparkeria Revealed by Pangenome Analysis. Microorganisms, 2022, 10, 724.	1.6	0
3736	In Vitro and In Silico Based Approaches to Identify Potential Novel Bacteriocins from the Athlete Gut Microbiome of an Elite Athlete Cohort. Microorganisms, 2022, 10, 701.	1.6	8
3737	Comparative Respiratory Tract Microbiome Between Carbapenem-Resistant Acinetobacter baumannii Colonization and Ventilator Associated Pneumonia. Frontiers in Microbiology, 2022, 13, 782210.	1.5	5
3738	Microbial Diversity and Sulfur Cycling in an Early Earth Analogue: From Ancient Novelty to Modern Commonality. MBio, 2022, 13, e0001622.	1.8	15
3739	Insights into carbon-fixation pathways through metagonomics in the sediments of deep-sea cold seeps. Marine Pollution Bulletin, 2022, 176, 113458.	2.3	15
3740	Phylogenetic diversity of NO reductases, new tools for nor monitoring, and insights into N2O production in natural and engineered environments. Frontiers of Environmental Science and Engineering, 2022, 16, 1.	3.3	2
3741	Complete Genome Resource of a Commonly Used Laboratory Substrain of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99^A. Plant Disease, 2022, 106, 1045-1048.	0.7	0
3742	Identification of active gaseous-alkane degraders at natural gas seeps. ISME Journal, 2022, 16, 1705-1716.	4.4	7
3743	Evidence of Genomic Diversification in a Natural Symbiotic Population Within Its Host. Frontiers in Microbiology, 2022, 13, 854355.	1.5	3
3744	Dataset for Genome Sequencing and De Novo Assembly of the Candidate Phyla Radiation in Supragingival Plaque. Canadian Journal of Infectious Diseases and Medical Microbiology, 2022, 2022, 1-10.	0.7	0
3745	The CIAMIB: a Large and Metabolically Diverse Collection of Inflammation-Associated Bacteria from the Murine Gut. MBio, 2022, , e0294921.	1.8	11
3747	Single-cell metabolite detection and genomics reveals uncultivated talented producer. , 2022, 1, .		15

#	Article	IF	Citations
3748	Draft Genome Sequences of Two <i>Sphingobium</i> Species Associated with Hexachlorocyclohexane (HCH) Degradation Isolated from an HCH-Contaminated Soil. Microbiology Resource Announcements, 2022, 11, e0088621.	0.3	2
3749	Quantification of archaea-driven freshwater nitrification from single cell to ecosystem levels. ISME Journal, 2022, 16, 1647-1656.	4.4	10
3750	Metagenomics reveals global-scale contrasts in nitrogen cycling and cyanobacterial light-harvesting mechanisms in glacier cryoconite. Microbiome, 2022, 10, 50.	4.9	10
3751	Infection strategy and biogeography distinguish cosmopolitan groups of marine jumbo bacteriophages. ISME Journal, 2022, 16, 1657-1667.	4.4	27
3752	Whole-Genome Sequence Resource of Indian Race 4 of <i>Xanthomonas campestris</i> pv. <i>campestris</i>, the Causal Agent of Black Rot Disease of <i>Brassica oleracea</i> var. <i>capitata</i>. Plant Disease, 2022, 106, 1502-1505.	0.7	5
3754	Anaerobic singleâ€cell dispensing facilitates the cultivation of human gut bacteria. Environmental Microbiology, 2022, 24, 3861-3881.	1.8	15
3755	A comparative whole-genome approach identifies bacterial traits for marine microbial interactions. Communications Biology, 2022, 5, 276.	2.0	18
3759	Isolation and characterization of Escherichia albertii originated from the broiler farms in Mississippi and Alabama. Veterinary Microbiology, 2022, 267, 109379.	0.8	7
3760	Draft genome sequence of â€˜Candidatus Phytoplasma australasiaâ€™, strain SS02 associated with sesame phyllody disease. 3 Biotech, 2022, 12, 107.	1.1	4
3761	Active lithoautotrophic and methane-oxidizing microbial community in an anoxic, sub-zero, and hypersaline High Arctic spring. ISME Journal, 2022, 16, 1798-1808.	4.4	14
3762	Development of a synbiotic that protects against ovariectomy-induced trabecular bone loss. American Journal of Physiology - Endocrinology and Metabolism, 2022, 322, E344-E354.	1.8	5
3763	Microbial and functional characterization of granulated sludge from full-scale UASB thermophilic reactor applied to sugarcane vinasse treatment. Environmental Technology (United Kingdom), 2023, 44, 3141-3160.	1.2	3
3764	From rags to enriched: metagenomic insights into ammoniaâ€oxidizing archaea following ammonia enrichment of a denuded oligotrophic soil ecosystem. Environmental Microbiology, 2022, 24, 3097-3110.	1.8	4
3765	Halorussus halobius sp. nov., Halorussus marinus sp. nov. and Halorussus pelagicus sp. nov., isolated from salted brown alga Laminaria. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	12
3766	Rhizobium cremeum sp. nov., isolated from sewage and capable of acquisition of heavy metal and aromatic compounds resistance genes. Systematic and Applied Microbiology, 2022, 45, 126322.	1.2	6
3767	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	9.0	133
3769	Genome Sequence Resource for <i>Bipolaris zeicola,</i> the Cause of Northern Corn Leaf Spot Disease. Phytopathology, 2022, , PHYTO05210196A.	1.1	2
3770	Mechanistic insights into consumption of the food additive xanthan gum by the human gut microbiota. Nature Microbiology, 2022, 7, 556-569.	5.9	21

#	Article	IF	Citations
3771	Recovering metagenome-assembled genomes from shotgun metagenomic sequencing data: Methods, applications, challenges, and opportunities. Microbiological Research, 2022, 260, 127023.	2.5	17
3772	Cloacimonadota metabolisms include adaptations in engineered environments that are reflected in the evolutionary history of the phylum. Environmental Microbiology Reports, 2022, 14, 520-529.	1.0	8
3773	Porcine gut microbiota in mediating host metabolic adaptation to cold stress. Npj Biofilms and Microbiomes, 2022, 8, 18.	2.9	17
3774	Strain Identification and Quantitative Analysis in Microbial Communities. Journal of Molecular Biology, 2022, 434, 167582.	2.0	15
3775	Halophilic Martelella sp. AD-3 enhanced phenanthrene degradation in a bioaugmented activated sludge system through syntrophic interaction. Water Research, 2022, 218, 118432.	5.3	7
3776	Paraburkholderia gardini sp. nov. and Paraburkholderia saeva sp. nov.: Novel aromatic compound degrading bacteria isolated from garden and forest soil samples. Systematic and Applied Microbiology, 2022, 45, 126318.	1.2	11
3777	A mixed blessing of viruses in wastewater treatment plants. Water Research, 2022, 215, 118237.	5.3	21
3778	Isolation, characterization and complete genome sequencing of fish pathogenic Aeromonas veronii from diseased Labeo rohita. Aquaculture, 2022, 553, 738085.	1.7	11
3779	Biogeochemical profiling and taxonomic characterization of municipal landfill site by metagenomic sequencing. Bioresource Technology, 2022, 351, 126936.	4.8	13
3780	Cold seeps alter the near-bottom biogeochemistry in the ultraoligotrophic Southeastern Mediterranean Sea. Deep-Sea Research Part I: Oceanographic Research Papers, 2022, 183, 103744.	0.6	9
3781	Genome sequence of five Zetaproteobacteria metagenome-assembled genomes recovered from hydrothermal vent Longqi, Southwest Indian Ridge. Marine Genomics, 2022, 63, 100936.	0.4	4
3782	Unraveling microbe-mediated degradation of lignin and lignin-derived aromatic fragments in the Pearl River Estuary sediments. Chemosphere, 2022, 296, 133995.	4.2	2
3783	Metagenomic assembled genomes unravel purple nonâ€‘sulfur bacteria (PNSB) involved in integrating C, N, P biotransformation. Science of the Total Environment, 2022, 830, 154591.	3.9	4
3784	Viral diversity and biogeochemical potential revealed in different prawn-culture sediments by virus-enriched metagenome analysis. Environmental Research, 2022, 210, 112901.	3.7	7
3785	Identification of bacterial antibiotic resistance genes in next-generation sequencing data (review of) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.2	1
3788	Identification of two novel HIV-1 circulating recombinant forms of CRF111_01C and CRF116_0108 in southwestern Yunnan, China. Virulence, 2022, 13, 19-29.	1.8	4
3789	Elioraea tepida, sp. nov., a Moderately Thermophilic Aerobic Anoxygenic Phototrophic Bacterium Isolated from the Mat Community of an Alkaline Siliceous Hot Spring in Yellowstone National Park, WY, USA. Microorganisms, 2022, 10, 80.	1.6	1
3790	Halorubrum salipaludis sp. nov., isolated from the salineâ€“alkaline soil. Archives of Microbiology, 2022, 204, 103.	1.0	1

#	Article	IF	Citations
3791	Omics-Inferred Partitioning and Expression of Diverse Biogeochemical Functions in a Low-O ₂ Cyanobacterial Mat Community. MSystems, 2021, 6, e0104221.	1.7	5
3792	Genomic and transcriptomic evidence for the diverse adaptations of <i>Synechococcus</i> subclusters 5.2 and 5.3 to mesoscale eddies. New Phytologist, 2022, 233, 1828-1842.	3.5	4
3793	Species-Level Analysis of the Human Gut Microbiome Shows Antibiotic Resistance Genes Associated With Colorectal Cancer. Frontiers in Microbiology, 2021, 12, 765291.	1.5	7
3794	Genetic Potential of Dissulfurimicrobium hydrothermale, an Obligate Sulfur-Disproportionating Thermophilic Microorganism. Microorganisms, 2022, 10, 60.	1.6	6
3795	Lineage-specific energy and carbon metabolism of sponge symbionts and contributions to the host carbon pool. ISME Journal, 2022, 16, 1163-1175.	4.4	13
3796	Draft genome sequence of the cyanobacterium Sphaerospermopsis aphanizomenoides BCCUSP55 from the Brazilian semiarid region reveals potential for anti-cancer applications. Archives of Microbiology, 2022, 204, 4.	1.0	0
3798	Genome-based reclassification of Evansella polygoni as a later heterotypic synonym of Evansella clarkii and transfer of Bacillus shivajii and Bacillus tamaricis to the genus Evansella as Evansella shivajii comb. nov. and Evansella tamaricis comb. nov. Archives of Microbiology, 2022, 204, 47.	1.0	21
3799	Gracilibacillus suaedae sp. nov., an indole acetic acid-producing endophyte isolated from a root of Suaeda salsa. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	10
3800	Croceicoccus gelatinilyticus sp. nov., isolated from a tidal flat sediment. Archives of Microbiology, 2022, 204, 93.	1.0	10
3801	The global population structure and evolutionary history of the acquisition of major virulence factor-encoding genetic elements in Shiga toxin-producing Escherichia coli O121:H19. Microbial Genomics, 2021, 7, .	1.0	9
3802	Biogeography of culturable marine bacteria from both poles reveals that â€˜everything is not everywhereâ€™ at the genomic level. Environmental Microbiology, 2022, 24, 98-109.	1.8	5
3803	Genomic adaptations of Campylobacter jejuni to long-term human colonization. Gut Pathogens, 2021, 13, 72.	1.6	5
3804	Halomonas populi sp. nov. isolated from Populus euphratica. Archives of Microbiology, 2022, 204, 86.	1.0	12
3806	The Archaeal Transcription Termination Factor aCPSF1 is a Robust Phylogenetic Marker for Archaeal Taxonomy. Microbiology Spectrum, 2021, 9, e0153921.	1.2	5
3808	Mesorhizobium comanense sp. nov., isolated from groundwater. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	10
3809	Anaerostipes hominis sp. nov., a novel butyrate-producing bacteria isolated from faeces of a patient with Crohn's disease. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	16
3810	Prevotella illustrans sp. nov., derived from human oropharyngeal abscess puncture fluid. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
3811	Lentilactobacillus fungorum sp. nov., isolated from spent mushroom substrates. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6

#	ARTICLE	IF	CITATIONS
3813	A Large-Scale Multiple Genome Comparison of Acidophilic Archaea (pH â‰ 5.0) Extends Our Understanding of Oxidative Stress Responses in Polyextreme Environments. Antioxidants, 2022, 11, 59.	2.2	3
3814	Amsterdam urban canals contain novel niches for methaneâ€cycling microorganisms. Environmental Microbiology, 2022, 24, 82-97.	1.8	8
3815	The Edible Plant Microbiome represents a diverse genetic reservoir with functional potential in the human host. Scientific Reports, 2021, 11, 24017.	1.6	14
3816	A Survey of Chinese Pig Farms and Human Healthcare Isolates Reveals Separate Human and Animal Methicillinâ€Resistant <i>Staphylococcus aureus</i> Populations. Advanced Science, 2022, 9, e2103388.	5.6	13
3817	Integrating cultivation and metagenomics for a multi-kingdom view of skin microbiome diversity and functions. Nature Microbiology, 2022, 7, 169-179.	5.9	58
3818	The economical lifestyle of CPR bacteria in groundwater allows little preference for environmental drivers. Environmental Microbiomes, 2021, 16, 24.	2.2	36
3821	Nocardioides donggukensis sp. nov. and Hyunsoonleella aquatilis sp. nov., isolated from Jeongbang Waterfall on Jeju Island. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	18
3822	Azospirillum tabaci sp. nov., a bacterium isolated from rhizosphere soil of Nicotiana tabacum L. Archives of Microbiology, 2022, 204, 80.	1.0	3
3823	Diverse ecophysiological adaptations of subsurface Thaumarchaeota in floodplain sediments revealed through genome-resolved metagenomics. ISME Journal, 2022, 16, 1140-1152.	4.4	28
3824	Complete Genome Sequences of <i>Kinneretia</i> sp. Strain XES5, <i>Shinella</i> sp. Strain XGS7, and <i>Vogesella</i> sp. Strain XCS3, Isolated from Xenopus laevis Skin. Microbiology Resource Announcements, 2021, 10, e0105021.	0.3	2
3825	Bacillus velezensis: A Treasure House of Bioactive Compounds of Medicinal, Biocontrol and Environmental Importance. Forests, 2021, 12, 1714.	0.9	25
3826	Phylogenomic Reappraisal of Fatty Acid Biosynthesis, Mycolic Acid Biosynthesis and Clinical Relevance Among Members of the Genus Corynebacterium. Frontiers in Microbiology, 2021, 12, 802532.	1.5	12
3827	Single-cell genomics-based analysis reveals a vital ecological role of Thiocapsa sp. LSW in the meromictic Lake Shunet, Siberia. Microbial Genomics, 2021, 7, .	1.0	1
3828	Three Novel Bacteria Associated with Two Centric Diatom Species from the Mediterranean Sea, Thalassiosira rotula and Skeletonema marinoi. International Journal of Molecular Sciences, 2021, 22, 13199.	1.8	5
3829	Desulfovibrio desulfuricans AY5 Isolated from a Patient with Autism Spectrum Disorder Binds Iron in Low-Soluble Greigite and Pyrite. Microorganisms, 2021, 9, 2558.	1.6	6
3830	Prochlorococcus have low global mutation rate and small effective population size. Nature Ecology and Evolution, 2022, 6, 183-194.	3.4	16
3832	Ecoâ€phylogenetic analyses reveal divergent evolution of vitamin <scp>B₁₂</scp> metabolism in the marine bacterial family â€˜<i>Psychromonadaceae</i>â€™. Environmental Microbiology Reports, 2022, 14, 147-163.	1.0	2
3834	Peat-Inhabiting Verrucomicrobia of the Order Methylacidiphilales Do Not Possess Methanotrophic Capabilities. Microorganisms, 2021, 9, 2566.	1.6	9

#	ARTICLE	IF	CITATIONS
3835	Draft Genome Sequence of <i>Desulfovibrio</i> sp. Strain CSMB_222, Isolated from Coal Seam Formation Water. Microbiology Resource Announcements, 2021, 10, e0056421.	0.3	2
3836	Hoyosella lacisalsi sp. nov., a halotolerant actinobacterium isolated from the Lake Gudzhirganskoe. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
3837	Aliidiomarina indica sp. nov., isolated from deep seawater. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	5
3838	Genome Sequence of the Reuterin-Producing Strain Limosilactobacillus reuteri INIA P572. Microbiology Resource Announcements, 2021, 10, e0098821.	0.3	0
3841	Dissecting the dominant hot spring microbial populations based on community-wide sampling at single-cell genomic resolution. ISME Journal, 2022, 16, 1337-1347.	4.4	15
3842	Specific gut microbiome signatures and the associated pro-inflamatory functions are linked to pediatric allergy and acquisition of immune tolerance. Nature Communications, 2021, 12, 5958.	5.8	77
3843	How clear is our current view on microbial dark matter? (Re-)assessing public MAG & SAG datasets with MDMcleaner. Nucleic Acids Research, 2022, 50, e76-e76.	6.5	19
3844	The National Ecological Observatory Networkâ€™s soil metagenomes: assembly and basic analysis. F1000Research, 0, 10, 299.	0.8	2
3845	Metagenomic investigation of the equine faecal microbiome reveals extensive taxonomic diversity. PeerJ, 2022, 10, e13084.	0.9	18
3846	Metagenomic data for Halichondria panicea from Illumina and nanopore sequencing and preliminary genome assemblies for the sponge and two microbial symbionts. BMC Research Notes, 2022, 15, 135.	0.6	5
3847	Identification of BgP, a Cutinase-Like Polyesterase From a Deep-Sea Sponge-Derived Actinobacterium. Frontiers in Microbiology, 2022, 13, 888343.	1.5	12
3848	Genomic and resistome analysis of Alcaligenes faecalis strain PGB1 by Nanopore MinION and Illumina Technologies. BMC Genomics, 2022, 23, 316.	1.2	8
3849	Temporal Transcriptional Responses of a Vibrio alginolyticus Strain to <i>Podoviridae</i> Phage HH109 Revealed by RNA-Seq. MSystems, 2022, 7, e0010622.	1.7	4
3850	Metagenomic signatures of balancing selection in the human gut. Molecular Ecology, 2023, 32, 2582-2591.	2.0	4
3851	Comprehensive Analysis of the Nocardia cyriacigeorgica Complex Reveals Five Species-Level Clades with Different Evolutionary and Pathogenicity Characteristics. MSystems, 2022, 7, e0140621.	1.7	5
3852	Genomic Evidence for the Recycling of Complex Organic Carbon by Novel <i>Thermoplasmatota</i> Clades in Deep-Sea Sediments. MSystems, 2022, , e0007722.	1.7	4
3853	Enhancing predictions of antimicrobial resistance of pathogens by expanding the potential resistance gene repertoire using a pan-genome-based feature selection approach. BMC Bioinformatics, 2022, 23, 131.	1.2	5
3854	Synthetic bacterial community derived from a desert rhizosphere confers salt stress resilience to tomato in the presence of a soil microbiome. ISME Journal, 2022, 16, 1907-1920.	4.4	54

#	ARTICLE	IF	CITATIONS
3855	Comparative genomics analysis of genus Leuconostoc resolves its taxonomy and elucidates its biotechnological importance. Food Microbiology, 2022, 106, 104039.	2.1	11
3857	Metagenomic evidence of a novel family of anammox bacteria in a subsea environment. Environmental Microbiology, 2022, 24, 2348-2360.	1.8	22
3858	In-depth genome analysis of Bacillus sp. BH32, a salt stress-tolerant endophyte obtained from a halophyte in a semiarid region. Applied Microbiology and Biotechnology, 2022, 106, 3113-3137.	1.7	11
3859	Phylogeny and Metabolic Potential of the Candidate Phylum SAR324. Biology, 2022, 11, 599.	1.3	8
3860	Litter Commensal Bacteria Can Limit the Horizontal Gene Transfer of Antimicrobial Resistance to Salmonella in Chickens. Applied and Environmental Microbiology, 2022, 88, e0251721.	1.4	13
3861	Single cell genome sequencing of laboratory mouse microbiota improves taxonomic and functional resolution of this model microbial community. PLoS ONE, 2022, 17, e0261795.	1.1	3
3862	Diversity and distribution of sulfur metabolic genes in the human gut microbiome and their association with colorectal cancer. Microbiome, 2022, 10, 64.	4.9	42
3864	Hydrogenophaga crocea sp. nov. associated with cyanobacterial mat isolated from farmland mud. Archives of Microbiology, 2022, 204, 265.	1.0	0
3865	Reevaluation of Parasynechococcus-like Strains and Genomic Analysis of Their Microsatellites and Compound Microsatellites. Plants, 2022, 11, 1060.	1.6	5
3866	Genomic and metabolic adaptations of biofilms to ecological windows of opportunity in glacier-fed streams. Nature Communications, 2022, 13, 2168.	5.8	25
3867	Genome Streamlining, Proteorhodopsin, and Organic Nitrogen Metabolism in Freshwater Nitrifiers. MBio, 2022, 13, e0237921.	1.8	7
3868	Secreted NF-Î°B suppressive microbial metabolites modulate gut inflammation. Cell Reports, 2022, 39, 110646.	2.9	22
3869	Phylogeny, distribution and potential metabolism of candidate bacterial phylum KSB1. PeerJ, 2022, 10, e13241.	0.9	3
3871	Comparative Genomics Reveals Genetic Diversity and Metabolic Potentials of the Genus <i>Qipengyuania</i> and Suggests Fifteen Novel Species. Microbiology Spectrum, 2022, 10, e0126421.	1.2	55
3872	Coral holobiont cues prime <i>Endozoicomonas</i> for a symbiotic lifestyle. ISME Journal, 2022, 16, 1883-1895.	4.4	36
3873	Draft Genome Sequence from a Putative New Genus and Species in the Family <i>M1A02</i> within the Phylum <i>Planctomycetes</i> , Isolated from Benthic Pinnacle Mats in Lake Untersee, Antarctica. Microbiology Resource Announcements, 2022, , e0119221.	0.3	0
3874	Comparative Genomic Analysis of Vibrio cincinnatiensis Provides Insights into Genetic Diversity, Evolutionary Dynamics, and Pathogenic Traits of the Species. International Journal of Molecular Sciences, 2022, 23, 4520.	1.8	3
3875	Genome-based, phenotypic and chemotaxonomic classification of Faecalibacterium strains: proposal of three novel species Faecalibacterium duncaniae sp. nov., Faecalibacterium hattorii sp. nov. and Faecalibacterium gallinarum sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	36

#	Article	IF	Citations
3876	Comparative Genomics of Members of the Genus Defluviicoccus With Insights Into Their Ecophysiological Importance. Frontiers in Microbiology, 2022, 13, 834906.	1.5	8
3877	Effect of sulfur sources on the competition between denitrification and DNRA. Environmental Pollution, 2022, 305, 119322.	3.7	26
4480	Integrative Genomics Sheds Light on Evolutionary Forces Shaping the Acidithiobacillia Class Acidophilic Lifestyle. Frontiers in Microbiology, 2021, 12, 822229.	1.5	10
4481	Metagenomic methylation patterns resolve bacterial genomes of unusual size and structural complexity. ISME Journal, 2022, 16, 1921-1931.	4.4	11
4482	Genome sequences of <i>Rhizopogon roseolus</i>, <i>Mariannaea elegans, Myrothecium verrucaria</i> and <i>Sphaerostilbella broomeana</i> and the identification of biosynthetic gene clusters for fungal peptide natural products. G3: Genes, Genomes, Genetics, 2022, , .	0.8	0
4483	Sabulibacter ruber gen. nov., sp. nov., a novel bacterium in the family Hymenobacteraceae, isolated from desert soil. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	8
4484	Companilactobacillus salsicarnum Zheng et al. 2020 is a later heterotypic synonym of Companilactobacillus mishanensis (Wei and Gu 2019) Zheng et al. 2020. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	3
4485	Pusillimonas minor sp. nov., a novel member of the genus Pusillimonas isolated from activated sludge. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	6
4486	Paenalcaligenes niemegkensis sp. nov., a novel species of the family Alcaligenaceae isolated from plastic waste. International Journal of Systematic and Evolutionary Microbiology, 2022, 71, .	0.8	1
4487	Luteimonas saliphila sp. nov. and Luteimonas salinisoli sp. nov., two novel strains isolated from saline soils. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	11
4488	Genomic and phenotypic analyses of diverse non-clinical Acinetobacter baumannii strains reveals strain-specific virulence and resistance capacity. Microbial Genomics, 2022, 8, .	1.0	7
4489	Characterisation of the symbionts in the Mediterranean fruit fly gut. Microbial Genomics, 2022, 8, .	1.0	3
4490	Into the darkness: the ecologies of novel â€˜microbial dark matterâ€™ phyla in an Antarctic lake. Environmental Microbiology, 2022, 24, 2576-2603.	1.8	9
4491	Precision Probiotics in Agroecosystems: Multiple Strategies of Native Soil Microbiotas for Conquering the Competitor Ralstonia solanacearum. MSystems, 2022, 7, e0115921.	1.7	4
4492	Whole-Genome Shotgun Metagenomic Sequencing Reveals Distinct Gut Microbiome Signatures of Obese Cats. Microbiology Spectrum, 2022, 10, e0083722.	1.2	15
4494	fIDBAC: A Platform for Fast Bacterial Genome Identification and Typing. Frontiers in Microbiology, 2021, 12, 723577.	1.5	9
4495	MetaCoAG: Binning Metagenomic Contigs viaÂComposition, Coverage andÂAssembly Graphs. Lecture Notes in Computer Science, 2022, , 70-85.	1.0	5
4497	Enhanced Cultured Diversity of the Mouse Gut Microbiota Enables Custom-Made Synthetic Communities. SSRN Electronic Journal, 0, , .	0.4	1

#	ARTICLE	IF	CITATIONS
4498	Ancient Diatom DNA. , 2022, , 87-108.		1
4499	CLMB: Deep Contrastive Learning forÂRobust Metagenomic Binning. Lecture Notes in Computer Science, 2022, , 326-348.	1.0	4
4500	Functional Insights of Salinity Stress-Related Pathways in Metagenome-Resolved <i>Methanothrix</i> Genomes. Applied and Environmental Microbiology, 2022, 88, e0244921.	1.4	8
4501	Comparative Genomics of Xylella fastidiosa Explores Candidate Host-Specificity Determinants and Expands the Known Repertoire of Mobile Genetic Elements and Immunity Systems. Microorganisms, 2022, 10, 914.	1.6	8
4502	The car tank lid bacteriome: a reservoir of bacteria with potential in bioremediation of fuel. Npj Biofilms and Microbiomes, 2022, 8, 32.	2.9	6
4503	ABO genotype alters the gut microbiota by regulating GalNAc levels in pigs. Nature, 2022, 606, 358-367.	13.7	67
4504	Impact of different organic matters on the occurrence of antibiotic resistance genes in activated sludge. Journal of Environmental Sciences, 2023, 127, 273-283.	3.2	6
4506	Metagenome-assembled genomes of phytoplankton microbiomes from the Arctic and Atlantic Oceans. Microbiome, 2022, 10, 67.	4.9	17
4507	A deep siamese neural network improves metagenome-assembled genomes in microbiome datasets across different environments. Nature Communications, 2022, 13, 2326.	5.8	47
4508	Nocardioides alcanivorans sp. nov., a novel hexadecane-degrading species isolated from plastic waste. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	6
4510	Genomic Sequencing of Bacillus cereus Sensu Lato Strains Isolated from Meat and Poultry Products in South Africa Enables Inter- and Intranational Surveillance and Source Tracking. Microbiology Spectrum, 2022, 10, e0070022.	1.2	4
4511	Evolution of the murine gut resistome following broad-spectrum antibiotic treatment. Nature Communications, 2022, 13, 2296.	5.8	16
4512	Comparative genomic analysis of <i>Thermus</i> provides insights into the evolutionary history of an incomplete denitrification pathway. , 0, , .		3
4513	Halalkalibacterium roseum gen. nov., sp. nov., a new member of the family Balneolaceae isolated from soil. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	9
4514	Discovery of Early-Branching Wolbachia Reveals Functional Enrichment on Horizontally Transferred Genes. Frontiers in Microbiology, 2022, 13, 867392.	1.5	6
4515	A Novel Isolate of Spherical Multicellular Magnetotactic Prokaryotes Has Two Magnetosome Gene Clusters and Synthesizes Both Magnetite and Greigite Crystals. Microorganisms, 2022, 10, 925.	1.6	1
4517	Metagenomic Insights Into Competition Between Denitrification and Dissimilatory Nitrate Reduction to Ammonia Within One-Stage and Two-Stage Partial-Nitritation Anammox Bioreactor Configurations. Frontiers in Microbiology, 2022, 13, 825104.	1.5	9
4518	Bioprospecting of Plant Growth-Promoting Traits of Pseudomonas sp. Strain C3 Isolated from the Atacama Desert: Molecular and Culture-Based Analysis. Diversity, 2022, 14, 388.	0.7	5

#	ARTICLE	IF	CITATIONS
4519	Sugars dominate the seagrass rhizosphere. Nature Ecology and Evolution, 2022, 6, 866-877.	3.4	27
4520	Qipengyuania thermophila sp. nov., isolated from a Chinese hot spring. Archives of Microbiology, 2022, 204, 305.	1.0	2
4521	Hybrid Plasmids Encoding Antimicrobial Resistance and Virulence Traits Among Hypervirulent Klebsiella pneumoniae ST2096 in India. Frontiers in Cellular and Infection Microbiology, 2022, 12, 875116.	1.8	15
4523	Microbiome â€œInceptionâ€: an Intestinal Cestode Shapes a Hierarchy of Microbial Communities Nested within the Host. MBio, 2022, 13, e0067922.	1.8	8
4524	Genomic diversity across the Rickettsia and â€˜Candidatus Megairaâ€™ genera and proposal of genus status for the Torix group. Nature Communications, 2022, 13, 2630.	5.8	22
4525	Complete Genome Sequence of <i>Bacillus</i> sp. Strain TM2, Isolated from Ground <i>Tetragnatha</i> Spider Extract. Microbiology Resource Announcements, 2022, , e0013022.	0.3	1
4527	Metagenome assembly of high-fidelity long reads with hifiasm-meta. Nature Methods, 2022, 19, 671-674.	9.0	56
4528	Novel Chloroflexi genomes from the deepest ocean reveal metabolic strategies for the adaptation to deep-sea habitats. Microbiome, 2022, 10, 75.	4.9	42
4529	Draft Genome Sequence of the Marine <i>Flavobacteriaceae</i> sp. Strain LSUCC0859. Microbiology Resource Announcements, 2022, 11, e0018622.	0.3	0
4530	The in-situ release of algal bloom populations and the role of prokaryotic communities in their establishment and growth. Water Research, 2022, 219, 118565.	5.3	13
4531	The coâ€occurrence of antibiotic resistance genes between dogs and their owners in families. , 2022, 1, .		14
4532	Recovery of Metagenome-Assembled Genomes from a Human Fecal Sample with Pacific Biosciences High-Fidelity Sequencing. Microbiology Resource Announcements, 2022, 11, e0025022.	0.3	3
4533	Enzymatically triggered delignification through a novel stable laccase: A mixed in-silico /in-vitro exploration of a complex environmental microbiota. International Journal of Biological Macromolecules, 2022, 211, 328-341.	3.6	9
4534	Complete Genome Sequences of Two Closely Related Paenarthrobacter nicotinovorans Strains. Microbiology Resource Announcements, 2022, 11, e0013322.	0.3	2
4535	Intracellular silicification by early-branching magnetotactic bacteria. Science Advances, 2022, 8, eabn6045.	4.7	11
4536	Whole genome sequencing of cyanobacterium Nostoc sp. CCCryo 231-06 using microfluidic single cell technology. IScience, 2022, 25, 104291.	1.9	6
4537	Comparative Analysis and Data Provenance for 1,113 Bacterial Genome Assemblies. MSphere, 2022, 7, e0007722.	1.3	4
4538	Comparative Genomic Analysis Revealed Distinct Molecular Components and Organization of CO2-Concentrating Mechanism in Thermophilic Cyanobacteria. Frontiers in Microbiology, 2022, 13, .	1.5	10

#	Article	IF	Citations
4539	Persisting uropathogenic Escherichia coli lineages show signatures of niche-specific within-host adaptation mediated by mobile genetic elements. Cell Host and Microbe, 2022, 30, 1034-1047.e6.	5.1	13
4540	<i>Escherichia coli</i> Strains from Patients with Inflammatory Bowel Diseases have Disease-specific Genomic Adaptations. Journal of Crohn's and Colitis, 2022, 16, 1584-1597.	0.6	5
4541	Variation in Root Exudate Composition Influences Soil Microbiome Membership and Function. Applied and Environmental Microbiology, 2022, 88, e0022622.	1.4	30
4542	Meta-Omics-Supervised Characterization of Respiration Activities Associated with Microbial Immigrants in Anaerobic Sludge Digesters. Environmental Science & Technology, 2022, 56, 6689-6698.	4.6	4
4543	Meta-Omics reveal the metabolic acclimation of freshwater anammox bacteria for saline wastewater treatment. Journal of Cleaner Production, 2022, 362, 132184.	4.6	5
4544	Pararoseburia lenta gen. nov., sp. nov. isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	10
4546	Microbially promoted calcite precipitation in the pelagic redoxcline: Elucidating the formation of the turbid layer. Geobiology, 2022, 20, 498-517.	1.1	5
4547	Discovery of lignin-transforming bacteria and enzymes in thermophilic environments using stable isotope probing. ISME Journal, 2022, 16, 1944-1956.	4.4	16
4548	High-Resolution Metagenomics of Human Gut Microbiota Generated by Nanopore and Illumina Hybrid Metagenome Assembly. Frontiers in Microbiology, 2022, 13, .	1.5	4
4549	Description of two novel anaerobic members in the family Clostridiaceae, Anaeromonas gelatinilytica gen.nov., sp. nov., and Anaeromonas frigoriresistens sp. nov., isolated from saline lake sediment. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	9
4550	Copranaerobaculum intestinale gen. nov., sp. nov., a novel anaerobic bacterium isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	6
4551	Pontibrevibacter nitratireducens gen. nov., sp. nov., a member of the family Rhodobacteraceae isolated from seawater of the Indian Ocean and intertidal zone. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	7
4552	Patterns and ecological drivers of viral communities in acid mine drainage sediments across Southern China. Nature Communications, 2022, 13, 2389.	5.8	25
4554	A putatively new family of alphaproteobacterial chloromethane degraders from a deciduous forest soil revealed by stable isotope probing and metagenomics. Environmental Microbiomes, 2022, 17, 24.	2.2	0
4556	Helicobacter cinaedi is a human-adapted lineage in the Helicobacter cinaedi/canicola/â€˜magdeburgensisâ€™ complex. Microbial Genomics, 2022, 8, .	1.0	4
4557	Phylogeny and Metabolic Potential of the Methanotrophic Lineage MO3 in Beijerinckiaceae from the Paddy Soil through Metagenome-Assembled Genome Reconstruction. Microorganisms, 2022, 10, 955.	1.6	3
4558	Draft Reference Genome Sequence of Corynebacterium mastitidis RC, an Ocular Commensal, Isolated from Mouse Conjunctiva. Microbiology Resource Announcements, 2022, , e0018722.	0.3	1
4559	Metagenomic exploration of antibiotic resistance genes and their hosts in aquaculture waters of the semi-closed Dongshan Bay (China). Science of the Total Environment, 2022, 838, 155784.	3.9	12

#	Article	IF	Citations
4560	Elevated temperature alters bacterial community composition and metabolism in seawaters of coral reef ecosystem: An evidence of laboratory experiment with Acropora digitifera bleaching. Ecological Indicators, 2022, 139, 108886.	2.6	5
4561	Revealing the microbial heritage of traditional Brazilian cheeses through metagenomics. Food Research International, 2022, 157, 111265.	2.9	12
4562	Extracellular fructooligosaccharide degradation in Anaerostipes hadrus for co-metabolism with non-fructooligosaccharide utilizers. Biochemical and Biophysical Research Communications, 2022, 613, 81-86.	1.0	7
4563	Investigation of microbial metabolisms in an extremely high pH marine-like terrestrial serpentinizing system: Ney Springs. Science of the Total Environment, 2022, 836, 155492.	3.9	15
4564	Holistic approach to chemical and microbiological quality of aquatic ecosystems impacted by wastewater effluent discharges. Science of the Total Environment, 2022, 835, 155388.	3.9	6
4565	Halorhabdus amylolytica sp. nov. and Halorhabdus salina sp. nov., isolated from hypersaline environments. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	7
4566	Comparative Genomic Analysis of Two Xanthomonas oryzae pv. oryzae Strains Isolated From Low Land and High Mountain Paddies in Guangxi, China. Frontiers in Microbiology, 2022, 13, 867633.	1.5	2
4567	Fibrella aquatilis sp. nov., Fibrella rubiginis sp. nov. and Fibrella forsythiae sp. nov., isolated from freshwater, rusty iron and forsythia flower. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	10
4568	Description and characterization of three endophytic Bacillaceae from the halophyte Suaeda salsa: Paenalkalicoccus suaedae gen. nov., sp. nov., Cytobacillus suaedae sp. nov., and Bacillus suaedae sp. nov. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	20
4569	Generation and application of pseudoâ€"long reads for metagenome assembly. GigaScience, 2022, 11, .	3.3	4
4570	Genetic and Phenotypic Study of the <i>Pectobacterium versatile</i> Beta-Lactamase, the Enzyme Most Similar to the Plasmid-Encoded TEM-1. Applied and Environmental Microbiology, 2022, 88, e0022022.	1.4	2
4571	Metagenomes from 25 Low-Abundance Microbes in a Partial Nitritation Anammox Microbiome. Microbiology Resource Announcements, 2022, 11, e0021222.	0.3	2
4572	Draft Genome Sequence of the Novel, Moderately Thermophilic, Iron- and Sulfur-Oxidizing Firmicute Strain Y002, Isolated from an Extremely Acidic Geothermal Environment. Microbiology Resource Announcements, 2022, , e0014922.	0.3	1
4573	Genomic, morphological, and biochemical analyses of a multi-metal resistant but multi-drug susceptible strain of Bordetella petrii from hospital soil. Scientific Reports, 2022, 12, 8439.	1.6	11
4574	Phenylobacterium glaciei sp. nov., isolated from Vestrebroggerbreen, a valley glacier in Svalbard, Arctic. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	5
4575	Vagococcus allomyrinae sp. nov. and Enterococcus larvae sp. nov., isolated from larvae of Allomyrina dichotoma. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	10
4576	Investigating plant disease outbreaks with long-read metagenomics: sensitive detection and highly resolved phylogenetic reconstruction applied to Xylella fastidiosa. Microbial Genomics, 2022, 8, .	1.0	5
4577	Draft Genome Sequence of Vibrio mediterranei Strain CyArs1. Microbiology Resource Announcements, 2022, , e0015522.	0.3	0

#	Article	IF	Citations
4578	Complete Genome Sequence of <i>Limosilactobacillus reuteri</i> Strain VHProbi E18, Isolated from Feces of an Old Man. Microbiology Resource Announcements, 2022, 11, e0121121.	0.3	2
4579	Phylogenetic and protein prediction analysis reveals the taxonomically diverse distribution of virulence factors in Bacillus cereus strains. PLoS ONE, 2022, 17, e0262974.	1.1	0
4586	MIntO: A Modular and Scalable Pipeline For Microbiome Metagenomic and Metatranscriptomic Data Integration. Frontiers in Bioinformatics, 2022, 2, .	1.0	5
4587	Effects of Spartina alterniflora Invasion on Nitrogen Fixation and Phosphorus Solubilization in a Subtropical Marine Mangrove Ecosystem. Microbiology Spectrum, 2022, 10, .	1.2	9
4589	Comparative Genomics of Acetic Acid Bacteria within the Genus Bombella in Light of Beehive Habitat Adaptation. Microorganisms, 2022, 10, 1058.	1.6	6
4591	Introducing <i>Candidatus</i> Bathyanammoxibiaceae, a family of bacteria with the anammox potential present in both marine and terrestrial environments. ISME Communications, 2022, 2, .	1.7	16
4592	Plume Layer Influences the Amazon Reef Sponge Microbiome Primary Producers. Frontiers in Marine Science, 2022, 9, .	1.2	3
4594	Effect of magnetite addition on transcriptional profiles of syntrophic <i>Bacteria</i> and <i>Archaea</i> during anaerobic digestion of propionate in wastewater sludge. Environmental Microbiology Reports, 2022, 14, 664-678.	1.0	4
4595	The functional evolution of termite gut microbiota. Microbiome, 2022, 10, .	4.9	35
4596	Phylogenomic Analyses of <i>Snodgrassella</i> Isolates from Honeybees and Bumblebees Reveal Taxonomic and Functional Diversity. MSystems, 2022, 7, .	1.7	19
4598	Ecological dynamics of the gut microbiome in response to dietary fiber. ISME Journal, 2022, 16, 2040-2055.	4.4	38
4599	Biofilm: A strategy for the dominance of comammox Nitrospira. Journal of Cleaner Production, 2022, 363, 132361.	4.6	9
4600	Isolation and Genome Analysis of an Amoeba-Associated Bacterium Dyella terrae Strain Ely Copper Mine From Acid Rock Drainage in Vermont, United States. Frontiers in Microbiology, 2022, 13, .	1.5	1
4601	Changes in the Metagenome-Encoded CAZymes of the Rumen Microbiome Are Linked to Feed-Induced Reductions in Methane Emission From Holstein Cows. Frontiers in Microbiology, 2022, 13, .	1.5	2
4603	Natronocalculus amylovorans gen. nov., sp. nov., and Natranaeroarchaeum aerophilus sp. nov., dominant culturable amylolytic natronoarchaea from hypersaline soda lakes in southwestern Siberia. Systematic and Applied Microbiology, 2022, 45, 126336.	1.2	4
4604	Draft Genome Sequences of Eight Bacilli Isolated from an Ancient Roman Amphora. Microbiology Resource Announcements, 0, , .	0.3	1
4605	Ecology and evolution of chlamydial symbionts of arthropods. ISME Communications, 2022, 2, .	1.7	8
4607	Apilactobacillus zhangqiuensis sp. nov. and Apilactobacillus xinyiensis sp. nov., isolated from the gut of honeybee (Apis mellifera). International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	9

#	ARTICLE	IF	CITATIONS
4608	Genome Evolution of Invasive Methicillin-Resistant Staphylococcus aureus in the Americas. Microbiology Spectrum, 2022, 10, .	1.2	4
4609	Bacterial colonisation dynamics of household plastics in a coastal environment. Science of the Total Environment, 2022, 838, 156199.	3.9	12
4610	Bifidobacterium mizhiense sp. nov., isolated from the gut of honeybee (Apis mellifera). International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	6
4611	Novosphingobium percolationis sp. nov. and Novosphingobium huizhouense sp. nov., isolated from landfill leachate of a domestic waste treatment plant. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	11
4613	Metagenomic, (bio)chemical, and microscopic analyses reveal the potential for the cycling of sulfated EPS in Shark Bay pustular mats. ISME Communications, 2022, 2, .	1.7	5
4615	Probiotics synergized with conventional regimen in managing Parkinsonâ€™s disease. Npj Parkinson's Disease, 2022, 8, .	2.5	39
4616	Prevotella species in the human gut is primarily comprised of Prevotella copri, Prevotella stercorea and related lineages. Scientific Reports, 2022, 12, .	1.6	28
4617	Draft Genome Sequence of Plesiomonas shigelloides Strain zfcc0051 (Phylum <i>Proteobacteria</i>). Microbiology Resource Announcements, 0, , .	0.3	0
4618	Pangenome analyses of Bacillus pumilus, Bacillus safensis, and Priestia megaterium exploring the plant-associated features of bacilli strains isolated from canola. Molecular Genetics and Genomics, 2022, 297, 1063-1079.	1.0	19
4620	Characteristics of Stenotrophomonas maltophilia isolates from cystic fibrosis patients in Russia. Klinicheschesкaya Laboratornaya Diagnostika, 2022, 67, 315-320.	0.2	0
4622	Algoriphagus algorifonticola sp. nov., a marine bacterium isolated from cold spring area of South China Sea. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	4
4623	Metagenomics Reveals Dominant Unusual Sulfur Oxidizers Inhabiting Active Hydrothermal Chimneys From the Southwest Indian Ridge. Frontiers in Microbiology, 2022, 13, .	1.5	4
4624	Metagenomes of Red Sea Subpopulations Challenge the Use of Marker Genes and Morphology to Assess Trichodesmium Diversity. Frontiers in Microbiology, 2022, 13, .	1.5	4
4627	Pseudomonas oligotrophica sp. nov., a Novel Denitrifying Bacterium Possessing Nitrogen Removal Capability Under Low Carbonâ€"Nitrogen Ratio Condition. Frontiers in Microbiology, 2022, 13, .	1.5	8
4628	CABGen: A Web Application for the Bioinformatic Analysis of Bacterial Genomes. Frontiers in Microbiology, 2022, 13, .	1.5	0
4630	Genome size distributions in bacteria and archaea are strongly linked to evolutionary history at broad phylogenetic scales. PLoS Genetics, 2022, 18, e1010220.	1.5	20
4632	Detection of a Novel Metallo-Î²-Lactamase, CAM-2, in a Metagenome-Assembled Genome from China. Microbiology Spectrum, 2022, 10, .	1.2	2
4633	A Dual Enrichment Strategy Provides Soil- and Digestate-Competent Nitrous Oxide-Respiring Bacteria for Mitigating Climate Forcing in Agriculture. MBio, 2022, 13, .	1.8	5

#	Article	IF	Citations
4634	Genomic Surveillance of Clinical Pseudomonas aeruginosa Isolates Reveals an Additive Effect of Carbapenemase Production on Carbapenem Resistance. Microbiology Spectrum, 2022, 10, .	1.2	4
4635	Mineralogical and Genomic Constraints on the Origin of Microbial Mn Oxide Formation in Complexed Microbial Community at the Terrestrial Hot Spring. Life, 2022, 12, 816.	1.1	1
4636	Antibiotic-resistant organisms establish reservoirs in new hospital built environments and are related to patient blood infection isolates. Communications Medicine, 2022, 2, .	1.9	21
4637	Water quality drives the distribution of freshwater cable bacteria. Science of the Total Environment, 2022, 841, 156468.	3.9	6
4639	High-throughput, single-microbe genomics with strain resolution, applied to a human gut microbiome. Science, 2022, 376, .	6.0	100
4640	HT-ARGfinder: A Comprehensive Pipeline for Identifying Horizontally Transferred Antibiotic Resistance Genes and Directionality in Metagenomic Sequencing Data. Frontiers in Environmental Science, 2022, 10, .	1.5	2
4641	Dynamics of Salmonella enterica and antimicrobial resistance in the Brazilian poultry industry and global impacts on public health. PLoS Genetics, 2022, 18, e1010174.	1.5	13
4642	Evansella halocellulosilytica sp. nov., an alkali-halotolerant and cellulose-dissolving bacterium isolated from bauxite residue. Extremophiles, 2022, 26, .	0.9	3
4643	Genomic and Physiological Characterization of Halophilic Bacteria of the Genera Halomonas and Marinobacter from Petroleum Reservoirs. Microbiology, 2022, 91, 235-248.	0.5	7
4644	Phylogenomic Analysis of Metagenome-Assembled Genomes Deciphered Novel Acetogenic Nitrogen-Fixing <i>Bathyarchaeota</i> from Hot Spring Sediments. Microbiology Spectrum, 2022, 10, .	1.2	5
4645	Recovery of metagenome-assembled genomes from the phyllosphere of 110 rice genotypes. Scientific Data, 2022, 9, .	2.4	5
4646	Micron-scale biogeography reveals conservative intra anammox bacteria spatial co-associations. Water Research, 2022, 220, 118640.	5.3	12
4647	Comparative analysis of nitrogen removals and microbial communities in air and pure oxygen aeration systems during treatment of municipal solid waste incineration (MSWI) leachate. Journal of Water Process Engineering, 2022, 48, 102900.	2.6	0
4648	Draft Genomes of Nitrogen-fixing<i> Frankia</i> Strains Ag45/Mut15 and AgPM24 Isolated from Root Nodules of <i>Alnus Glutinosa</i>. Journal of Genomics, 2022, 10, 49-56.	0.6	4
4650	Diversity of <i>Candidatus</i> Patescibacteria in Activated Sludge Revealed by a Size-â€Fractionation Approach. Microbes and Environments, 2022, 37, n/a.	0.7	3
4651	Textile Industry Wastewater Microbiome: Recovery of Metagenome Assembled Genomes (Mags) Using Shotgun Sequencing Approach from Jetpur, Gujarat, India. SSRN Electronic Journal, 0, , .	0.4	0
4652	Binning Metagenomic Contigs Using Unsupervised Clustering and Reference Databases. Interdisciplinary Sciences, Computational Life Sciences, 0, , .	2.2	0
4653	Marinilactibacillus kalidii sp. nov., an Indole Acetic Acid-Producing Endophyte Isolated from a Shoot of Halophyte Kalidium cuspidatum. Current Microbiology, 2022, 79, .	1.0	10

#	ARTICLE	IF	CITATIONS
4655	Denitrification in foraminifera has an ancient origin and is complemented by associated bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	9
4656	MarkerMAG: linking metagenome-assembled genomes (MAGs) with 16S rRNA marker genes using paired-end short reads. Bioinformatics, 2022, 38, 3684-3688.	1.8	6
4657	Genome-based reclassification of Streptococcus ursoris as a later heterotypic synonym of Streptococcus ratti. Archives of Microbiology, 2022, 204, .	1.0	0
4659	Cultured Bacteria Provide Insight into the Functional Potential of the Coral-Associated Microbiome. MSystems, 2022, 7, .	1.7	14
4660	An Isolated Arthrobacter sp. Enhances Rice (Oryza sativa L.) Plant Growth. Microorganisms, 2022, 10, 1187.	1.6	14
4661	Lignocellulose degradation in Protaetia brevitarsis larvae digestive tract: refining on a tightly designed microbial fermentation production line. Microbiome, 2022, 10, .	4.9	18
4662	How Microbiome Composition Correlates with Biochemical Changes during Sauerkraut Fermentation: a Focus on Neglected Bacterial Players and Functionalities. Microbiology Spectrum, 2022, 10, .	1.2	14
4663	Genomic analysis of Acinetobacter pittii CEP14 reveals its extensive biodegradation capabilities, including cometabolic degradation of cis-1,2-dichloroethene. Antonie Van Leeuwenhoek, 2022, 115, 1041-1057.	0.7	3
4664	Genomic Characterization of Mobile Genetic Elements Associated With Carbapenem Resistance of Acinetobacter baumannii From India. Frontiers in Microbiology, 0, 13, .	1.5	9
4666	Mutual Exclusion of <i>Methanobrevibacter</i> Species in the Human Gut Microbiota Facilitates Directed Cultivation of a <i>Candidatus</i> Methanobrevibacter Intestini Representative. Microbiology Spectrum, 2022, 10, .	1.2	6
4667	A metagenomic portrait of the microbial community responsible for two decades of bioremediation of poly-contaminated groundwater. Water Research, 2022, 221, 118767.	5.3	11
4668	Rhodococcus oxybenzonivorans sp. nov., a benzophenone-3-degrading bacterium, isolated from stream sediment. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	6
4669	Gramella crocea sp. nov., isolated from activated sludge of a seafood processing plant. Antonie Van Leeuwenhoek, 2022, 115, 969-978.	0.7	3
4670	Endosymbiont population genomics sheds light on transmission mode, partner specificity, and stability of the scaly-foot snail holobiont. ISME Journal, 2022, 16, 2132-2143.	4.4	6
4671	Rheinheimera maricola sp. nov., isolated from seawater of the Yellow Sea. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	8
4672	Genome Sequence and Characterization of a Xanthorhodopsin-Containing, Aerobic Anoxygenic Phototrophic Rhodobacter Species, Isolated from Mesophilic Conditions at Yellowstone National Park. Microorganisms, 2022, 10, 1169.	1.6	3
4674	Functional and phylogenetic analyses of camel rumen microbiota associated with different lignocellulosic substrates. Npj Biofilms and Microbiomes, 2022, 8, .	2.9	15
4675	Complete Genome Sequences of Four Bacteria Isolated from the Gut of a Spiny Ant (<i>Polyrhachis) Tj ETQq1 1 0.784314 rgBT /Overl	0.3	1

#	Article	IF	Citations
4676	Globally distributed mining-impacted environments are underexplored hotspots of multidrug resistance genes. ISME Journal, 2022, 16, 2099-2113.	4.4	35
4677	Robust variation in infant gut microbiome assembly across a spectrum of lifestyles. Science, 2022, 376, 1220-1223.	6.0	63
4678	Disturbance-based management of ecosystem services and disservices in partial nitritation-anammox biofilms. Npj Biofilms and Microbiomes, 2022, 8, .	2.9	5
4679	Halomonas jincaotanensis sp. nov., isolated from the Pamir Plateau degrading polycyclic aromatic hydrocarbon. Archives of Microbiology, 2022, 204, .	1.0	4
4680	Complete Genome Sequences of Rhizobium gallicum M101 and Two Potential New <i>Rhizobium</i> Species Isolated from Soils in Central Canada. Microbiology Resource Announcements, 2022, 11, .	0.3	1
4681	Growth of nitriteâ€oxidizing <i>Nitrospira</i> and ammoniaâ€oxidizing <i>Nitrosomonas</i> in marine recirculating trickling biofilter reactors. Environmental Microbiology, 2022, 24, 3735-3750.	1.8	4
4682	Genomic characterization of Streptococcus parasuis, a close relative of Streptococcus suis and also a potential opportunistic zoonotic pathogen. BMC Genomics, 2022, 23, .	1.2	6
4683	Genome-Scale Mutational Analysis of Cathode-Oxidizing Thioclava electrotropha ElOx9T. Frontiers in Microbiology, 0, 13, .	1.5	0
4684	Characterization of Kordiimonas marina sp. nov. and Kordiimonas laminariae sp. nov. and Comparative Genomic Analysis of the Genus Kordiimonas, A Marine-Adapted Taxon. Frontiers in Marine Science, 0, 9, .	1.2	11
4685	Combined read- and assembly-based metagenomics to reconstruct a <i>Dehalococcoides mccartyi</i> genome from PCB-contaminated sediments and evaluate functional differences among organohalide-respiring consortia in the presence of different halogenated contaminants. FEMS Microbiology Ecology, 2022, 98, .	1.3	3
4686	500 metagenome-assembled microbial genomes from 30 subtropical estuaries in South China. Scientific Data, 2022, 9, .	2.4	9
4687	MAGNETO: An Automated Workflow for Genome-Resolved Metagenomics. MSystems, 2022, 7, .	1.7	7
4688	Disentangling the genetic basis of rhizosphere microbiome assembly in tomato. Nature Communications, 2022, 13, .	5.8	53
4689	Genome Sequence of Ralstonia pseudosolanacearum SL1931, a Causal Phytopathogen of Bacterial Wilt Disease in Capsicum annuum and Nicotiana benthamiana. Microbiology Resource Announcements, 0, , .	0.3	0
4690	CleanSeq: A Pipeline for Contamination Detection, Cleanup, and Mutation Verifications from Microbial Genome Sequencing Data. Applied Sciences (Switzerland), 2022, 12, 6209.	1.3	3
4691	Whole-Genome Sequencing of <i>Staphylococcus aureus</i> and <i>Staphylococcus haemolyticus</i> Clinical Isolates from Egypt. Microbiology Spectrum, 2022, 10, .	1.2	7
4692	Pangenome Evolution in Environmentally Transmitted Symbionts of Deep-Sea Mussels Is Governed by Vertical Inheritance. Genome Biology and Evolution, 2022, 14, .	1.1	5
4693	The OceanDNA MAG catalog contains over 50,000 prokaryotic genomes originated from various marine environments. Scientific Data, 2022, 9, .	2.4	29

#	Article	IF	Citations
4694	Metagenome-Assembled Genomes of Bacterial Symbionts Associated with Insecticide-Resistant and -Susceptible Individuals of the Glassy-Winged Sharpshooter (Homalodisca vitripennis). Microbiology Resource Announcements, 2022, 11, .	0.3	4
4695	Sphingopyxis lutea sp. nov., a novel moderately halotolerant bacterium isolated from pebbles. Archives of Microbiology, 2022, 204, .	1.0	1
4696	The CRISPR/Cas Machinery Evolution and Gene Flow in the Hot Spring Cyanobacterium Thermostichus. Diversity, 2022, 14, 502.	0.7	2
4697	Introduction to the principles and methods underlying the recovery of metagenomeâ€assembled genomes from metagenomic data. MicrobiologyOpen, 2022, 11, .	1.2	8
4698	The Distinguishing Bacterial Features From Active and Remission Stages of Ulcerative Colitis Revealed by Paired Fecal Metagenomes. Frontiers in Microbiology, 0, 13, .	1.5	1
4699	Differentiated Evolutionary Strategies of Genetic Diversification in Atlantic and Pacific Thaumarchaeal Populations. MSystems, 2022, 7, .	1.7	3
4701	Physiologic, Genomic, and Electrochemical Characterization of Two Heterotrophic Marine Sediment Microbes from the Idiomarina Genus. Microorganisms, 2022, 10, 1219.	1.6	0
4702	Genome-Resolved Characterization of Structure and Potential Functions of the Zebrafish Stool Microbiome. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	3
4703	Moraxella tetraodonis sp. nov., isolated from freshwater pufferfish (Tetraodon cutcutia) skin. Archives of Microbiology, 2022, 204, .	1.0	2
4704	Unique pool of carbohydrate-degrading enzymes in novel bacteria assembled from cow and buffalo rumen metagenomes. Applied Microbiology and Biotechnology, 2022, 106, 4643-4654.	1.7	4
4705	Recovery of High Quality Metagenome-Assembled Genomes From Full-Scale Activated Sludge Microbial Communities in a Tropical Climate Using Longitudinal Metagenome Sampling. Frontiers in Microbiology, 0, 13, .	1.5	8
4707	Metagenomics to characterize sediment microbial biodiversity associated with fishing exposure within the Stellwagen Bank National Marine Sanctuary. Scientific Reports, 2022, 12, .	1.6	6
4710	The Microbial Community and Functional Potential in the Midland Basin Reveal a Community Dominated by Both Thiosulfate and Sulfate-Reducing Microorganisms. Microbiology Spectrum, 2022, 10, .	1.2	5
4711	Flavobacterium taihuense sp. nov., a bacterium isolated from lake sediment. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	4
4712	The complete and closed genome of the facultative generalist <i>Candidatus</i> Endoriftia persephone from deepâ€sea hydrothermal vents. Molecular Ecology Resources, 2022, 22, 3106-3123.	2.2	7
4713	Microbiome Restructuring: Dominant Coral Bacterium <i>Endozoicomonas</i> Species Respond Differentially to Environmental Changes. MSystems, 2022, 7, .	1.7	11
4714	Turnover in Life-Strategies Recapitulates Marine Microbial Succession Colonizing Model Particles. Frontiers in Microbiology, 0, 13, .	1.5	5
4715	Biosynthetic potential of the global ocean microbiome. Nature, 2022, 607, 111-118.	13.7	128

#	Article	IF	Citations
4717	Common and distinctive genomic features of Klebsiella pneumoniae thriving in the natural environment or in clinical settings. Scientific Reports, 2022, 12, .	1.6	18
4718	Large Scale Genome-Centric Metagenomic Data from the Gut Microbiome of Food-Producing Animals and Humans. Scientific Data, 2022, 9, .	2.4	1
4719	Reclassification of Streptococcus ilei as a later heterotypic synonym of Streptococcus koreensis based on whole-genome sequence analysis. Archives of Microbiology, 2022, 204, .	1.0	1
4720	Evolutionary Divergence of Marinobacter Strains in Cryopeg Brines as Revealed by Pangenomics. Frontiers in Microbiology, 0, 13, .	1.5	6
4721	Draft Genome Sequences of <i>Flavobacterium covae</i> Strains LSU-066-04 and LV-359-01. Microbiology Resource Announcements, 2022, 11, .	0.3	1
4723	Triculamin: An Unusual Lasso Peptide with Potent Antimycobacterial Activity. Journal of Natural Products, 2022, 85, 1514-1521.	1.5	7
4724	Genome Sequence of <i>Salipaludibacillus</i> sp. Strain CUR1, Isolated from an Alkaline-Saline Lake in Rajasthan, India. Microbiology Resource Announcements, 0, , .	0.3	0
4725	Cecal Microbial Hydrogen Cycling Potential Is Linked to Feed Efficiency Phenotypes in Chickens. Frontiers in Veterinary Science, 0, 9, .	0.9	2
4726	Identification of <i>nosZ</i>-expressing microorganisms consuming trace N2O in microaerobic chemostat consortia dominated by an uncultured <i>Burkholderiales</i>. ISME Journal, 2022, 16, 2087-2098.	4.4	12
4727	Composition and Ecological Roles of the Core Microbiome along the Abyssal-Hadal Transition Zone Sediments of the Mariana Trench. Microbiology Spectrum, 2022, 10, .	1.2	11
4728	Agriterribacter soli sp. nov., isolated from herbicide-contaminated soil. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	4
4729	Strain Tracking of â€˜<i>Candidatus</i> Liberibacter asiaticusâ€™, the Citrus Greening Pathogen, by High-Resolution Microbiome Analysis of Asian Citrus Psyllids. Phytopathology, 2022, 112, 2273-2287.	1.1	4
4730	Nocardioides carbamazepini sp. nov., an ibuprofen degrader isolated from a biofilm bacterial community enriched on carbamazepine. Systematic and Applied Microbiology, 2022, 45, 126339.	1.2	10
4731	Anthropogenic impacts on antibiotic resistance genes and their hosts from pristine to urban river using metagenomic and binning approaches. Aquatic Toxicology, 2022, 249, 106221.	1.9	13
4732	Genome analysis uncovers the prolific antagonistic and plant growth-promoting potential of endophyte Bacillus velezensis K1. Gene, 2022, 836, 146671.	1.0	15
4733	Metagenomic assembly and binning analyses the prevalence and spread of antibiotic resistome in water and fish gut microbiomes along an environmental gradient. Journal of Environmental Management, 2022, 318, 115521.	3.8	13
4734	Microbial metabolic routes in metagenome assembled genomes are mirrored by the mass balance of polycyclic aromatic hydrocarbons in a high altitude lake. Environmental Pollution, 2022, 308, 119592.	3.7	0
4735	Genomic insights to facilitate the construction of a high-xylose-utilization Enterococcus faecalis OPS2 for 2,3-BDO production. Chemical Engineering Journal, 2022, 448, 137617.	6.6	5

#	Article	IF	Citations
4736	Metabolic Potential of the Superphylum <i>Patescibacteria</i> Reconstructed from Activated Sludge Samples from a Municipal Wastewater Treatment Plant. Microbes and Environments, 2022, 37, n/a.	0.7	11
4739	Nitrogen fixation in cyanobacteria. , 2022, , 29-45.		9
4740	Citrobacter Sp. Y3 Harboring a Novel Gene Hbcd-Hd-1 Mineralizes Hexabromocyclododecane (Hbcd) with New Metabolic Pathways Based on Multi-Omics Characterization. SSRN Electronic Journal, 0, , .	0.4	0
4741	Metagenomes, Metagenome-Assembled Genomes, and Metatranscriptomes from Polychlorinated Biphenyl-Contaminated Sediment Microcosms. Microbiology Resource Announcements, 2022, 11, .	0.3	2
4742	A genome and gene catalog of glacier microbiomes. Nature Biotechnology, 2022, 40, 1341-1348.	9.4	50
4743	Draft Genome Sequences of Five Putatively Novel <i>Saccharibacteria</i> Species Assembled from the Human Oral Metagenome. Microbiology Resource Announcements, 0, , .	0.3	0
4744	Insights into plastic biodegradation: community composition and functional capabilities of the superworm (Zophobas morio) microbiome in styrofoam feeding trials. Microbial Genomics, 2022, 8, .	1.0	11
4745	An essential role for tungsten in the ecology and evolution of a previously uncultivated lineage of anaerobic, thermophilic Archaea. Nature Communications, 2022, 13, .	5.8	16
4746	High-Quality Genome Assembly of Nannochloris desiccata 2437 and Its Associated Bacterial Community. Microbiology Resource Announcements, 2022, 11, .	0.3	2
4747	Three families of Asgard archaeal viruses identified in metagenome-assembled genomes. Nature Microbiology, 2022, 7, 962-973.	5.9	21
4748	Proposal for transfer Bacillus alkalicola to the genus Evansella as Evansella alkalicola comb. nov. Archives of Microbiology, 2022, 204, .	1.0	0
4749	Arabinoxylan and Pectin Metabolism in Crohnâ€™s Disease Microbiota: An In Silico Study. International Journal of Molecular Sciences, 2022, 23, 7093.	1.8	9
4750	A critical evaluation of Mycobacterium bovis pangenomics, with reference to its utility in outbreak investigation. Microbial Genomics, 2022, 8, .	1.0	7
4751	Acinetobacter baumannii Sampled from Cattle and Pigs Represent Novel Clones. Microbiology Spectrum, 2022, 10, .	1.2	9
4753	Spontaneous Riboflavin-Overproducing Limosilactobacillus reuteri for Biofortification of Fermented Foods. Frontiers in Nutrition, 0, 9, .	1.6	14
4754	Genomes of six viruses that infect Asgard archaea from deep-sea sediments. Nature Microbiology, 2022, 7, 953-961.	5.9	17
4755	Metagenomes and Metagenome-Assembled Genomes from Microbial Communities Fermenting Ultrafiltered Milk Permeate. Microbiology Resource Announcements, 2022, 11, .	0.3	2
4757	Draft Whole-Genome Sequences of the Polar Cyanobacterium <i>Leptolyngbya</i> sp. Strain Cla-17 and Its Associated Flavobacterium. Microbiology Resource Announcements, 2022, 11, .	0.3	2

#	Article	IF	Citations
4758	Potential metabolic and genetic interaction among viruses, methanogen and methanotrophic archaea, and their syntrophic partners. ISME Communications, 2022, 2, .	1.7	5
4759	Aurantiacibacter sediminis sp. nov., a marine bacterium isolated from a tidal flat. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	4
4760	Guidelines for reporting Whole Genome Sequencingâ€based typing data through the EFSA One Health WGS System. EFSA Supporting Publications, 2022, 19, .	0.3	5
4762	Emergence of plasmid-mediated tigecycline, Î²-lactam and florfenicol resistance genes tet(X), blaOXA-347 and floR in Riemerella anatipestifer isolated in China. Poultry Science, 2022, 101, 102057.	1.5	7
4763	Genomic analysis of heavy metal-resistant Halobacterium salinarum isolated from Sfax solar saltern sediments. Extremophiles, 2022, 26, .	0.9	6
4764	Diversity of novel archaeal viruses infecting methanogens discovered through coupling of stable isotope probing and metagenomics. Environmental Microbiology, 2022, 24, 4853-4868.	1.8	12
4765	Dominance of <i>Sulfurospirillum</i> in Metagenomes Associated with the Methane Ice Worm (Sirsoe) Tj ETQq0 0 0 rgBT /Overlock 10	1.4	2
4767	Corynebacterium kalidii sp. nov, an endophyte from a shoot of the halophyte Kalidium cuspidatum. Archives of Microbiology, 2022, 204, .	1.0	5
4768	Longâ€Term Dietary Effects on Human Gut Microbiota Composition Employing Shotgun Metagenomics Data Analysis. Molecular Nutrition and Food Research, 2023, 67, .	1.5	4
4769	Î±-cyanobacteria possessing form IA RuBisCO globally dominate aquatic habitats. ISME Journal, 2022, 16, 2421-2432.	4.4	14
4771	Brachybacterium kimchii sp. nov. and Brachybacterium halotolerans subsp. kimchii subsp. nov., isolated from the Korean fermented vegetables, kimchi, and description of Brachybacterium halotolerans subsp. halotolerans subsp. nov.. Journal of Microbiology, 2022, 60, 678-688.	1.3	11
4772	Expanding the phylogenetic distribution of cytochrome <i>b</i>-containing methanogenic archaea sheds light on the evolution of methanogenesis. ISME Journal, 2022, 16, 2373-2387.	4.4	12
4773	Draft Genome Sequence of <i>Helicobacter</i> sp. Strain CaF467b, Isolated from a Pig Manure Storage Tank. Microbiology Resource Announcements, 0, , .	0.3	0
4774	Fictibacillus marinisediminis sp. nov., a nitrate-reducing bacterium isolated from marine sediment in Hupo Basin, Republic of Korea. Archives of Microbiology, 2022, 204, .	1.0	3
4775	Compositional and Metabolic Responses of Autotrophic Microbial Community to Salinity in Lacustrine Environments. MSystems, 2022, 7, .	1.7	15
4776	Diverse Genomic Traits Differentiate Sinking-Particle-Associated versus Free-Living Microbes throughout the Oligotrophic Open Ocean Water Column. MBio, 2022, 13, .	1.8	21
4777	Deep-Sea Sediments from the Southern Gulf of Mexico Harbor a Wide Diversity of PKS I Genes. Antibiotics, 2022, 11, 887.	1.5	0
4778	Uptake of Phytoplankton-Derived Carbon and Cobalamins by Novel <i>Acidobacteria</i> Genera in <i>Microcystis</i> Blooms Inferred from Metagenomic and Metatranscriptomic Evidence. Applied and Environmental Microbiology, 2022, 88, .	1.4	7

#	Article	IF	Citations
4779	Heterotrophic Bacteria Dominate Catalase Expression during <i>Microcystis</i> Blooms. Applied and Environmental Microbiology, 2022, 88, .	1.4	14
4780	Comparative Genomics of Thaumarchaeota From Deep-Sea Sponges Reveal Their Niche Adaptation. Frontiers in Microbiology, 0, 13, .	1.5	3
4781	Genome Analysis Coupled With Transcriptomics Reveals the Reduced Fitness of a Hot Spring Cyanobacterium Mastigocladus laminosus UU774 Under Exogenous Nitrogen Supplement. Frontiers in Microbiology, 0, 13, .	1.5	2
4782	Nocardioides nematodiphilus sp. nov., isolated from rhizosphere of Arabidopsis thaliana. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	6
4783	Changes in the Species and Functional Composition of Activated Sludge Communities Revealed Mechanisms of Partial Nitrification Established by Ultrasonication. Frontiers in Microbiology, 0, 13, .	1.5	0
4784	Metagenomic insight into the microbial degradation of organic compounds in fermented plant leaves. Environmental Research, 2022, 214, 113902.	3.7	18
4785	An expanded reference map of the human gut microbiome reveals hundreds of previously unknown species. Nature Communications, 2022, 13, .	5.8	31
4786	Genomic Insights Into the Interspecific Diversity and Evolution of Mobiluncus, a Pathogen Associated With Bacterial Vaginosis. Frontiers in Microbiology, 0, 13, .	1.5	0
4788	Oxford Nanopore R10.4 long-read sequencing enables the generation of near-finished bacterial genomes from pure cultures and metagenomes without short-read or reference polishing. Nature Methods, 2022, 19, 823-826.	9.0	152
4789	Recovery of Lutacidiplasmatales archaeal order genomes suggests convergent evolution in Thermoplasmatota. Nature Communications, 2022, 13, .	5.8	10
4790	Diversity and Ecophysiology of the Genus OLB8 and Other Abundant Uncultured Saprospiraceae Genera in Global Wastewater Treatment Systems. Frontiers in Microbiology, 0, 13, .	1.5	32
4791	Metagenomic insights into the antibiotic resistome in freshwater and seawater from an Antarctic ice-free area. Environmental Pollution, 2022, 309, 119738.	3.7	7
4792	Distribution of ESBL/AmpC-Escherichia coli on a Dairy Farm. Antibiotics, 2022, 11, 940.	1.5	5
4793	Conserved and lineage-specific hypothetical proteins may have played a central role in the rise and diversification of major archaeal groups. BMC Biology, 2022, 20, .	1.7	4
4794	Salt flat microbial diversity and dynamics across salinity gradient. Scientific Reports, 2022, 12, .	1.6	4
4795	Selection of <i>Anabaena</i> sp. PCC 7938 as a Cyanobacterium Model for Biological ISRU on Mars. Applied and Environmental Microbiology, 2022, 88, .	1.4	10
4797	Greater functional diversity and redundancy of coral endolithic microbiomes align with lower coral bleaching susceptibility. ISME Journal, 2022, 16, 2406-2420.	4.4	21
4798	New-Generation Sequencing Technology in Diagnosis of Fungal Plant Pathogens: A Dream Comes True?. Journal of Fungi (Basel, Switzerland), 2022, 8, 737.	1.5	14

#	ARTICLE	IF	CITATIONS
4799	Co-Occurrence of Francisella, Spotted Fever Group Rickettsia, and Midichloria in Avian-Associated Hyalomma rufipes. Microorganisms, 2022, 10, 1393.	1.6	5
4800	Bacillus licheniformis MCC 2514 genome sequencing and functional annotation for providing genetic evidence for probiotic gut adhesion properties and its applicability as a bio-preservative agent. Gene, 2022, 840, 146744.	1.0	6
4801	Genomic diversity of genus Limosilactobacillus. Microbial Genomics, 2022, 8, .	1.0	4
4802	Unraveling diverse survival strategies of microorganisms to vanadium stress in aquatic environments. Water Research, 2022, 221, 118813.	5.3	71
4803	Shotgun metagenomic sequencing of bulk tank milk filters reveals the role of Moraxellaceae and Enterobacteriaceae as carriers of antimicrobial resistance genes. Food Research International, 2022, 158, 111579.	2.9	6
4804	Genome-centric metagenomics analysis revealed the metabolic function of abundant microbial communities in thermal hydrolysis-assisted thermophilic anaerobic digesters under propionate stress. Bioresource Technology, 2022, 360, 127574.	4.8	12
4805	Longitudinal surveillance and comparative characterization of Escherichia albertii in wild raccoons in the United States. Microbiological Research, 2022, 262, 127109.	2.5	3
4806	Diversity, function and assembly of the Trifolium repens L. root-associated microbiome under lead stress. Journal of Hazardous Materials, 2022, 438, 129510.	6.5	12
4807	Characterization of two novel pentose-fermenting and GABA-producing species: Levilactobacillus tujiorum sp. nov. and Secundilactobacillus angelensis sp. nov. Isolated from a solid-state fermented zha-chili. Systematic and Applied Microbiology, 2022, 45, 126344.	1.2	11
4808	Localized intensification of arsenic methylation within landfill leachate-saturated zone. Science of the Total Environment, 2022, 842, 156979.	3.9	0
4809	Preliminary investigation of microorganisms potentially involved in microplastics degradation using an integrated metagenomic and biochemical approach. Science of the Total Environment, 2022, 843, 157017.	3.9	13
4810	Unraveling the skatole biodegradation process in an enrichment consortium using integrated omics and culture-dependent strategies. Journal of Environmental Sciences, 2023, 127, 688-699.	3.2	12
4811	Phylogenomic analysis of the genus Leuconostoc. Frontiers in Microbiology, 0, 13, .	1.5	6
4812	The Histidine Kinase CckA Is Directly Inhibited by a Response Regulator-like Protein in a Negative Feedback Loop. MBio, 2022, 13, .	1.8	1
4813	Systematic whole-genome sequencing reveals an unexpected diversity among actinomycetoma pathogens and provides insights into their antibacterial susceptibilities. PLoS Neglected Tropical Diseases, 2022, 16, e0010128.	1.3	4
4814	Efficient management of the nitritation-anammox microbiome through intermittent aeration: absence of the NOB guild and expansion and diversity of the NOx reducing guild suggests a highly reticulated nitrogen cycle. Environmental Microbiomes, 2022, 17, .	2.2	1
4816	Draft Genome Sequence of Nocardioides alcanivorans NGK65 ^T , a Hexadecane-Degrading Bacterium. Microbiology Resource Announcements, 2022, 11, .	0.3	1
4817	Core Genome Multilocus Sequence Typing Scheme for Improved Characterization and Epidemiological Surveillance of Pathogenic Brucella. Journal of Clinical Microbiology, 2022, 60, .	1.8	15

#	ARTICLE	IF	CITATIONS
4819	Metagenomics: An Approach for Unraveling the Community Structure and Functional Potential of Activated Sludge of a Common Effluent Treatment Plant. Frontiers in Microbiology, 0, 13, .	1.5	1
4820	Proteogenomics identification of TBBPA degraders in anaerobic bioreactor. Environmental Pollution, 2022, 310, 119786.	3.7	2
4821	High-resolution spatial and genomic characterization of coral-associated microbial aggregates in the coral <i>Stylophora pistillata</i>. Science Advances, 2022, 8, .	4.7	27
4822	Draft Genome Sequence of <i>Lysinibacillus</i> sp. Strain BPa_S21, Isolated from Petroleum-Contaminated Soil in Delta State, Nigeria. Microbiology Resource Announcements, 0, , .	0.3	1
4823	A temporal view of the water kefir microbiota and flavour attributes. Innovative Food Science and Emerging Technologies, 2022, 80, 103084.	2.7	15
4824	Metagenomes and Metagenome-Assembled Genomes from Microbiomes Metabolizing Thin Stillage from an Ethanol Biorefinery. Microbiology Resource Announcements, 2022, 11, .	0.3	2
4825	Ruegeria alba sp. nov., Isolated from a Tidal Flat Sediment. Current Microbiology, 2022, 79, .	1.0	5
4826	Insights from cyanobacterial genomic and transcriptomic analyses into adaptation strategies in terrestrial environments. Genomics, 2022, , 110438.	1.3	1
4827	Metagenome-Assembled Genomes from a Microbiome Grown in Dairy Manure Hydrolysate. Microbiology Resource Announcements, 2022, 11, .	0.3	2
4828	Genome-resolved metagenomics reveals novel archaeal and bacterial genomes from Amazonian forest and pasture soils. Microbial Genomics, 2022, 8, .	1.0	5
4829	Supercarriers of antibiotic resistome in a worldâ€™s large river. Microbiome, 2022, 10, .	4.9	20
4830	Incipient Sympatric Speciation and Evolution of Soil Bacteria Revealed by Metagenomic and Structured Non-Coding RNAs Analysis. Biology, 2022, 11, 1110.	1.3	3
4831	Convergence of virulence and antimicrobial resistance in increasingly prevalent Escherichia coli ST131 papGII+ sublineages. Communications Biology, 2022, 5, .	2.0	19
4832	Coastal Transient Niches Shape the Microdiversity Pattern of a Bacterioplankton Population with Reduced Genomes. MBio, 2022, 13, .	1.8	1
4834	Metagenomic binning and assembled genome analysis revealed the distinct composition of resistome and mobilome in the Ili River. Ecotoxicology and Environmental Safety, 2022, 242, 113886.	2.9	5
4835	Complete genome sequences of Lacticaseibacillus paracasei INIA P272 (CECT 8315) and Lacticaseibacillus rhamnosus INIA P344 (CECT 8316) isolated from breast-fed infants reveal probiotic determinants. Gene, 2022, 840, 146743.	1.0	4
4836	Characterization of Lactiplantibacillus plantarum Tw226 strain and its use for the production of a new membrane-bound biosurfactant. Journal of Molecular Liquids, 2022, 363, 119889.	2.3	1
4837	mOTUpan: a robust Bayesian approach to leverage metagenome-assembled genomes for core-genome estimation. NAR Genomics and Bioinformatics, 2022, 4, .	1.5	6

#	Article	IF	Citations
4838	Comparative analysis of assembly algorithms to optimize biosynthetic gene cluster identification in novel marine actinomycete genomes. Frontiers in Marine Science, 0, 9, .	1.2	2
4839	Strains Associated with Two 2020 Welder Anthrax Cases in the United States Belong to Separate Lineages within Bacillus cereus sensu lato. Pathogens, 2022, 11, 856.	1.2	2
4840	Highly Virulent and Multidrug-Resistant Escherichia coli Sequence Type 58 from a Sausage in Germany. Antibiotics, 2022, 11, 1006.	1.5	7
4841	Analysis of the Diversity of Xylophilus ampelinus Strains Held in CIRM-CFBP Reveals a Strongly Homogenous Species. Microorganisms, 2022, 10, 1531.	1.6	2
4842	Novel Insights into the Pig Gut Microbiome Using Metagenome-Assembled Genomes. Microbiology Spectrum, 2022, 10, .	1.2	16
4843	Oceanospirillales containing the DMSP lyase DddD are key utilisers of carbon from DMSP in coastal seawater. Microbiome, 2022, 10, .	4.9	6
4846	Genome-Resolved Metaproteomics Decodes the Microbial and Viral Contributions to Coupled Carbon and Nitrogen Cycling in River Sediments. MSystems, 2022, 7, .	1.7	10
4847	Metagenomic insights into the microbe-mediated B and K2 vitamin biosynthesis in the gastrointestinal microbiome of ruminants. Microbiome, 2022, 10, .	4.9	18
4848	Non-random genetic alterations in the cyanobacterium Nostoc sp. exposed to space conditions. Scientific Reports, 2022, 12, .	1.6	2
4849	Unveiling degradation mechanism of PAHs by a <i>Sphingobium</i> strain from a microbial consortium. , 2022, 1, 287-302.		6
4850	Metagenomic Insights into Pathogenic Characterization of ST410 Acinetobacter nosocomialis Prevalent in China. Pathogens, 2022, 11, 838.	1.2	1
4851	Comparative Genomic Analysis of Antarctic Pseudomonas Isolates with 2,4,6-Trinitrotoluene Transformation Capabilities Reveals Their Unique Features for Xenobiotics Degradation. Genes, 2022, 13, 1354.	1.0	12
4852	Historical contingencies and phage induction diversify bacterioplankton communities at the microscale. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	15
4853	Phylogenomic analysis and metabolic role reconstruction of mutualistic <i>Rhizobiales</i> hindgut symbionts of <i>Acromyrmex</i> leaf-cutting ants. FEMS Microbiology Ecology, 2022, 98, .	1.3	1
4854	Methanol utilizers of the rhizosphere and phyllosphere of a common grass and forb host species. Environmental Microbiomes, 2022, 17, .	2.2	1
4856	Genome characteristics of clinical Salmonella enterica population from a state public health laboratory, New Hampshire, USA, 2017â€“2020. BMC Genomics, 2022, 23, .	1.2	5
4857	Metagenome-Assembled Genomes of <i>Komagataeibacter</i> from Kombucha Exposed to Mars-Like Conditions Reveal the Secrets in Tolerating Extraterrestrial Stresses. Journal of Microbiology and Biotechnology, 2022, , .	0.9	1
4858	Giant virus biology and diversity in the era of genome-resolved metagenomics. Nature Reviews Microbiology, 2022, 20, 721-736.	13.6	48

#	Article	IF	Citations
4859	Competition-cooperation in the chemoautotrophic ecosystem of Movile Cave: first metagenomic approach on sediments. Environmental Microbiomes, 2022, 17, .	2.2	10
4861	Uncovering the structure and function of specialist bacterial lineages in environments routinely exposed to explosives. Letters in Applied Microbiology, 0, , .	1.0	0
4864	Complete Genome Sequence from an Uncultivated Freshwater <i>Elusimicrobiota</i> Lineage. Microbiology Resource Announcements, 2022, 11, .	0.3	1
4865	A balanced gut microbiota is essential to maintain health in captive sika deer. Applied Microbiology and Biotechnology, 2022, 106, 5659-5674.	1.7	4
4866	Geological processes mediate a microbial dispersal loop in the deep biosphere. Science Advances, 2022, 8, .	4.7	17
4867	Microbial paracetamol degradation involves a high diversity of novel amidase enzyme candidates. Water Research X, 2022, 16, 100152.	2.8	22
4868	Investigation of Antibiotic Resistome in Hospital Wastewater during the COVID-19 Pandemic: Is the Initial Phase of the Pandemic Contributing to Antimicrobial Resistance?. Environmental Science & Technology, 2022, 56, 15007-15018.	4.6	24
4869	(Meta)Genomic Analysis Reveals Diverse Energy Conservation Strategies Employed by Globally Distributed<i>Gemmatimonadota</i>. MSystems, 2022, 7, .	1.7	6
4870	High impact of bacterial predation on cyanobacteria in soil biocrusts. Nature Communications, 2022, 13, .	5.8	12
4871	A thousand metagenome-assembled genomes of Akkermansia reveal phylogroups and geographical and functional variations in the human gut. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	6
4872	Complete gammaproteobacterial endosymbiont genome assembly from a seep tubeworm Lamellibrachia satsuma. Journal of Microbiology, 2022, 60, 916-927.	1.3	1
4874	Pelagibacterium xiamenense sp. nov., isolated from intertidal sediment. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	1
4876	Genomic insights into symbiosis and host adaptation of an ascidian-associated bacterium Bacillus aryabhattai MCCB 387. Symbiosis, 0, , .	1.2	0
4877	Exploring strain diversity of dominant human skin bacterial species using single-cell genome sequencing. Frontiers in Microbiology, 0, 13, .	1.5	6
4878	Genome Sequence of <i>Erysipelothrix</i> sp. Strain Poltava, Isolated from Acute Septic Erysipelas of Swine in Ukraine. Microbiology Resource Announcements, 2022, 11, .	0.3	1
4881	Metagenome sequencing and 768 microbial genomes from cold seep in South China Sea. Scientific Data, 2022, 9, .	2.4	12
4883	Parvicella tangerina gen. nov., sp. nov. (Parvicellaceae fam. nov., Flavobacteriales), first cultured representative of the marine clade UBA10066, and Lysobacter luteus sp. nov., from activated sludge of a seawater-processing wastewater treatment plant. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	2
4884	Analysis of the anaerobic digestion metagenome under environmental stresses stimulating prophage induction. Microbiome, 2022, 10, .	4.9	11

#	ARTICLE	IF	CITATIONS
4887	Nonâ€ribosomal peptide biosynthetic potential of the nematode symbiont <i>Photorhabdus</i>. Environmental Microbiology Reports, 0, , .	1.0	2
4888	Sphingomonas folii sp. nov., Sphingomonas citri sp. nov. and Sphingomonas citricola sp. nov., isolated from citrus phyllosphere. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	1
4890	New insights into lincomycin biodegradation by Conexibacter sp. LD01: Genomics characterization, biodegradation kinetics and pathways. Journal of Hazardous Materials, 2023, 441, 129824.	6.5	6
4891	Draft genome sequencing data of the moderately halophilic bacterium, Allobacillus halotolerans SKP2-8 from shrimp paste (ka-pi). Data in Brief, 2022, , 108549.	0.5	0
4892	Multi-omics analyses of airway hostâ€“microbe interactions in chronic obstructive pulmonary disease identify potential therapeutic interventions. Nature Microbiology, 2022, 7, 1361-1375.	5.9	43
4893	Phototrophy and carbon fixation in Chlorobi postdate the rise of oxygen. PLoS ONE, 2022, 17, e0270187.	1.1	2
4894	Quadrisphaera setariae sp. nov., polyphosphate-accumulating bacterium occurring as tetrad or aggregate cocci and isolated from Setaria viridis. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	4
4895	Microbial diversity and adaptive strategies in the Marsâ€like Qaidam Basin, North Tibetan Plateau, China. Environmental Microbiology Reports, 2022, 14, 873-885.	1.0	11
4896	Draft Genome Sequence of Multidrug Resistant Klebsiella pneumoniae Strain C43 Isolated from Environmental Water Sample. Microbiology Resource Announcements, 0, , .	0.3	0
4897	Metagenomic binning with assembly graph embeddings. Bioinformatics, 2022, 38, 4481-4487.	1.8	14
4899	First Report of Bartonella spp. in Marsupials from Brazil, with a Description of Bartonella harrusi sp. nov. and a New Proposal for the Taxonomic Reclassification of Species of the Genus Bartonella. Microorganisms, 2022, 10, 1609.	1.6	12
4900	Pseudovibrio flavus sp. nov. isolated from the sea sponge Verongula gigantea. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	0
4901	Metagenomic views on taxonomic and functional profiles of the Himalayan Tsomgo cold lake and unveiling its deterzome potential. Current Genetics, 2022, 68, 565-579.	0.8	3
4902	Atmospheric chemosynthesis is phylogenetically and geographically widespread and contributes significantly to carbon fixation throughout cold deserts. ISME Journal, 2022, 16, 2547-2560.	4.4	18
4903	Insights into Evolutionary, Genomic, and Biogeographic Characterizations of Chryseobacterium nepalense Represented by a Polyvinyl Alcohol-Degrading Bacterium, AC3. Microbiology Spectrum, 2022, 10, .	1.2	1
4904	Description of Aestuariivivens marinum sp. nov., Aestuariivivens sediminis sp. nov. and Aestuariivivens sediminicola sp. nov., three new species isolated from the upper layer of tidal flat sediment. Systematic and Applied Microbiology, 2022, 45, 126355.	1.2	1
4905	Tenacibaculum aquimarinum sp. nov., isolated from a marine alga and seawater. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	5
4906	Metabolism Interactions Promote the Overall Functioning of the Episymbiotic Chemosynthetic Community of Shinkaia crosnieri of Cold Seeps. MSystems, 2022, 7, .	1.7	5

#	ARTICLE	IF	CITATIONS
4907	Long-Read-Resolved, Ecosystem-Wide Exploration of Nucleotide and Structural Microdiversity of Lake Bacterioplankton Genomes. MSystems, 2022, 7, .	1.7	11
4909	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. Research in Microbiology, 2023, 174, 103988.	1.0	7
4911	Phylogenetically and catabolically diverse diazotrophs reside in deep-sea cold seep sediments. Nature Communications, 2022, 13, .	5.8	29
4912	Attempts to Stimulate Leaching Activity of Acidithiobacillus ferrooxidans Strain TFBk. Minerals (Basel,) Tj ETQq1 1 0.784314 rgBT /Overl	0.8	5
4913	Metabolic Strategies Shared by Basement Residents of the Lost City Hydrothermal Field. Applied and Environmental Microbiology, 2022, 88, .	1.4	14
4914	Draft Genome Sequence of the Thermophilic Unicellular Cyanobacterium <i>Synechococcus</i> sp. Strain C9. Microbiology Resource Announcements, 2022, 11, .	0.3	5
4915	Oceanobacillus saliphilus sp. nov., Isolated from Salineâ˜Alkali Soil in Heilongjiang Province, China. Current Microbiology, 2022, 79, .	1.0	0
4916	Culturomics of Bacteria from Radon-Saturated Water of the Worldâ€™s Oldest Radium Mine. Microbiology Spectrum, 2022, 10, .	1.2	5
4917	In Situ Genomics and Transcriptomics of SAR202 Subclusters Revealed Subtle Distinct Activities in Deep-Sea Water. Microorganisms, 2022, 10, 1629.	1.6	2
4918	Coupled Aerobic Methane Oxidation and Arsenate Reduction Contributes to Soil-Arsenic Mobilization in Agricultural Fields. Environmental Science & Technology, 2022, 56, 11845-11856.	4.6	8
4919	Genome analysis of the candidate phylum MBNT15 bacterium from a boreal peatland predicted its respiratory versatility and dissimilatory iron metabolism. Frontiers in Microbiology, 0, 13, .	1.5	9
4920	Metagenome-Assembled Genome of a <i>Pseudanabaena</i> sp. from a Crimson Cyanobacterial Bloom in Lake Salubria, New York, USA. Microbiology Resource Announcements, 0, , .	0.3	0
4921	Detection of interphylum transfers of the magnetosome gene cluster in magnetotactic bacteria. Frontiers in Microbiology, 0, 13, .	1.5	7
4922	MetaTrass: A highâ€quality metagenome assembler of the human gut microbiome by cobarcoding sequencing reads. , 2022, 1, .		2
4923	Metaproteome plasticity sheds light on the ecology of the rumen microbiome and its connection to host traits. ISME Journal, 2022, 16, 2610-2621.	4.4	4
4924	Four <i>Lentisphaerae</i> Family Metagenome-Assembled Genomes from the South Atlantic Ocean. Microbiology Resource Announcements, 0, , .	0.3	0
4925	Elucidating the picocyanobacteria salinity divide through ecogenomics of new freshwater isolates. BMC Biology, 2022, 20, .	1.7	7
4926	Acetate reprograms gut microbiota during alcohol consumption. Nature Communications, 2022, 13, .	5.8	34

#	Article	IF	Citations
4927	BinSPreader: Refine binning results for fuller MAG reconstruction. IScience, 2022, 25, 104770.	1.9	5
4928	Probiogenomic Analysis of LactiplantibacillusÂsp. LM14-2 from Fermented Mussel (Hoi-dong), and Evaluation of its Cholesterol-lowering and Immunomodulation Effects. Probiotics and Antimicrobial Proteins, 2023, 15, 1206-1220.	1.9	5
4929	Bioremediation of a Polluted Groundwater: Microbial Community Comparison of Treated and Untreated Aquifer through Next Generation Sequencing. Water (Switzerland), 2022, 14, 2456.	1.2	1
4931	Metabacillus rhizolycopersici sp. nov., Isolated from the Rhizosphere Soil of Tomato Plants. Current Microbiology, 2022, 79, .	1.0	0
4932	The microbiome of a bacterivorous marine choanoflagellate contains a resource-demanding obligate bacterial associate. Nature Microbiology, 2022, 7, 1466-1479.	5.9	5
4933	A widely distributed genus of soil Acidobacteria genomically enriched in biosynthetic gene clusters. ISME Communications, 2022, 2, .	1.7	6
4934	The Polar Fox Lagoon in Siberia harbours a community of Bathyarchaeota possessing the potential for peptide fermentation and acetogenesis. Antonie Van Leeuwenhoek, 2022, 115, 1229-1244.	0.7	4
4935	Morphine and high-fat diet differentially alter the gut microbiota composition and metabolic function in lean versus obese mice. ISME Communications, 2022, 2, .	1.7	4
4938	Complete Genome Sequence of Micrococcus yunnanensis TT9, Isolated from a Healthy Volunteer. Microbiology Resource Announcements, 0, , .	0.3	1
4939	Comprehensive investigation of antibiotic resistance gene content in cfiA-harboring Bacteroides fragilis isolates of human and animal origins by whole genome sequencing. International Journal of Medical Microbiology, 2022, 312, 151559.	1.5	8
4940	Arm race among closely-related carbapenem-resistant <i>Klebsiella pneumoniae</i> clones. ISME Communications, 2022, 2, .	1.7	3
4941	Microbial functional genes are driven by gradients in sediment stoichiometry, oxygen, and salinity across the Baltic benthic ecosystem. Microbiome, 2022, 10, .	4.9	12
4942	Facilitating the adoption of highâ€throughput sequencing technologies as a plant pest diagnostic test in laboratories: AÂstepâ€byâ€step description. EPPO Bulletin, 2022, 52, 394-418.	0.6	24
4943	Higher pathogen load in children from Mozambique vs. USA revealed by comparative fecal microbiome profiling. ISME Communications, 2022, 2, .	1.7	4
4945	Nitrogen cycling and microbial cooperation in the terrestrial subsurface. ISME Journal, 2022, 16, 2561-2573.	4.4	41
4946	Nitrogen Fixation Activity and Genome Analysis of a Moderately Haloalkaliphilic Anoxygenic Phototrophic Bacterium Rhodovulum tesquicola. Microorganisms, 2022, 10, 1615.	1.6	1
4947	Bacillus paralicheniformis isolated from a hypersaline sediment of Lake Texcoco, draft genome sequence of strain TXO7B-1SG6. Microbiology Resource Announcements, 2022, 11, .	0.3	0
4948	Complete Genome Sequence of Staphylococcus edaphicus Strain CCM 8731. Microbiology Resource Announcements, 0, , .	0.3	0

#	Article	IF	Citations
4949	Open pangenome of Lactococcus lactis generated by a combination of metagenome-assembled genomes and isolate genomes. Frontiers in Microbiology, 0, 13, .	1.5	3
4950	Complete Reductive Dechlorination of 4-Hydroxy-chlorothalonil by <i>Dehalogenimonas</i> Populations. Environmental Science & Technology, 2022, 56, 12237-12246.	4.6	9
4951	Metagenome-Assembled Genome Sequence of Marine <i>Rhizobiaceae</i> sp. Strain MnEN-MB40S, Obtained from Manganese-Oxidizing Enrichment Culture. Microbiology Resource Announcements, 2022, 11, .	0.3	1
4952	Machine learning algorithm to characterize antimicrobial resistance associated with the International Space Station surface microbiome. Microbiome, 2022, 10, .	4.9	14
4953	Novel Long-Chain Fatty Acid (LCFA)-Degrading Bacteria and Pathways in Anaerobic Digestion Promoted by Hydrochar as Revealed by Genome-Centric Metatranscriptomics Analysis. Applied and Environmental Microbiology, 2022, 88, .	1.4	8
4954	Comparative genome analysis of Vagococcus fluvialis reveals abundance of mobile genetic elements in sponge-isolated strains. BMC Genomics, 2022, 23, .	1.2	5
4955	Oceanobacillus alkalisoli sp. nov., an alkaliphilic bacterium isolated from saline-alkaline soil. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	0
4956	Wildfire-dependent changes in soil microbiome diversity and function. Nature Microbiology, 2022, 7, 1419-1430.	5.9	51
4959	Draft Genome Sequence of the Alkaliphilic, Lithoautotrophic Homoacetogen Fuchsiella alkaliacetigena Z-7100 ^T. Microbiology Resource Announcements, 2022, 11, .	0.3	0
4962	Soil metatranscriptome demonstrates a shift in C, N, and S metabolisms of a grassland ecosystem in response to elevated atmospheric CO2. Frontiers in Microbiology, 0, 13, .	1.5	6
4963	Genome assembly of the chemosynthetic endosymbiont of the hydrothermal vent snail <i>Alviniconcha adamantis</i> from the Mariana Arc. G3: Genes, Genomes, Genetics, 0, , .	0.8	1
4965	Draft Metagenome-Assembled Genome Sequences of Three Novel Ammonia-Oxidizing <i>Nitrososphaera</i> Strains Recovered from Agricultural Soils in Western Colorado. Microbiology Resource Announcements, 0, , .	0.3	0
4967	Aestuariicella albida sp. nov., isolated from surface water of the Yellow Sea, and proposal of the genus Aestuariicella as a member of the family Cellvibrionaceae. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	3
4968	Glutamate Enhances Osmoadaptation of Anammox Bacteria under High Salinity: Genomic Analysis and Experimental Evidence. Environmental Science & Technology, 2022, 56, 11310-11322.	4.6	11
4969	Designing a Novel Peptide-Based Multi-Epitope Vaccine to Evoke a Robust Immune Response against Pathogenic Multidrug-Resistant Providencia heimbachae. Vaccines, 2022, 10, 1300.	2.1	11
4970	Integrating Genome-Resolved Metagenomics with Trait-Based Process Modeling to Determine Biokinetics of Distinct Nitrifying Communities within Activated Sludge. Environmental Science & Technology, 2022, 56, 11670-11682.	4.6	6
4971	Coral and Seawater Metagenomes Reveal Key Microbial Functions to Coral Health and Ecosystem Functioning Shaped at Reef Scale. Microbial Ecology, 2023, 86, 392-407.	1.4	9
4972	Whole Genome Sequencing Suggests that â€œNonpathogenicity on Banana (NPB)â€•Is the Ancestral State of the <i>Ralstonia solanacearum</i> IIB-4 Lineage. PhytoFrontiers, 2023, 3, 262-267.	0.8	3

#	ARTICLE	IF	CITATIONS
4973	Desulfuromonas sp. 'CSMB_57â€™, isolation and genomic insights from the most abundant bacterial taxon in eastern Australian coals. Microbial Genomics, 2022, 8, .	1.0	0
4974	Distribution and Genomic Variation of Thermophilic Cyanobacteria in Diverse Microbial Mats at the Upper Temperature Limits of Photosynthesis. MSystems, 2022, 7, .	1.7	9
4976	Insights into the microbial response mechanisms to ciprofloxacin during sulfur-mediated biological wastewater treatment using a metagenomics approach. Water Research, 2022, 223, 118995.	5.3	13
4977	Genome sequence of freshwater nontoxigenic Limnoraphis associated with microcystin-producing blooms.. Harmful Algae, 2022, 118, 102309.	2.2	2
4978	Trade-off for survival: Microbiome response to chemical exposure combines activation of intrinsic resistances and adapted metabolic activity. Environment International, 2022, 168, 107474.	4.8	1
4979	Food safety assessment and toxicity study of the synbiotic consortium SBD111. Food and Chemical Toxicology, 2022, 168, 113329.	1.8	1
4980	Nitrite oxidation in oxygen-deficient conditions during landfill leachate treatment. Environmental Research, 2022, 214, 114090.	3.7	3
4981	Metagenomic analysis of Fe(II)-oxidizing bacteria for Fe(III) mineral formation and carbon assimilation under microoxic conditions in paddy soil. Science of the Total Environment, 2022, 851, 158068.	3.9	10
4982	Xanthomonas indica sp. nov., a Novel Member of Non-Pathogenic Xanthomonas Community from Healthy Rice Seeds. Current Microbiology, 2022, 79, .	1.0	11
4983	Metaomics unveils the contribution of Alteromonas bacteria to carbon cycling in marine oxygen minimum zones. Frontiers in Marine Science, 0, 9, .	1.2	3
4984	Syntrophic Acetate-Oxidizing Microbial Consortia Enriched from Full-Scale Mesophilic Food Waste Anaerobic Digesters Showing High Biodiversity and Functional Redundancy. MSystems, 2022, 7, .	1.7	15
4985	Significant compositional and functional variation reveals the patterns of gut microbiota evolution among the widespread Asian honeybee populations. Frontiers in Microbiology, 0, 13, .	1.5	5
4988	Absolute quantification and genome-centric analyses elucidate the dynamics of microbial populations in anaerobic digesters. Water Research, 2022, 224, 119049.	5.3	9
4989	Effects of a Carnobacterium maltaromaticum strain at natural contamination levels on the microbiota of vacuum-packaged beef steaks during chilled storage. LWT - Food Science and Technology, 2022, 168, 113944.	2.5	2
4990	Deciphering discriminative antibiotic resistance genes and pathogens in agricultural soil following chemical and organic fertilizer. Journal of Environmental Management, 2022, 322, 116110.	3.8	5
4991	Characterization of arsenic-metabolizing bacteria in an alkaline soil. Environmental Pollution, 2022, 312, 120040.	3.7	6
4992	CYP108N12 initiates p-cymene biodegradation in Rhodococcus globerulus. Archives of Biochemistry and Biophysics, 2022, 730, 109410.	1.4	4
4993	Rhodopirellula aestuarii sp. nov., a novel member of the genus Rhodopirellula isolated from brackish sediments collected in the Tagus River estuary, Portugal. Systematic and Applied Microbiology, 2022, 45, 126360.	1.2	3

#	ARTICLE	IF	CITATIONS
4994	Genome-based taxonomic classification of the closest-to-Comamonadaceae group supports a new family Sphaerotilaceae fam. nov. and taxonomic revisions. Systematic and Applied Microbiology, 2022, 45, 126352.	1.2	12
4995	The divergent genome of Scorpion Group 1 (SG1) intracellular bacterium from the venom glands of Vaejovis smithi (Scorpiones: Vaejovidae). Systematic and Applied Microbiology, 2022, 45, 126358.	1.2	0
4996	Region-specific genomic signatures of multidrug-resistant Helicobacter pylori isolated from East and South India. Gene, 2022, 847, 146857.	1.0	4
4997	Community and shotgun metagenomic analysis of Alligator mississippiensis oral cavity and GI tracts reveal complex ecosystems and potential reservoirs of antibiotic resistance. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2022, 274, 111319.	0.8	1
4998	Microbiome structure in biofilms from a volcanic island in Maritime Antarctica investigated by genome-centric metagenomics and metatranscriptomics. Microbiological Research, 2022, 265, 127197.	2.5	3
4999	Alternative nitrogenase of Paenibacillus sonchi genomovar Riograndensis: An insight in the origin of Fe-nitrogenase in the Paenibacillaceae family. Molecular Phylogenetics and Evolution, 2022, 177, 107624.	1.2	2
5000	Mangrove microbial community recovery and their role in early stages of forest recolonization within shrimp ponds. Science of the Total Environment, 2023, 855, 158863.	3.9	5
5001	The plastisphere microbiome in alpine soils alters the microbial genetic potential for plastic degradation and biogeochemical cycling. Journal of Hazardous Materials, 2023, 441, 129941.	6.5	17
5002	Assembling a Reference Phylogenomic Tree of Bacteria and Archaea by Summarizing Many Gene Phylogenies. Methods in Molecular Biology, 2022, , 137-165.	0.4	1
5003	Rooting Species Trees Using Gene Tree-Species Tree Reconciliation. Methods in Molecular Biology, 2022, , 189-211.	0.4	3
5004	Reconstruction of Archaeal Genomes from Short-Read Metagenomes. Methods in Molecular Biology, 2022, , 487-527.	0.4	0
5005	Carbon Substrate Selects for Different Lineages of N2O Reducing Communities in Soils Under Anoxic Conditions. SSRN Electronic Journal, 0, , .	0.4	0
5006	Metagenome-assembled Genomes of Six Novel Ammonia-oxidizing Archaea (AOA) from Agricultural Upland Soil. Microbes and Environments, 2022, 37, n/a.	0.7	1
5007	New-Age Genomic Measures for Uncovering Plant-Microbiome Interactions: Tools, Pipelines and Guidance Map for Genomic Data Mining. , 2022, , 207-232.		0
5008	Impact of beaver ponds on biogeochemistry of organic carbon and nitrogen along a fire-impacted stream. Environmental Sciences: Processes and Impacts, 2022, 24, 1661-1677.	1.7	2
5009	Assessing a Role of Genetic Drift for Deep-Time Evolutionary Events. Methods in Molecular Biology, 2022, , 343-359.	0.4	0
5010	Draft Genomes of Symbiotic<i> Frankia</i> Strains AgB32 and AgKG'84/4 from Root Nodules of <i>Alnus Glutinosa</i> growing under Contrasted Environmental Conditions. Journal of Genomics, 2022, 10, 61-68.	0.6	3
5011	Tools to Study Gut Microbiome. , 2022, , 253-270.		0

#	Article	IF	Citations
5012	Citrobacter sp. Y3 harbouring novel gene HBCD-hd-1 mineralizes hexabromocyclododecane via new metabolic pathways according to multi-omics characterization. Journal of Hazardous Materials, 2023, 442, 130071.	6.5	2
5013	Revealing the diversity of bacteria and fungi in the active layer of permafrost at Spitsbergen island (Arctic) â€“ Combining classical microbiology and metabarcoding for ecological and bioprospecting exploration. Science of the Total Environment, 2023, 856, 159072.	3.9	4
5014	Metagenomic approaches for understanding microbial communities in contaminated environments: Bioinformatic tools, case studies and future outlook. , 2023, , 103-156.		1
5015	Long-term partial substitution of chemical fertilizer by organic amendments influences soil microbial functional diversity of phosphorus cycling and improves phosphorus availability in greenhouse vegetable production. Agriculture, Ecosystems and Environment, 2023, 341, 108193.	2.5	17
5016	Genomic and transcriptomic characterization of the <i>Collimonas</i> quorum sensing genes and regulon. FEMS Microbiology Ecology, 0, , .	1.3	0
5017	Metagenome-Assembled Genomes of Bacteria Associated with Massospora cicadina Fungal Plugs from Infected Brood VIII Periodical Cicadas. Microbiology Resource Announcements, 2022, 11, .	0.3	3
5018	Genome-Resolved Metagenomics Informs the Functional Ecology of Uncultured Acidobacteria in Redox Oscillated <i>Sphagnum</i> Peat. MSystems, 2022, 7, .	1.7	5
5019	Isolation of Saccharibacillus WB17 strain from wheat bran phyllosphere and genomic insight into the cellulolytic and hemicellulolytic complex of the Saccharibacillus genus. Brazilian Journal of Microbiology, 0, , .	0.8	0
5020	Systematic Analysis of Mobile Genetic Elements Mediating Î²-Lactamase Gene Amplification in Noncarbapenemase-Producing Carbapenem-Resistant <i>Enterobacterales</i> Bloodstream Infections. MSystems, 2022, 7, .	1.7	12
5022	Genomic Characterization of Salmonella Typhimurium Isolated from Guinea Pigs with Salmonellosis in Lima, Peru. Microorganisms, 2022, 10, 1726.	1.6	1
5025	Acesulfame Anoxic Biodegradation Coupled to Nitrate Reduction by Enriched Consortia and Isolated <i>Shinella</i> spp.. Environmental Science & Technology, 2022, 56, 13096-13106.	4.6	10
5026	Complete Genome Sequence of Lacticaseibacillus paracasei Strain VHProbi F22, Isolated from Cheese. Microbiology Resource Announcements, 0, , .	0.3	0
5027	Draft Genome Sequence of Paenalcaligenes niemegkensis NGK35 ^T , Isolated from Plastic-Polluted Soil of an Abandoned Landfill. Microbiology Resource Announcements, 0, , .	0.3	0
5028	Insights into the Genomic Potential of a Methylocystis sp. from Amazonian Floodplain Sediments. Microorganisms, 2022, 10, 1747.	1.6	0
5029	Strain-level profiling with picodroplet microfluidic cultivation reveals host-specific adaption of honeybee gut symbionts. Microbiome, 2022, 10, .	4.9	6
5031	Prokaryotes of renowned Karlovy Vary (Carlsbad) thermal springs: phylogenetic and cultivation analysis. Environmental Microbiomes, 2022, 17, .	2.2	7
5032	Prevalence and diversity of type VI secretion systems in a model beneficial symbiosis. Frontiers in Microbiology, 0, 13, .	1.5	3
5034	Metagenomics-resolved genomics provides novel insights into chitin turnover, metabolic specialization, and niche partitioning in the octocoral microbiome. Microbiome, 2022, 10, .	4.9	17

#	Article	IF	Citations
5035	The panâ€genome of Splendidus clade species in the family<i>Vibrionaceae</i>: Insights into evolution, adaptation, and pathogenicity. Environmental Microbiology, 2022, 24, 4587-4606.	1.8	7
5036	Validation of the application of gel beads-based single-cell genome sequencing platform to soil and seawater. ISME Communications, 2022, 2, .	1.7	15
5037	Draft Genome Sequence of Pseudomonas aeruginosa AS_23, Isolated from Petroleum-Contaminated Soil in Delta State, Nigeria. Microbiology Resource Announcements, 0, , .	0.3	0
5038	Draft Genome Sequences of Robbsia andropogonis Isolated from Sorghum bicolor Exhibiting Bacterial Leaf Stripe in Australia. Microbiology Resource Announcements, 0, , .	0.3	0
5039	In silico identification of bacterial seaweed-degrading bioplastic producers. Microbial Genomics, 2022, 8, .	1.0	3
5041	Genome-guided prediction of acid resistance mechanisms in acidophilic methanotrophs of phylogenetically deep-rooted Verrucomicrobia isolated from geothermal environments. Frontiers in Microbiology, 0, 13, .	1.5	1
5042	Active antibiotic resistome in soils unraveled by single-cell isotope probing and targeted metagenomics. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	13
5043	Identification and characterization of a novel metallo Î²-lactamase, SZM-1, in Shenzhen Bay, South China. Frontiers in Microbiology, 0, 13, .	1.5	3
5047	Novel bacterial taxa in a minimal lignocellulolytic consortium and their potential for lignin and plastics transformation. ISME Communications, 2022, 2, .	1.7	5
5048	Genome Sequences of the Human-Skin-Originated Brevundimonas albigilva TT17 and the Soil-Originated B. albigilva KEME 9005-016 ^T. Microbiology Resource Announcements, 0, , .	0.3	1
5049	Genome analysis of a new sulphur disproportionating species Thermosulfurimonas strain F29 and comparative genomics of sulfur-disproportionating bacteria from marine hydrothermal vents. Microbial Genomics, 2022, 8, .	1.0	1
5050	Dissecting the role of the human microbiome in COVID-19 via metagenome-assembled genomes. Nature Communications, 2022, 13, .	5.8	24
5051	Variability of strain engraftment and predictability of microbiome composition after fecal microbiota transplantation across different diseases. Nature Medicine, 2022, 28, 1913-1923.	15.2	81
5052	Evidence for Assimilatory Nitrate Reduction as a Previously Overlooked Pathway of Reactive Nitrogen Transformation in Estuarine Suspended Particulate Matter. Environmental Science & Technology, 2022, 56, 14852-14866.	4.6	16
5053	Complete Genome Sequence of the Radioresistant Bacterium Deinococcus aetherius ST0316, Isolated from Air Dust Collected in the Lower Stratosphere above Japan. Microbiology Resource Announcements, 2022, 11, .	0.3	1
5054	Proposal to transfer Bacillus lacisalsi Dong et al. 2021 to the genus Alteribacter as Alteribacter lacisalsi comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	0
5055	High-quality metagenome-assembled genomes from proximal colonic microbiomes of synbiotic-treated korean native black pigs reveal changes in functional capacity. Scientific Reports, 2022, 12, .	1.6	2
5056	Genome collection of Shewanella spp. isolated from spoiled lamb. Frontiers in Microbiology, 0, 13, .	1.5	3

#	Article	IF	Citations
5057	Lithoautotrophic lifestyle of the widespread genus <i>Roseovarius</i> revealed by physiological and genomic characterization of <i>Roseovarius autotrophicus</i> sp. nov.. FEMS Microbiology Ecology, 0, , .	1.3	6
5058	Genomic features of <i>Pseudomonas</i> sp. <scp>RGM2144</scp> correlates with increased survival of rainbow trout infected by <i>Flavobacterium psychrophilum</i>. Journal of Fish Diseases, 0, , .	0.9	1
5059	Aeromonas allosaccharophila Strain AE59-TE2 Is Highly Antagonistic towards Multidrug-Resistant Human Pathogens, What Does Its Genome Tell Us?. Life, 2022, 12, 1492.	1.1	1
5060	Ancestral archaea expanded the genetic code with pyrrolysine. Journal of Biological Chemistry, 2022, 298, 102521.	1.6	10
5061	Possible involvement of extracellular polymeric substrates of Antarctic cyanobacterium Nostoc sp. strain SO-36 in adaptation to harsh environments. Journal of Plant Research, 2022, 135, 771-784.	1.2	5
5062	Subsurface Archaea associated with rapid geobiological change in a model Yellowstone hot spring. Communications Earth & Environment, 2022, 3, .	2.6	7
5063	Discovery of a new genus of anaerobic ammonium oxidizing bacteria with a mechanism for oxygen tolerance. Water Research, 2022, 226, 119165.	5.3	19
5064	Hybrid metagenome assemblies link carbohydrate structure with function in the human gut microbiome. Communications Biology, 2022, 5, .	2.0	4
5066	Genome Sequencing of Methicillin-Resistant and Methicillin-Susceptible <i>Mammaliicoccus sciuri</i> from Diseased Animals. Microbiology Resource Announcements, 0, , .	0.3	0
5067	Uncovering Lasonolide A Biosynthesis Using Genome-Resolved Metagenomics. MBio, 2022, 13, .	1.8	7
5068	Draft Genome Sequence of Cupriavidus basilensis SRS, a Bacterium Isolated from Stream Sediments. Microbiology Resource Announcements, 0, , .	0.3	0
5070	Critical assessment of pan-genomic analysis of metagenome-assembled genomes. Briefings in Bioinformatics, 2022, 23, .	3.2	6
5071	Culexarchaeia, a novel archaeal class of anaerobic generalists inhabiting geothermal environments. ISME Communications, 2022, 2, .	1.7	4
5072	Using Genomes and Evolutionary Analyses to Screen for Host-Specificity and Positive Selection in the Plant Pathogen Xylella fastidiosa. Applied and Environmental Microbiology, 2022, 88, .	1.4	6
5073	Colonization dynamics of extended-spectrum beta-lactamase-producing Enterobacterales in the gut of Malawian adults. Nature Microbiology, 2022, 7, 1593-1604.	5.9	9
5074	Genome analysis and phenotypic characterization of Halomonas hibernica isolated from a traditional food process with novel quorum quenching and catalase activities. Microbiology (United Kingdom), 2022, 168, .	0.7	0
5077	Conservation of Energetic Pathways for Electroautotrophy in the Uncultivated Candidate Order <i>Tenderiales</i>. MSphere, 2022, 7, .	1.3	3
5078	Metagenomic and metatranscriptomic insights into sulfate-reducing bacteria in a revegetated acidic mine wasteland. Npj Biofilms and Microbiomes, 2022, 8, .	2.9	2

#	ARTICLE	IF	CITATIONS
5079	Whole-Genome Sequencing of the Tropical Marine Bacterium Nocardiopsis dassonvillei NCIM 5124, Containing the Ectoine Biosynthesis Gene Cluster <i>ectABC</i>. Microbiology Resource Announcements, 2022, 11, .	0.3	4
5080	A global phylogenomic and metabolic reconstruction of the large intestine bacterial community of domesticated cattle. Microbiome, 2022, 10, .	4.9	6
5082	Novel species identification and deep functional annotation of electrogenic biofilms, selectively enriched in a microbial fuel cell array. Frontiers in Microbiology, 0, 13, .	1.5	3
5083	Imaging sensitive and drug-resistant bacterial infection with [11C]-trimethoprim. Journal of Clinical Investigation, 2022, 132, .	3.9	16
5084	In silico prediction of the enzymes involved in the degradation of the herbicide molinate by Gulosibacter molinativorax ON4T. Scientific Reports, 2022, 12, .	1.6	0
5085	A stable home for an equine pathogen: valid publication of the binomial Prescottella equi gen. nov., comb. nov., and reclassification of four rhodococcal species into the genus Prescottella.. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	11
5087	Selective Enrichment of Comammox <i>Nitrospira</i> in a Moving Bed Biofilm Reactor with Sufficient Oxygen Supply. Environmental Science & Technology, 2022, 56, 13338-13346.	4.6	21
5088	Seasonal microbial dynamics in the ocean inferred from assembled and unassembled data: a view on the unknown biosphere. ISME Communications, 2022, 2, .	1.7	1
5089	Functionally diverse microbial communities show resilience in response to a record-breaking rain event. ISME Communications, 2022, 2, .	1.7	4
5091	Apilactobacillus apisilvae sp. nov., Nicolia spurrieriana gen. nov. sp. nov., Bombilactobacillus folatiphilus sp. nov. and Bombilactobacillus thymidiniphilus sp. nov., four new lactic acid bacterial isolates from stingless bees Tetragonula carbonaria and Austroplebeia australis. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	11
5092	Dyella sedimenti sp. nov., Isolated from the Sediment of a Winery. Current Microbiology, 2022, 79, .	1.0	0
5093	Siteâ€tropism of streptococci in the oral microbiome. Molecular Oral Microbiology, 2022, 37, 229-243.	1.3	8
5094	Pan-cancer analyses reveal cancer-type-specific fungal ecologies and bacteriome interactions. Cell, 2022, 185, 3789-3806.e17.	13.5	163
5095	Phylogenomic characterization and pangenomic insights into the surfactin-producing bacteria Bacillus subtilis strain RI4914. Brazilian Journal of Microbiology, 2022, 53, 2051-2063.	0.8	1
5096	Metabolic framework of spontaneous and synthetic sourdough metacommunities to reveal microbial players responsible for resilience and performance. Microbiome, 2022, 10, .	4.9	15
5097	Codiversification of gut microbiota with humans. Science, 2022, 377, 1328-1332.	6.0	67
5098	Insights into community assembly mechanisms, biogeography, and metabolic potential of particle-associated and free-living prokaryotes in tropical oligotrophic surface oceans. Frontiers in Marine Science, 0, 9, .	1.2	3
5099	A compendium of 32,277 metagenome-assembled genomes and over 80 million genes from the early-life human gut microbiome. Nature Communications, 2022, 13, .	5.8	23

#	ARTICLE	IF	CITATIONS
5100	Genomic sequence of the non-pathogen Neisseria sp. strain MA1-1 with antibiotic resistance and virulence factors isolated from a head and neck cancer patient. Archives of Microbiology, 2022, 204, .	1.0	1
5101	Draft Genome Sequences of 25 Mycobacterium marinum Strains Isolated from Animals and Environmental Components in Aquaria and an Aquaculture Farm. Microbiology Resource Announcements, 0, , .	0.3	1
5102	Whole-Genome Sequencing and Comparative Genomic Analysis of Enterococcus spp. Isolated from Dairy Products: Genomic Diversity, Functional Characteristics, and Pathogenic Potential. Applied Sciences (Switzerland), 2022, 12, 9620.	1.3	2
5103	Integrated identification of growth pattern and taxon of bacterium in gut microbiota via confocal fluorescence imagingâ€oriented singleâ€cell sequencing. , 2022, 1, 350-358.		1
5104	Comparative Genome Analysis of a Novel Alkaliphilic Actinobacterial Species <i>Nesterenkonia haasae</i>. Polish Journal of Microbiology, 2022, 71, 453-461.	0.6	2
5105	Design, construction, and inÂvivo augmentation of a complex gut microbiome. Cell, 2022, 185, 3617-3636.e19.	13.5	84
5106	Drivers and determinants of strain dynamics following fecal microbiota transplantation. Nature Medicine, 2022, 28, 1902-1912.	15.2	54
5107	Complete Genome Sequence of an Uncultivated Freshwater <i>Flavobacterium</i> sp. Strain. Microbiology Resource Announcements, 0, , .	0.3	0
5110	Clinically relevant pathogens on surfaces display differences in survival and transcriptomic response in relation to probiotic and traditional cleaning strategies. Npj Biofilms and Microbiomes, 2022, 8, .	2.9	3
5112	Insect Gut Isolate Pseudomonas sp. Strain Nvir Degrades the Toxic Plant Metabolite Nitropropionic Acid. Applied and Environmental Microbiology, 2022, 88, .	1.4	2
5113	First Genome of Rock Lizard Darevskia valentini Involved in Formation of Several Parthenogenetic Species. Genes, 2022, 13, 1569.	1.0	4
5114	Deep metagenomic characterization of gut microbial community and function in preeclampsia. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	12
5115	Metagenomic analysis reveals the microbiome and antibiotic resistance genes in indigenous Chinese yellow-feathered chickens. Frontiers in Microbiology, 0, 13, .	1.5	6
5116	Circular Metagenome-Assembled Genome of <i>Methanobacterium</i> sp. Strain ERen5, a Putative Methanogenic, H ₂ -Utilizing Terrestrial Subsurface Archaeon. Microbiology Resource Announcements, 0, , .	0.3	0
5117	Deep-branching ANME-1c archaea grow at the upper temperature limit of anaerobic oxidation of methane. Frontiers in Microbiology, 0, 13, .	1.5	12
5118	Study of Complete Genome Sequence of Uncultivated <i>Hyphomonadaceae</i> sp.. Microbiology Resource Announcements, 0, , .	0.3	0
5121	Salmonella enterica Newserovar Abeokuta Genome Sequence, Strain OG19FER4 Isolated from Poultry Feed in Nigeria. Microbiology Resource Announcements, 0, , .	0.3	0
5123	Complete Genome Sequence of an Uncultivated Freshwater Bacteroidota Lineage. Microbiology Resource Announcements, 2022, 11, .	0.3	2

#	ARTICLE	IF	CITATIONS
5124	Marine DNA methylation patterns are associated with microbial community composition and inform virus-host dynamics. Microbiome, 2022, 10, .	4.9	8
5125	Vitamin B12 biosynthesis of Cetobacterium ceti isolated from the intestinal content of captive common bottlenose dolphins (Tursiops truncatus). Microbiology (United Kingdom), 2022, 168, .	0.7	6
5126	Microbial communities of stratified aquatic ecosystems of Kandalaksha Bay (White Sea) shed light on the evolutionary history of green and brown morphotypes of<i>Chlorobiota</i>. FEMS Microbiology Ecology, 2022, 98, .	1.3	3
5127	Inherent tendency of <i>Synechococcus</i> and heterotrophic bacteria for mutualism on long-term coexistence despite environmental interference. Science Advances, 2022, 8, .	4.7	8
5128	Duganella vulcania sp. nov., Rugamonas fusca sp. nov., Rugamonas brunnea sp. nov. and Rugamonas apoptosis sp. nov., isolated from subtropical streams, and phylogenomic analyses of the genera Janthinobacterium, Duganella, Rugamonas, Pseudoduganella and Massilia. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	3
5130	Rothia santali sp. nov., endophytic bacteria isolated from sandalwood (Santalum album L.) seedling. Archives of Microbiology, 2022, 204, .	1.0	3
5131	High genomic differentiation and limited gene flow indicate recent cryptic speciation within the genus Laspinema (cyanobacteria). Frontiers in Microbiology, 0, 13, .	1.5	7
5132	The Structure of Stable Cellulolytic Consortia Isolated from Natural Lignocellulosic Substrates. International Journal of Molecular Sciences, 2022, 23, 10779.	1.8	9
5133	Environmental Adaptability and Organic Pollutant Degradation Capacity of a Novel Rhodococcus Species Derived from Soil in the Uninhabited Area of the Qinghai-Tibet Plateau. Microorganisms, 2022, 10, 1935.	1.6	1
5134	Pan-genome evolution and its association with divergence of metabolic functions in Bifidobacterium genus. World Journal of Microbiology and Biotechnology, 2022, 38, .	1.7	1
5135	Basaltic Lava Tube Hosts a Putative Novel Genus in the Family <i>Solirubrobacteraceae</i>. Microbiology Resource Announcements, 2022, 11, .	0.3	1
5136	Anaeromyxobacter oryzae sp. nov., Anaeromyxobacter diazotrophicus sp. nov. and Anaeromyxobacter paludicola sp. nov., isolated from paddy soils. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	4
5138	Stromatolite formation by Anaerolineae-dominated microbial communities in hot spring travertine in North Sumatra, Indonesia. Sedimentary Geology, 2022, 440, 106263.	1.0	2
5139	Exploring AI-2-mediated interspecies communications within rumen microbial communities. Microbiome, 2022, 10, .	4.9	5
5140	Metagenome-Assembled Genome of <i>Acidibrevibacterium fodinaquatile</i> FLA01 from Fumarole Sediments from the Los Azufres Geothermal Field. Microbiology Resource Announcements, 2022, 11, .	0.3	2
5141	Ammonia oxidation by novel â€œCandidatus Nitrosacidococcus urinaeâ€• is sensitive to process disturbances at low pH and to iron limitation at neutral pH. Water Research X, 2022, 17, 100157.	2.8	9
5142	Microbially enhanced methane uptake under warming enlarges ecosystem carbon sink in a Tibetan alpine grassland. Global Change Biology, 2022, 28, 6906-6920.	4.2	7
5143	Mining the equine gut metagenome: poorly-characterized taxa associated with cardiovascular fitness in endurance athletes. Communications Biology, 2022, 5, .	2.0	7

#	Article	IF	Citations
5144	Novel trends of genomeÂevolution in highly complex tropical sponge microbiomes. Microbiome, 2022, 10, .	4.9	9
5145	Genome dynamics mediated by repetitive and mobile elements in Xanthomonas citri pv. durantae. Access Microbiology, 2022, 4, .	0.2	1
5146	Shotgun metagenomics of fecal samples from children in Peru reveals frequent complex co-infections with multiple Campylobacter species. PLoS Neglected Tropical Diseases, 2022, 16, e0010815.	1.3	5
5147	Bartonella choladocola sp. nov. and Bartonella apihabitans sp. nov., two novel species isolated from honey bee gut. Systematic and Applied Microbiology, 2022, 45, 126372.	1.2	6
5148	Size-fractionated microbiome observed during an eight-month long sampling in Jiaozhou Bay and the Yellow Sea. Scientific Data, 2022, 9, .	2.4	0
5149	Enhanced cultured diversity of the mouse gut microbiota enables custom-made synthetic communities. Cell Host and Microbe, 2022, 30, 1630-1645.e25.	5.1	26
5150	Niche differentiation and symbiotic association among ammonia/nitrite oxidizers in a full-scale rotating biological contactor. Water Research, 2022, 225, 119137.	5.3	3
5151	Past and present giant viruses diversity explored through permafrost metagenomics. Nature Communications, 2022, 13, .	5.8	17
5153	Prophage-encoded immune evasion factors are critical for Staphylococcus aureus host infection, switching, and adaptation. Cell Genomics, 2022, , 100194.	3.0	11
5156	Insight into co-hosts of nitrate reduction genes and antibiotic resistance genes in an urban river of the qinghai-tibet plateau. Water Research, 2022, 225, 119189.	5.3	12
5158	Draft Genome Sequence of Cold-Tolerant Pseudomonas sp. Strain NKUCC02_KPG, Isolated from Old Alexandria Reservoir in Northern Kentucky, USA. Microbiology Resource Announcements, 0, , .	0.3	0
5159	Viruses direct carbon cycling in lake sediments under global change. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	8
5160	Carbon fixation pathways across the bacterial and archaeal tree of life. , 2022, 1, .		12
5161	Draft Genome Sequences of <i>Dickeya</i> Species Associated with Soft Rot Diseases in Pineapple (Ananas comosus) and Banana (<i>Musa</i> spp.). Microbiology Resource Announcements, 0, , .	0.3	0
5162	Pharmaceutical Biotransformation is Influenced by Photosynthesis and Microbial Nitrogen Cycling in a Benthic Wetland Biomat. Environmental Science & Technology, 2022, 56, 14462-14477.	4.6	8
5163	Characterization and Identification of Probiotic Features in Lacticaseibacillus Paracasei Using a Comparative Genomic Analysis Approach. Probiotics and Antimicrobial Proteins, 2022, 14, 1211-1224.	1.9	5
5165	Phylogenetic and functional diverse ANME-1 thrive in Arctic hydrothermal vents. FEMS Microbiology Ecology, 2022, 98, .	1.3	1
5166	Pan-genomic and comparative analysis of Pediococcus pentosaceus focused on the in silico assessment of pediocin-like bacteriocins. Computational and Structural Biotechnology Journal, 2022, 20, 5595-5606.	1.9	2

#	Article	IF	Citations
5167	Exploring the biodiversity of <scp><i>Bifidobacterium asteroides</i></scp> among honey bee microbiomes. Environmental Microbiology, 2022, 24, 5666-5679.	1.8	4
5168	Unique H2-utilizing lithotrophy in serpentinite-hosted systems. ISME Journal, 2023, 17, 95-104.	4.4	11
5169	An ancient respiratory system in the widespread sedimentary archaea Thermoprofundales. Molecular Biology and Evolution, 0, , .	3.5	2
5170	Description of five novel thermophilic species of the genus Thermus: Thermus hydrothermalis sp. nov., Thermus neutrinimicus sp. nov., Thermus thalpophilus sp. nov., Thermus albus sp. nov., and Thermus altitudinis sp. nov., isolated from hot spring sediments. Systematic and Applied Microbiology, 2022, 45, 126361.	1.2	2
5171	Identification of 146 Metagenome-assembled Genomes from the Rumen Microbiome of Cattle in Japan. Microbes and Environments, 2022, 37, n/a.	0.7	4
5172	A novel species of lactic acid bacteria, Ligilactobacillus pabuli sp. nov., isolated from alfalfa silage. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	3
5173	Fidelity varies in the symbiosis between a gutless marine worm and its microbial consortium. Microbiome, 2022, 10, .	4.9	6
5174	Insights on Microbial Communities Inhabiting Non-Volcanic Hot Springs. International Journal of Molecular Sciences, 2022, 23, 12241.	1.8	3
5175	Granulimonas faecalis gen. nov., sp. nov., and Leptogranulimonas caecicola gen. nov., sp. nov., novel lactate-producing Atopobiaceae bacteria isolated from mouse intestines, and an emended description of the family Atopobiaceae. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	3
5176	Description of Halosolutus amylolyticus gen. nov., sp. nov., Halosolutus halophilus sp. nov. and Halosolutus gelatinilyticus sp. nov., and genome-based taxonomy of genera Natribaculum and Halovarius. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	11
5178	Halorussus vallis sp. nov., Halorussus aquaticus sp. nov., Halorussus gelatinilyticus sp. nov., Halorussus limi sp. nov., Halorussus salilacus sp. nov., Halorussus salinisoli sp. nov.: six extremely halophilic archaea isolated from solar saltern, salt lake and saline soil. Extremophiles, 2022, 26, .	0.9	10
5179	Deinococcus betulae sp. nov. and Deinococcus arboris sp. nov., novel bacteria isolated from bark of birch tree (Betula platyphylla). International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	2
5181	Population analysis of heavy metal and biocide resistance genes in Salmonella enterica from human clinical cases in New Hampshire, United States. Frontiers in Microbiology, 0, 13, .	1.5	5
5182	Disturbances in microbial skin recolonization and cutaneous immune response following allogeneic stem cell transfer. Leukemia, 2022, 36, 2705-2714.	3.3	3
5185	<tt>MAGScoT</tt>: a fast, lightweight and accurate bin-refinement tool. Bioinformatics, 2022, 38, 5430-5433.	1.8	3
5186	A Clinical Outcome of the Anti-PD-1 Therapy of Melanoma in Polish Patients Is Mediated by Population-Specific Gut Microbiome Composition. Cancers, 2022, 14, 5369.	1.7	3
5187	Deciphering chloramphenicol biotransformation mechanisms and microbial interactions via integrated multi-omics and cultivation-dependent approaches. Microbiome, 2022, 10, .	4.9	8
5188	Deep-branching acetogens in serpentinized subsurface fluids of Oman. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	18

#	Article	IF	Citations
5189	HiFi metagenomic sequencing enables assembly of accurate and complete genomes from human gut microbiota. Nature Communications, 2022, 13, .	5.8	22
5191	Enhanced terrestrial Fe(II) mobilization identified through a novel mechanism of microbially driven cave formation in Fe(III)-rich rocks. Scientific Reports, 2022, 12, .	1.6	1
5192	Sphingomicrobium nitratireducens sp. nov., isolated from a tidal flat in Guangxi. Archives of Microbiology, 2022, 204, .	1.0	1
5194	Genome-centric analysis of short and long read metagenomes reveals uncharacterized microbiome diversity in Southeast Asians. Nature Communications, 2022, 13, .	5.8	16
5195	Adaptations to high pressure of <scp> <i>Nautilia</i> </scp> sp. strain <scp>PV</scp> â€1, a piezophilic Campylobacterium (aka Epsilonproteobacterium) isolated from a deepâ€sea hydrothermal vent. Environmental Microbiology, 0, , .	1.8	3
5196	Complete Genome Sequence of Limosilactobacillus reuteri Strain VHProbi M07, Isolated from Breast Milk. Microbiology Resource Announcements, 0, , .	0.3	0
5197	Agarose gel microcapsules enable easy-to-prepare, picolitre-scale, single-cell genomics, yielding high-coverage genome sequences. Scientific Reports, 2022, 12, .	1.6	3
5198	Functional differentiation determines the molecular basis of the symbiotic lifestyle of Ca. Nanohaloarchaeota. Microbiome, 2022, 10, .	4.9	8
5199	2,5-Diketo-D-Gluconate Hyperproducing Gluconobacter sphaericus SJF2-1 with Reporting Multiple Genes Encoding the Membrane-Associated Flavoprotein-Cytochrome c Complexed Dehydrogenases. Microorganisms, 2022, 10, 2130.	1.6	5
5201	Single-cell Raman-activated sorting and cultivation (scRACS-Culture) for assessing and mining in situ phosphate-solubilizing microbes from nature. ISME Communications, 2022, 2, .	1.7	5
5202	Recovery and genome reconstruction of novel magnetotactic <i>Elusimicrobiota</i> from bog soil. ISME Journal, 2023, 17, 204-214.	4.4	5
5203	Comparative genome analysis of mycobacteria focusing on tRNA and non-coding RNA. BMC Genomics, 2022, 23, .	1.2	2
5204	Genome-centric investigation of bile acid metabolizing microbiota of dairy cows and associated diet-induced functional implications. ISME Journal, 2023, 17, 172-184.	4.4	16
5205	Lysobacter selenitireducens sp. nov., isolated from river sediment. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	1
5206	Composition and niche-specific characteristics of microbial consortia colonizing Marsberg copper mine in the Rhenish Massif. Biogeosciences, 2022, 19, 4883-4902.	1.3	3
5207	Chemolithoautotroph distributions across the subsurface of a convergent margin. ISME Journal, 2023, 17, 140-150.	4.4	15
5208	Draft Genome of <i>Frankia</i> sp. Strain R82, an Isolate from Root Nodules of Myrica gale. Microbiology Resource Announcements, 0, , .	0.3	0
5209	Identification of shared bacterial strains in the vaginal microbiota of related and unrelated reproductive-age mothers and daughters using genome-resolved metagenomics. PLoS ONE, 2022, 17, e0275908.	1.1	5

#	Article	IF	Citations
5210	Predominance of Methanomicrobiales and diverse hydrocarbonâ€degrading taxa in the Appalachian coalbed biosphere revealed through metagenomics and genomeâ€resolved metabolisms. Environmental Microbiology, 2022, 24, 5984-5997.	1.8	2
5212	Microbial Community Structure and Metabolic Potential at the Initial Stage of Soil Development of the Glacial Forefields in Svalbard. Microbial Ecology, 2023, 86, 933-946.	1.4	2
5213	Sharing of Antimicrobial Resistance Genes between Humans and Food Animals. MSystems, 2022, 7, .	1.7	9
5214	<scp>PM</scp> 7/151 (1) Considerations for the use of high throughput sequencing in plant health diagnostics¹. EPPO Bulletin, 2022, 52, 619-642.	0.6	8
5215	Vibrio ostreae sp. nov., a novel gut bacterium isolated from a Yellow Sea oyster. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	4
5216	Limibaculum sediminis sp. nov., isolated from mangrove sediment. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	0
5217	Microbial diversity and biogeochemical cycling potential in deep-sea sediments associated with seamount, trench, and cold seep ecosystems. Frontiers in Microbiology, 0, 13, .	1.5	1
5218	<i>Brucella ceti</i> and <i>Brucella pinnipedialis</i> genome characterization unveils genetic features that highlight their zoonotic potential. MicrobiologyOpen, 2022, 11, .	1.2	2
5219	Single-cell Genomics for Uncovering Relationships between Bacteriophages and their Hosts. , 0, , .		0
5221	Dongia deserti sp. nov., Isolated from the Gurbantunggut Desert Soil. Current Microbiology, 2022, 79, .	1.0	3
5222	Multidrug-Resistant High-Risk Escherichia coli and Klebsiella pneumoniae Clonal Lineages Occur in Black-Headed Gulls from Two Conservation Islands in Germany. Antibiotics, 2022, 11, 1357.	1.5	4
5223	Genomic insights into the physiology of Quinella, an iconic uncultured rumen bacterium. Nature Communications, 2022, 13, .	5.8	10
5224	Fontivita pretiosa gen. nov., sp. nov., a thermophilic planctomycete of the order Tepidisphaerales from a hot spring of Baikal lake region. Systematic and Applied Microbiology, 2022, , 126375.	1.2	3
5225	VEBA: a modular end-to-end suite for in silico recovery, clustering, and analysis of prokaryotic, microeukaryotic, and viral genomes from metagenomes. BMC Bioinformatics, 2022, 23, .	1.2	7
5226	Tabrizicola rongguiensis sp. nov., isolated from the sediment of a river in Ronggui, Foshan city, China. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	0
5227	Potential autotrophic carbon-fixer and Fe(II)-oxidizer Alcanivorax sp. MM125-6 isolated from Wocan hydrothermal field. Frontiers in Microbiology, 0, 13, .	1.5	2
5229	Zavarzinia marina sp. nov., a novel hydrocarbon-degrading bacterium isolated from deep chlorophyll maximum layer seawater of the West Pacific Ocean and emended description of the genus Zavarzinia. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	0
5230	Draft Genome Sequence of Delftia tsuruhatensis Strain 45.2.2, Colonizer of Zebrafish, Danio rerio, Skin Mucus. Microbiology Resource Announcements, 2022, 11, .	0.3	1

#	ARTICLE	IF	CITATIONS
5231	Anaerobic oxidation of propane coupled to nitrate reduction by a lineage within the class Symbiobacteriia. Nature Communications, 2022, 13, .	5.8	9
5233	Bioinformatic approaches for studying the microbiome of fermented food. Critical Reviews in Microbiology, 2023, 49, 693-725.	2.7	9
5234	High-Quality Draft Genome Sequence of Fischerella thermalis JSC-11, a Siderophilic Cyanobacterium with Bioremediation Potential. Microbiology Resource Announcements, 0, , .	0.3	0
5235	Comparative genomics and pangenomics of vancomycin-resistant and susceptible Enterococcus faecium from Irish hospitals. Journal of Medical Microbiology, 2022, 71, .	0.7	4
5236	Tumour microbiomes and Fusobacterium genomics in Vietnamese colorectal cancer patients. Npj Biofilms and Microbiomes, 2022, 8, .	2.9	9
5237	Metagenome-Assembled Genomes from Amazonian Soil Microbial Consortia. Microbiology Resource Announcements, 2022, 11, .	0.3	1
5238	<i>binny</i>: an automated binning algorithm to recover high-quality genomes from complex metagenomic datasets. Briefings in Bioinformatics, 2022, 23, .	3.2	5
5241	Genome-centric insight into metabolically active microbial population in shallow-sea hydrothermal vents. Microbiome, 2022, 10, .	4.9	2
5242	Pan-Genome Analysis Reveals Functional Divergences in Gut-Restricted Gilliamella and Snodgrassella. Bioengineering, 2022, 9, 544.	1.6	5
5243	Expression of divergent methyl/alkyl coenzyme M reductases from uncultured archaea. Communications Biology, 2022, 5, .	2.0	11
5244	Thermal Endurance by a Hot-Spring-Dwelling Phylogenetic Relative of the Mesophilic <i>Paracoccus</i>. Microbiology Spectrum, 2022, 10, .	1.2	2
5245	Plastic leachates impair picophytoplankton and dramatically reshape the marine microbiome. Microbiome, 2022, 10, .	4.9	12
5246	High-Quality Genome Sequences of Six Actinobacterial Strains Isolated from Granite, Granodiorite, and Tourmaline Rock Surfaces Sampled from Tamil Nadu, India, and New England, United States. Microbiology Resource Announcements, 0, , .	0.3	0
5247	Metagenomic Features Characterized with Microbial Iron Oxidoreduction and Mineral Interaction in Southwest Indian Ridge. Microbiology Spectrum, 2022, 10, .	1.2	7
5248	Complete Genome Sequence of <i>Lactiplantibacillus plantarum</i> VHProbi O10, Isolated from Kimchi. Microbiology Resource Announcements, 0, , .	0.3	0
5250	Metagenome-Assembled Genome of a Putative Chemoheterotroph from Volcanic Terrain in Hawaii. Microbiology Resource Announcements, 2022, 11, .	0.3	2
5251	Identification of PKS Gene Clusters from Metagenomic Libraries Using a Next-Generation Sequencing Approach. Methods in Molecular Biology, 2023, , 73-90.	0.4	0
5252	Geno- and Phenotypic Characteristics of a Klebsiella pneumoniae ST20 Isolate with Unusual Colony Morphology. Microorganisms, 2022, 10, 2063.	1.6	6

#	Article	IF	Citations
5253	Genomic and functional analysis of phageâ€mediated horizontal gene transfer in <i>Pseudomonas syringae</i> on the plant surface. New Phytologist, 2023, 237, 959-973.	3.5	4
5255	Epidermal Microbiomes of Leopard Sharks (Triakis semifasciata) Are Consistent across Captive and Wild Environments. Microorganisms, 2022, 10, 2081.	1.6	3
5257	Multiple sources of aerobic methane production in aquatic ecosystems include bacterial photosynthesis. Nature Communications, 2022, 13, .	5.8	15
5258	Stieleria sedimenti sp. nov., a Novel Member of the Family Pirellulaceae with Antimicrobial Activity Isolated in Portugal from Brackish Sediments. Microorganisms, 2022, 10, 2151.	1.6	3
5260	Epidemiological links and antimicrobial resistance of clinical Salmonella enterica ST198 isolates: a nationwide microbial population genomic study in Switzerland. Microbial Genomics, 2022, 8, .	1.0	3
5261	Genome-Resolved Metagenomics and Metatranscriptomics Reveal that Aquificae Dominates Arsenate Reduction in Tengchong Geothermal Springs. Environmental Science & Technology, 2022, 56, 16473-16482.	4.6	11
5262	Complete Genome Sequence of the Probiotic Strain <i>Lacticaseibacillus rhamnosus</i> VHProbi M14, Isolated from Cheese. Microbiology Resource Announcements, 0, , .	0.3	0
5263	A Novel Inovirus Reprograms Metabolism and Motility of Marine <i>Alteromonas</i>. Microbiology Spectrum, 2022, 10, .	1.2	1
5265	Psychroflexus curvus sp. nov., Psychroflexus longus sp. nov. and Psychroflexus montanilacus sp. nov., isolated from salt lakes on the Tibetan Plateau. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	0
5266	Glycoside hydrolase subfamily GH5_57 features a highly redesigned catalytic interface to process complex hetero-Î²-mannans. Acta Crystallographica Section D: Structural Biology, 2022, 78, 1358-1372.	1.1	1
5267	Ideonella alba sp. nov. and Ideonella aquatica sp. nov. isolated from an aquaculture farm. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	1
5268	Comparative Genomic Insights into the Evolution of <i>Halobacteria</i> -Associated â€œ <i>Candidatus</i> Nanohaloarchaeotaâ€• MSystems, 2022, 7, .	1.7	6
5269	Distributional Pattern of Bacteria, Protists, and Diatoms in Ocean according to Water Depth in the Northern South China Sea. Microbiology Spectrum, 2022, 10, .	1.2	3
5270	A low-cost genomics workflow enables isolate screening and strain-level analyses within microbiomes. Genome Biology, 2022, 23, .	3.8	6
5271	Vanadate reducing bacteria and archaea may use different mechanisms to reduce vanadate in vanadium contaminated riverine ecosystems as revealed by the combination of DNA-SIP and metagenomic-binning. Water Research, 2022, 226, 119247.	5.3	9
5272	Massively parallel single-cell genomics of microbiomes in rice paddies. Frontiers in Microbiology, 0, 13, .	1.5	4
5273	The Assessment of the Risk Ranking and Mobility Potential Associated with Environmental Resistomes in Wastewater Using Metagenomic Assembly. Sustainability, 2022, 14, 14292.	1.6	1
5274	Phylogenomic analysis of a metagenome-assembled genome indicates a new taxon of an anoxygenic phototroph bacterium in the family Chromatiaceae and the proposal of â€œCandidatus Thioaporhodococcusâ€•gen. nov. Archives of Microbiology, 2022, 204, .	1.0	2

#	ARTICLE	IF	CITATIONS
5275	Life Underground: Investigating Microbial Communities and Their Biomarkers in Marsâ€Analog Lava Tubes at Craters of the Moon National Monument and Preserve. Journal of Geophysical Research E: Planets, 2022, 127, .	1.5	5
5276	A distinct clade of Bifidobacterium longum in the gut of Bangladeshi children thrives during weaning. Cell, 2022, 185, 4280-4297.e12.	13.5	26
5277	Portibacter marinus sp. nov., isolated from the sediment on the surface of plastics and proposal of a novel genus Neolewinella gen. nov. based on the genome-based phylogeny of the family Lewinellaceae. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	1
5278	Comammox biogeography subject to anthropogenic interferences along a high-altitude river. Water Research, 2022, 226, 119225.	5.3	5
5279	In silico, in vitro and in vivo characterization of host-associated Latilactobacillus curvatus strains for potential probiotic applications in farmed Atlantic salmon (Salmo salar). Scientific Reports, 2022, 12, .	1.6	2
5280	Influences of carbon sources on N2O production during denitrification in freshwaters: Activity, isotopes and functional microbes. Water Research, 2022, 226, 119315.	5.3	14
5281	A Catalog of over 5,000 Metagenome-Assembled Microbial Genomes from the Caprinae Gut Microbiota. Microbiology Spectrum, 2022, 10, .	1.2	3
5282	Metagenome-Assembled Genome of a Putative Methanogenic <i>Methanosarcina</i> sp. Strain Enriched from Terrestrial High-CO ₂ Subsurface Sediments. Microbiology Resource Announcements, 0, , .	0.3	0
5283	Methanotrophy by a Mycobacterium species that dominates a cave microbial ecosystem. Nature Microbiology, 2022, 7, 2089-2100.	5.9	22
5284	Methylobacter couples methane oxidation and N2O production in hypoxic wetland soil. Soil Biology and Biochemistry, 2022, 175, 108863.	4.2	6
5285	A preliminary study on the feasibility of industrialization for n-caproic acid recovery from food wastewater: From lab to pilot. Bioresource Technology, 2022, 366, 128154.	4.8	6
5286	Sediment metagenomics reveals the impacts of poultry industry wastewater on antibiotic resistance and nitrogen cycling genes in tidal creek ecosystems. Science of the Total Environment, 2023, 857, 159496.	3.9	8
5287	Bioaugmentation of intertidal sludge enhancing the development of salt-tolerant aerobic granular sludge. Journal of Environmental Management, 2023, 325, 116394.	3.8	2
5288	Phytostabilization mitigates antibiotic resistance gene enrichment in a copper mine tailings pond. Journal of Hazardous Materials, 2023, 443, 130255.	6.5	3
5289	Thiobacillus spp. and Anaeromyxobacter spp. mediate arsenite oxidation-dependent biological nitrogen fixation in two contrasting types of arsenic-contaminated soils. Journal of Hazardous Materials, 2023, 443, 130220.	6.5	13
5290	Isolation and characterization of a thermophilic chain elongating bacterium that produces the high commodity chemical n-caproate from polymeric carbohydrates. Bioresource Technology, 2023, 367, 128170.	4.8	5
5291	Biofilm formation, sodium hypochlorite susceptibility and genetic diversity of Vibrio parahaemolyticus. International Journal of Food Microbiology, 2023, 385, 110011.	2.1	11
5292	Food provisioning results in functional, but not compositional, convergence of the gut microbiomes of two wild Rhinopithecus species: Evidence of functional redundancy in the gut microbiome. Science of the Total Environment, 2023, 858, 159957.	3.9	7

#	Article	IF	Citations
5293	High-resolution shotgun metagenomics: the more data, the better?. Briefings in Bioinformatics, 2022, 23, .	3.2	6
5294	Function-Based Rhizosphere Assembly along a Gradient of Desiccation in the Former Aral Sea. MSystems, 2022, 7, .	1.7	6
5295	Defining Composition and Function of the Rhizosphere Microbiota of Barley Genotypes Exposed to Growth-Limiting Nitrogen Supplies. MSystems, 2022, 7, .	1.7	12
5296	Frequent Occurrence and Metabolic Versatility of <i>Marinifilaceae</i> Bacteria as Key Players in Organic Matter Mineralization in Global Deep Seas. MSystems, 2022, 7, .	1.7	7
5297	metaMIC: reference-free misassembly identification and correction of de novo metagenomic assemblies. Genome Biology, 2022, 23, .	3.8	12
5298	Host diet shapes functionally differentiated gut microbiomes in sympatric speciation of blind mole rats in Upper Galilee, Israel. Frontiers in Microbiology, 0, 13, .	1.5	2
5299	Bifidobacterium lactis Probio-M8 improves bone metabolism in patients with postmenopausal osteoporosis, possibly by modulating the gut microbiota. European Journal of Nutrition, 0, , .	1.8	4
5300	Functional and Safety Characterization of Weissella paramesenteroides Strains Isolated from Dairy Products through Whole-Genome Sequencing and Comparative Genomics. Dairy, 2022, 3, 799-813.	0.7	9
5301	Concordance between Antimicrobial Resistance Phenotype and Genotype of Staphylococcus pseudintermedius from Healthy Dogs. Antibiotics, 2022, 11, 1625.	1.5	5
5302	Constructing metagenome-assembled genomes for almost all components in a real bacterial consortium for binning benchmarking. BMC Genomics, 2022, 23, .	1.2	4
5303	A <i>Mollicutes</i> Metagenome-Assembled Genome from the Gut of the Pteropod <i>Limacina rangii</i>. Microbiology Resource Announcements, 0, , .	0.3	0
5304	Idiomarina rhizosphaerae sp. nov. isolated from rhizosphere soil of Kalidium cuspidatum, and reclassification of Idiomarina andamanensis as Pseudidiomarina andamanensis comb. nov., and Idiomarina mangrovi as Pseudidiomarina mangrovi comb. nov. Archives of Microbiology, 2022, 204, .	1.0	3
5305	Years After a Fire, Biocrust Microbial Communities are Similar to Unburned Communities in a Coastal Grassland. Microbial Ecology, 0, , .	1.4	1
5306	Whole-genome sequence of the filamentous diazotrophic cyanobacterium Tolypothrix sp. PCC 7712 and its comparison with non-diazotrophic Tolypothrix sp. PCC 7601. Frontiers in Microbiology, 0, 13, .	1.5	2
5307	Characterization of antibiotic-resistance traits in Akkermansia muciniphila strains of human origin. Scientific Reports, 2022, 12, .	1.6	5
5309	Decoding the microbiome and metabolome of the <i>Panchagavya</i>â€”An indigenous fermented bioâ€formulation. , 2022, 1, .		4
5310	Accurate Binning of Metagenomic Contigs Using Composition, Coverage, and Assembly Graphs. Journal of Computational Biology, 2022, 29, 1357-1376.	0.8	6
5311	Expanding the genomic encyclopedia of Actinobacteria with 824 isolate reference genomes. Cell Genomics, 2022, 2, 100213.	3.0	16

#	Article	IF	Citations
5314	Complete Genome Sequence of Xanthomonas arboricola pv. <i>pruni</i> Strain Xcp1 Isolated in 1984 from a Bacterial Spot Spring Canker on Prunus persica var. <i>nucipersica</i> cv. â€œRedgoldâ€. Microbiology Resource Announcements, 2022, 11, .	0.3	1
5315	Exploring clade differentiation of the Faecalibacterium prausnitzii complex. IScience, 2022, 25, 105533.	1.9	0
5316	Paracrocinitomix mangrovi gen. nov., sp. nov., isolated from a mangrove sediment: proposal of two new families, Phaeocystidibacteraceae fam. nov. and Owenweeksiaceae fam. nov., and emended description of the family Schleiferiaceae. Antonie Van Leeuwenhoek, 2023, 116, 171-184.	0.7	2
5318	Marinobacterium sedimentorum sp. nov., Isolated from the Bottom Sediments of the Okhotsk Sea. Diversity, 2022, 14, 944.	0.7	1
5319	Discovery of integrons in Archaea: Platforms for cross-domain gene transfer. Science Advances, 2022, 8, .	4.7	8
5321	Genomic analysis of Paenibacillus sp. MDMC362 from the Merzouga desert leads to the identification of a potentially thermostable catalase. Antonie Van Leeuwenhoek, 2023, 116, 21-38.	0.7	1
5322	Metagenome-assembled genome extraction and analysis from microbiomes using KBase. Nature Protocols, 2023, 18, 208-238.	5.5	7
5324	Metabolic Potential of Microbial Communities in the Hypersaline Sediments of the Bonneville Salt Flats. MSystems, 2022, 7, .	1.7	4
5325	Advanced prokaryotic systematics: the modern face of an ancient science. New Microbes and New Infections, 2022, 49-50, 101036.	0.8	4
5327	Key players in syntrophic propionate oxidation revealed by metagenome-assembled genomes from anaerobic digesters bioaugmented with propionic acid enriched microbial consortia. Frontiers in Microbiology, 0, 13, .	1.5	0
5328	Metagenomics revealing molecular profiles of microbial community structure and metabolic capacity in Bamucuo lake, Tibet. Environmental Research, 2023, 217, 114847.	3.7	2
5329	Adaptation of a microbial community to demand-oriented biological methanation. , 2022, 15, .		4
5330	Cross-generational bacterial strain transfer to an infant after fecal microbiota transplantation to a pregnant patient: a case report. Microbiome, 2022, 10, .	4.9	5
5331	Viral community-wide auxiliary metabolic genes differ by lifestyles, habitats, and hosts. Microbiome, 2022, 10, .	4.9	35
5332	TbasCO: trait-based comparative â€˜omics identifies ecosystem-level and niche-differentiating adaptations of an engineered microbiome. ISME Communications, 2022, 2, .	1.7	5
5333	Genomic analysis and biochemical profiling of an unaxenic strain of Synechococcus sp. isolated from the Peruvian Amazon Basin region. Frontiers in Genetics, 0, 13, .	1.1	1
5334	Moorella sulfitireducens sp. nov., a thermophilic anaerobic bacterium isolated from a terrestrial thermal spring. Extremophiles, 2022, 26, .	0.9	2
5335	Genomic remnants of ancestral methanogenesis and hydrogenotrophy in Archaea drive anaerobic carbon cycling. Science Advances, 2022, 8, .	4.7	17

#	ARTICLE	IF	CITATIONS
5336	Perchlorate reduction kinetics and genome-resolved metagenomics identify metabolic interactions in acclimated saline lake perchlorate-reducing consortia. Water Research, 2022, 227, 119343.	5.3	2
5341	Heterotrophic denitrification: An overlooked factor that contributes to nitrogen removal in n-DAMO mixed culture. Environmental Research, 2023, 216, 114802.	3.7	4
5342	Evidence of virulence and antibiotic resistance genes from the microbiome mapping in minimally processed vegetables producing facilities. Food Research International, 2022, 162, 112202.	2.9	7
5344	Monsoon affects the distribution of antibiotic resistome in Tibetan glaciers. Environmental Pollution, 2023, 317, 120809.	3.7	11
5345	Draft Genomes of <i>Frankia</i> strains AiPa1 and AiPs1 Retrieved from Soil with Monocultures of <i>Picea abies</i> or <i>Pinus sylvestris</i> using <i>Alnus incana</i> as Capture Plant. Journal of Genomics, 2023, 11, 1-8.	0.6	0
5346	A survey of the biosynthetic potential and specialized metabolites of archaea and understudied bacteria. Current Research in Biotechnology, 2023, 5, 100117.	1.9	5
5347	Interactions among deep-sea mussels and their epibiotic and endosymbiotic chemoautotrophic bacteria: Insights from multi-omics analysis. Zoological Research, 2023, 44, 106-125.	0.9	4
5348	Taxonomic proposal for a deep branching bacterial phylogenetic lineage: transfer of the family Thermodesulfobiaceae to Thermodesulfobiales ord. nov., Thermodesulfobiia classis nov. and Thermodesulfobiota phyl. nov. Systematic and Applied Microbiology, 2023, 46, 126388.	1.2	6
5349	Pyrite-enhanced Sludge Digestion via Stimulation of Direct Interspecies Electron Transfer between Syntrophic Propionate- and Sulfur-oxidizing Bacteria and Methanogens: Genome-centric Metagenomics Evidence. Chemical Engineering Journal, 2023, 456, 141089.	6.6	15
5350	Microbiome enrichment from contaminated marine sediments unveils novel bacterial strains for petroleum hydrocarbon and heavy metal bioremediation. Environmental Pollution, 2023, 317, 120772.	3.7	6
5351	Whole genome sequence data of a marine bacterium, Marinobacter adhaerens PBVC038, associated with toxic harmful algal bloom. Data in Brief, 2023, 46, 108768.	0.5	0
5352	Structural, metagenomic and metabolic shifts in multispecies freshwater biofilm models exposed to silver nanoparticles. Journal of Environmental Chemical Engineering, 2023, 11, 109162.	3.3	2
5353	C-N-S synergy in a pilot-scale mainstream anammox fluidized-bed membrane bioreactor for treating chemically enhanced primary treatment saline sewage. Water Research, 2023, 229, 119475.	5.3	15
5354	Carbon substrate selects for different lineages of N2O reducing communities in soils under anoxic conditions. Soil Biology and Biochemistry, 2023, 177, 108909.	4.2	2
5355	Low diversity and microdiversity of comammox bacteria in wastewater systems suggest specific adaptations within the Ca. Nitrospira nitrosa cluster. Water Research, 2023, 229, 119497.	5.3	8
5356	A comparative analysis employing a gene- and genome-centric metagenomic approach reveals changes in composition, function, and activity in waterworks with different treatment processes and source water in Finland. Water Research, 2023, 229, 119495.	5.3	7
5357	Unravelling microbial drivers of the sulfate-reduction process inside landfill using metagenomics. Chemosphere, 2023, 313, 137537.	4.2	3
5358	Textile industry wastewater microbiome: Recovery of metagenome assembled genomes (MAGs) using shotgun sequencing approach from Jetpur, Gujarat, India. Ecological Genetics and Genomics, 2023, 26, 100155.	0.3	1

#	Article	IF	Citations
5359	Coupling effects of nitrate reduction and sulfur oxidation in a subtropical marine mangrove ecosystem with Spartina alterniflora invasion. Science of the Total Environment, 2023, 862, 160930.	3.9	52
5360	Improved microbial genomes and gene catalog of the chicken gut from metagenomic sequencing of high-fidelity long reads. GigaScience, 2022, 11, .	3.3	12
5361	pH-Dependent Hydrogenotrophic Denitratation Based on Self-Alkalization. Environmental Science & Technology, 2023, 57, 685-696.	4.6	10
5363	Complete circularized genome resources of seven strains of <i>Xylella fastidiosa</i> subsp. <i>fastidiosa</i> using hybrid assembly reveals unknown plasmids. Phytopathology, 0, , .	1.1	1
5365	Novel application of metagenomics for the strain-level detection of bacterial contaminants within non-sterile industrial products â€“ a retrospective, real-time analysis. Microbial Genomics, 2022, 8, .	1.0	0
5366	Zunongwangia pacifica sp. nov., isolated from surface seawater of the Western Pacific Ocean. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	0
5367	Bifidobacterium animalis subsp. lactis Probio-M8 undergoes host adaptive evolution by glcU mutation and translocates to the infantâ€™s gut via oral-/entero-mammary routes through lactation. Microbiome, 2022, 10, .	4.9	4
5368	Characterization, genome analysis and genetic tractability studies of a new nanocellulose producing Komagataeibacter intermedius isolate. Scientific Reports, 2022, 12, .	1.6	5
5369	Insights into the diversity of transcription activator-like effectors (TALEs) in Indian pathotype strains of Xanthomonas oryzae pv. oryzae. Phytopathology, 0, , .	1.1	0
5371	Deciphering the community structure and the functional potential of a hypersaline marsh microbial mat community. FEMS Microbiology Ecology, 2022, 98, .	1.3	1
5372	Complete genome sequence resource of <i>Pantoea anthophila</i> CL1 causing soft rot disease in <i>Clausena lansium</i> (Wampee) in China. Plant Disease, 0, , .	0.7	2
5373	Colwellia maritima sp. nov. and Polaribacter marinus sp. nov., isolated from seawater. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	0
5374	Genomic analysis and in vivo efficacy of Pediococcus acidilactici as a potential probiotic to prevent hyperglycemia, hypercholesterolemia and gastrointestinal infections. Scientific Reports, 2022, 12, .	1.6	8
5375	Unexpected absence of ribosomal protein genes from metagenome-assembled genomes. ISME Communications, 2022, 2, .	1.7	13
5376	Metagenome-Based Exploration of Bacterial Communities Associated with Cyanobacteria Strains Isolated from Thermal Muds. Microorganisms, 2022, 10, 2337.	1.6	3
5378	A longitudinal census of the bacterial community in raw milk correlated with Staphylococcus aureus clinical mastitis infections in dairy cattle. Animal Microbiome, 2022, 4, .	1.5	3
5379	HT-SIP: a semi-automated stable isotope probing pipeline identifies cross-kingdom interactions in the hyphosphere of arbuscular mycorrhizal fungi. Microbiome, 2022, 10, .	4.9	22
5380	Ancient oral microbiomes support gradual Neolithic dietary shifts towards agriculture. Nature Communications, 2022, 13, .	5.8	13

#	ARTICLE	IF	CITATIONS
5381	Roseicella aerolata sp. nov., isolated from bioaerosols of electronic waste. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	1
5382	Metagenomic insights into the functions of microbial communities in sulfur-rich sediment of a shallow-water hydrothermal vent off Kueishan Island. Frontiers in Microbiology, 0, 13, .	1.5	1
5383	proGenomes3: approaching one million accurately and consistently annotated high-quality prokaryotic genomes. Nucleic Acids Research, 2023, 51, D760-D766.	6.5	15
5384	Adaptations of endolithic communities to abrupt environmental changes in a hyper-arid desert. Scientific Reports, 2022, 12, .	1.6	2
5385	Anianabacter salinae gen. nov., sp. nov. ASV31T, a Facultative Alkaliphilic and Extremely Halotolerant Bacterium Isolated from Brine of a Millennial Continental Saltern. Diversity, 2022, 14, 1009.	0.7	2
5386	Nitrogen-metabolising microorganism analysis in rapid sand filters from drinking water treatment plant. Environmental Science and Pollution Research, 2023, 30, 29458-29475.	2.7	3
5387	A step forward for Shiga toxin-producing Escherichia coli identification and characterization in raw milk using long-read metagenomics. Microbial Genomics, 2022, 8, .	1.0	2
5388	Metagenomic Characterization of Multiple Genetically Modified Bacillus Contaminations in Commercial Microbial Fermentation Products. Life, 2022, 12, 1971.	1.1	3
5389	Complete Genome Sequence Resource of <i>Pectobacterium colocasium</i> strain F1-1 that Causes Soft Rot Disease of Taro. Plant Disease, 0, , .	0.7	0
5391	Coupling continuous poly(3-hydroxybutyrate) synthesis with piperazine-contained wastewater treatment: Fermentation performance and microbial contamination deciphering. International Journal of Biological Macromolecules, 2023, 226, 1523-1532.	3.6	1
5392	Nutrient niche specificity for glycosaminoglycans is reflected in polysaccharide utilization locus architecture of gut Bacteroides species. Frontiers in Microbiology, 0, 13, .	1.5	1
5393	Genomic profiling of Nitrospira species reveals ecological success of comammox Nitrospira. Microbiome, 2022, 10, .	4.9	13
5394	Lacticaseibacillus kribbianus sp. nov., isolated from pig farm faeces dump. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	5
5395	Distribution Patterns of Antibiotic Resistance Genes and Their Bacterial Hosts in a Manure Lagoon of a Large-Scale Swine Finishing Facility. Microorganisms, 2022, 10, 2301.	1.6	5
5396	Analyzing rare mutations in metagenomes assembled using long and accurate reads. Genome Research, 0, , .	2.4	2
5397	Limnobacter parvus sp. nov., a Thiosulfate-Oxidizing Bacterium Isolated from Lake Water. Current Microbiology, 2023, 80, .	1.0	3
5398	Nanopore long-read-only metagenomics enables complete and high-quality genome reconstruction from mock and complex metagenomes. Microbiome, 2022, 10, .	4.9	28
5399	Genome Sequence of the Euphotic Hawaiian Gammaproteobacterium HetDA_MAG_MS8, in the Order <i>Nevskiales</i> , Family <i>Oceanococcaceae</i> , Genus <i>Oceanococcus</i>. Microbiology Resource Announcements, 0, , .	0.3	0

#	ARTICLE	IF	CITATIONS
5400	An improved workflow for accurate and robust healthcare environmental surveillance using metagenomics. Microbiome, 2022, 10, .	4.9	3
5401	Genome Sequence of a Heterocystous Diazotroph Isolated from a <i>Trichodesmium</i> Consortium from the North Pacific Subtropical Gyre. Microbiology Resource Announcements, 0, , .	0.3	0
5402	Comparative genomics of Campylobacter jejuni from clinical campylobacteriosis stool specimens. Gut Pathogens, 2022, 14, .	1.6	4
5403	Large-scale comparative genomics to refine the organization of the global Salmonella enterica population structure. Microbial Genomics, 2022, 8, .	1.0	1
5404	Genome-resolved insight into the reservoir of antibiotic resistance genes in aquatic microbial community. Scientific Reports, 2022, 12, .	1.6	0
5405	Comparison of Metagenomics and Metatranscriptomics Tools: A Guide to Making the Right Choice. Genes, 2022, 13, 2280.	1.0	9
5406	Cyclitol metabolism is a central feature of <scp><i>Burkholderia</i></scp> leaf symbionts. Environmental Microbiology, 2023, 25, 454-472.	1.8	5
5407	Genetic manipulation of the human gut bacterium Eggerthella lenta reveals a widespread family of transcriptional regulators. Nature Communications, 2022, 13, .	5.8	15
5408	A regulatory hydrogenase gene cluster observed in the thioautotrophic symbiont of Bathymodiolus mussel in the East Pacific Rise. Scientific Reports, 2022, 12, .	1.6	0
5409	Proposal to reclassify Aquiflexum aquatile into a novel genus as Cognataquiflexum aquatile gen. nov., comb. nov., and description of Cognataquiflexum nitidum sp. nov. and Cognataquiflexum rubidum sp. nov., isolated from freshwater lakes on the Tibetan Plateau. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	0
5413	A metagenomic insight into the microbiomes of geothermal springs in the Subantarctic Kerguelen Islands. Scientific Reports, 2022, 12, .	1.6	4
5414	Microbiome and metagenomic analysis of Lake Hillier Australia reveals pigment-rich polyextremophiles and wide-ranging metabolic adaptations. Environmental Microbiomes, 2022, 17, .	2.2	3
5415	Decoupling of respiration rates and abundance in marine prokaryoplankton. Nature, 2022, 612, 764-770.	13.7	19
5416	Metagenomic binning analyses of pig manure composting reveal potential antibiotic-degrading bacteria and their risk of antibiotic resistance genes. Bioresource Technology, 2023, 371, 128540.	4.8	2
5417	Nitrifiers Cooperate to Produce Nitrous Oxide in Plateau Wetland Sediments. Environmental Science & Technology, 2023, 57, 810-821.	4.6	3
5418	Plant microbiomes harbor potential to promote nutrient turnover in impoverished substrates of a Brazilian biodiversity hotspot. ISME Journal, 2023, 17, 354-370.	4.4	14
5419	Human microbiota drives hospital-associated antimicrobial resistance dissemination in the urban environment and mirrors patient case rates. Microbiome, 2022, 10, .	4.9	12
5420	Metagenome-Assembled Genome of a <i>Cyclobacteriaceae</i> Bacterium, HetDA_MAG_MS6, Isolated from a <i>Trichodesmium</i> Consortium from Station ALOHA. Microbiology Resource Announcements, 0, , .	0.3	0

#	ARTICLE	IF	CITATIONS
5421	High Level of Interaction between Phages and Bacteria in an Artisanal Raw Milk Cheese Microbial Community. MSystems, 2023, 8, .	1.7	5
5422	Emiliania huxleyiâ€"Bacteria Interactions under Increasing CO2 Concentrations. Microorganisms, 2022, 10, 2461.	1.6	0
5423	Draft Genome Sequences of Phytase Active Endophytic and Epiphytic Erwinia gerundensis Isolated from Wheat (Triticum aestivum) Seeds. Microbiology Resource Announcements, 0, , .	0.3	0
5424	Adaptive genetic traits in pelagic freshwater microbes. Environmental Microbiology, 2023, 25, 606-641.	1.8	12
5425	Pangenome and genomic taxonomy analyses of Leuconostoc gelidum and Leuconostoc gasicomitatum. BMC Genomics, 2022, 23, .	1.2	0
5426	The draft genome of Andean Rhodopseudomonas sp. strain AZUL predicts genome plasticity and adaptation to chemical homeostasis. BMC Microbiology, 2022, 22, .	1.3	0
5427	Impact of international travel and diarrhea on gut microbiome and resistome dynamics. Nature Communications, 2022, 13, .	5.8	9
5428	Levilactobacillus humaensis sp. nov. and Lapidilactobacillus luobeiensis sp. nov., isolated from traditional Chinese pickle. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	1
5429	Epidemiological Investigation of Hospital Transmission of Corynebacterium striatum Infection by Core Genome Multilocus Sequence Typing Approach. Microbiology Spectrum, 2023, 11, .	1.2	3
5430	Gordonia tangerina sp. nov., isolated from seawater. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	2
5431	Targeted single-cell genomics reveals novel host adaptation strategies of the symbiotic bacteria Endozoicomonas in Acropora tenuis coral. Microbiome, 2022, 10, .	4.9	6
5432	Metagenome-Assembled Genomes for â€œ <i>Candidatus</i> Phormidium sp. Strain AB48â€•and Co-occurring Microorganisms from an Industrial Photobioreactor Environment. Microbiology Resource Announcements, 2022, 11, .	0.3	1
5433	New globally distributed bacterial phyla within the FCB superphylum. Nature Communications, 2022, 13, .	5.8	4
5434	Widespread formation of intracellular calcium carbonates by the bloomâ€forming cyanobacterium <scp><i>Microcystis</i></scp>. Environmental Microbiology, 2023, 25, 751-765.	1.8	1
5435	Genome-based analyses of the genus Acidovorax: proposal of the two novel genera Paracidovorax gen. nov., Paenacidovorax gen. nov. and the reclassification of Acidovorax antarcticus as Comamonas antarctica comb. nov. and emended description of the genus Acidovorax. Archives of Microbiology, 2023, 205, .	1.0	4
5436	Dynamics of extended-spectrum cephalosporin resistance genes in Escherichia coli from Europe and North America. Nature Communications, 2022, 13, .	5.8	17
5437	Long-read genome sequence data of pomegranate bacterial blight pathogen Xanthomonas citri pv. punicae 119. Data in Brief, 2022, , 108849.	0.5	0
5438	Constraining the composition and quantity of organic matter used by abundant marine Thaumarchaeota. Environmental Microbiology, 2023, 25, 689-704.	1.8	5

#	ARTICLE	IF	CITATIONS
5440	A bacterium from a mountain lake harvests light using both proton-pumping xanthorhodopsins and bacteriochlorophyll-based photosystems. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	12
5441	<i>Vulcanimicrobium alpinus</i> gen. nov. sp. nov., the first cultivated representative of the candidate phylum â€œEremiobacterotaâ€, is a metabolically versatile aerobic anoxygenic phototroph. ISME Communications, 2022, 2, .	1.7	8
5442	Actin cytoskeleton and complex cell architecture in an Asgard archaeon. Nature, 2023, 613, 332-339.	13.7	55
5444	Chryseolinea lacunae sp. nov. and Piscinibacter lacus sp. nov. Isolated from Artificial Pond Water. Current Microbiology, 2023, 80, .	1.0	0
5445	Prokaryotic and viral genomes recovered from 787 Japanese gut metagenomes revealed microbial features linked to diets, populations, and diseases. Cell Genomics, 2022, 2, 100219.	3.0	8
5448	Soil Collected from a Single Great Smoky Mountains Trail Contains a Diversity of Listeria monocytogenes and<i>Listeria</i>spp.. Microbiology Spectrum, 2023, 11, .	1.2	2
5449	Acidobacteria in Fens: Phylogenetic Diversity and Genome Analysis of the Key Representatives. Microbiology, 2022, 91, 662-670.	0.5	2
5450	Complete Genome Sequence of Lactococcus garvieae MS210922A, Isolated from Farmed Greater Amberjack (Seriola dumerili) in Japan. Microbiology Resource Announcements, 2022, 11, .	0.3	2
5451	Metagenomic-based surveillance systems for antibiotic resistance in non-clinical settings. Frontiers in Microbiology, 0, 13, .	1.5	8
5452	Microvirga terrae sp. nov., Isolated from Soil. Current Microbiology, 2023, 80, .	1.0	2
5453	Metagenomics and metatranscriptomics reveal broadly distributed, active, novel methanotrophs in the Gulf of Mexico hypoxic zone and in the marine water column. FEMS Microbiology Ecology, 2023, 99, .	1.3	5
5455	Taxonomic, Genomic, and Functional Variation in the Gut Microbiomes of Wild Spotted Hyenas Across 2 Decades of Study. MSystems, 0, , .	1.7	1
5456	Mobile genetic elements from the maternal microbiome shape infant gut microbial assembly and metabolism. Cell, 2022, 185, 4921-4936.e15.	13.5	33
5458	High-Quality Genome Sequences of Two Octocoral-Associated Bacteria, Endozoicomonas euniceicola EF212 ^T and Endozoicomonas gorgoniicola PS125 ^T. Microbiology Resource Announcements, 0, , .	0.3	0
5459	Environmental predictors of electroactive bacterioplankton in small boreal lakes. Environmental Microbiology, 2023, 25, 705-720.	1.8	3
5460	Long-Read Metagenome-Assembled Genomes Improve Identification of Novel Complete Biosynthetic Gene Clusters in a Complex Microbial Activated Sludge Ecosystem. MSystems, 2022, 7, .	1.7	11
5461	Long-Read Sequencing Improves Recovery of Picoeukaryotic Genomes and Zooplankton Marker Genes from Marine Metagenomes. MSystems, 2022, 7, .	1.7	7
5462	Identification and Genomic Characterization of Escherichia albertii in Migratory Birds from Poyang Lake, China. Pathogens, 2023, 12, 9.	1.2	3

#	ARTICLE	IF	CITATIONS
5463	Disentangling the lipid divide: Identification of key enzymes for the biosynthesis of membrane-spanning and ether lipids in Bacteria. Science Advances, 2022, 8, .	4.7	6
5464	Metaproteomics reveals methyltransferases implicated in dichloromethane and glycine betaine fermentation by â€˜Candidatus Formimonas warabiyaâ€™ strain DCMF. Frontiers in Microbiology, 0, 13, .	1.5	0
5465	Genome-based taxonomic rearrangement of Oceanobacter-related bacteria including the description of Thalassolituus hydrocarbonoclasticus sp. nov. and Thalassolituus pacificus sp. nov. and emended description of the genus Thalassolituus. Frontiers in Microbiology, 0, 13, .	1.5	4
5466	Mining of novel secondary metabolite biosynthetic gene clusters from acid mine drainage. Scientific Data, 2022, 9, .	2.4	3
5467	Genomic Legacies of Ancient Adaptation Illuminate GC-Content Evolution in Bacteria. Microbiology Spectrum, 2023, 11, .	1.2	7
5469	Silent gene clusters encode magnetic organelle biosynthesis in a non-magnetotactic phototrophic bacterium. ISME Journal, 2023, 17, 326-339.	4.4	6
5470	Virus diversity and interactions with hosts in deep-sea hydrothermal vents. Microbiome, 2022, 10, .	4.9	12
5471	Global patterns of diversity and metabolism of microbial communities in deep-sea hydrothermal vent deposits. Microbiome, 2022, 10, .	4.9	23
5472	Diverse Methylmercury (MeHg) Producers and Degraders Inhabit Acid Mine Drainage Sediments, but Few Taxa Correlate with MeHg Accumulation. MSystems, 2023, 8, .	1.7	1
5473	Cultivation-independent genomes greatly expand taxonomic-profiling capabilities of mOTUs across various environments. Microbiome, 2022, 10, .	4.9	22
5475	Chemolithotrophic Biological Nitrogen Fixation Fueled by Antimonite Oxidation May Be Widespread in Sb-Contaminated Habitats. Environmental Science & Technology, 2023, 57, 231-243.	4.6	8
5476	Devosia oryzisoli sp. nov., a novel moderately halotolerant bacterium isolated from the roots of rice plants and genome mining revealed the biosynthesis potential as plant growth promoter. Antonie Van Leeuwenhoek, 2023, 116, 231-242.	0.7	0
5478	Improved Assembly of Metagenome-Assembled Genomes and Viruses in Tibetan Saline Lake Sediment by HiFi Metagenomic Sequencing. Microbiology Spectrum, 2023, 11, .	1.2	3
5479	Metatranscriptomes reveal the diverse responses of <scp> <i>Thaumarchaeota</i> </scp> ecotypes to environmental variations in the northern slope of the South China Sea. Environmental Microbiology, 0, , .	1.8	2
5480	Cave <i>Thiovulum</i> (<i>Candidatus</i> Thiovulum stygium) differs metabolically and genomically from marine species. ISME Journal, 2023, 17, 340-353.	4.4	3
5481	Comparative genomic analyses of four novel Ramlibacter species and the cellulose-degrading properties of Ramlibacter cellulosilyticus sp. nov.. Scientific Reports, 2022, 12, .	1.6	5
5483	New perspectives on an old grouping: The genomic and phenotypic variability of Oxalobacter formigenes and the implications for calcium oxalate stone prevention. Frontiers in Microbiology, 0, 13, .	1.5	2
5484	Gut microbiota contributes to lignocellulose deconstruction and nitrogen fixation of the larva of Apriona swainsoni. Frontiers in Physiology, 0, 13, .	1.3	2

#	ARTICLE	IF	CITATIONS
5485	Identification of Novel Viruses and Their Microbial Hosts from Soils with Long-Term Nitrogen Fertilization and Cover Cropping Management. MSystems, 2022, 7, .	1.7	3
5486	Sphingomonas liriopis sp. nov., Sphingomonas donggukensis sp. nov., and Sphingomonas tagetis sp. nov., isolated from Liriope platyphylla fruit, soil, and Tagetes patula roots. Archives of Microbiology, 2023, 205, .	1.0	2
5488	Occurrence, Diversity, and Genomes of â€œ <i>Candidatus</i> Patescibacteriaâ€•along the Early Diagenesis of Marine Sediments. Applied and Environmental Microbiology, 2022, 88, .	1.4	2
5489	SnakeMAGs: a simple, efficient, flexible and scalable workflow to reconstruct prokaryotic genomes from metagenomes. F1000Research, 0, 11, 1522.	0.8	0
5491	Isolation and Genomics of <i>Futiania mangrovii</i> gen. nov., sp. nov., a Rare and Metabolically Versatile Member in the Class <i>Alphaproteobacteria</i>. Microbiology Spectrum, 2023, 11, .	1.2	2
5492	Comparative Genomic and Metagenomic Investigations of the Corynebacterium tuberculostearicum Species Complex Reveals Potential Mechanisms Underlying Associations To Skin Health and Disease. Microbiology Spectrum, 2023, 11, .	1.2	5
5493	Metabolic reconstruction of the near complete microbiome of the model sponge <scp><i>Ianthella basta</i></scp>. Environmental Microbiology, 2023, 25, 646-660.	1.8	4
5495	Degradation pathways for organic matter of terrestrial origin are widespread and expressed in Arctic Ocean microbiomes. Microbiome, 2022, 10, .	4.9	7
5496	Characteristics and adaptability of Flavobacterium panici BSSL-CR3 in tidal flat revealed by comparative genomic and enzymatic analysis. Archives of Microbiology, 2023, 205, .	1.0	2
5497	Campylobacter majalis sp. nov. and Campylobacter suis sp. nov., novel Campylobacter species isolated from porcine gastrointestinal mucosa. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	5
5498	Draft Genome Sequence of <i>Pyrobaculum</i> sp. Strain 3827-6, a Hyperthermophilic Crenarchaeon, Isolated from a Kamchatka Hot Spring. Microbiology Resource Announcements, 2023, 12, .	0.3	1
5499	Complete Genome Sequence of Streptococcus thermophilus VHProbi R08, Isolated from Fermented Sour Porridge. Microbiology Resource Announcements, 2023, 12, .	0.3	1
5500	Draft Genome Sequence and Annotation of Priestia aryabhattai Strain BD1 Isolated from a Dye Sediment. Microbiology Resource Announcements, 2023, 12, .	0.3	2
5501	Taxonomic Assignment-Based Genome Reconstruction from Apical Periodontal Metagenomes to Identify Antibiotic Resistance and Virulence Factors. Life, 2023, 13, 194.	1.1	2
5502	Genome Sequences of <i>Metabacillus</i> sp. Strain B2-18, Isolated from Human Skin, and Metabacillus endolithicus KCTC 33579 ^T. Microbiology Resource Announcements, 0, , .	0.3	1
5503	Complete Genome Sequence of Vibrio natriegens Strain PWH3a. Microbiology Resource Announcements, 0, , .	0.3	0
5504	Novel integrative elements and genomic plasticity in ocean ecosystems. Cell, 2023, 186, 47-62.e16.	13.5	25
5505	Proteiniphilum and Methanothrix harundinacea became dominant acetate utilizers in a methanogenic reactor operated under strong ammonia stress. Frontiers in Microbiology, 0, 13, .	1.5	10

#	ARTICLE	IF	CITATIONS
5506	Potential for mercury methylation by Asgard archaea in mangrove sediments. ISME Journal, 2023, 17, 478-485.	4.4	6
5508	Predictive Power of Long-Read Whole-Genome Sequencing for Rapid Diagnostics of Multidrug-Resistant Brachyspira hyodysenteriae Strains. Microbiology Spectrum, 2023, 11, .	1.2	5
5509	Longitudinal, Multi-Platform Metagenomics Yields a High-Quality Genomic Catalog and Guides an <i>In Vitro</i> Model for Cheese Communities. MSystems, 2023, 8, .	1.7	4
5510	Metagenomics Shines Light on the Evolution of â€œSunscreenâ€•Pigment Metabolism in the<i>Teloschistales</i>(Lichen-Forming Ascomycota). Genome Biology and Evolution, 2023, 15, .	1.1	8
5511	Capturing variation in metagenomic assembly graphs with MetaCortex. Bioinformatics, 2023, 39, .	1.8	0
5512	Relationships between fluid mixing, biodiversity, and chemosynthetic primary productivity in Yellowstone hot springs. Environmental Microbiology, 2023, 25, 1022-1040.	1.8	4
5513	Halorarius litoreus gen. nov., sp. nov., Halorarius halobius sp. nov., Haloglomus halophilum sp. nov., Haloglomus salinum sp. nov., and Natronomonas marina sp. nov., extremely halophilic archaea isolated from tidal flat and marine solar salt. Frontiers in Marine Science, 0, 10, .	1.2	8
5514	Expanded catalogue of metagenome-assembled genomes reveals resistome characteristics and athletic performance-associated microbes in horse. Microbiome, 2023, 11, .	4.9	8
5515	Deciphering basic and key traits of antibiotic resistome in influent and effluent of hospital wastewater treatment systems. Water Research, 2023, 231, 119614.	5.3	23
5516	Octadecabacter algicola sp. nov. and Octadecabacter dasysiphoniae sp. nov., isolated from a marine red alga and emended description of the genus Octadecabacter. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	3
5517	Pseudarthrobacter humi sp. nov., an actinobacterium isolated from soil. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	2
5518	Genomic and Transcriptomic Insights into Salinity Tolerance-Based Niche Differentiation of <i>Synechococcus</i> Clades in Estuarine and Coastal Waters. MSystems, 2023, 8, .	1.7	2
5519	Culturomics- and metagenomics-based insights into the microbial community and function of rhizosphere soils in Sinai desert farming systems. Environmental Microbiomes, 2023, 18, .	2.2	5
5520	Into the darkness of the microbial dark matter in situ activities through expression profiles of Patescibacteria populations. Frontiers in Microbiology, 0, 13, .	1.5	5
5521	Viral Community Structure and Potential Functions in the Dried-Out Aral Sea Basin Change along a Desiccation Gradient. MSystems, 2023, 8, .	1.7	1
5523	<i>Microcystis</i> pangenome reveals cryptic diversity within and across morphospecies. Science Advances, 2023, 9, .	4.7	18
5524	A Cross-Validated Feature Selection (CVFS) approach for extracting the most parsimonious feature sets and discovering potential antimicrobial resistance (AMR) biomarkers. Computational and Structural Biotechnology Journal, 2023, 21, 769-779.	1.9	3
5525	Genomic study and lipidomic bioassay of Leeuwenhoekiella parthenopeia: A novel rare biosphere marine bacterium that inhibits tumor cell viability. Frontiers in Microbiology, 0, 13, .	1.5	3

#	Article	IF	Citations
5526	Analyzing the genetic diversity and biotechnological potential of Leuconostoc pseudomesenteroides by comparative genomics. Frontiers in Microbiology, 0, 13, .	1.5	3
5527	The person-to-person transmission landscape of the gut and oral microbiomes. Nature, 2023, 614, 125-135.	13.7	111
5531	The Early Microbial Colonizers of a Short-Lived Volcanic Island in the Kingdom of Tonga. MBio, 2023, 14, .	1.8	3
5532	Combining Flow Cytometry and Metagenomics Improves Recovery of Metagenome-Assembled Genomes in a Cell Culture from Activated Sludge. Microorganisms, 2023, 11, 175.	1.6	6
5533	<i>Limosilactobacillus walteri</i> sp. nov., a novel probiotic antimicrobial lipopeptide-producing bacterium. FEMS Microbiology Letters, 2023, 370, .	0.7	4
5535	Anaerobic methanotroph â€˜Candidatus Methanoperedens nitroreducensâ€™ has a pleomorphic life cycle. Nature Microbiology, 2023, 8, 321-331.	5.9	10
5536	Maritalea mediterranea sp. nov., isolated from marine plastic residues. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	1
5537	Hiding in Plain Sight: Characterization of Aeromonas Species Isolated from a Recreational Estuary Reveals the Carriage and Putative Dissemination of Resistance Genes. Antibiotics, 2023, 12, 84.	1.5	4
5538	Metatranscriptomics-guided genome-scale metabolic modeling of microbial communities. Cell Reports Methods, 2023, 3, 100383.	1.4	7
5539	Genomic characterization and assessment of pathogenic potential of Legionella spp. isolates from environmental monitoring. Frontiers in Microbiology, 0, 13, .	1.5	6
5540	Phylogenomic Analysis Supports the Transfer of 20 Pathovars from Xanthomonas campestris into Xanthomonas euvesicatoria. Taxonomy, 2023, 3, 29-45.	0.4	3
5541	Biohydrogenation of 1,3-Butadiene to 1-Butene under Acetogenic Conditions by <i>Acetobacterium wieringae</i>. Environmental Science & Technology, 2023, 57, 1637-1645.	4.6	0
5542	A high-quality genome compendium of the human gut microbiome of Inner Mongolians. Nature Microbiology, 2023, 8, 150-161.	5.9	11
5543	Deterministic Effect of pH on Shaping Soil Resistome Revealed by Metagenomic Analysis. Environmental Science & Technology, 2023, 57, 985-996.	4.6	22
5544	Comparative Genomics Revealed a Potential Threat of AeromonasÂrivipollensis G87 Strain and Its Antibiotic Resistance. Antibiotics, 2023, 12, 131.	1.5	1
5545	In Silico Prediction of Secondary Metabolites and Biosynthetic Gene Clusters Analysis of Streptomyces thinghirensis HM3 Isolated from Arid Soil. Fermentation, 2023, 9, 65.	1.4	3
5546	Bacteriophages playing nice: Lysogenic bacteriophage replication stable in the human gut microbiota. IScience, 2023, 26, 106007.	1.9	11
5547	Strategies and tools in illumina and nanoporeâ€integrated metagenomic analysis of microbiome data. , 2023, 2, .		3

#	Article	IF	Citations
5548	Differential carbon utilization enables co-existence of recently speciated Campylobacteraceae in the cow rumen epithelial microbiome. Nature Microbiology, 2023, 8, 309-320.	5.9	4
5550	Flavihumibacter fluminis sp. nov., a novel thermotolerant bacterium isolated from river silt. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	1
5551	Bacteroides faecium sp. nov. isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5552	Phylogenomic analysis of the genus Alcanivorax: proposal for division of this genus into the emended genus Alcanivorax and two novel genera Alloalcanivorax gen. nov. and Isoalcanivorax gen. nov.. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5553	Legionella maioricensis sp. nov., a new species isolated from the hot water distribution systems of a hospital and a shopping center during routine sampling. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	3
5554	MetaBinner: a high-performance and stand-alone ensemble binning method to recover individual genomes from complex microbial communities. Genome Biology, 2023, 24, .	3.8	14
5555	Microbial Motility at the Bottom of North America: Digital Holographic Microscopy and Genomic Motility Signatures in Badwater Spring, Death Valley National Park. Astrobiology, 0, , .	1.5	1
5556	Draft Metagenome-Assembled Genome Sequence of a Novel <i>Citricoccus</i> Species from Agricultural Soil in Western Colorado. Microbiology Resource Announcements, 0, , .	0.3	0
5557	Natural Recombination among Type I Restriction-Modification Systems Creates Diverse Genomic Methylation Patterns among Xylella fastidiosa Strains. Applied and Environmental Microbiology, 2023, 89, .	1.4	1
5558	Recovery of metagenome-assembled microbial genomes from a full-scale biogas plant of food waste by pacific biosciences high-fidelity sequencing. Frontiers in Microbiology, 0, 13, .	1.5	2
5559	Gene loss and symbiont switching during adaptation to the deep sea in a globally distributed symbiosis. ISME Journal, 2023, 17, 453-466.	4.4	6
5560	Comprehensive characterization of aerobic groundwater biotreatment media. Water Research, 2023, 230, 119587.	5.3	2
5561	Impacts of organic loading rate and hydraulic retention time on organics degradation, interspecies interactions and functional traits in thermophilic anaerobic co-digestion of food waste and sewage sludge. Bioresource Technology, 2023, 370, 128578.	4.8	3
5562	Exploring diversity patterns and driving mechanisms of the antibiotic resistome and microbiome in saline groundwater. Journal of Hazardous Materials, 2023, 446, 130734.	6.5	8
5563	Potential bacterial isolation by dosing metabolites in cross-feedings. Water Research, 2023, 231, 119589.	5.3	9
5564	Antioxidant prodigiosin-producing cold-adapted Janthinobacterium sp. ERMR3:09 from a glacier moraine: Genomic elucidation of cold adaptation and pigment biosynthesis. Gene, 2023, 857, 147178.	1.0	1
5565	Genome-resolved metagenomics reveals depth-related patterns of microbial community structure and functions in a highly stratified, AMD overlaying mine tailings. Journal of Hazardous Materials, 2023, 447, 130774.	6.5	4
5566	Composite carrier enhanced bacterial adhesion and nitrogen removal in partial nitrification/anammox process. Science of the Total Environment, 2023, 868, 161659.	3.9	2

#	Article	IF	Citations
5567	Multi-Omics Analyses Identify Signatures in Patients with Liver Cirrhosis and Hepatocellular Carcinoma. Cancers, 2023, 15, 210.	1.7	2
5568	Metagenomic analysis reveals unexplored diversity of archaeal virome in the human gut. Nature Communications, 2022, 13, .	5.8	14
5569	A <i>Salmonella enterica</i> Serovar Oranienburg Clone Caused a Cluster of Bacteremia Cases in Persons With No Recognizable Underlying Diseases in Japan. Open Forum Infectious Diseases, 2023, 10, .	0.4	0
5570	Hybrid Genomic Analysis of Salmonella enterica Serovar Enteritidis SE3 Isolated from Polluted Soil in Brazil. Microorganisms, 2023, 11, 111.	1.6	2
5571	To assemble or not to assemble: metagenomic profiling of microbially mediated biogeochemical pathways in complex communities. Briefings in Bioinformatics, 2023, 24, .	3.2	2
5572	Flavobacterium potami sp. nov., a multi-metal resistance genes harbouring bacterium isolated from shallow river silt. Antonie Van Leeuwenhoek, 2023, 116, 265-280.	0.7	1
5573	Systems biology approach for analysis of mobile genetic elements in chicken gut microbiome. , 2022, , .		1
5574	Diversity of Mixotrophic Neutrophilic Thiosulfate- and Iron-Oxidizing Bacteria from Deep-Sea Hydrothermal Vents. Microorganisms, 2023, 11, 100.	1.6	2
5575	Postglacial adaptations enabled colonization and quasi-clonal dispersal of ammonia-oxidizing archaea in modern European large lakes. Science Advances, 2023, 9, .	4.7	12
5576	Melaminivora suipulveris sp. nov., isolated from pigpen dust. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5577	Multifactorial Microvariability of the Italian Raw Milk Cheese Microbiota and Implication for Current Regulatory Scheme. MSystems, 2023, 8, .	1.7	5
5578	High-resolution metagenomic reconstruction of the freshwater spring bloom. Microbiome, 2023, 11, .	4.9	9
5579	Variable impact of geochemical gradients on the functional potential of bacteria, archaea, and phages from the permanently stratified Lac Pavin. Microbiome, 2023, 11, .	4.9	4
5580	Site Specialization of Human Oral <i>Veillonella</i> Species. Microbiology Spectrum, 2023, 11, .	1.2	5
5581	The gastrointestinal microbiome in dairy cattle is constrained by the deterministic driver of the region and the modified effect of diet. Microbiome, 2023, 11, .	4.9	12
5582	Genomic Characterization of Three Novel Bartonella Strains in a Rodent and Two Bat Species from Mexico. Microorganisms, 2023, 11, 340.	1.6	2
5584	Luteibacter flocculans sp. nov., Isolated from a Eutrophic Pond and Isolation and Characterization of Luteibacter Phage vB_LflM-Pluto. Microorganisms, 2023, 11, 307.	1.6	4
5585	Arbuscular mycorrhizal fungi enhance plant phosphorus uptake through stimulating hyphosphere soil microbiome functional profiles for phosphorus turnover. New Phytologist, 2023, 238, 2578-2593.	3.5	18

#	Article	IF	Citations
5586	Paenibacillus rhizolycopersici sp. nov., an oligotrophic bacterium isolated from a tomato plant in China. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	2
5587	Biotin pathway in novel Fodinibius salsisoli sp. nov., isolated from hypersaline soils and reclassification of the genus Aliifodinibius as Fodinibius. Frontiers in Microbiology, 0, 13, .	1.5	7
5590	Nanopore-based enrichment of antimicrobial resistance genes â€“ aÂcase-based study. GigaByte, 0, 2023, 1-15.	0.0	3
5591	Selective enrichment, identification, and isolation of diclofenac, ibuprofen, and carbamazepine degrading bacteria from a groundwater biofilm. Environmental Science and Pollution Research, 2023, 30, 44518-44535.	2.7	6
5594	<i>Chrysosporum ovalisporum</i> is synonymous with the trueâ€branching cyanobacterium <i>Umezakia natans</i> (Nostocales/Aphanizomenonaceae). Journal of Phycology, 2023, 59, 326-341.	1.0	1
5595	Vibrio sinus sp. nov., a marine bacterium isolated from coastal seawater. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5596	Viruses Regulate Microbial Community Assembly Together with Environmental Factors in Acid Mine Drainage. Applied and Environmental Microbiology, 2023, 89, .	1.4	1
5597	The origin and evolution of methanogenesis and <i>Archaea</i> are intertwined. , 2023, 2, .		7
5598	Hypersaline Lake Urmia: a potential hotspot for microbial genomic variation. Scientific Reports, 2023, 13, .	1.6	5
5599	Strains Colonizing Different Intestinal Sites within an Individual Are Derived from a Single Founder Population. MBio, 2023, 14, .	1.8	1
5600	Evolutionary diversification of methanotrophic ANME-1 archaea and their expansive virome. Nature Microbiology, 2023, 8, 231-245.	5.9	14
5601	Genome Sequence of the <i>Streptomyces</i> Strain AgN23 Revealed Expansion and Acquisition of Gene Repertoires Potentially Involved in Biocontrol Activity and Rhizosphere Colonization. PhytoFrontiers, 0, , .	0.8	1
5602	ViralCC retrieves complete viral genomes and virus-host pairs from metagenomic Hi-C data. Nature Communications, 2023, 14, .	5.8	4
5603	Metagenome-Assembled Genome HetDA_MAG_MH13 of the Family <i>Devosiaceae</i> , from a Marine N2-fixing Cyanobacterial Enrichment Culture. Microbiology Resource Announcements, 0, , .	0.3	0
5604	Actinomadura terrae sp. nov. and Actinomadura litoris OS3-89, isolated from rhizosphere soil of cactus. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5605	Draft Genome Sequence of Seven Pigmented Strains of <i>Xanthomonas citri</i> pv. <i>anacardii</i>, the Causal Agent of Cashew Angular Spot. Phytopathology, 0, , .	1.1	0
5606	Complete Genome Sequence of Lactobacillus bulgaricus VHProbi R03, a Potential Fermentation Strain Isolated from Fermented Milk. Microbiology Resource Announcements, 0, , .	0.3	0
5607	Metagenome-Assembled Genome of an Alphaproteobacterium Isolated from an HetDA Enrichment from the North Pacific Subtropical Gyre. Microbiology Resource Announcements, 0, , .	0.3	0

#	ARTICLE	IF	CITATIONS
5608	Genomic and physiological characterization of Novosphingobium terrae sp. nov., an alphaproteobacterium isolated from Cerrado soil containing a mega-sized chromid. Brazilian Journal of Microbiology, 2023, 54, 239-258.	0.8	1
5609	Genome-centered metagenomics illuminates adaptations of core members to a partial Nitritationâ€"Anammox bioreactor under periodic microaeration. Frontiers in Microbiology, 0, 14, .	1.5	2
5612	Methanocaldococcus lauensis sp. nov., a novel deep-sea hydrothermal vent hyperthermophilic methanogen. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5613	Genetic and Structural Diversity of Prokaryotic Ice-Binding Proteins from the Central Arctic Ocean. Genes, 2023, 14, 363.	1.0	5
5615	Randomized clinical trial to test the safety and tolerability of SBD111, an optimized synbiotic medical food combination designed for the dietary management of the metabolic processes underlying osteopenia and osteoporosis. Journal of Microbiology & Experimentation, 2023, 11, 1-11.	0.1	0
5616	Genomic-based phylogenetic and metabolic analyses of the genus Natronomonas, and description of Natronomonas aquatica sp. nov.. Frontiers in Microbiology, 0, 14, .	1.5	4
5617	Draft Genome Assemblies of Phage AP50c-Resistant Derivatives of Bacillus anthracis Sterne Strain 7702 Lacking Plasmid pXO2. Microbiology Resource Announcements, 0, , .	0.3	1
5619	Harnessing Novel Soil Bacteria for Beneficial Interactions with Soybean. Microorganisms, 2023, 11, 300.	1.6	2
5620	Exploring the Potential Molecular Mechanisms of Interactions between a Probiotic Consortium and Its Coral Host. MSystems, 2023, 8, .	1.7	4
5621	Metagenome-Assembled Genome of a Novel <i>Cyclobacteriaceae</i> Epibiont of a Heterotrophic Diazotroph. Microbiology Resource Announcements, 0, , .	0.3	0
5625	Ecophysiology and genomics of the brackish water adapted SAR11 subclade IIIa. ISME Journal, 2023, 17, 620-629.	4.4	10
5626	Nanopore-only assemblies for genomic surveillance of the global priority drug-resistant pathogen, Klebsiella pneumoniae. Microbial Genomics, 2023, 9, .	1.0	10
5627	Secondary Metabolite Production Potential in a Microbiome of the Freshwater Sponge Spongilla lacustris. Microbiology Spectrum, 2023, 11, .	1.2	6
5628	Genomic view of the diversity and functional role of archaea and bacteria in the skeleton of the reef-building corals<i>Porites lutea</i>and<i>Isopora palifera</i>. GigaScience, 2022, 12, .	3.3	10
5629	Genome editing of microbes for degradation of pesticides. , 2023, , 167-200.		2
5630	Microbial Genome Sequencing and Assembly Using Nanopore Sequencers. Methods in Molecular Biology, 2023, , 31-39.	0.4	2
5631	Unitig level assembly graph based metagenome-assembled genome refiner (UGMAGrefiner): A tool to increase completeness and resolution of metagenome-assembled genomes. Computational and Structural Biotechnology Journal, 2023, 21, 2394-2404.	1.9	0
5632	Genome-centric view of the microbiome in a new deep-sea glass sponge species Bathydorus sp.. Frontiers in Microbiology, 0, 14, .	1.5	2

#	ARTICLE	IF	CITATIONS
5633	Reduction, evolutionary pattern and positive selection of genes encoding formate dehydrogenase in <scp>Woodâ€“Ljungdahl</scp> pathway of gastrointestinal acetogens suggests their adaptation to formateâ€rich habitats. Environmental Microbiology Reports, 2023, 15, 129-141.	1.0	2
5634	The media composition as a crucial element in high-throughput metabolic network reconstruction. Interface Focus, 2023, 13, .	1.5	1
5636	Infrequent intrahousehold transmission of <i>Clostridioides difficile</i> between pet owners and their pets. Zoonoses and Public Health, 2023, 70, 341-351.	0.9	3
5639	Panguiarchaeum symbiosum, a potential hyperthermophilic symbiont in the TACK superphylum. Cell Reports, 2023, 42, 112158.	2.9	3
5640	Discovery of the Streamlined Haloarchaeon <i>Halorutilus salinus</i> , Comprising a New Order Widespread in Hypersaline Environments across the World. MSystems, 2023, 8, .	1.7	5
5641	Genome enrichment of rare and unknown species from complicated microbiomes by nanopore selective sequencing. Genome Research, 2023, 33, 612-621.	2.4	3
5642	Cable bacteria with electric connection to oxygen attract flocks of diverse bacteria. Nature Communications, 2023, 14, .	5.8	10
5643	Deep Divergence and Genomic Diversification of Gut Symbionts of Neotropical Stingless Bees. MBio, 2023, 14, .	1.8	5
5644	Functional characterization and taxonomic classification of novel gammaproteobacterial diversity in sponges. Systematic and Applied Microbiology, 2023, 46, 126401.	1.2	0
5645	Microbial Communities of Flor Velums and the Genetic Stability of Flor Yeasts Used for a Long Time for the Industrial Production of Sherry-like Wines. Fermentation, 2023, 9, 367.	1.4	2
5646	Draft Genome Sequences of Coral-Associated Bacterium <i>Hoeflea</i> sp. Strain E7-10 and Dinoflagellate-Associated Bacterium Hoeflea prorocentri PM5-8. Microbiology Resource Announcements, 0, , .	0.3	1
5647	Probio-X Relieves Symptoms of Hyperlipidemia by Regulating Patientsâ€™ Gut Microbiome, Blood Lipid Metabolism, and Lifestyle Habits. Microbiology Spectrum, 2023, 11, .	1.2	2
5648	Genetic basis for the biodegradation of a polyether-polyurethane-acrylic copolymer by a landfill microbial community inferred by metagenomic deconvolution analysis. Science of the Total Environment, 2023, 881, 163367.	3.9	7
5650	Metagenomic Insight into Microbiome and Antibiotic Resistance Genes of High Clinical Concern in Urban and Rural Hospital Wastewater of Northern India Origin: a Major Reservoir of Antimicrobial Resistance. Microbiology Spectrum, 2023, 11, .	1.2	7
5651	Microbial life in 25-m-deep boreholes in ancient permafrost illuminated by metagenomics. Environmental Microbiomes, 2023, 18, .	2.2	1
5652	Genome-resolved metagenomics revealed metal-resistance, geochemical cycles in a Himalayan hot spring. Applied Microbiology and Biotechnology, 2023, 107, 3273-3289.	1.7	1
5653	Replicated life-history patterns and subsurface origins of the bacterial sister phyla <i>Nitrospirota</i> and <i>Nitrospinota</i>. ISME Journal, 2023, 17, 891-902.	4.4	7
5654	Diversity of Microbiomes Across a 13,000-Year-Old Amazon Sediment. Microbial Ecology, 0, , .	1.4	0

#	Article	IF	Citations
5655	CRISPR-resolved virus-host interactions in a municipal landfill include non-specific viruses, hyper-targeted viral populations, and interviral conflicts. Scientific Reports, 2023, 13, .	1.6	3
5656	Dominance of mixed ether/ester, intact polar membrane lipids in five species of the order Rubrobacterales: Another group of bacteria not obeying the â€œlipid divideâ€. Systematic and Applied Microbiology, 2023, 46, 126404.	1.2	5
5657	Effects of the oversized microplastic pollution layer on soil aggregates and organic carbon at different soil depths. Journal of Hazardous Materials, 2023, 450, 131014.	6.5	9
5658	Effect of the probiotic strain, Lactiplantibacillus plantarum P9, on chronic constipation: A randomized, double-blind, placebo-controlled study. Pharmacological Research, 2023, 191, 106755.	3.1	7
5659	Transcriptionally active nitrogen fixation and biosynthesis of diverse secondary metabolites by Dolichospermum and Aphanizomenon-like Cyanobacteria in western Lake Erie Microcystis blooms. Harmful Algae, 2023, 124, 102408.	2.2	7
5660	Delineation of the complex microbial nitrogen-transformation network in an anammox-driven full-scale wastewater treatment plant. Water Research, 2023, 235, 119799.	5.3	9
5661	Phylogenomics reveals insights into the functional evolution of the genus Agrobacterium and enables the description of Agrobacterium divergens sp. nov. Systematic and Applied Microbiology, 2023, 46, 126420.	1.2	2
5662	Govania unica gen. nov., sp. nov., a rare biosphere bacterium that represents a novel family in the class Alphaproteobacteria. Systematic and Applied Microbiology, 2023, 46, 126405.	1.2	0
5663	Genome-centric metagenomics revealed the effect of pH on the microbiome involved in short-chain fatty acids and ethanol production. Bioresource Technology, 2023, 377, 128920.	4.8	5
5664	CRISPR-Cas phage defense systems and prophages in Candidatus Accumulibacter. Water Research, 2023, 235, 119906.	5.3	6
5665	Woronichinia naegeliana: A common nontoxigenic component of temperate freshwater cyanobacterial blooms with 30% of its genome in transposons. Harmful Algae, 2023, 125, 102433.	2.2	2
5666	Deep sequencing reveals comprehensive insight into the prevalence, mobility, and hosts of antibiotic resistance genes in mangrove ecosystems. Journal of Environmental Management, 2023, 335, 117580.	3.8	2
5667	Conductive materials enhance microbial salt-tolerance in anaerobic digestion of food waste: Microbial response and metagenomics analysis. Environmental Research, 2023, 227, 115779.	3.7	5
5668	Lebanese fermented goat milk products: From tradition to meta-omics. Food Research International, 2023, 168, 112762.	2.9	4
5669	Cost-effective hybrid long-short read assembly delineates alternative GC-rich Streptomyces hosts for natural product discovery. Synthetic and Systems Biotechnology, 2023, 8, 253-261.	1.8	0
5670	Microbial isolation and characterization from two flex lines from the urine processor assembly onboard the International Space Station. Biofilm, 2023, 5, 100108.	1.5	1
5671	Clinical NEC prevention practices drive different microbiome profiles and functional responses in the preterm intestine. Nature Communications, 2023, 14, .	5.8	3
5672	Hot spring distribution and survival mechanisms of thermophilic comammox <i>Nitrospira</i>. ISME Journal, 2023, 17, 993-1003.	4.4	4

#	ARTICLE	IF	CITATIONS
5675	Potential reservoirs of antimicrobial resistance in livestock waste and treated wastewater that can be disseminated to agricultural land. Science of the Total Environment, 2023, 872, 162194.	3.9	15
5676	Dissolved storage glycans shaped the community composition of abundant bacterioplankton clades during a North Sea spring phytoplankton bloom. Microbiome, 2023, 11, .	4.9	10
5677	Metagenomic surveillance of antibiotic resistome in influent and effluent of wastewater treatment plants located on the Qinghai-Tibetan Plateau. Science of the Total Environment, 2023, 870, 162031.	3.9	8
5678	Genome-centric metagenomics revealed functional traits in high-solids anaerobic co-digestion of restaurant food waste, household food waste and rice straw. Bioresource Technology, 2023, 376, 128926.	4.8	5
5679	Bacterial benz(a)anthracene catabolic networks in contaminated soils and their modulation by other co-occurring HMW-PAHs. Environmental Pollution, 2023, 328, 121624.	3.7	4
5684	Deciphering risks of resistomes and pathogens in intensive laying hen production chain. Science of the Total Environment, 2023, 869, 161790.	3.9	1
5685	Metagenome-assembled genomes indicate that antimicrobial resistance genes are highly prevalent among urban bacteria and multidrug and glycopeptide resistances are ubiquitous in most taxa. Frontiers in Microbiology, 0, 14, .	1.5	3
5686	Closed genomes uncover a saltwater species of <i>Candidatus</i> Electronema and shed new light on the boundary between marine and freshwater cable bacteria. ISME Journal, 2023, 17, 561-569.	4.4	10
5688	Zeimonas sediminis sp. nov., isolated from mangrove sediment. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5690	The persistence of time: the lifespan of Bacillus anthracis spores in environmental reservoirs. Research in Microbiology, 2023, 174, 104029.	1.0	8
5691	Metagenomic analysis characterizes resistomes of an acidic, multimetal(loid)-enriched coal source mine drainage treatment system. Journal of Hazardous Materials, 2023, 448, 130898.	6.5	2
5692	Airborne antibiotic resistome and human health risk in railway stations during COVID-19 pandemic. Environment International, 2023, 172, 107784.	4.8	3
5693	PorinPredict: <i>In Silico</i> Identification of OprD Loss from WGS Data for Improved Genotype-Phenotype Predictions of P. aeruginosa Carbapenem Resistance. Microbiology Spectrum, 2023, 11, .	1.2	4
5694	High abundance of hydrocarbon-degrading <i>Alcanivorax</i> in plumes of hydrothermally active volcanoes in the South Pacific Ocean. ISME Journal, 2023, 17, 600-610.	4.4	5
5695	Complete Genome Sequences of Caldicellulosiruptor acetigenus DSM 7040, Caldicellulosiruptor morganii DSM 8990 (RT8.B8), and Caldicellulosiruptor naganoensis DSM 8991 (NA10). Microbiology Resource Announcements, 2023, 12, .	0.3	2
5696	Comparative metagenomics at Solfatara and Pisciarelli hydrothermal systems in Italy reveal that ecological differences across substrates are not ubiquitous. Frontiers in Microbiology, 0, 14, .	1.5	0
5697	Comparative Genomic Analysis Reveals the Functional Traits and Safety Status of Lactic Acid Bacteria Retrieved from Artisanal Cheeses and Raw Sheep Milk. Foods, 2023, 12, 599.	1.9	5
5698	Characterization of metagenome-assembled genomes of two endo-archaea of Candida tropicalis. , 0, 1, .		0

#	Article	IF	Citations
5699	Core single nucleotide polymorphism analysis reveals transmission of <i>Mycobacterium marinum</i> between animal and environmental sources in two aquaria. Journal of Fish Diseases, 2023, 46, 507-516.	0.9	1
5700	Genomic epidemiology of Mycobacterium avium subsp. paratuberculosis isolates from Canadian dairy herds provides evidence for multiple infection events. Frontiers in Genetics, 0, 14, .	1.1	6
5701	Acidaminococcus homini s sp. nov., Amedibacillus hominis sp. nov., Lientehia hominis gen. nov. sp. nov., Merdimmobilis hominis gen. nov. sp. nov., and Paraeggerthella hominis sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	4
5703	A novel sulfate-reducing and nitrogen-fixing bacterium Fundidesulfovibrio soli sp. nov., isolated from paddy soils. Archives of Microbiology, 2023, 205, .	1.0	1
5705	Proteus mirabilis isolated from untreated hospital wastewater, Ibadan, Southwestern Nigeria showed low-level resistance to fluoroquinolone and carried qnrD3 on Col3M plasmids. Environmental Science and Pollution Research, 2023, 30, 47158-47167.	2.7	0
5706	CrAssphage May Be Viable Markers of Contamination in Pristine and Contaminated River Water. MSystems, 2023, 8, .	1.7	2
5707	Comparative Genomic Study of Streptococcus anginosus Reveals Distinct Group of Urinary Strains. MSphere, 2023, 8, .	1.3	2
5708	Diverse secondary metabolites are expressed in particle-associated and free-living microorganisms of the permanently anoxic Cariaco Basin. Nature Communications, 2023, 14, .	5.8	10
5709	Molecular hydrogen in seawater supports growth of diverse marine bacteria. Nature Microbiology, 2023, 8, 581-595.	5.9	17
5710	Deduplication Improves Cost-Efficiency and Yields of <i>De Novo</i> Assembly and Binning of Shotgun Metagenomes in Microbiome Research. Microbiology Spectrum, 2023, 11, .	1.2	1
5711	Metagenomic Profiling of Pathogens in Simulated Reclaimed Water Distribution Systems Operated at Elevated Temperature Reveals Distinct Response of Mycobacteria to Filtration and Disinfection Conditions. ACS ES&T Water, 2023, 3, 720-732.	2.3	2
5712	Guild-Level Microbiome Signature Associated with COVID-19 Severity and Prognosis. MBio, 2023, 14, .	1.8	6
5713	Insights into the genome of Methylobacterium sp. NMS14P, a novel bacterium for growth promotion of maize, chili, and sugarcane. PLoS ONE, 2023, 18, e0281505.	1.1	4
5714	Complete Genome Sequences of Two Thermophilic Indigenous Bacteria Isolated from Wheat Straw, Thermoclostridium stercorarium subsp. Strain RKWS1 and <i>Thermoanaerobacter</i> sp. Strain RKWS2. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5715	A Genomic Survey of the Natural Product Biosynthetic Potential of Actinomycetes Isolated from New Zealand Lichens. MSystems, 2023, 8, .	1.7	2
5716	A nontuberculous mycobacterium could solve the mystery of the lady from the Franciscan church in Basel, Switzerland. BMC Biology, 2023, 21, .	1.7	1
5717	Aliidiomarina quisquiliarum sp. nov., isolated from landfill leachate. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5719	Corynebacterium megadyptis sp. nov. with two subspecies, Corynebacterium megadyptis subsp. megadyptis subsp. nov. and Corynebacterium megadyptis subsp. dunedinense subsp. nov. isolated from yellow-eyed penguins. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	3

#	ARTICLE	IF	CITATIONS
5720	Pseudomonas nunensis sp. nov. isolated from a suppressive potato field in Greenland. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	2
5722	Metagenomic Analysis of Anaerobic Microbial Communities Degrading Short-Chain Fatty Acids as Sole Carbon Sources. Microorganisms, 2023, 11, 420.	1.6	4
5724	One to host them all: genomics of the diverse bacterial endosymbionts of the spider Oedothorax gibbosus. Microbial Genomics, 2023, 9, .	1.0	1
5725	Singleâ€amplified genomes reveal most streamlined freeâ€living marine bacteria. Environmental Microbiology, 2023, 25, 1136-1154.	1.8	5
5726	Genetic mapping of microbial and host traits reveals production of immunomodulatory lipids by Akkermansia muciniphila in the murine gut. Nature Microbiology, 2023, 8, 424-440.	5.9	12
5727	Salinity determines performance, functional populations, and microbial ecology in consortia attenuating organohalide pollutants. ISME Journal, 2023, 17, 660-670.	4.4	15
5728	The mechanismÂof promoting rhizosphere nutrient turnover for arbuscular mycorrhizal fungi attributes to recruited functional bacterial assembly. Molecular Ecology, 2023, 32, 2335-2350.	2.0	6
5729	Trait biases in microbial reference genomes. Scientific Data, 2023, 10, .	2.4	4
5730	Seasonal variation of microbial community and methane metabolism in coalbed water in the Erlian Basin, China. Frontiers in Microbiology, 0, 14, .	1.5	1
5732	Sucralose biodegradation and enriched degrading consortia revealed by combining Illumina and Nanopore sequencing. Chemical Engineering Journal, 2023, 461, 141766.	6.6	0
5733	<scp>uBin:</scp> A manual refining tool for genomes from metagenomes. Environmental Microbiology, 2023, 25, 1077-1083.	1.8	13
5734	Genome Sequences of Alkalihalobacillus clausii, Bacillus safensis, Escherichia coli, and Pasteurella multocida Isolates from the Rumen, Nasopharynx, Vagina, and Uterus of Healthy Beef Cattle. Microbiology Resource Announcements, 2023, 12, .	0.3	1
5736	Metagenome-Assembled Genomes from Murine Fecal Microbiomes Dominated by Uncharacterized Bacteria. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5737	Nonomuraea sediminis sp. nov., a novel actinobacterium with antimicrobial activity, isolated from sediment of Dianchi Lake. Archives of Microbiology, 2023, 205, .	1.0	0
5738	Whole Genome Sequences of Nine <i>Xanthomonas</i> Strains Responsible for Common Bacterial Blight of Bean. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5739	A Nanopore Sequencing Course for Graduate School Curriculum. Methods in Molecular Biology, 2023, , 113-127.	0.4	0
5740	Electric-Inducive Microbial Interactions in a Thermophilic Anaerobic Digester Revealed by High-Throughput Sequencing of Micron-Scale Single Flocs. Environmental Science & Technology, 2023, 57, 4367-4378.	4.6	5
5741	Diverse Populations of Staphylococcus pseudintermedius Colonize the Skin of Healthy Dogs. Microbiology Spectrum, 2023, 11, .	1.2	3

#	Article	IF	Citations
5742	Dataset of 143 metagenome-assembled genomes from the Arctic and Atlantic Oceans, including 21 for eukaryotic organisms. Data in Brief, 2023, 47, 108990.	0.5	1
5743	Complete Genome Sequence of <i>Roseibium</i> sp. Strain Sym1, a Bacterial Associate of Symbiodinium linucheae, the Microalgal Symbiont of the Anemone <i>Aiptasia</i>. Microbiology Resource Announcements, 2023, 12, .	0.3	1
5745	Monthly dynamics of microbial communities and variation of nitrogen-cycling genes in an industrial-scale expanded granular sludge bed reactor. Frontiers in Microbiology, 0, 14, .	1.5	1
5746	Draft Genome Sequence of <i>Afifella</i> sp. Strain JA880, Isolated from a Salt Pond. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5747	Comparative genome identification of accessory genes associated with strong biofilm formation in Vibrio parahaemolyticus. Food Research International, 2023, 166, 112605.	2.9	4
5748	Genomic diversity in Fructobacillus spp. isolated from fructose-rich niches. PLoS ONE, 2023, 18, e0281839.	1.1	3
5749	MGnify Genomes: A Resource for Biome-specific Microbial Genome Catalogues. Journal of Molecular Biology, 2023, 435, 168016.	2.0	6
5750	Impact of microbial genome completeness on metagenomic functional inference. ISME Communications, 2023, 3, .	1.7	11
5751	Metagenome-Assembled Genomes of Four Southern Ocean Archaea Harbor Multiple Genes Linked to Polyethylene Terephthalate and Polyhydroxybutyrate Plastic Degradation. Microbiology Resource Announcements, 2023, 12, .	0.3	1
5752	Genomic characterization of coexisting anatoxin-producing and non-toxigenic Microcoleus subspecies in benthic mats from the Wolastoq, New Brunswick, Canada. Harmful Algae, 2023, 124, 102405.	2.2	6
5753	Challenges and opportunities of strain diversity in gut microbiome research. Frontiers in Microbiology, 0, 14, .	1.5	4
5754	Ultra-small bacteria and archaea exhibit genetic flexibility towards groundwater oxygen content, and adaptations for attached or planktonic lifestyles. ISME Communications, 2023, 3, .	1.7	3
5755	Extreme Niche Partitioning and Microbial Dark Matter in a Mauna Loa Lava Tube. Journal of Geophysical Research E: Planets, 2023, 128, .	1.5	3
5757	Genome-resolved metagenomics inferred novel insights into the microbial community, metabolic pathways, and biomining potential of Malanjkhand acidic copper mine tailings. Environmental Science and Pollution Research, 2023, 30, 50864-50882.	2.7	1
5758	Computational Insight into Intraspecies Distinctions in Pseudoalteromonas distincta: Carotenoid-like Synthesis Traits and Genomic Heterogeneity. International Journal of Molecular Sciences, 2023, 24, 4158.	1.8	2
5760	High-throughput microbial culturomics using automation and machine learning. Nature Biotechnology, 2023, 41, 1424-1433.	9.4	39
5761	Genome-centric metagenomic insights into the role of Chloroflexi in anammox, activated sludge and methanogenic reactors. BMC Microbiology, 2023, 23, .	1.3	18
5762	Genomic Insights of Alnus-Infective Frankia Strains Reveal Unique Genetic Features and New Evidence on Their Host-Restricted Lifestyle. Genes, 2023, 14, 530.	1.0	2

#	ARTICLE	IF	CITATIONS
5763	A Guide to Geneâ€Centric Analysis Using TreeSAPP. Current Protocols, 2023, 3, .	1.3	0
5764	Genomic Epidemiological Analysis of Antimicrobial-Resistant Bacteria with Nanopore Sequencing. Methods in Molecular Biology, 2023, , 227-246.	0.4	0
5765	Bioinformatic Tools for NGS-Based Metagenomics to Improve the Clinical Diagnosis of Emerging, Re-Emerging and New Viruses. Viruses, 2023, 15, 587.	1.5	7
5766	Genome Sequence of Pseudomonas sp. Strain So3.2b, Isolated from a Soil Sample from Robert Island (Antarctic Specially Protected Area 112), Antarctic. Microbiology Resource Announcements, 2023, 12, .	0.3	2
5767	Draft Genome Sequences of Spacecraft-Associated Microbes Isolated from Six NASA Missions. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5768	Draft Genome Sequence of a Mycobacterium chelonae subsp. <i>bovis</i> Strain Isolated from a Baikal Seal (Pusa sibirica) in Captivity. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5769	Extracellular DNA includes an important fraction of high-risk antibiotic resistance genes in treated wastewaters. Environmental Pollution, 2023, 323, 121325.	3.7	5
5770	Meta-omics elucidates key degraders in a bacterial tris(2-butoxyethyl) phosphate (TBOEP)-degrading enrichment culture. Water Research, 2023, 233, 119774.	5.3	4
5771	Metagenomic and machine learning-aided identification of biomarkers driving distinctive Cd accumulation features in the root-associated microbiome of two rice cultivars. ISME Communications, 2023, 3, .	1.7	13
5772	Whole-Genome Sequence of <i>Thermodesulfomicrobium</i> sp. Strain WS, Isolated from Onikobe Geothermal Field in Japan. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5773	Composition and Metabolic Potential of Fe(III)-Reducing Enrichment Cultures of Methanotrophic ANME-2a Archaea and Associated Bacteria. Microorganisms, 2023, 11, 555.	1.6	4
5774	Draft Genome Sequence of Lactococcus lactis Strain 12-16-PSH, Isolated from Prostokvasha from the Arkhangelsk Region of Russia. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5775	Draft Genome Sequence of <i>Thermomicrobium</i> sp. Strain 4228-Ro, a Thermophilic Bacterium Isolated from a Kamchatka Hot Spring. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5776	Draft Genome Sequences of Three Bacterial Species from Aquatic Habitats near Washington, DC. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5778	Improved Genomic Prediction of Staphylococcus epidermidis Isolation Sources with a Novel Polygenic Score. Journal of Clinical Microbiology, 2023, 61, .	1.8	0
5779	Importance of mobile genetic element immunity in numerically abundant <i>Trichodesmium</i> clades. ISME Communications, 2023, 3, .	1.7	4
5781	A novel and diverse group of Candidatus Patescibacteria from bathypelagic Lake Baikal revealed through long-read metagenomics. Environmental Microbiomes, 2023, 18, .	2.2	2
5782	Non-Toxigenic Clostridioides difficile Strain E4 (NTCD-E4) Prevents Establishment of Primary C. difficile Infection by Epidemic PCR Ribotype 027 in an In Vitro Human Gut Model. Antibiotics, 2023, 12, 435.	1.5	2

#	Article	IF	Citations
5783	Extending and improving metagenomic taxonomic profiling with uncharacterized species using MetaPhlAn 4. Nature Biotechnology, 2023, 41, 1633-1644.	9.4	132
5784	Seasonal activities of the phyllosphere microbiome of perennial crops. Nature Communications, 2023, 14, .	5.8	13
5785	Metagenomic analysis reveals patterns and hosts of antibiotic resistance in different pig farms. Environmental Science and Pollution Research, 2023, 30, 52087-52106.	2.7	3
5786	Revealing within-species diversity in uncultured human gut bacteria with single-cell long-read sequencing. Frontiers in Microbiology, 0, 14, .	1.5	5
5788	Draft genomes of three closely related low light-adapted Prochlorococcus. BMC Genomic Data, 2023, 24, .	0.7	1
5789	Thermomonas paludicola sp. nov., isolated from a lotus wetland. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	1
5790	Actively replicating gut bacteria identified by 5-ethynyl-2â€™-deoxyuridine (EdU) click chemistry and cell sorting. Gut Microbes, 2023, 15, .	4.3	2
5793	Chitinophaga horti sp. nov., Isolated from Garden Soil. Current Microbiology, 2023, 80, .	1.0	1
5794	Comparative Genomics of Halobacterium salinarum Strains Isolated from Salted Foods Reveals Protechnological Genes for Food Applications. Microorganisms, 2023, 11, 587.	1.6	1
5795	SnakeMAGs: a simple, efficient, flexible and scalable workflow to reconstruct prokaryotic genomes from metagenomes. F1000Research, 0, 11, 1522.	0.8	0
5796	Trimming and decontamination of metagenomic data can significantly impact assembly and binning metrics, phylogenomic and functional analysis. Current Bioinformatics, 2023, 18, .	0.7	0
5797	Nitrate-Stimulated Release of Naturally Occurring Sedimentary Uranium. Environmental Science & Technology, 2023, 57, 4354-4366.	4.6	9
5798	Pan-Chromosome and Comparative Analysis of <i>Agrobacterium fabrum</i> Reveal Important Traits Concerning the Genetic Diversity, Evolutionary Dynamics, and Niche Adaptation of the Species. Microbiology Spectrum, 2023, 11, .	1.2	0
5799	Molecular Characterization and Clinical Relevance of Taxonomic Reassignment of Staphylococcus schleiferi Subspecies into Two Separate Species, Staphylococcus schleiferi and Staphylococcus <i>coagulans</i>. Microbiology Spectrum, 2023, 11, .	1.2	4
5800	Complete Genome Sequence of <i>Flavobacterium</i> sp. Strain GSB-24, Isolated from inside <i>Dendrobium</i> Roots. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5801	A Genome-Scale Metabolic Model of Marine Heterotroph Vibrio splendidus Strain 1A01. MSystems, 0, , .	1.7	0
5802	A thermophilic chemolithoautotrophic bacterial consortium suggests a mutual relationship between bacteria in extreme oligotrophic environments. Communications Biology, 2023, 6, .	2.0	1
5803	The majority of microorganisms in gas hydrate-bearing subseafloor sediments ferment macromolecules. Microbiome, 2023, 11, .	4.9	7

#	ARTICLE	IF	CITATIONS
5804	Antimicrobial resistance in Campylobacter fetus: emergence and genomic evolution. Microbial Genomics, 2023, 9, .	1.0	1
5805	Stingray epidermal microbiomes are species-specific with local adaptations. Frontiers in Microbiology, 0, 14, .	1.5	1
5806	Evolutionary ecology of microbial populations inhabiting deep sea sediments associated with cold seeps. Nature Communications, 2023, 14, .	5.8	9
5807	Variety of rumen microbial populations involved in biohydrogenation related to individual milk fat percentage of dairy cows. Frontiers in Veterinary Science, 0, 10, .	0.9	2
5808	Hot moment of N2O emissions in seasonally frozen peatlands. ISME Journal, 2023, 17, 792-802.	4.4	3
5809	Diversity and potential function of pig gut DNA viruses. Heliyon, 2023, 9, e14020.	1.4	2
5810	Rickettsia felis DNA recovered from a child who lived in southern Africa 2000 years ago. Communications Biology, 2023, 6, .	2.0	2
5811	Blastopirellula sediminis sp. nov. a new member of Pirellulaceae isolated from the Andaman and Nicobar Islands. Antonie Van Leeuwenhoek, 0, , .	0.7	0
5812	Alterations in faecal microbiome and resistome in Chinese international travellers: a metagenomic analysis. Journal of Travel Medicine, 2023, 30, .	1.4	3
5813	Ecological divergence of syntopic marine bacterial species is shaped by gene content and expression. ISME Journal, 2023, 17, 813-822.	4.4	3
5814	Surface-layer protein is a public-good matrix exopolymer for microbial community organisation in environmental anammox biofilms. ISME Journal, 2023, 17, 803-812.	4.4	7
5815	Genome Sequence Analysis of a Wohlfahrtiimonas chitiniclastica Strain Isolated from a Septic Wound of a Hospitalized Patient in Uganda. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5816	Genomic Features Predict Bacterial Life History Strategies in Soil, as Identified by Metagenomic Stable Isotope Probing. MBio, 2023, 14, .	1.8	4
5820	Complete Genome Sequence of <i>Dyella</i> sp. Strain GSA-30, a Predominant Endophytic Bacterium of <i>Dendrobium</i> Plants. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5821	Draft Genome Sequences of Endophytic Pseudomonas Strains, Isolated from the Interior of <i>Brassicaceae</i> Plants. Microbiology Resource Announcements, 2023, 12, .	0.3	1
5823	An active microbiome in Old Faithful geyser. , 2023, 2, .		2
5824	Abundance and composition of particles and their attached microbiomes along an Atlantic Meridional Transect. Frontiers in Marine Science, 0, 10, .	1.2	4
5825	The terrestrial isopod symbiont â€˜<i>Candidatus</i> Hepatincola porcellionumâ€™ is a potential nutrient scavenger related to <i>Holosporales</i> symbionts of protists. ISME Communications, 2023, 3, .	1.7	2

#	ARTICLE	IF	CITATIONS
5827	Hologenome analysis reveals independent evolution to chemosymbiosis by deep-sea bivalves. BMC Biology, 2023, 21, .	1.7	2
5829	An untargeted exometabolomics approach to characterize dissolved organic matter in groundwater of the Samail Ophiolite. Frontiers in Microbiology, 0, 14, .	1.5	1
5830	A hydrogenotrophic Sulfurimonas is globally abundant in deep-sea oxygen-saturated hydrothermal plumes. Nature Microbiology, 2023, 8, 651-665.	5.9	5
5837	Acinetobacter nematophilus sp. nov., Alcaligenes nematophilus sp. nov., Enterobacter nematophilus sp. nov., and Kaistia nematophila sp. nov., Isolated from Soil-Borne Nematodes and Proposal for the Elevation of Alcaligenes faecalis subsp. faecalis, Alcaligenes faecalis subsp. parafaecalis, and Alcaligenes faecalis subsp. phenolicus to the Species Level. Taxonomy, 2023, 3, 148-168.	0.4	5
5838	Characterization of a bloom-associated alphaproteobacterial lineage, â€˜<i>Candidatus</i> Phycosociusâ€™: insights into freshwater algal-bacterial interactions. ISME Communications, 2023, 3, .	1.7	1
5839	Comammox <i>Nitrospira</i> and Ammonia-Oxidizing Archaea Are Dominant Ammonia Oxidizers in Sediments of an Acid Mine Lake Containing High Ammonium Concentrations. Applied and Environmental Microbiology, 2023, 89, .	1.4	2
5840	Genome Analysis of Two Pseudomonas syringae pv. <i>aptata</i> Strains with Different Virulence Capacity Isolated from Sugar Beet: Features of Successful Pathogenicity in the Phyllosphere Microbiome. Microbiology Spectrum, 2023, 11, .	1.2	4
5841	Change in the Gut Microbiome and Immunity by Lacticaseibacillusrhamnosus Probio-M9. Microbiology Spectrum, 2023, 11, .	1.2	2
5842	Characterization and Antibiotic Resistance of Listeria monocytogenes Strains Isolated from Greek Myzithra Soft Whey Cheese and Related Food Processing Surfaces over Two-and-a-Half Years of Safety Monitoring in a Cheese Processing Facility. Foods, 2023, 12, 1200.	1.9	4
5843	Co-Occurrence and Cooperation between Comammox and Anammox Bacteria in a Full-Scale Attached Growth Municipal Wastewater Treatment Process. Environmental Science & Technology, 2023, 57, 5013-5023.	4.6	10
5844	Secondary Metabolic Potential of <i>Kutzneria</i>. Journal of Natural Products, 2023, 86, 1120-1127.	1.5	3
5845	Benchmarking genome assembly methods on metagenomic sequencing data. Briefings in Bioinformatics, 2023, 24, .	3.2	4
5846	Temporal disturbance of a model stream ecosystem by high microbial diversity from treated wastewater. MicrobiologyOpen, 2023, 12, .	1.2	2
5848	Phylogenomic analysis of the genus Rosenbergiella and description of Rosenbergiella gaditana sp. nov., Rosenbergiella metrosideri sp. nov., Rosenbergiella epipactidis subsp. epipactidis subsp. nov., Rosenbergiella epipactidis subsp. californiensis subsp. nov., Rosenbergiella epipactidis subsp. japonicus subsp. nov., Rosenbergiella nectarea subsp. nectarea subsp. nov. and Rosenbergiella nectarea subsp. apis subsp. nov., isolated from floral nectar and insects. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	2
5849	A holobiont approach towards polysaccharide degradation by the highly compartmentalised gut system of the soil-feeding higher termite Labiotermes labralis. BMC Genomics, 2023, 24, .	1.2	3
5850	Ligilactobacillus ubinensis sp. nov., a novel species isolated from the wild ferment of a durian fruit (Durio zibethinus). International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	3
5851	Neobacillus terrae sp. nov., isolated from mountain soil. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5852	Characterization of Molecular Diversity and Organization of Phycobilisomes in Thermophilic Cyanobacteria. International Journal of Molecular Sciences, 2023, 24, 5632.	1.8	2

#	ARTICLE	IF	CITATIONS
5853	Draft Genome Sequences of <i>Algoriphagus</i> sp. Strain PAP.12 and <i>Roseivirga</i> sp. Strain PAP.19, Isolated from Marine Samples from Papua, Indonesia. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5854	Bioinformatic and Statistical Analysis of Microbiome Data. Methods in Molecular Biology, 2023, , 183-229.	0.4	2
5855	'Candidatus Megaira' are diverse symbionts of algae and ciliates with the potential for defensive symbiosis. Microbial Genomics, 2023, 9, .	1.0	2
5856	Mobile genetic elements drive the multidrug resistance and spread of Salmonella serotypes along a poultry meat production line. Frontiers in Microbiology, 0, 14, .	1.5	3
5857	Cytobacillus citreus sp. nov., isolated from citrus rhizosphere soil. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	1
5858	Genomic Insights into Niche Partitioning across Sediment Depth among Anaerobic Methane-Oxidizing Archaea in Global Methane Seeps. MSystems, 2023, 8, .	1.7	4
5859	Hyperactive nanobacteria with host-dependent traits pervade Omnitrophota. Nature Microbiology, 2023, 8, 727-744.	5.9	9
5860	Assembly of novel microbial genomes from gut metagenomes of rhesus macaque (<i>Macaca) Tj ETQq1 1 0.784314 rgBT /Overlock 10	4.3	5
5861	Salinibacterium sedimenticola sp. nov., Isolated from Tidal Flat Sediment. Current Microbiology, 2023, 80, .	1.0	1
5862	<i>De novo</i>genomic analysis of<i>Enterobacter asburiae</i>EBRJ12, a plant growth-promoting rhizobacteria isolated from the rhizosphere of<i>Phaseolus vulgaris</i>L. Journal of Applied Microbiology, 2023, 134, .	1.4	6
5863	Metagenomic sequencing reveals swine lung microbial communities and metagenome-assembled genomes associated with lung lesionsâ€"a pilot study. International Microbiology, 0, , .	1.1	0
5864	Draft Genome Sequence of Agrobacterium radiobacter Strain MD22b, Isolated from a Grape Plant in Tajikistan. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5867	Applications of Microbial Consortia and Microbiome Interactions for Augmenting Sustainable Agrobiology. Microorganisms for Sustainability, 2023, , 275-316.	0.4	1
5868	Micromonospora thermarum sp. nov., an actinobacterium isolated from hot spring soil. Archives of Microbiology, 2023, 205, .	1.0	1
5869	Diversity of the genus Cryobacterium and proposal of 19 novel species isolated from glaciers. Frontiers in Microbiology, 0, 14, .	1.5	2
5870	Metagenomic Discovery of â€œ <i>Candidatus</i> Parvarchaealesâ€•Related Lineages Sheds Light on Adaptation and Diversification from Neutral-Thermal to Acidic-Mesothermal Environments. MSystems, 0, , .	1.7	1
5871	Draft Genome Sequence of <i>Sinomicrobium</i> sp. Strain PAP.21, Isolated from a Coast Sample of Papua, Indonesia. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5872	Lacticaseibacillus parakribbianus sp. nov., isolated from a pig farm faeces dump. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	2

#	Article	IF	Citations
5874	Evidence for a Putative Isoprene Reductase in Acetobacterium wieringae. MSystems, 0, , .	1.7	0
5875	Isolation and characterisation of novel Methanocorpusculum species indicates the genus is ancestrally host-associated. BMC Biology, 2023, 21, .	1.7	5
5877	Genome-centric metagenomics reveals the host-driven dynamics and ecological role of CPR bacteria in an activated sludge system. Microbiome, 2023, 11, .	4.9	11
5878	Draft Genome Sequence of Pectobacterium brasiliense Isolated from Potato in South Africa. Microbiology Resource Announcements, 2023, 12, .	0.3	1
5879	Diversity and function of methyl-coenzyme M reductase-encoding archaea in Yellowstone hot springs revealed by metagenomics and mesocosm experiments. ISME Communications, 2023, 3, .	1.7	10
5881	The phylogeny and metabolic potentials of an n-alkane-degrading Venatorbacter bacterium isolated from deep-sea sediment of the Mariana Trench. Frontiers in Microbiology, 0, 14, .	1.5	2
5882	Recovery of metagenomic data from the Aedes aegypti microbiome using a reproducible snakemake pipeline: MINUUR. Wellcome Open Research, 0, 8, 131.	0.9	1
5883	The risk of pig and chicken farming for carriage and transmission of Escherichia coli containing extended-spectrum beta-lactamase (ESBL) and mobile colistin resistance (mcr) genes in Thailand. Microbial Genomics, 2023, 9, .	1.0	0
5884	A Complete Genome of the Alphaproteobacterial Methanotroph Methylocystis parvus OBBP. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5885	Draft Genome Sequence of Fusobacterium vincentii CNGBCC1850030, Isolated from Healthy Human Feces. Microbiology Resource Announcements, 2023, 12, .	0.3	0
5887	Metagenomics reveals the diversity and role of surface-water microbes in biogeochemical cycles in lakes at different terrain ladders. Frontiers in Environmental Science, 0, 11, .	1.5	1
5888	Global population structure, genomic diversity and carbohydrate fermentation characteristics of clonal complex 119 (CC119), an understudied Shiga toxin-producing E. coli (STEC) lineage including O165:H25 and O172:H25. Microbial Genomics, 2023, 9, .	1.0	0
5889	Shouchella tritolerans sp. nov., a facultative anaerobic bacterium isolated from marine sediments. Archives of Microbiology, 2023, 205, .	1.0	1
5890	Gordonia aquimaris sp. nov., a novel marine actinobacterium isolated from seawater in the upper gulf of Thailand. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	1
5891	New insights into the neuroprotective and beta-secretase1 inhibitor profiles of tirandamycin B isolated from a newly found Streptomyces composti sp. nov.. Scientific Reports, 2023, 13, .	1.6	0
5892	Discovery of diphenyl etherâ€“degrading Streptomyces strains by direct screening based on ether bondâ€“cleaving activity. Journal of Bioscience and Bioengineering, 2023, , .	1.1	1
5893	Microbial community structure and exploration of bioremediation enzymes: functional metagenomics insight into Arabian Sea sediments. Molecular Genetics and Genomics, 0, , .	1.0	0
5894	The genomic landscape of reference genomes of cultivated human gut bacteria. Nature Communications, 2023, 14, .	5.8	12

#	Article	IF	Citations
5895	Genomic analysis of Vibrio harveyi strain PH1009, a potential multi-drug resistant pathogen due to acquisition of toxin genes. Heliyon, 2023, 9, e14926.	1.4	1
5897	Altered infective competence of the human gut microbiome in COVID-19. Microbiome, 2023, 11, .	4.9	5
5898	Potato root-associated microbiomes adapt to combined water and nutrient limitation and have a plant genotype-specific role for plant stress mitigation. Environmental Microbiomes, 2023, 18, .	2.2	15
5899	Nanopore Sequencing Discloses Compositional Quality of Commercial Probiotic Feed Supplements. Scientific Reports, 2023, 13, .	1.6	0
5900	Linking prokaryotic genome size variation to metabolic potential and environment. ISME Communications, 2023, 3, .	1.7	1
5901	The Origins of ST11 KL64 Klebsiella pneumoniae: a Genome-Based Study. Microbiology Spectrum, 2023, 11, .	1.2	3
5902	The microbial dark matter and â€œwanted listâ€•in worldwide wastewater treatment plants. Microbiome, 2023, 11, .	4.9	10
5904	Soil conditions and the plant microbiome boost the accumulation of monoterpenes in the fruit of Citrus reticulata â€˜Chachiâ€™. Microbiome, 2023, 11, .	4.9	14
5905	Description of a Novel Fish Pathogen, Plesiomonas shigelloides subsp. oncorhynchi, Isolated from Rainbow Trout (Oncorhynchus mykiss): First Genome Analysis and Comparative Genomics. Fishes, 2023, 8, 179.	0.7	4
5906	Genome-resolved analyses of oligotrophic groundwater microbial communities along phenol pollution in a continuous-flow biodegradation model system. Frontiers in Microbiology, 0, 14, .	1.5	3
5907	Unexpected genetic and microbial diversity for arsenic cycling in deep sea cold seep sediments. Npj Biofilms and Microbiomes, 2023, 9, .	2.9	3
5908	Nitrite accumulation and anammox bacterial niche partitioning in Arctic Mid-Ocean Ridge sediments. ISME Communications, 2023, 3, .	1.7	6
5909	Abundance, classification and genetic potential of Thaumarchaeota in metagenomes of European agricultural soils: a meta-analysis. Environmental Microbiomes, 2023, 18, .	2.2	5
5910	Responses to organic pollutants in the tropical Pacific and subtropical Atlantic Oceans by pelagic marine bacteria. Frontiers in Environmental Science, 0, 11, .	1.5	0
5911	Prevalence and Molecular Characterization of Methicillin-Resistant Staphylococci (MRS) and Mammaliicocci (MRM) in Dromedary Camels from Algeria: First Detection of SCCmec-mecC Hybrid in Methicillin-Resistant Mammaliicoccus lentus. Antibiotics, 2023, 12, 674.	1.5	3
5912	Phylogenic position and low genomic diversity of â€œ<i>Candidatus Rickettsia kotlanii</i>â€•inferred by complete genome sequences of two Japanese isolates. Microbiology and Immunology, 2023, 67, 275-280.	0.7	1
5913	Maternal diet modulates the infant microbiome and intestinal Flt3L necessary for dendritic cell development and immunity to respiratory infection. Immunity, 2023, 56, 1098-1114.e10.	6.6	9
5914	Parapedobacter tibetensis sp. nov., isolated from shore soil of saline lake in Tibet of China and its genome mining of secondary metabolite. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0

#	ARTICLE	IF	CITATIONS
5915	Membranihabitans maritimus sp. nov., a marine bacterium isolated from deep seawater. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5918	Tsuneonella litorea sp. nov., a novel carotenoid-producing bacterium isolated from coastal sediment. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	1
5919	A social niche breadth score reveals niche range strategies of generalists and specialists. Nature Ecology and Evolution, 2023, 7, 768-781.	3.4	15
5920	Comprehensive Functional Annotation of Metagenomes and Microbial Genomes Using a Deep Learning-Based Method. MSystems, 2023, 8, .	1.7	3
5921	Alcanivorax xiamenensis sp. nov., a novel marine hydrocarbonoclastic bacterium isolated from surface seawater. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5922	Roseomonas fluvialis sp. nov., an aerobic bacteriochlorophyll a-containing freshwater bacterium isolated from river epilithic biofilm. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5923	Draft Genome Sequence of Lactobacillus oris BE7N, Isolated from a Healthy Centenarian in Hainan, China. Microbiology Resource Announcements, 0, , .	0.3	0
5924	Metagenomes and Metagenome-Assembled Genome Sequences from Nitrogen-Fixing Alder Nodules. Microbiology Resource Announcements, 0, , .	0.3	0
5926	Metagenome-Assembled Genomes from Appalachian Acid Mine Drainage Sites. Microbiology Resource Announcements, 2023, 12, .	0.3	2
5927	Comprehensive genomic analysis of hypocholesterolemic probiotic Enterococcus faecium LR13 reveals unique proteins involved in cholesterol-assimilation. Frontiers in Nutrition, 0, 10, .	1.6	1
5928	Bioinformatic analysis of structures and encoding genes of Escherichia coli surface polysaccharides sheds light on the heterologous biosynthesis of glycans. BMC Genomics, 2023, 24, .	1.2	2
5929	Paraburkholderia tagetis sp. nov., a novel species isolated from roots of Tagetes patula enhances the growth and yield of Solanum lycopersicum L. (tomato). Frontiers in Microbiology, 0, 14, .	1.5	5
5931	Bee breweries: The unusually fermentative, lactobacilli-dominated brood cell microbiomes of cellophane bees. Frontiers in Microbiology, 0, 14, .	1.5	3
5932	Vertically stratified methane, nitrogen and sulphur cycling and coupling mechanisms in mangrove sediment microbiomes. Microbiome, 2023, 11, .	4.9	7
5933	Unveiling the role of emerging metagenomics for the examination of hypersaline environments. Biotechnology and Genetic Engineering Reviews, 0, , 1-39.	2.4	2
5934	Whole genome sequencing to study antimicrobial resistance and RTX virulence genes in equine Actinobacillus isolates. Veterinary Research, 2023, 54, .	1.1	2
5936	Sulfate reduction and homoacetogenesis at various hypersaline conditions: Implications for H2 underground gas storage. Frontiers in Energy Research, 0, 11, .	1.2	2
5937	Spontaneously Produced Lysogenic Phages Are an Important Component of the Soybean <i>Bradyrhizobium</i> Mobilome. MBio, 2023, 14, .	1.8	2

#	Article	IF	Citations
5938	Isolation and pan-genome analysis of Enterobacter hormaechei Z129, a ureolytic bacterium, from the rumen of dairy cow. Frontiers in Microbiology, 0, 14, .	1.5	2
5939	Whole-Genome Sequence of Salmonella enterica Serovar Bispebjerg from Turkey Reveals Its Pathogenic Potential. Microbiology Resource Announcements, 0, , .	0.3	0
5940	Viruses interact with hosts that span distantly related microbial domains in dense hydrothermal mats. Nature Microbiology, 2023, 8, 946-957.	5.9	15
5941	GutAliveÂ® enables DNA-based microbiome analysis without disrupting the original composition and diversity. Frontiers in Microbiology, 0, 14, .	1.5	2
5942	Metagenomic insights into the composition and function of the gut microbiota of mice infected with Toxoplasma gondii. Frontiers in Immunology, 0, 14, .	2.2	2
5943	Mesophilic and thermophilic viruses are associated with nutrient cycling during hyperthermophilic composting. ISME Journal, 2023, 17, 916-930.	4.4	18
5944	Phylogenomics and molecular marker-based analyses of the order Nevskiales: proposal for the creation of Steroidobacterales ord. nov. and Peristeroidobacter gen. nov. Research in Microbiology, 2023, 174, 104057.	1.0	3
5947	Distribution and abundance of tetraether lipid cyclization genes in terrestrial hot springs reflect <scp>pH</scp>. Environmental Microbiology, 2023, 25, 1644-1658.	1.8	2
5948	Genome Sequence of <i>Arthrobacter</i> sp. Strain ATA002, a Seed Endophytic Bacterium from the Atacama Desert. Microbiology Resource Announcements, 0, , .	0.3	0
5949	The GEN-ERA toolbox: unified and reproducible workflows for research in microbial genomics. GigaScience, 2022, 12, .	3.3	3
5950	Aurantimonas marianensis sp. nov., isolated from deep-sea sediment of the Mariana Trench. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5951	Thermophilic <i>Dehalococcoidia</i> with unusual traits shed light on an unexpected past. ISME Journal, 2023, 17, 952-966.	4.4	5
5952	Draft Genomes of Halophilic <i>Chromohalobacter</i> and <i>Halomonas</i> Strains Isolated from Brines of The Carpathian Foreland, Poland. Journal of Genomics, 2023, 11, 14-19.	0.6	1
5953	Facilitative interaction networks in experimental microbial community dynamics. Frontiers in Microbiology, 0, 14, .	1.5	4
5955	Aestuariibaculum lutulentum sp. nov., a marine bacterium isolated from coastal sediment in Beihai. Archives of Microbiology, 2023, 205, .	1.0	3
5956	Staphylococcal diversity in atopic dermatitis from an individual to a global scale. Cell Host and Microbe, 2023, 31, 578-592.e6.	5.1	9
5957	Arthrobacter caoxuetaonis sp. nov., Arthrobacter zhangbolii sp. nov. and Arthrobacter gengyunqii sp. nov., isolated from Marmota himalayana faeces from Qinghai-Tibet Plateau. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	1
5958	Microbial Niche Differentiation during Nitrite-Dependent Anaerobic Methane Oxidation. Environmental Science & Technology, 2023, 57, 7029-7040.	4.6	4

#	Article	IF	Citations
5959	Draft genomes of halophilic Archaea strains isolated from brines of the Carpathian Foreland, Poland. Journal of Genomics, 2023, 11, 20-25.	0.6	0
5960	CRISPR detection in metagenome-assembled genomes (MAGs) of coal mine. Functional and Integrative Genomics, 2023, 23, .	1.4	1
5961	Draft Genome Sequence Resource of <i>Erwinia</i> sp. Strain INIA01, a Phytopathogen Isolated from a Diseased Stalk of Peruvian Maize. Microbiology Resource Announcements, 0, , .	0.3	0
5962	Dynamic Development of Viral and Bacterial Diversity during Grass Silage Preservation. Viruses, 2023, 15, 951.	1.5	0
5963	Previously uncharacterized rectangular bacterial structures in the dolphin mouth. Nature Communications, 2023, 14, .	5.8	1
5964	Escherichia cryptic clade I is an emerging source of human intestinal pathogens. BMC Biology, 2023, 21, .	1.7	0
5965	Genomic and metabolic analyses reveal antagonistic lanthipeptides in archaea. Microbiome, 2023, 11, .	4.9	4
5966	<i>Lacticaseibacillus rhamnosus</i> Probio-M9 may be vertically transmitted from mother to infant during lactation based on faeces metagenomics. , 2024, 13, 721-728.		0
5967	Species-Level Taxonomic Characterization of Uncultured Core Gut Microbiota of Plateau Pika. Microbiology Spectrum, 0, , .	1.2	1
5968	A comprehensive genomic analysis provides insights on the high environmental adaptability of Acinetobacter strains. Frontiers in Microbiology, 0, 14, .	1.5	3
5969	Variation in Sphingomonas traits across habitats and phylogenetic clades. Frontiers in Microbiology, 0, 14, .	1.5	0
5970	Fecal Metagenomes and Metagenome-Assembled Genomes from the South American Sea Lion (Otaria) Tj ETQq1 1 0.784314 rgBT /Ove	0.3	0
5971	Phosphorus Removal and Storage Polymer Synthesis by <i>Tetrasphaera</i>-Related Bacteria with Different Carbon Sources. ACS ES&T Water, 2023, 3, 1374-1384.	2.3	3
5972	Three marine species of the genus Fulvivirga, rich sources of carbohydrate-active enzymes degrading alginate, chitin, laminarin, starch, and xylan. Scientific Reports, 2023, 13, .	1.6	3
5974	Identification of diverse antibiotic resistant bacteria in agricultural soil with H218O stable isotope probing combined with high-throughput sequencing. Environmental Microbiomes, 2023, 18, .	2.2	3
5975	Virotyping and genetic antimicrobial susceptibility testing of porcine ETEC/STEC strains and associated plasmid types. Frontiers in Microbiology, 0, 14, .	1.5	5
5976	Expression of <i>Microcystis</i> Biosynthetic Gene Clusters in Natural Populations Suggests Temporally Dynamic Synthesis of Novel and Known Secondary Metabolites in Western Lake Erie. Applied and Environmental Microbiology, 2023, 89, .	1.4	2
5977	Genomic features, antimicrobial susceptibility, and epidemiological insights into Burkholderia cenocepacia clonal complex 31 isolates from bloodstream infections in India. Frontiers in Cellular and Infection Microbiology, 0, 13, .	1.8	0

#	ARTICLE	IF	CITATIONS
5978	Rheinheimera faecalis sp. nov., isolated from Ceratotherium simum feces. Archives of Microbiology, 2023, 205, .	1.0	0
5979	Genomic insight of sulfate reducing bacterial genus Desulfofaba reveals their metabolic versatility in biogeochemical cycling. BMC Genomics, 2023, 24, .	1.2	0
5980	Microbulbifer zhoushanensis sp. nov., Microbulbifer sediminum sp. nov. and Microbulbifer guangxiensis sp. nov., three marine bacteria isolated from a tidal flat. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5981	Viruses of sulfur oxidizing phototrophs encode genes for pigment, carbon, and sulfur metabolisms. Communications Earth & Environment, 2023, 4, .	2.6	3
5982	Clinical Diagnostics of Bacterial Infections and Their Resistance to Antibioticsâ€"Current State and Whole Genome Sequencing Implementation Perspectives. Antibiotics, 2023, 12, 781.	1.5	9
5983	Antimicrobial resistome during the transition from an integrated to a monoculture aquaculture farm in southern China. Science of the Total Environment, 2023, 882, 163511.	3.9	0
5984	Genome-based reclassification of Picrophilus torridus Zillig et al. 1996 as a later heterotypic synonym of Picrophilus oshimae Schleper et al. 1996. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5985	Sphingomicrobium sediminis sp. nov., isolated from marine sediment in the Republic of Korea. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	1
5986	Aridibaculum aurantiacum gen. nov., sp. nov., isolated from the Kumtag Desert soil. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5987	Comparative genomic insights into habitat adaptation of coral-associated Prosthecochloris. Frontiers in Microbiology, 0, 14, .	1.5	1
5988	Dyadobacter pollutisoli sp. nov., isolated from plastic waste landfill soil. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5989	Extensive genome analysis identifies novel plasmid families in Clostridium perfringens. Microbial Genomics, 2023, 9, .	1.0	0
5991	Genomic analysis of the population structure of Paenibacillus larvae in New Zealand. Frontiers in Microbiology, 0, 14, .	1.5	2
5992	Anaerobic degradation of organic carbon supports uncultured microbial populations in estuarine sediments. Microbiome, 2023, 11, .	4.9	1
5993	Spirosoma oryzicola sp. nov., isolated from dried rice husk. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	0
5994	Aeoliella straminimaris sp. nov., a novel member of the phylum Planctomycetota with an unusual filamentous structure. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	1
5996	Gut microbiome responds compositionally and functionally to the seasonal diet variations in wild gibbons. Npj Biofilms and Microbiomes, 2023, 9, .	2.9	4
5998	Cuticle supplementation and nitrogen recycling by a dual bacterial symbiosis in a family of xylophagous beetles. ISME Journal, 2023, 17, 1029-1039.	4.4	1

#	ARTICLE	IF	CITATIONS
5999	Pelosinus baikalensis sp. nov., an Iron-Reducing Bacterium Isolated from a Cold Freshwater Lake. Microbiology, 2023, 92, 137-145.	0.5	0
6000	iPHoP: An integrated machine learning framework to maximize host prediction for metagenome-derived viruses of archaea and bacteria. PLoS Biology, 2023, 21, e3002083.	2.6	57
6001	Diurnal Methane Dynamics in the Cyanobacterial Community of Soda Lake Bitter 1 (Kulunda Steppe,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.5	1
6003	Identification of novel Carnobacterium maltaromaticum strains in bone marrow samples of patients with acute myeloid leukemia using a metagenomic binning approach. International Microbiology, 2023, 26, 1033-1040.	1.1	1
6010	Long-Read Metagenomics and CAZyme Discovery. Methods in Molecular Biology, 2023, , 253-284.	0.4	0
6043	New Developments in Techniques Like Metagenomics and Metaproteomics for Isolation, Identification, and Characterization of Microbes from Varied Environment. Rhizosphere Biology, 2023, , 487-496.	0.4	0
6088	Bioinformatics Analysis Tools for Studying Microbiomes at the DOE Joint Genome Institute. Journal of the Indian Institute of Science, 2023, 103, 857-875.	0.9	3
6092	Metagenomic next generation sequencing for studying antibiotic resistance genes in the environment. Advances in Applied Microbiology, 2023, , .	1.3	0
6099	Recovery and Analysis of Long-Read Metagenome-Assembled Genomes. Methods in Molecular Biology, 2023, , 235-259.	0.4	0
6105	DIAMOND +â€‰ MEGAN Microbiome Analysis. Methods in Molecular Biology, 2023, , 107-131.	0.4	2
6172	VollstÃndige Shotgun-DNA-Metagenomik. , 2023, , 187-200.		0
6176	Comparative Genomics Using the Integrated Microbial Genomes and Microbiomes (IMG/M) System: A Deinococcus Use Case. Journal of the Indian Institute of Science, 0, , .	0.9	2
6209	Using De Novo Metagenome Assembly for Improved Metagenomic Classification. , 2023, , .		0
6322	Role of co-infections in modulating disease severities and clinical phenotypes. , 2023, , 151-186.		0
6531	Fast and robust metagenomic sequence comparison through sparse chaining with skani. Nature Methods, 2023, 20, 1661-1665.	9.0	3
6558	Tools for microbial single-cell genomics for obtaining uncultured microbial genomes. Biophysical Reviews, 0, , .	1.5	4
6658	Description of Tellurirhabdus bombi sp. nov., Isolated from Bumblebee. Current Microbiology, 2023, 80, .	1.0	1
6750	Clostridium brassicae sp. nov., A Strictly Anaerobic Bacterium Isolated from High-Salt Industrial Wastewater. Current Microbiology, 2023, 80, .	1.0	0

#	ARTICLE	IF	CITATIONS
6770	Parerythrobacter aestuarii sp. nov., Isolated from Seawater in the Tidal Region of Taizhou. Current Microbiology, 2023, 80, .	1.0	0
6885	Omics Technologies in the Plantâ€"Microbe Interactions. Microorganisms for Sustainability, 2023, , 257-282.	0.4	0
6931	Ready Reckoner for Using Bioinformatics Tools in Fish and Shellfish Microbiome Analysis. , 2023, , 93-120.		0
6970	Proposal to Reclassify Companilactobacillus futsaii subsp. chongqingensis as a Later Heterotypic Synonym of Companilactobacillus futsaii subsp. futsaii. Current Microbiology, 2024, 81, .	1.0	0
6971	Detection and Analysis of Wolbachia in Plant-Parasitic Nematodes and Insights into Wolbachia Evolution. Methods in Molecular Biology, 2024, , 115-134.	0.4	0
6975	Full Shotgun DNA Metagenomics. Learning Materials in Biosciences, 2023, , 183-200.	0.2	0
7119	Molecular and associated approaches for studying soil biota and their functioning. , 2024, , 161-192.		0
7250	Pelagibacterium flavum sp. nov., Isolated from Soil Sample. Current Microbiology, 2024, 81, .	1.0	0
7290	Parendozoicomonas callyspongiae sp. nov. Isolated from a Marine Sponge, Callyspongia elongate, and Reclassification of Sansalvadorimonas verongulae as Parendozoicomonas verongulae comb. nov.. Current Microbiology, 2024, 81, .	1.0	0
7372	Genomics of the Thermophilic Bacterium Thermosulfidibacter takaii Reveals Novel Lineage of Deep-Branching Bacterial Phylum. Indian Journal of Microbiology, 0, , .	1.5	0