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677	Proposal of Litorimonas haliclonae sp. nov., isolated from a marine sponge of the genus Haliclona. 2018 , 68, 835-843	6
676	Marinicrinis lubricantis sp. nov., isolated from a coolant lubricant. 2018 , 68, 1018-1022	2
675	Halomonas malpeensis sp. nov., isolated from rhizosphere sand of a coastal sand dune plant. 2018 , 68, 1037-1046	9
674	Comamonas aquatilis sp. nov., isolated from a garden pond. 2018 , 68, 1210-1214	5
673	sp. nov., a member of the family from lichen-dominated forested tundra. 2018 , 68, 1265-1270	10
672	Deinococcus lacus sp. nov., a gamma radiation-resistant bacterium isolated from an artificial freshwater pond. 2018 , 68, 1372-1377	1
671	Novosphingobium lubricantis sp. nov., isolated from a coolant lubricant emulsion. 2018 , 68, 1560-1564	3
670	Flavobacterium lacicola sp. nov., isolated from a freshwater lake. 2018 , 68, 1565-1570	5
669	Proposal for a new classification of a deep branching bacterial phylogenetic lineage: transfer of Coprothermobacter proteolyticus and Coprothermobacter platensis to Coprothermobacteraceae fam. nov., within Coprothermobacterales ord. nov., Coprothermobacteria classis nov. and	24
668	Coprothermobacterota phyl. nov. and emended description of the family Thermodesulfobiaceae. Winogradskyella pocilloporae sp. nov. isolated from healthy tissue of the coral Pocillopora damicornis. 2018 , 68, 1689-1696	7
667	Marinicaulis flavus gen. nov., sp. nov., a novel stalked bacterium of the family Parvularculaceae. 2018 , 68, 2061-2067	4
666	Sulfurovum denitrificans sp. nov., an obligately chemolithoautotrophic sulfur-oxidizing epsilonproteobacterium isolated from a hydrothermal field. 2018 , 68, 2183-2187	27
665	Vicinamibacteraceae fam. nov., the first described family within the subdivision 6 Acidobacteria. 2018 , 68, 2331-2334	14
664	Ruegeria denitrificans sp. nov., a marine bacterium in the family Rhodobacteraceae with the potential ability for cyanophycin synthesis. 2018 , 68, 2515-2522	15
663	Marinobacter fuscus sp. nov., a marine bacterium of Gammaproteobacteria isolated from surface seawater. 2018 , 68, 3156-3162	6
662	Spirosoma pollinicola sp. nov., isolated from pollen of common hazel (Corylus avellana L.). 2018 , 68, 3248-325	541

661	Winogradskyella aurantiaca sp. nov., isolated from seawater. 2018 , 68, 3260-3265	2
660	Sphingomonas floccifaciens sp. nov., isolated from subterranean sediment. 2019 , 69, 1531-1536	2
659	Halorubrum chaoviator Mancinelli et al. 2009 is a later, heterotypic synonym of Halorubrum ezzemoulense Kharroub et al. 2006. Emended description of Halorubrum ezzemoulense Kharroub et al. 2006. 2018 , 68, 3657-3665	3
658	Eubacterium maltosivorans sp. nov., a novel human intestinal acetogenic and butyrogenic bacterium with a versatile metabolism. 2018 ,	3
657	Refining the taxonomic structure of the phylum Acidobacteria. 2018 , 68, 3796-3806	45
656	Erythrobacter zhengii sp. nov., a bacterium isolated from deep-sea sediment. 2019 , 69, 241-248	9
655	Kocuria tytonis sp. nov., isolated from the uropygial gland of an American barn owl (Tyto furcata). 2019 , 69, 447-451	6
654	Trichococcus shcherbakoviae sp. nov., isolated from a laboratory-scale anaerobic EGSB bioreactor operated at low temperature. 2019 , 69, 529-534	11
653	Aromatoleum gen. nov., a novel genus accommodating the phylogenetic lineage including Azoarcus evansii and related species, and proposal of Aromatoleum aromaticum sp. nov., Aromatoleum petrolei sp. nov., Aromatoleum bremense sp. nov., Aromatoleum toluolicum sp. nov. and	27
652	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.	5
651	Granulicella sibirica sp. nov., a psychrotolerant acidobacterium isolated from an organic soil layer in forested tundra, West Siberia. 2019 , 69, 1195-1201	6
650	Methanofervidicoccus abyssi gen. nov., sp. nov., a hydrogenotrophic methanogen, isolated from a hydrothermal vent chimney in the Mid-Cayman Spreading Center, the Caribbean Sea. 2019 , 69, 1225-1230	5
649	Halonotius aquaticus sp. nov., a new haloarchaeon isolated from a marine saltern. 2019 , 69, 1306-1312	3
648	Azoarcus pumilus sp. nov., isolated from seawater in Sanya, China. 2019 , 69, 1459-1464	5
647	Altererythrobacter aerophilus sp. nov., isolated from deep-sea water of the north-west Pacific. 2019 , 69, 1689-1695	7
646	sp. nov., isolated from tidal flat sediment. 2019 , 69, 2651-2657	1
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644	sp. nov., isolated from a large freshwater lake. 2019 , 69, 3135-3140	5

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642	gen. nov., sp. nov., isolated from a marine red alga. 2019 , 69, 3544-3550	2
641	gen. nov., sp. nov., a D-arabinose-utilizing bacterium isolated from faeces of C57BL/6J mice that is a close relative of species ASF 502. 2019 , 69, 3616-3622	2
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639	sp. nov., isolated from fresh water. 2019 , 69, 3903-3909	6
638	sp. nov. isolated from the penguin. 2020 , 70, 211-219	5
637	gen. nov., sp. nov., a moderately thermophilic heterotrophic aggregating bacterium isolated from microbial mats at a terrestrial hot spring. 2020 , 70, 1117-1121	2
636	gen. nov., sp. nov., a novel freshwater planctomycete with a giant genome from the family. 2020 , 70, 1240-1249	14
635	gen. nov., sp. nov., a novel member of the family. 2020 , 70, 1231-1239	7
634	Taxonomic reassessment of the genus using whole genome sequencing: is a later heterotypic synonym of and description of sp. nov. 2020 , 70, 1315-1320	3
633	Genome-based analyses reveal a synonymy among Zvyagintseva and Tarasov 1989; Oren and Ventosa 1996, Ventosa . 2004, Xu . 2007 and Cui . 2007. Emended description of Zvyagintseva and Tarasov 1989; Oren and Ventosa 1996. 2020 , 70, 1698-1705	2
632	gen. nov., sp. nov., isolated from a sea tidal flat and proposal of fam. nov. 2020 , 70, 2239-2246	5
631	sp. nov., isolated from coastal seawater. 2020 , 70, 1868-1875	3
630	Proposal to reclassify into a novel genus as gen. nov., comb. nov. 2020 , 70, 2084-2088	1
629	Proposal to reclassify into a novel genus as gen. nov., comb. nov. 2020 , 70, 2366-2368	2
628	Leon . 2017 is a later heterotypic synonym of Leon . 2016. Reclassification of Menes . 2016 as comb. nov. 2020 , 70, 2873-2878	1
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616	Synechococcus diversity along a trophic gradient in the Osterseen Lake District, Bavaria. 2016 , 162, 2053-2063	3 18
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614	290 Metagenome-assembled Genomes from the Mediterranean Sea: a resource for marine microbiology.	2
613	AmoA-targeted polymerase chain reaction primers for the specific detection and quantification of comammoxNitrospirain the environment.	4
612	Nitrogen-fixing populations of Planctomycetes and Proteobacteria are abundant in the surface ocean.	18
611	Rice paddyNitrospiraeencode and express genes related to sulfate respiration: proposal of the new genusCandidatusSulfobium.	1
610	Highly parallelized microfluidic droplet cultivation and prioritization on antibiotic producers from complex natural microbial communities.	1
609	Lateral gene transfer drives metabolic flexibility in the anaerobic methane oxidising archaeal family Methanoperedenaceae.	1
608	Experimentally-validated correlation analysis reveals new anaerobic methane oxidation partnerships with consortium-level heterogeneity in diazotrophy.	1

607	Connecting structure to function with the recovery of over 1000 high-quality activated sludge metagenome-assembled genomes encoding full-length rRNA genes using long-read sequencing.	15
606	Chloroflexi persisting for millions of years in oxic and anoxic deep-sea clay.	3
605	Microdiversity and phylogeographic diversification of bacterioplankton in pelagic freshwater systems revealed through long-read amplicon sequencing.	3
604	Novel taxa of Acidobacteriota involved in seafloor sulfur cycling.	5
603	Landidatus Dechloromonas phosphatisland Landidatus Dechloromonas phosphovora∏two novel polyphosphate accumulating organisms abundant in wastewater treatment systems.	3
602	Metabolic potential for reductive acetogenesis and a novel energy-converting [NiFe] hydrogenase in Bathyarchaeia from termite guts 🛭 genome-centric analysis.	1
601	TaxAss: Leveraging a Custom Freshwater Database Achieves Fine-Scale Taxonomic Resolution.	4
600	Automated high throughput animal DNA metabarcode classification.	2
599	A proposal for a standardized bacterial taxonomy based on genome phylogeny.	32
598	Marine sponges as Chloroflexi hot-spots: Genomic insights and high resolution visualization of an abundant and diverse symbiotic clade.	3
597	The ecology of the Chloroflexi in full-scale activated sludge wastewater treatment plants.	2
596	Asgard archaea are diverse, ubiquitous, and transcriptionally active microbes.	9
595	Pyrite formation from FeS and H2S is mediated by a novel type of microbial energy metabolism.	3
594	Trait-based approach to bacterial growth efficiency.	5
593	Insights into the microbiota of Asian seabass (Lates calcarifer) with tenacibaculosis symptoms and description of sp. nov. Tenacibaculum singaporense.	3
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468	Biogeochemical processes and microbial diversity of the Gullfaks and Tommeliten methane seeps (Northern North Sea).	10
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83	Genome analysis and 2Fucosyllactose utilization characteristics of a new Akkermansia muciniphila strain isolated from mice feces.	1
82	The root zone of graminoids: A niche for H2-consuming acetogens in a minerotrophic peatland. 13,	
81	Metabolic responses of thermophilic endospores to sudden heat-induced perturbation in marine sediment samples. 13,	2
80	Variations in Atlantic water influx and sea-ice cover drive taxonomic and functional shifts in Arctic marine bacterial communities.	
79	Assembly of root-associated N2O-reducing communities of annual crops is governed by selection for nosZ clade I over clade II. 2022 , 98,	0
78	Propagule limitation affects the response of soil methane oxidizer community to increased salinity. 2022 , 426, 116082	
77	Convergent community assembly among globally separated acidic cave biofilms.	0
76	Specific Localization and Quantification of the Oligo-Mouse-Microbiota (OMM 12) by Fluorescence In Situ Hybridization (FISH). 2022 , 2,	O
75	Carbon Substrate Selects for Different Lineages of N2O Reducing Communities in Soils Under Anoxic Conditions.	0
74	Distinct stages of the intestinal bacterial community of Ampullaceana balthica after salinization. 13,	O
73	Grazers affect the composition of dissolved storage glycans and thereby bacterioplankton composition during a biphasic North Sea spring algae bloom.	0
72	Paenibacillus allorhizoplanae sp. nov. from the rhizoplane of a Zea mays root. 2022 , 204,	2
71	Exploring the Healthy Eye Microbiota Niche in a Multicenter Study. 2022 , 23, 10229	2
70	Microorganisms associated with Sporobolus anglicus, an invasive dimethylsulfoniopropionate producing salt marsh plant, are an unrecognized sink for dimethylsulfide. 13,	O
69	Deep-branching ANME-1c archaea grow at the upper temperature limit of anaerobic oxidation of methane. 13,	2
68	Colitis caused by Entamoeba histolytica identified by real-time-PCR and fluorescence in situ hybridization from formalin-fixed, paraffin-embedded tissue. 2022 , 12, 84-91	O

67	Microbial communities from weathered outcrops of a sulfide-rich ultramafic intrusion, and implications for mine waste management.	О
66	Microarray-Based Detection and Identification of Bacterial and Viral Plant Pathogens. 2022 , 47-69	O
65	Adaptations to high pressure of Nautilia sp. strain PV -1, a piezophilic Campylobacterium (aka Epsilonproteobacterium) isolated from a deep-sea hydrothermal vent.	1
64	Genomic insights into the physiology of Quinella, an iconic uncultured rumen bacterium. 2022, 13,	0
63	Anaerobic oxidation of propane coupled to nitrate reduction by a lineage within the class Symbiobacteriia. 2022 , 13,	О
62	Screening of Spore-Forming Bacteria with Probiotic Potential in Pristine Algerian Caves. 2022 , 10,	O
61	Closed genomes uncover a saltwater species of Candidatus Electronema and shed new light on the boundary between marine and freshwater cable bacteria.	О
60	Sutcliffiella rhizosphaerae sp. nov. isolated from roots. 2022 , 72,	O
59	Neobacillus rhizosphaerae sp. nov., isolated from the rhizosphere, and reclassification of Bacillus dielmonensis as Neobacillus dielmonensis comb. nov 2022 , 72,	1
58	Nitrogen cycling activities during decreased stratification in the coastal oxygen minimum zone off Namibia.	O
57	Shell Disease Syndrome Is Associated with Reduced and Shifted Epibacterial Diversity on the Carapace of the Crustacean Cancer pagurus.	О
56	Arbuscular Mycorrhiza Support Plant Sulfur Supply through Organosulfur Mobilizing Bacteria in the Hypho- and Rhizosphere. 2022 , 11, 3050	O
55	Targeted metagenomics using probe capture detects a larger diversity of nitrogen and methane cycling genes in complex microbial communities than traditional metagenomics.	О
54	Seasonal variation in the community distribution of protists off Wakasa Bay, Southern Sea of Japan. 2023 , 253, 104898	O
53	Carbon substrate selects for different lineages of N2O reducing communities in soils under anoxic conditions. 2023 , 177, 108909	О
52	Distinct responses of soil methanotrophy in hummocks and hollows to simulated glacier meltwater and temperature rise in Tibetan glacier foreland. 2023 , 862, 160888	O
51	FISHing for ciliates: Catalyzed reporter deposition fluorescence in situ hybridization for the detection of planktonic freshwater ciliates. 13,	О
50	Coupled C, H, N, S and Fe biogeochemical cycles operating in the continental deep subsurface of the Iberian Pyrite Belt.	O

49	A metagenomic insight into the microbiomes of geothermal springs in the Subantarctic Kerguelen Islands. 2022 , 12,	O
48	New globally distributed bacterial phyla within the FCB superphylum. 2022, 13,	O
47	Actin cytoskeleton and complex cell architecture in an Asgard archaeon.	O
46	Revealing the transfer pathways of cyanobacterial-fixed N into the boreal forest through the feather-moss microbiome. 13,	O
45	Faunimonas pinastri gen. nov., sp. nov., an endophyte from a pine tree of the family Pleomorphomonadaceae, class Alphaproteobacteria. 2022 , 72,	O
44	Distribution and environmental drivers of fungal denitrifiers in global soils.	O
43	Microbial diversity gradients in the geothermal mud volcano underlying the hypersaline Urania Basin. 13,	O
42	Contaminant Removal from Wastewater by Microalgal Photobioreactors and Modeling by Artificial Neural Network. 2022 , 14, 4046	O
41	The maternal microbiome regulates infant respiratory disease susceptibility via intestinal Flt3L expression and plasmacytoid dendritic cell hematopoiesis.	O
40	Convergent Community Assembly among Globally Separated Acidic Cave Biofilms.	O
39	Anaerobic methanotroph Candidatus Methanoperedens nitroreducens Chas a pleomorphic life cycle.	O
38	Molecular characterization of Dictyocaulus nematodes in wild red deer Cervus elaphus in two areas of the Italian Alps.	O
37	Diversity of the holopelagic Sargassum microbiome from the Great Atlantic Sargassum Belt to coastal stranding locations. 2023 , 122, 102369	O
36	Biotin pathway in novel Fodinibius salsisoli sp. nov., isolated from hypersaline soils and reclassification of the genus Aliifodinibius as Fodinibius. 13,	O
35	Evolutionary diversification of methanotrophic ANME-1 archaea and their expansive virome. 2023 , 8, 231-245	O
34	New insights into the coevolutionary history of termites and their gut flagellates: Description of Retractinympha glossotermitis gen. nov. sp. nov. (Retractinymphidae fam. nov.). 11,	O
33	Phosphorus Solubilization by Biological Acidification of Pig Slurry Using Agri-Food Waste: ´Efficiency and Underpinning Chemical and Microbiological Parameters.	О
32	Genomic-based phylogenetic and metabolic analyses of the genus Natronomonas, and description of Natronomonas aquatica sp. nov 14,	O

31	RickettsialesIdeep evolutionary history sheds light on the emergence of intracellular lifestyles.	O
30	Secondary Metabolite Production Potential in a Microbiome of the Freshwater Sponge Spongilla lacustris.	O
29	Nitrogen cycling activities during decreased stratification in the coastal oxygen minimum zone off Namibia. 14,	0
28	Dietary Effects of a Short-Term Administration of Microalgae Blend on Growth Performance, Tissue Fatty Acids, and Predominant Intestinal Microbiota in Sparus aurata. 2023 , 11, 463	O
27	Microbiota Phenotype Promotes Anastomotic Leakage in a Model of Rats with Ischemic Colon Resection. 2023 , 11, 680	1
26	Description of two cultivated and two uncultivated new Salinibacter species, one named following the rules of the bacteriological code: Salinibacter grassmerensis sp. nov.; and three named following the rules of the SeqCode: Salinibacter pepae sp. nov., Salinibacter abyssi sp. nov., and	O
25	Seed treatment with plant-defense elicitors decreases the abundance of ammonia oxidizers associated with winter wheat roots. 2023 , 180, 109016	0
24	Dissolved storage glycans shaped the community composition of abundant bacterioplankton clades during a North Sea spring phytoplankton bloom. 2023 , 11,	O
23	Characterization of Short-chain fatty acid-producing and cholesterol assimilation potential probiotic Lactic acid bacteria from Chinese fermented rice. 2023 , 52, 102404	0
22	Closed genomes uncover a saltwater species of Candidatus Electronema and shed new light on the boundary between marine and freshwater cable bacteria. 2023 , 17, 561-569	O
21	High abundance of hydrocarbon-degrading Alcanivorax in plumes of hydrothermally active volcanoes in the South Pacific Ocean. 2023 , 17, 600-610	O
20	Identification of key virusprokaryote infection pairs that contribute to viral shunt in a freshwater lake.	O
19	Aminithiophilus ramosus gen. nov., sp. nov., a sulphur-reducing bacterium isolated from a pyrite-forming enrichment culture, and taxonomic revision of the family Synergistaceae. 2023 , 73,	O
18	Dark Fermentation of Arundo donax: Characterization of the Anaerobic Microbial Consortium. 2023 , 16, 1813	O
17	Fine-scale evaluation of two standard 16S rRNA gene amplicon primer pairs for analysis of total prokaryotes and archaeal nitrifiers in differently managed soils. 14,	0
16	A New Parasitic Archamoeba Causing Systemic Granulomatous Disease in Goldfish Extends the Diversity of Pathogenic Endolimax spp 2023 , 13, 935	O
15	Abundance and composition of particles and their attached microbiomes along an Atlantic Meridional Transect. 10,	О
14	A hydrogenotrophic Sulfurimonas is globally abundant in deep-sea oxygen-saturated hydrothermal plumes. 2023 , 8, 651-665	O

13	Quantitative 16S rRNA Gene Amplicon Sequencing for Comprehensive Pathogenic Bacterial Tracking in a Municipal Wastewater Treatment Plant. 2023 , 3, 923-933	O
12	Metabolic Versatility of the Family Halieaceae Revealed by the Genomics of Novel Cultured Isolates. 2023 , 11,	O
11	Spatial profiling of microbial communities by sequential FISH with error-robust encoding. 2023, 14,	O
10	Mare-MAGE curated reference database of fish mitochondrial genes. 2023 , 24,	O
9	Cultivation of SAR202 Bacteria from the Ocean.	0
8	Maternal diet modulates the infant microbiome and intestinal Flt3L necessary for dendritic cell development and immunity to respiratory infection. 2023 ,	O
7	Isolation and physiological properties of methanogenic archaea that degrade tetramethylammonium hydroxide. 2023 , 107, 3047-3056	O
6	Paenibacillus auburnensis sp. nov. and Paenibacillus pseudetheri sp. nov., isolated from the rhizosphere of Zea mays. 2023 , 73,	O
5	Identification of Pseudo-nitzschia Cryptic Species Collected in the Gulf of Naples Using Whole-Cell Fluorescent In Situ Hybridization: From Cultured Sample to Field Test. 2023 , 15, 521	O
4	Phyloecology ofnrfA-ammonifiers and their relative importance with denitrifiers in global terrestrial biomes.	O
3	Molecular Epidemiology of Sars-CoV-2 in the Pityusic Islands, a Touristic Worldwide Hotspot in the Western Mediterranean.	O
2	A comparison between Greengenes, SILVA, RDP, and NCBI reference databases in four published microbiota datasets.	O
1	Genomic insight of sulfate reducing bacterial genus Desulfofaba reveals their metabolic versatility in biogeochemical cycling. 2023 , 24,	O