

# CITATION REPORT

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**Insights into the phylogeny and coding potential of microbial dark matter**

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#	Paper	IF	Citations
2073	Geochemistry articles □July 2013. <b>2013</b> , 63, e1-e33		
2072	Environmental microbiology: Exploring diversity with single-cell genomics. <b>2013</b> , 11, 598		6
2071	Microbial planet. <b>2013</b> , 10, 826		1
2070	Regulation of the immune system by biodiversity from the natural environment: an ecosystem service essential to health. <b>2013</b> , 110, 18360-7		416
2069	Sequencing the human microbiome in health and disease. <b>2013</b> , 22, R88-94		89
2068	Microbiology. Genomes from metagenomics. <b>2013</b> , 342, 1057-8		112
2067	Stabilizing the foundation of the house that 'omics builds: the evolving value of cultured isolates to marine microbiology. <b>2013</b> , 16, 618-24		14
2066	Genomes of "Spiribacter", a streamlined, successful halophilic bacterium. <b>2013</b> , 14, 787		37
2065	The PVC superphylum: exceptions to the bacterial definition?. <b>2013</b> , 104, 451-66		39
2064	Single-cell and metagenomic analyses indicate a fermentative and saccharolytic lifestyle for members of the OP9 lineage. <b>2013</b> , 4, 1854		143
2063	Using phage display selected antibodies to dissect microbiomes for complete de novo genome sequencing of low abundance microbes. <b>2013</b> , 13, 270		9
2062	Small genomes and sparse metabolisms of sediment-associated bacteria from four candidate phyla. <b>2013</b> , 4, e00708-13		204
2061	Microbial diversity in the era of omic technologies. <b>2013</b> , 2013, 958719		45
2060	Expanding the marine virosphere using metagenomics. <b>2013</b> , 9, e1003987		183
2059	Being Aquifex aeolicus: Untangling a hyperthermophile's checkered past. <b>2013</b> , 5, 2478-97		15
2058	Functional genome analysis of unculturable microbial species as genetic resources . <b>2013</b> , 24, 167-173		
2057	Isolation and characterization of two novel bacteria Afipia cberi and Mesorhizobium hominis from blood of a patient afflicted with fatal pulmonary illness. <b>2013</b> , 8, e82673		7

2056	Wide distribution of autochthonous branched glycerol dialkyl glycerol tetraethers (bGDGTs) in U.S. Great Basin hot springs. <b>2013</b> , 4, 222	11
2055	The distribution and abundance of archaeal tetraether lipids in U.S. Great Basin hot springs. <b>2013</b> , 4, 247	5
2054	Bespoke microbiome therapy to manage plant diseases. <b>2013</b> , 4, 355	57
2053	Close encounters of the third domain: the emerging genomic view of archaeal diversity and evolution. <b>2013</b> , 2013, 202358	19
2052	Researchers glimpse microbial 'dark matter'. <i>Nature</i> , <b>2013</b> ,	50.4
2051	The first complete genome sequence of the class Fimbriimonadia in the phylum Armatimonadetes. <b>2014</b> , 9, e100794	8
2050	IM-TORNADO: a tool for comparison of 16S reads from paired-end libraries. <b>2014</b> , 9, e114804	76
2049	Advancements toward a systems level understanding of the human oral microbiome. <b>2014</b> , 4, 98	45
2048	Pan-genome analyses identify lineage- and niche-specific markers of evolution and adaptation in Epsilonproteobacteria. <b>2014</b> , 5, 110	45
2047	Evolutionary ecology of the marine Roseobacter clade. <b>2014</b> , 78, 573-87	165
2046	Metagenomics and novel gene discovery: promise and potential for novel therapeutics. <b>2014</b> , 5, 399-412	80
2045	Gut microbiome of the Hadza hunter-gatherers. <b>2014</b> , 5, 3654	780
2044	Metagenomic systems biology and metabolic modeling of the human microbiome: from species composition to community assembly rules. <b>2014</b> , 5, 265-70	30
2043	Planning considerations related to the organic contamination of Martian samples and implications for the Mars 2020 Rover. <b>2014</b> , 14, 969-1027	22
2042	Global phylogenomic analysis disentangles the complex evolutionary history of DNA replication in archaea. <b>2014</b> , 6, 192-212	58
2041	A metagenomic study of the microbial communities in four parallel biogas reactors. <b>2014</b> , 7, 146	98
2040	IMG/M 4 version of the integrated metagenome comparative analysis system. <b>2014</b> , 42, D568-73	212
2039	Archaeal "dark matter" and the origin of eukaryotes. <b>2014</b> , 6, 474-81	74

2038	Advantages and Applications of Gel-Free Proteomic Approaches in the Study of Prokaryotes. <b>2014</b> , 64, 157-200	1
2037	Single cell genomic study of Dehalococcoidetes species from deep-sea sediments of the Peruvian Margin. <b>2014</b> , 8, 1831-42	59
2036	Metagenomic ventures into outer sequence space. <b>2014</b> , 4, e979664	22
2035	Bacteria in Soil. <b>2014</b> ,	
2034	Metagenomic insights into particles and their associated microbiota in a coastal margin ecosystem. <b>2014</b> , 5, 466	40
2033	A taxonomy of bacterial microcompartment loci constructed by a novel scoring method. <b>2014</b> , 10, e1003898	170
2032	ExaBayes: massively parallel bayesian tree inference for the whole-genome era. <b>2014</b> , 31, 2553-6	289
2031	Pangenome evidence for extensive interdomain horizontal transfer affecting lineage core and shell genes in uncultured planktonic thaumarchaeota and euryarchaeota. <b>2014</b> , 6, 1549-63	69
2030	Recoding of the stop codon UGA to glycine by a BD1-5/SN-2 bacterium and niche partitioning between Alpha- and Gammaproteobacteria in a tidal sediment microbial community naturally selected in a laboratory chemostat. <b>2014</b> , 5, 231	26
2029	Grappling archaea: ultrastructural analyses of an uncultivated, cold-loving archaeon, and its biofilm. <b>2014</b> , 5, 397	23
2028	Illuminating microbial dark matter in meromictic Sakinaw Lake. <b>2014</b> , 80, 6807-18	79
2027	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <b>2014</b> , 12, e1001920	146
2026	Robust identification of noncoding RNA from transcriptomes requires phylogenetically-informed sampling. <b>2014</b> , 10, e1003907	35
2025	Hidden diversity in honey bee gut symbionts detected by single-cell genomics. <b>2014</b> , 10, e1004596	102
2024	Single-cell genomics reveals features of a Colwellia species that was dominant during the Deepwater Horizon oil spill. <b>2014</b> , 5, 332	72
2023	Metagenomic evidence for metabolism of trace atmospheric gases by high-elevation desert Actinobacteria. <b>2014</b> , 5, 698	47
2022	Inter-species interconnections in acid mine drainage microbial communities. <b>2014</b> , 5, 367	39
2021	Hidden state prediction: a modification of classic ancestral state reconstruction algorithms helps unravel complex symbioses. <b>2014</b> , 5, 431	14

2020	The Marine Microbial Eukaryote Transcriptome Sequencing Project (MMETSP): illuminating the functional diversity of eukaryotic life in the oceans through transcriptome sequencing. <b>2014</b> , 12, e1001889	617
2019	Emerging methods to study bacteriophage infection at the single-cell level. <b>2014</b> , 5, 724	28
2018	Linking geology and microbiology: inactive pockmarks affect sediment microbial community structure. <b>2014</b> , 9, e85990	9
2017	6. Quantifying microbes in the marine subseafloor: some notes of caution.	2
2016	7. Archaea in deep marine subsurface sediments.	2
2015	2. Life in the Oceanic Crust.	3
2014	Biology of a widespread uncultivated archaeon that contributes to carbon fixation in the subsurface. <b>2014</b> , 5, 5497	86
2013	Revolutionizing Prokaryotic Systematics Through Next-Generation Sequencing. <b>2014</b> , 75-101	6
2012	The Family Nitrospinaceae. <b>2014</b> , 231-237	7
2011	Metaproteomics reveals differential modes of metabolic coupling among ubiquitous oxygen minimum zone microbes. <b>2014</b> , 111, 11395-400	115
2010	Horizontal gene acquisitions by eukaryotes as drivers of adaptive evolution. <b>2014</b> , 36, 9-20	97
2009	Diversity and genomic insights into the uncultured Chloroflexi from the human microbiota. <b>2014</b> , 16, 2635-43	38
2008	Cataloguing the taxonomic origins of sequences from a heterogeneous sample using phylogenomics: applications in adventitious agent detection. <b>2014</b> , 68, 602-18	5
2007	Effects of sample treatments on genome recovery via single-cell genomics. <b>2014</b> , 8, 2546-9	25
2006	Single-cell RNA-seq: advances and future challenges. <b>2014</b> , 42, 8845-60	478
2005	Culture-dependent and culture-independent analyses reveal no prokaryotic community shifts or recovery of <i>Serratia marcescens</i> in <i>Acropora palmata</i> with white pox disease. <b>2014</b> , 88, 457-67	26
2004	Analysis of plant microbe interactions in the era of next generation sequencing technologies. <b>2014</b> , 5, 216	150
2003	Concatenated alignments and the case of the disappearing tree. <b>2014</b> , 14, 266	36

2002	DNA-dependent RNA polymerase detects hidden giant viruses in published databanks. <b>2014</b> , 6, 1603-10	33
2001	Genetic Evidence of Subseafloor Microbial Communities. <b>2014</b> , 7, 85-125	6
2000	A quantitative comparison of single-cell whole genome amplification methods. <b>2014</b> , 9, e105585	215
1999	Host-associated bacterial taxa from Chlorobi, Chloroflexi, GN02, Synergistetes, SR1, TM7, and WPS-2 Phyla/candidate divisions. <b>2014</b> , 6,	55
1998	Species-level deconvolution of metagenome assemblies with Hi-C-based contact probability maps. <b>2014</b> , 4, 1339-46	120
1997	IMG 4 version of the integrated microbial genomes comparative analysis system. <b>2014</b> , 42, D560-7	444
1996	Ecological understanding of root-infecting fungi using trait-based approaches. <b>2014</b> , 19, 432-8	56
1995	Dynamics in the microbial cytochrome single cell analytics in natural systems. <b>2014</b> , 27, 134-41	32
1994	Non-model organisms, a species endangered by proteogenomics. <b>2014</b> , 105, 5-18	116
1993	Then and now: a systematic review of the systematics of prokaryotes in the last 80 years. <b>2014</b> , 106, 43-56	67
1992	Intestinal microbiome and digoxin inactivation: meal plan for digoxin users?. <b>2014</b> , 30, 791-9	6
1991	Progress and perspective on frontiers of geobiology. <b>2014</b> , 57, 855-868	13
1990	Every cell is special: genome-wide studies add a new dimension to single-cell biology. <b>2014</b> , 157, 8-11	136
1989	Taxonomic identification of algae (morphological and molecular): species concepts, methodologies, and their implications for ecological bioassessment. <b>2014</b> , 50, 409-24	53
1988	Single-cell genomics reveals hundreds of coexisting subpopulations in wild <i>Prochlorococcus</i> . <b>2014</b> , 344, 416-20	361
1987	Phylogeny, culturing, and metagenomics of the human gut microbiota. <b>2014</b> , 22, 267-74	148
1986	Obtaining genomes from uncultivated environmental microorganisms using FACS-based single-cell genomics. <b>2014</b> , 9, 1038-48	177
1985	'Geoarchaeote NAG1' is a deeply rooting lineage of the archaeal order Thermoproteales rather than a new phylum. <b>2014</b> , 8, 1353-7	19

1984	Activating hotspot L205R mutation in PRKACA and adrenal Cushing's syndrome. <b>2014</b> , 344, 913-7	160
1983	Stop codon reassignments in the wild. <b>2014</b> , 344, 909-13	83
1982	The hybrid nature of the Eukaryota and a consilient view of life on Earth. <b>2014</b> , 12, 449-55	95
1981	Mind the PVCs. <b>2014</b> , 16, 1217-21	16
1980	<i>Thermoflexus hugenholtzii</i> gen. nov., sp. nov., a thermophilic, microaerophilic, filamentous bacterium representing a novel class in the Chloroflexi, <i>Thermoflexia</i> classis nov., and description of Thermoflexaceae fam. nov. and Thermoflexales ord. nov. <b>2014</b> , 64, 2119-2127	36
1979	Syntrophic biodegradation of hydrocarbon contaminants. <b>2014</b> , 27, 21-9	167
1978	An environmental bacterial taxon with a large and distinct metabolic repertoire. <i>Nature</i> , <b>2014</b> , 506, 58-63	421
1977	Evolution. Searching for new branches on the tree of life. <b>2014</b> , 346, 698-9	17
1976	Determining microbial products and identifying molecular targets in the human microbiome. <b>2014</b> , 20, 731-741	68
1975	Impact of single-cell genomics and metagenomics on the emerging view of extremophile "microbial dark matter". <b>2014</b> , 18, 865-75	96
1974	Mosaic aneuploidy in <i>Leishmania</i> : the perspective of whole genome sequencing. <b>2014</b> , 30, 554-5	14
1973	Key roles for freshwater Actinobacteria revealed by deep metagenomic sequencing. <b>2014</b> , 23, 6073-90	104
1972	Single-cell enabled comparative genomics of a deep ocean SAR11 bathytype. <b>2014</b> , 8, 1440-51	76
1971	Rapid succession of uncultured marine bacterial and archaeal populations in a denitrifying continuous culture. <b>2014</b> , 16, 3275-86	17
1970	Adding genomic 'foliage' to the tree of life. <b>2014</b> , 12, 78	9
1969	Integrating genomics into the taxonomy and systematics of the Bacteria and Archaea. <b>2014</b> , 64, 316-324	327
1968	Microbial genome-enabled insights into plant-microorganism interactions. <b>2014</b> , 15, 797-813	135
1967	Endospore-enriched sequencing approach reveals unprecedented diversity of Firmicutes in sediments. <b>2014</b> , 6, 631-9	34

1966	Capturing and cultivating single bacterial cells in gel microdroplets to obtain near-complete genomes. <b>2014</b> , 9, 608-21	28
1965	RefSeq microbial genomes database: new representation and annotation strategy. <b>2014</b> , 42, D553-9	327
1964	A germ theory for glacial systems?. <b>2014</b> , 1, 331-340	17
1963	Unveiling viral-host interactions within the 'microbial dark matter'. <b>2014</b> , 5, 4542	49
1962	Insights into secondary metabolism from a global analysis of prokaryotic biosynthetic gene clusters. <b>2014</b> , 158, 412-421	587
1961	Recent advances in genomic DNA sequencing of microbial species from single cells. <b>2014</b> , 15, 577-84	118
1960	Biosynthesis: bioinformatics bolster a renaissance. <b>2014</b> , 10, 798-800	8
1959	Diverse sulfate-reducing bacteria of the Desulfosarcina/Desulfococcus clade are the key alkane degraders at marine seeps. <b>2014</b> , 8, 2029-44	134
1958	A hidden pitfall in the preparation of agar media undermines microorganism cultivability. <b>2014</b> , 80, 7659-66	133
1957	Mutational analysis of the (p)ppGpp synthetase activity of the Rel enzyme of Mycobacterium tuberculosis. <b>2014</b> , 196, 575-88	14
1956	Niche specialization of novel Thaumarchaeota to oxic and hypoxic acidic geothermal springs of Yellowstone National Park. <b>2014</b> , 8, 938-51	62
1955	Controlling factors of temporal variation of soil respiration in a natural beech forest as revealed by natural incubation experiments. <b>2014</b> , 29, 789-799	4
1954	Metaproteomic analysis of a winter to spring succession in coastal northwest Atlantic Ocean microbial plankton. <b>2014</b> , 8, 1301-13	50
1953	Mapping the inner workings of the microbiome: genomic- and metagenomic-based study of metabolism and metabolic interactions in the human microbiome. <b>2014</b> , 20, 742-752	60
1952	Single-cell genomics reveals potential for magnetite and greigite biomineralization in an uncultivated multicellular magnetotactic prokaryote. <b>2014</b> , 6, 524-31	25
1951	Distinct microbial communities thriving in gas hydrate-associated sediments from the eastern Japan Sea. <b>2014</b> , 90, 243-249	19
1950	Seasonal fluctuations in ionic concentrations drive microbial succession in a hypersaline lake community. <b>2014</b> , 8, 979-90	58
1949	MetaRef: a pan-genomic database for comparative and community microbial genomics. <b>2014</b> , 42, D617-24	46



1948	Nitrososphaera viennensis gen. nov., sp. nov., an aerobic and mesophilic, ammonia-oxidizing archaeon from soil and a member of the archaeal phylum Thaumarchaeota. <b>2014</b> , 64, 2738-2752	174
1947	Deciphering diversity and ecological function from marine metagenomes. <b>2014</b> , 227, 107-16	6
1946	Opportunities and challenges in deriving phytoplankton diversity measures from individual trait-based data obtained by scanning flow-cytometry. <b>2014</b> , 5, 324	14
1945	Localized electron transfer rates and microelectrode-based enrichment of microbial communities within a phototrophic microbial mat. <b>2014</b> , 5, 11	25
1944	Policy: An intergovernmental panel on antimicrobial resistance. <i>Nature</i> , <b>2014</b> , 509, 555-7	50.4 101
1943	PATTERNS OF UNCULTURED BACTERIA PHYLA IN DIFFERENT WASTEWATER TREATMENT SLUDGES. <b>2014</b> , 70, 42-52	1
1942	Metagenomic analysis of microbial consortium from natural crude oil that seeps into the marine ecosystem offshore Southern California. <b>2014</b> , 9, 1259-74	28
1941	Archaeal ancestors of eukaryotes: not so elusive any more. <b>2015</b> , 13, 84	50
1940	Assessing Chemical Diversity through Metagenomics. <b>2015</b> , 3-22	
1939	- Hydrosphere as Microbial Habitat. <b>2015</b> , 112-143	
1938	Earth as a Microbial Habitat. <b>2015</b> , 22-33	1
1937	Metagenomic insights into strategies of aerobic and anaerobic carbon and nitrogen transformation in boreal lakes. <b>2015</b> , 5, 12102	25
1936	Introduction: Mesocosms and Microcosms. <b>2015</b> , 1-13	2
1935	Anaerobic Cultivation. <b>2015</b> , 2.1.2-1-2.1.2-12	1
1934	Heterotrophic Planktonic Microbes: Virus, Bacteria, Archaea, and Protozoa. <b>2015</b> , 4.2.2-1-4.2.2-34	3
1933	Life in High-Temperature Environments. <b>2015</b> , 4.3.4-1-4.3.4-15	3
1932	Environmental Systems Microbiology of Contaminated Environments. <b>2015</b> , 5.1.6-1-5.1.6-10	1
1931	Back to Basics--The Influence of DNA Extraction and Primer Choice on Phylogenetic Analysis of Activated Sludge Communities. <b>2015</b> , 10, e0132783	294

1930	An assessment of the amount of untapped fold level novelty in under-sampled areas of the tree of life. <b>2015</b> , 5, 14717	3
1929	An Aquatic Microbial Metaproteomics Workflow: From Cells to Tryptic Peptides Suitable for Tandem Mass Spectrometry-based Analysis. <b>2015</b> ,	2
1928	Large-scale contamination of microbial isolate genomes by Illumina PhiX control. <b>2015</b> , 10, 18	85
1927	Highly divergent ancient gene families in metagenomic samples are compatible with additional divisions of life. <b>2015</b> , 10, 64	12
1926	Advancing understanding of microbial bioenergy conversion processes by activity-based protein profiling. <b>2015</b> , 8, 156	17
1925	Dominant ectosymbiotic bacteria of cellulolytic protists in the termite gut also have the potential to digest lignocellulose. <b>2015</b> , 17, 4942-53	37
1924	The Sanford Underground Research Facility at Homestake. <b>2015</b> , 606, 012015	26
1923	Metaproteomics of aquatic microbial communities in a deep and stratified estuary. <b>2015</b> , 15, 3566-79	21
1922	Shedding light on microbial dark matter: a TM6 bacterium as natural endosymbiont of a free-living amoeba. <b>2015</b> , 7, 970-8	29
1921	Oligoflexia, the Newest Class of the Phylum Proteobacteria, Consisting of only One Cultured Species and Uncultured Bacterial Phylotypes from Diverse Habitats. <b>2015</b> , 03,	
1920	Non-Standard Genetic Codes Define New Concepts for Protein Engineering. <b>2015</b> , 5, 1610-28	22
1919	Single-Cell Genome Sequencing for Viral-Host Interactions. <b>2015</b> , 8,	1
1918	Microbiological Confinement of Two Adjacent Water Wells in Lake Karla Basin, Greece. <b>2015</b> , 7, 5272-5283	
1917	Long-Read, Single Molecule, Real-Time (SMRT) DNA Sequencing for Metagenomic Applications. <b>2015</b> , 25-38	1
1916	Wiretapping into microbial interactions by single cell genomics. <b>2015</b> , 6, 258	14
1915	Combining genomic sequencing methods to explore viral diversity and reveal potential virus-host interactions. <b>2015</b> , 6, 265	47
1914	Synergistic function of four novel thermostable glycoside hydrolases from a long-term enriched thermophilic methanogenic digester. <b>2015</b> , 6, 509	16
1913	The reduced genomes of Parcubacteria (OD1) contain signatures of a symbiotic lifestyle. <b>2015</b> , 6, 713	176

1912	The universal tree of life: an update. <b>2015</b> , 6, 717	89
1911	Toward the identification of methanogenic archaeal groups as targets of methane mitigation in livestock animals. <b>2015</b> , 6, 776	17
1910	Rational and combinatorial tailoring of bioactive cyclic dipeptides. <b>2015</b> , 6, 785	44
1909	Abundant Atribacteria in deep marine sediment from the Adlle Basin, Antarctica. <b>2015</b> , 6, 872	52
1908	Nitrate and ammonia as nitrogen sources for deep subsurface microorganisms. <b>2015</b> , 6, 1079	31
1907	Taxonomic and functional characteristics of microbial communities and their correlation with physicochemical properties of four geothermal springs in Odisha, India. <b>2015</b> , 6, 1166	45
1906	Metagenome and Metatranscriptome Revealed a Highly Active and Intensive Sulfur Cycle in an Oil-Immersed Hydrothermal Chimney in Guaymas Basin. <b>2015</b> , 6, 1236	13
1905	Comparative Genomic Insights into Ecophysiology of Neutrophilic, Microaerophilic Iron Oxidizing Bacteria. <b>2015</b> , 6, 1265	61
1904	Metagenome-Based Metabolic Reconstruction Reveals the Ecophysiological Function of Epsilonproteobacteria in a Hydrocarbon-Contaminated Sulfidic Aquifer. <b>2015</b> , 6, 1396	24
1903	PCR-activated cell sorting for cultivation-free enrichment and sequencing of rare microbes. <b>2015</b> , 10, e0113549	38
1902	The unique chemistry of Eastern Mediterranean water masses selects for distinct microbial communities by depth. <b>2015</b> , 10, e0120605	40
1901	In Silico Analysis of the Metabolic Potential and Niche Specialization of Candidate Phylum "Latescibacteria" (WS3). <b>2015</b> , 10, e0127499	69
1900	Current overview on the study of bacteria in the rhizosphere by modern molecular techniques: a mini-review. <b>2015</b> , 0-0	13
1899	Viral dark matter and virus-host interactions resolved from publicly available microbial genomes. <b>2015</b> , 4,	274
1898	Paper Essentials. <b>2015</b> , 105-140	
1897	Bioinformation and Omic Approaches for Characterization of Environmental Microorganisms. <b>2015</b> , 483-505	1
1896	Advances and applications of single-cell sequencing technologies. <b>2015</b> , 58, 598-609	341
1895	Marine biology. Uncovering hidden worlds of ocean biodiversity. <b>2015</b> , 348, 865-7	21

1894	Predominance of archaea-derived hydrocarbons in an Early Triassic microbialite. <b>2015</b> , 85, 66-75	14
1893	Dispersing misconceptions and identifying opportunities for the use of 'omics' in soil microbial ecology. <b>2015</b> , 13, 439-46	168
1892	Rooting the domain archaea by phylogenomic analysis supports the foundation of the new kingdom Proteoarchaeota. <b>2014</b> , 7, 191-204	92
1891	Classification and identification of pigmented cocci bacteria relevant to the soil environment via Raman spectroscopy. <b>2015</b> , 22, 19317-25	20
1890	Metagenomics as a tool for the investigation of uncultured microorganisms. <b>2015</b> , 51, 431-439	16
1889	Archaeal Clusters of Orthologous Genes (arCOGs): An Update and Application for Analysis of Shared Features between Thermococcales, Methanococcales, and Methanobacteriales. <b>2015</b> , 5, 818-40	125
1888	Insights into the life of an oxygenic phototroph. <b>2015</b> , 112, 14747-8	1
1887	Complete Genome Sequence of the Bacterium Aalborg_AAW-1, Representing a Novel Family within the Candidate Phylum SR1. <b>2015</b> , 3,	5
1886	. <b>2015</b> ,	3
1885	Captured metagenomics: large-scale targeting of genes based on 'sequence capture' reveals functional diversity in soils. <b>2015</b> , 22, 451-60	19
1884	Genomic and transcriptomic evidence for scavenging of diverse organic compounds by widespread deep-sea archaea. <b>2015</b> , 6, 8933	98
1883	4. Starving Artists: Bacterial Oligotrophic Heterotrophy in Caves.	8
1882	CVTree3 Web Server for Whole-genome-based and Alignment-free Prokaryotic Phylogeny and Taxonomy. <b>2015</b> , 13, 321-31	124
1881	Computational Tools for Taxonomic Microbiome Profiling of Shotgun Metagenomes. <b>2015</b> , 67-80	1
1880	Antibiotics: An irresistible newcomer. <i>Nature</i> , <b>2015</b> , 517, 442-4	50.4 45
1879	The rebirth of culture in microbiology through the example of culturomics to study human gut microbiota. <b>2015</b> , 28, 237-64	490
1878	Current and past strategies for bacterial culture in clinical microbiology. <b>2015</b> , 28, 208-36	239
1877	The Bacteria and Archaea. <b>2015</b> , 41-76	6

1876	Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. <b>2015</b> , 25, 534-43	96
1875	Temporal patterns of rarity provide a more complete view of microbial diversity. <b>2015</b> , 23, 335-40	78
1874	A putative greigite-type magnetosome gene cluster from the candidate phylum Latescibacteria. <b>2015</b> , 7, 237-42	45
1873	High-throughput metagenomic technologies for complex microbial community analysis: open and closed formats. <b>2015</b> , 6,	265
1872	The effects of variable sample biomass on comparative metagenomics. <b>2015</b> , 17, 2239-53	19
1871	Single cell biotechnology to shed a light on biological 'dark matter' in nature. <b>2015</b> , 8, 15-6	19
1870	Extending the conserved phylogenetic core of archaea disentangles the evolution of the third domain of life. <b>2015</b> , 32, 1242-54	44
1869	Microbial dark matter ecogenomics reveals complex synergistic networks in a methanogenic bioreactor. <b>2015</b> , 9, 1710-22	232
1868	Phylogeny of genetic codes and punctuation codes within genetic codes. <b>2015</b> , 129, 36-43	37
1867	Normalization of environmental metagenomic DNA enhances the discovery of under-represented microbial community members. <b>2015</b> , 60, 359-66	6
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1660	Label-free isolation and deposition of single bacterial cells from heterogeneous samples for clonal culturing. <b>2016</b> , 6, 32837	14
1659	Draft genome sequence of strain Hudgins isolated from human skin implicates metabolic versatility and several virulence determinants. <b>2016</b> , 10, 91-96	1
1658	The landscape of microbial phenotypic traits and associated genes. <b>2016</b> , 44, 10074-10090	51
1657	Methanogenesis: Ecology. <b>2016</b> , 1-9	
1656	Metabolic traits of an uncultured archaeal lineage--MSBL1--from brine pools of the Red Sea. <b>2016</b> , 6, 19181	51
1655	LCA*: an entropy-based measure for taxonomic assignment within assembled metagenomes. <b>2016</b> , 32, 3535-3542	11
1654	Genome sequence and overview of Shr3 in the eighth class of the phylum. <b>2016</b> , 11, 90	6
1653	Gastroenvironmental distress: metaphorical antecedents of the gut microbiome. <b>2016</b> , 42, 121-7	3
1652	Applying theories of microbial metabolism for induction of targeted enzyme activity in a methanogenic microbial community at a metabolic steady state. <b>2016</b> , 100, 7989-8002	8
1651	Comparison of archaeal and bacterial communities in two sponge species and seawater from an Indonesian coral reef environment. <b>2016</b> , 29, 69-80	15
1650	Status of the Archaeal and Bacterial Census: an Update. <b>2016</b> , 7,	97
1649	Sensitivity and correlation of hypervariable regions in 16S rRNA genes in phylogenetic analysis. <b>2016</b> , 17, 135	246
1648	Taxonomer: an interactive metagenomics analysis portal for universal pathogen detection and host mRNA expression profiling. <b>2016</b> , 17, 111	113
1647	Culture-Independent Diagnostics for Health Security. <b>2016</b> , 14, 122-42	24
1646	Archaeal communities of Arctic methane-containing permafrost. <b>2016</b> , 92,	28
1645	Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. <b>2016</b> , 10, 1589-601	146
1644	Sporulation, bacterial cell envelopes and the origin of life. <b>2016</b> , 14, 535-542	52
1643	Prokaryotic diversity in biodeteriorated wood coming from the BłkBrzy fossil forest. <b>2016</b> , 108, 181-190	6

1642	The bright side of microbial dark matter: lessons learned from the uncultivated majority. <b>2016</b> , 31, 217-226	142
1641	Genome Evolution and Nitrogen Fixation in Bacterial Ectosymbionts of a Protist Inhabiting Wood-Feeding Cockroaches. <b>2016</b> , 82, 4682-4695	30
1640	Novel function discovery through sequence and structural data mining. <b>2016</b> , 38, 53-61	22
1639	Metagenomic analysis of a high carbon dioxide subsurface microbial community populated by chemolithoautotrophs and bacteria and archaea from candidate phyla. <b>2016</b> , 18, 1686-703	59
1638	Examining the diversity of microbes in a deep-sea coral community impacted by the Deepwater Horizon oil spill. <b>2016</b> , 129, 157-166	18
1637	Single-cell genome sequencing: current state of the science. <b>2016</b> , 17, 175-88	795
1636	Single-Cell Genomics and Epigenomics. <b>2016</b> , 257-301	2
1635	Genomic reconstruction of a novel, deeply branched sediment archaeal phylum with pathways for acetogenesis and sulfur reduction. <b>2016</b> , 10, 1696-705	128
1634	Essentials of Single-Cell Analysis. <b>2016</b> ,	23
1633	Computational approaches to predict bacteriophage-host relationships. <b>2016</b> , 40, 258-72	235
1632	Synthetic long-read sequencing reveals intraspecies diversity in the human microbiome. <b>2016</b> , 34, 64-9	75
1631	Single-Cell-Genomics-Facilitated Read Binning of Candidate Phylum EM19 Genomes from Geothermal Spring Metagenomes. <b>2016</b> , 82, 992-1003	16
1630	Genome-Based Microbial Taxonomy Coming of Age. <b>2016</b> , 8,	50
1629	Consortia of low-abundance bacteria drive sulfate reduction-dependent degradation of fermentation products in peat soil microcosms. <b>2016</b> , 10, 2365-75	87
1628	Codon reassignment to facilitate genetic engineering and biocontainment in the chloroplast of <i>Chlamydomonas reinhardtii</i> . <b>2016</b> , 14, 1251-60	30
1627	Critical biogeochemical functions in the subsurface are associated with bacteria from new phyla and little studied lineages. <b>2016</b> , 18, 159-73	111
1626	Metagenomic investigation of the geologically unique Hellenic Volcanic Arc reveals a distinctive ecosystem with unexpected physiology. <b>2016</b> , 18, 1122-36	24
1625	Future Perspectives and Challenges of Fungal Systematics in the Age of Big Data. <b>2016</b> , 25-46	9

1624	Novel microbial assemblages inhabiting crustal fluids within mid-ocean ridge flank subsurface basalt. <b>2016</b> , 10, 2033-47	40
1623	High-resolution phylogenetic microbial community profiling. <b>2016</b> , 10, 2020-32	161
1622	Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. <b>2016</b> , 7, 10613	129
1621	Microbial diversity in European alpine permafrost and active layers. <b>2016</b> , 92,	139
1620	Archaeal community in a human-disturbed watershed in southeast China: diversity, distribution, and responses to environmental changes. <b>2016</b> , 100, 4685-98	19
1619	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <b>2016</b> , 7, 10476	90
1618	A comprehensive benchmarking study of protocols and sequencing platforms for 16S rRNA community profiling. <b>2016</b> , 17, 55	237
1617	Advanced tools in marine natural drug discovery. <b>2016</b> , 42, 13-23	33
1616	Archaeal Distribution in Moonmilk Deposits from Alpine Caves and Their Ecophysiological Potential. <b>2016</b> , 71, 686-99	15
1615	Comparative Genomics of Candidate Phylum TM6 Suggests That Parasitism Is Widespread and Ancestral in This Lineage. <b>2016</b> , 33, 915-27	50
1614	Polytheonamide biosynthesis showcasing the metabolic potential of sponge-associated uncultivated 'Entotheonella' bacteria. <b>2016</b> , 31, 8-14	40
1613	Subglacial Lake Whillans microbial biogeochemistry: a synthesis of current knowledge. <b>2016</b> , 374,	43
1612	Early Microbial Evolution: The Age of Anaerobes. <b>2015</b> , 8, a018127	57
1611	Prokaryotic Community Structure Driven by Salinity and Ionic Concentrations in Plateau Lakes of the Tibetan Plateau. <b>2016</b> , 82, 1846-1858	50
1610	Genome Reconstruction from Metagenomic Data Sets Reveals Novel Microbes in the Brackish Waters of the Caspian Sea. <b>2016</b> , 82, 1599-1612	29
1609	Genomic and metagenomic surveys of hydrogenase distribution indicate H <sub>2</sub> is a widely utilised energy source for microbial growth and survival. <b>2016</b> , 10, 761-77	319
1608	Tritagonist as a new term for uncharacterised microorganisms in environmental systems. <b>2016</b> , 10, 1-3	99
1607	Identification and Resolution of Microdiversity through Metagenomic Sequencing of Parallel Consortia. <b>2016</b> , 82, 255-67	34

1606	Predicting microbial traits with phylogenies. <b>2016</b> , 10, 959-67	88
1605	Acoelomorpha: earliest branching bilaterians or deuterostomes?. <b>2016</b> , 16, 391-399	15
1604	ProDeGe: a computational protocol for fully automated decontamination of genomes. <b>2016</b> , 10, 269-72	48
1603	Ecophysiology of an uncultivated lineage of Aigarchaeota from an oxic, hot spring filamentous 'streamer' community. <b>2016</b> , 10, 210-24	33
1602	Single-cell genomics of uncultivated deep-branching magnetotactic bacteria reveals a conserved set of magnetosome genes. <b>2016</b> , 18, 21-37	69
1601	Insights in the ecology and evolutionary history of the Miscellaneous Crenarchaeotic Group lineage. <b>2016</b> , 10, 665-77	70
1600	Experimental insights into the importance of aquatic bacterial community composition to the degradation of dissolved organic matter. <b>2016</b> , 10, 533-45	197
1599	Refining the phylum Chlorobi by resolving the phylogeny and metabolic potential of the representative of a deeply branching, uncultivated lineage. <b>2016</b> , 10, 833-45	38
1598	Phylogeny and physiology of candidate phylum 'Atribacteria' (OP9/JS1) inferred from cultivation-independent genomics. <b>2016</b> , 10, 273-86	118
1597	Competitive strategies differentiate closely related species of marine actinobacteria. <b>2016</b> , 10, 478-90	36
1596	Next-generation sequencing (NGS) in the microbiological world: How to make the most of your money. <b>2017</b> , 138, 60-71	78
1595	Regulation of infection efficiency in a globally abundant marine Bacteriodes virus. <b>2017</b> , 11, 284-295	33
1594	Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO concentrations. <b>2017</b> , 19, 459-474	116
1593	Endophytic bacteria in Miscanthus seed: implications for germination, vertical inheritance of endophytes, plant evolution and breeding. <b>2017</b> , 9, 57-77	64
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1591	Development of a facile droplet-based single-cell isolation platform for cultivation and genomic analysis in microorganisms. <b>2017</b> , 7, 41192	51
1590	Cheating fosters species co-existence in well-mixed bacterial communities. <b>2017</b> , 11, 1179-1188	42
1589	Ecology of the Oral Microbiome: Beyond Bacteria. <b>2017</b> , 25, 362-374	123

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1587	The gut microbiome in human neurological disease: A review. <b>2017</b> , 81, 369-382	283
1586	High-resolution sequencing reveals unexplored archaeal diversity in freshwater wetland soils. <b>2017</b> , 19, 2192-2209	34
1585	New Allometric Scaling Laws Revealed for Microorganisms. <b>2017</b> , 32, 400-402	3
1584	Tropical Meromictic Lakes: Specifics of Meromixis and Case Studies of Lakes Tanganyika, Malawi, and Matano. <b>2017</b> , 277-323	6
1583	Symbiosis in eukaryotic evolution. <b>2017</b> , 434, 20-33	85
1582	Genetic technologies for extremely thermophilic microorganisms of Sulfolobus, the only genetically tractable genus of crenarchaea. <b>2017</b> , 60, 370-385	39
1581	SAG-QC: quality control of single amplified genome information by subtracting non-target sequences based on sequence compositions. <b>2017</b> , 18, 152	4
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1579	Validation of Metagenomic Next-Generation Sequencing Tests for Universal Pathogen Detection. <b>2017</b> , 141, 776-786	204
1578	Unveiling microbial interactions in stratified mat communities from a warm saline shallow pond. <b>2017</b> , 19, 2405-2421	22
1577	Mechanisms of gene flow in archaea. <b>2017</b> , 15, 492-501	52
1576	Empirical genome evolution models root the tree of life. <b>2017</b> , 138, 137-155	18
1575	Metagenomic technologies of detecting genetic resources of microorganisms. <b>2017</b> , 87, 115-119	1
1574	Tracking microbial colonization in fecal microbiota transplantation experiments via genome-resolved metagenomics. <b>2017</b> , 5, 50	51
1573	Emulating Host-Microbiome Ecosystem of Human Gastrointestinal Tract in Vitro. <b>2017</b> , 13, 321-334	46
1572	Activity-based protein profiling as a robust method for enzyme identification and screening in extremophilic Archaea. <b>2017</b> , 8, 15352	27
1571	Akaryotes and Eukaryotes are independent descendants of a universal common ancestor. <b>2017</b> , 138, 168-183	17

1570	Binning_refiner: improving genome bins through the combination of different binning programs. <b>2017</b> , 33, 1873-1875	36
1569	The metabolic potential of the single cell genomes obtained from the Challenger Deep, Mariana Trench within the candidate superphylum Parcubacteria (OD1). <b>2017</b> , 19, 2769-2784	50
1568	Finding Genes in Genome Sequence. <b>2017</b> , 1525, 271-291	1
1567	Shotgun Metagenomic Sequencing Analysis of Soft-Rot Enterobacteriaceae in Polymicrobial Communities. <b>2017</b> , 1539, 85-97	2
1566	Variability in Metagenomic Count Data and Its Influence on the Identification of Differentially Abundant Genes. <b>2017</b> , 24, 311-326	14
1565	Analyses of 16S rRNA and cpn60 gene sequences provide complementary information about potentially useful and harmful oil field microbiota. <b>2017</b> , 123, 320-327	5
1564	Comparative genomics of the DNA damage-inducible network in the Patescibacteria. <b>2017</b> , 19, 3465-3474	26
1563	Unusual respiratory capacity and nitrogen metabolism in a Parcubacterium (OD1) of the Candidate Phyla Radiation. <b>2017</b> , 7, 40101	56
1562	Bioprospecting challenges in unusual environments. <b>2017</b> , 10, 671-673	8
1561	Establishment of thermophilic anaerobic terephthalic acid degradation system through one-step temperature increase startup strategy - Revealed by Illumina Miseq Sequencing. <b>2017</b> , 184, 951-959	13
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1559	Energy and carbon metabolisms in a deep terrestrial subsurface fluid microbial community. <b>2017</b> , 11, 2319-2333	59
1558	Unexpected genomic features in widespread intracellular bacteria: evidence for motility of marine chlamydiae. <b>2017</b> , 11, 2334-2344	16
1557	Novel approaches in function-driven single-cell genomics. <b>2017</b> , 41, 538-548	17
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1555	Integrative modeling of gene and genome evolution roots the archaeal tree of life. <b>2017</b> , 114, E4602-E4611	140
1554	RNA-Dependent Cysteine Biosynthesis in Bacteria and Archaea. <b>2017</b> , 8,	16
1553	Kisameet Glacial Clay: an Unexpected Source of Bacterial Diversity. <b>2017</b> , 8,	14

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1551	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <b>2017</b> , 35, 676-683	161
1550	Retroelement-guided protein diversification abounds in vast lineages of Bacteria and Archaea. <b>2017</b> , 2, 17045	42
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1545	Microbial Ecology of Extreme Environments. <b>2017</b> ,	3
1544	Ecogenomics of Deep-Ocean Microbial Bathotypes. <b>2017</b> , 7-50	6
1543	New Insights into the Microbial Diversity of Polar Desert Soils: A Biotechnological Perspective. <b>2017</b> , 169-183	6
1542	Streamlining the Design-to-Build Transition with Build-Optimization Software Tools. <b>2017</b> , 6, 485-496	32
1541	New CRISPR-Cas systems from uncultivated microbes. <i>Nature</i> , <b>2017</b> , 542, 237-241	50.4 320
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1539	Gaia and her microbiome. <b>2017</b> , 93,	19
1538	pH-gradient ion-exchange microbial cell chromatography as a simple method for microbial separation. <b>2017</b> , 123, 431-436	6
1537	Bioprospecting. <b>2017</b> ,	3
1536	Metagenomic assembly unravel microbial response to redox fluctuation in acid sulfate soil. <b>2017</b> , 105, 244-252	13
1535	Strategies to improve reference databases for soil microbiomes. <b>2017</b> , 11, 829-834	57

1534	A report on extensive lateral genetic reciprocation between arsenic resistant <i>Bacillus subtilis</i> and <i>Bacillus pumilus</i> strains analyzed using RAPD-PCR. <b>2017</b> , 107, 443-454	4
1533	Bioprospecting Archaea: Focus on Extreme Halophiles. <b>2017</b> , 81-112	7
1532	Finding life's missing pieces. <b>2017</b> , 2, 1458-1459	
1531	The trajectory of microbial single-cell sequencing. <b>2017</b> , 14, 1045-1054	77
1530	Stepwise impact of urban wastewater treatment on the bacterial community structure, antibiotic contents, and prevalence of antimicrobial resistance. <b>2017</b> , 231, 1578-1585	37
1529	Meta-analysis of Liver and Heart Transcriptomic Data for Functional Annotation Transfer in Mammalian Orthologs. <b>2017</b> , 15, 425-432	3
1528	Functional Metagenomics: Tools and Applications. <b>2017</b> ,	6
1527	The Possible Emergence of Life and Differentiation of a Shallow Biosphere on Irradiated Icy Worlds: The Example of Europa. <b>2017</b> , 17, 1265-1273	42
1526	Metabolic Roles of Uncultivated Bacterioplankton Lineages in the Northern Gulf of Mexico "Dead Zone". <b>2017</b> , 8,	46
1525	Individual Patterns of Complexity in Cystic Fibrosis Lung Microbiota, Including Predator Bacteria, over a 1-Year Period. <b>2017</b> , 8,	25
1524	Bioinformatics for Microbiome Research: Concepts, Strategies, and Advances. <b>2017</b> , 111-123	2
1523	An Expedition to the Mechanism of Plant-Microbe Interaction by Utilization of Different Molecular Biology Tools. <b>2017</b> , 431-446	
1522	Challenges and Opportunities in Discovery of Secondary Metabolites Using a Functional Metagenomic Approach. <b>2017</b> , 119-138	3
1521	Enhancing Functional Metagenomics of Complex Microbial Communities Using Stable Isotopes. <b>2017</b> , 139-150	1
1520	Genomic variation in microbial populations inhabiting the marine subseafloor at deep-sea hydrothermal vents. <b>2017</b> , 8, 1114	34
1519	Many More Microbes in Humans: Enlarging the Microbiome Repertoire. <b>2017</b> , 65, S20-S29	17
1518	Stress and stability: applying the Anna Karenina principle to animal microbiomes. <b>2017</b> , 2, 17121	326
1517	Bacterial diversity of the outflows of a Polichnitos (Lesvos, Greece) hot spring, laboratory studies of a <i>Cyanobacterium</i> sp. strain and potential medical applications. <b>2017</b> , 67, 643-654	6



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1515	Hiding in Plain Sight: Mining Bacterial Species Records for Phenotypic Trait Information. <b>2017</b> , 2,	43
1514	Novel arsenic-transforming bacteria and the diversity of their arsenic-related genes and enzymes arising from arsenic-polluted freshwater sediment. <b>2017</b> , 7, 11231	68
1513	Evaluation of single-cell genomics to address evolutionary questions using three SAGs of the choanoflagellate <i>Monosiga brevicollis</i> . <b>2017</b> , 7, 11025	16
1512	Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. <b>2017</b> , 2, 1533-1542	764
1511	Shotgun metagenomics, from sampling to analysis. <b>2017</b> , 35, 833-844	643
1510	Actinobacterial Rare Biospheres and Dark Matter Revealed in Habitats of the Chilean Atacama Desert. <b>2017</b> , 7, 8373	41
1509	The Brazilian Microbiome. <b>2017</b> ,	0
1508	Database and Bioinformatics Studies of Probiotics. <b>2017</b> , 65, 7599-7606	10
1507	Unusual metabolic diversity of hyperalkaliphilic microbial communities associated with subterranean serpentinization at The Cedars. <b>2017</b> , 11, 2584-2598	35
1506	Marine archaeal dynamics and interactions with the microbial community over 5 years from surface to seafloor. <b>2017</b> , 11, 2510-2525	28
1505	Present and Future of Culturing Bacteria. <b>2017</b> , 71, 711-730	113
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1503	Modules for metabolic engineering: Pathway assembly for bio-based production of value-added chemicals. <b>2017</b> , 2, 65-74	27
1502	Soil bacteria and archaea change rapidly in the first century of Fennoscandian boreal forest development. <b>2017</b> , 114, 160-167	17
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1500	Dynamics of archaea at fine spatial scales in Shark Bay mat microbiomes. <b>2017</b> , 7, 46160	46
1499	Improved genome recovery and integrated cell-size analyses of individual uncultured microbial cells and viral particles. <b>2017</b> , 8, 84	91

1498	Prokaryotic diversity and community composition in the Salar de Uyuni, a large scale, chaotropic salt flat. <b>2017</b> , 19, 3745-3754	33
1497	Metabolic potential and in situ activity of marine Marinimicrobia bacteria in an anoxic water column. <b>2017</b> , 19, 4392-4416	26
1496	Grape pomace compost harbors organohalide-respiring Dehalogenimonas species with novel reductive dehalogenase genes. <b>2017</b> , 11, 2767-2780	65
1495	Methane-metabolizing microbial communities in sediments of the Haima cold seep area, northwest slope of the South China Sea. <b>2017</b> , 93,	20
1494	Genomic exploration of the diversity, ecology, and evolution of the archaeal domain of life. <b>2017</b> , 357,	166
1493	The growing tree of Archaea: new perspectives on their diversity, evolution and ecology. <b>2017</b> , 11, 2407-2425	210
1492	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <b>2017</b> , 35, 725-731	648
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1487	Increased Biosynthetic Gene Dosage in a Genome-Reduced Defensive Bacterial Symbiont. <b>2017</b> , 2,	28
1486	First Insights into the Diverse Human Archaeome: Specific Detection of Archaea in the Gastrointestinal Tract, Lung, and Nose and on Skin. <b>2017</b> , 8,	108
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1484	Geochemical and Microbial Community Attributes in Relation to Hyporheic Zone Geological Facies. <b>2017</b> , 7, 12006	19
1483	Diverse Marinimicrobia bacteria may mediate coupled biogeochemical cycles along eco-thermodynamic gradients. <b>2017</b> , 8, 1507	56
1482	Ammonia-oxidising archaea living at low pH: Insights from comparative genomics. <b>2017</b> , 19, 4939-4952	57
1481	The First Microbial Colonizers of the Human Gut: Composition, Activities, and Health Implications of the Infant Gut Microbiota. <b>2017</b> , 81,	626

1480	Spatial Distribution Characteristics of Microorganisms in Constructed Wetland System with New Matrix and Its Effect on Sewage Purification. <b>2017</b> , 34, 828-834	1
1479	Raman-Activated Droplet Sorting (RADS) for Label-Free High-Throughput Screening of Microalgal Single-Cells. <b>2017</b> , 89, 12569-12577	76
1478	The development of permafrost bacterial communities under submarine conditions. <b>2017</b> , 122, 1689-1704	13
1477	Accessing the genomic information of unculturable oceanic picoeukaryotes by combining multiple single cells. <b>2017</b> , 7, 41498	39
1476	25 years of serving the community with ribosomal RNA gene reference databases and tools. <b>2017</b> , 261, 169-176	294
1475	Massively parallel whole genome amplification for single-cell sequencing using droplet microfluidics. <b>2017</b> , 7, 5199	69
1474	'ARMAN' archaea depend on association with euryarchaeal host in culture and in situ. <b>2017</b> , 8, 60	56
1473	Unexplored diversity and strain-level structure of the skin microbiome associated with psoriasis. <b>2017</b> , 3, 14	96
1472	ICoVeR - an interactive visualization tool for verification and refinement of metagenomic bins. <b>2017</b> , 18, 233	15
1471	Evolutionary Origins of Two-Barrel RNA Polymerases and Site-Specific Transcription Initiation. <b>2017</b> , 71, 331-348	20
1470	Impact of 6:2 fluorotelomer alcohol aerobic biotransformation on a sediment microbial community. <b>2017</b> , 575, 1361-1368	34
1469	Genomes OnLine Database (GOLD) v.6: data updates and feature enhancements. <b>2017</b> , 45, D446-D456	128
1468	Gifted microbes for genome mining and natural product discovery. <b>2017</b> , 44, 573-588	137
1467	Influence of Process Parameters on Anaerobic Digestion Microbiome in Bioenergy Production: Towards an Improved Understanding. <b>2017</b> , 10, 288-303	22
1466	Diversity and temporal patterns of planktonic protist assemblages at a Mediterranean Long Term Ecological Research site. <b>2017</b> , 93,	78
1465	Quest for Ancestors of Eukaryal Cells Based on Phylogenetic Analyses of Aminoacyl-tRNA Synthetases. <b>2017</b> , 84, 51-66	16
1464	Improvement of phytoplankton culture isolation using single cell sorting by flow cytometry. <b>2017</b> , 53, 271-282	15
1463	All together now: experimental multispecies biofilm model systems. <b>2017</b> , 19, 42-53	55

1462	Bacterial Communities Predominant in the Degradation of <sup>13</sup> C-Labeled Pyrene in Red Soil. <b>2017</b> , 26, 709-721	3
1461	Microbial Biodiversity: Straight from the Dolphin's Mouth. <b>2017</b> , 27, R1307-R1309	
1460	Visualization of Microorganisms in Bioprocesses. <b>2017</b> , 13-26	1
1459	Organismal and spatial partitioning of energy and macronutrient transformations within a hypersaline mat. <b>2017</b> , 93,	14
1458	9. Assessing metabolic activity at methane seeps: a testing ground for slow growing environmental systems. <b>2017</b> ,	
1457	Decontaminating eukaryotic genome assemblies with machine learning. <b>2017</b> , 18, 533	12
1456	Towards a balanced view of the bacterial tree of life. <b>2017</b> , 5, 140	44
1455	Introductory Chapter: A Brief Overview of Archaeal Applications. <b>2017</b> ,	1
1454	Characterization of Reconstructed Ancestral Proteins Suggests a Change in Temperature of the Ancient Biosphere. <b>2017</b> , 7,	16
1453	Mare Incognitum: A Glimpse into Future Plankton Diversity and Ecology Research. <b>2017</b> , 4,	4
1452	Geological and Geochemical Controls on Subsurface Microbial Life in the Samail Ophiolite, Oman. <b>2017</b> , 8, 56	61
1451	Mineralizing Filamentous Bacteria from the Prony Bay Hydrothermal Field Give New Insights into the Functioning of Serpentinization-Based Subseafloor Ecosystems. <b>2017</b> , 8, 57	21
1450	Genomic Analysis of , the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum. <b>2017</b> , 8, 195	30
1449	Molecular Taxonomic Profiling of Bacterial Communities in a Gilthead Seabream ( ) Hatchery. <b>2017</b> , 8, 204	29
1448	Untangling Genomes of Novel and Species from Monterey Bay Kelp Forest Metagenomes by Refined Binning. <b>2017</b> , 8, 472	42
1447	Comparative Genomic Analysis of the Class and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). <b>2017</b> , 8, 682	188
1446	Diversity of Metabolically Active in Water-Flooded High-Temperature Heavy Oil Reservoir. <b>2017</b> , 8, 707	30
1445	Novel Large Sulfur Bacteria in the Metagenomes of Groundwater-Fed Chemosynthetic Microbial Mats in the Lake Huron Basin. <b>2017</b> , 8, 791	16

1444	Technological Microbiology: Development and Applications. <b>2017</b> , 8, 827	49
1443	A Small Number of Low-abundance Bacteria Dominate Plant Species-specific Responses during Rhizosphere Colonization. <b>2017</b> , 8, 975	53
1442	Influence of Igneous Basement on Deep Sediment Microbial Diversity on the Eastern Juan de Fuca Ridge Flank. <b>2017</b> , 8, 1434	17
1441	Bacterial, Archaeal, and Eukaryotic Diversity across Distinct Microhabitats in an Acid Mine Drainage. <b>2017</b> , 8, 1756	55
1440	Tools for Genomic and Transcriptomic Analysis of Microbes at Single-Cell Level. <b>2017</b> , 8, 1831	24
1439	Genomic Comparison of Two Family-Level Groups of the Uncultivated NAG1 Archaeal Lineage from Chemically and Geographically Disparate Hot Springs. <b>2017</b> , 8, 2082	4
1438	Rokubacteria: Genomic Giants among the Uncultured Bacterial Phyla. <b>2017</b> , 8, 2264	55
1437	Bacterial Succession on Sinking Particles in the Ocean's Interior. <b>2017</b> , 8, 2269	24
1436	Archaeal S-Layers: Overview and Current State of the Art. <b>2017</b> , 8, 2597	48
1435	PALADIN: protein alignment for functional profiling whole metagenome shotgun data. <b>2017</b> , 33, 1473-1478	16
1434	Archaeal Diversity and CO Fixers in Carbonate-/Siliciclastic-Rock Groundwater Ecosystems. <b>2017</b> , 2017, 2136287	21
1433	Spatiotemporal analysis of microbial community dynamics during seasonal stratification events in a freshwater lake (Grand Lake, OK, USA). <b>2017</b> , 12, e0177488	28
1432	Lokiarchaea are close relatives of Euryarchaeota, not bridging the gap between prokaryotes and eukaryotes. <b>2017</b> , 13, e1006810	101
1431	Comparing and Evaluating Metagenome Assembly Tools from a Microbiologist's Perspective - Not Only Size Matters!. <b>2017</b> , 12, e0169662	125
1430	Phylogenomics of Cas4 family nucleases. <b>2017</b> , 17, 232	36
1429	Legacy effects of continuous chloropicrin-fumigation for 3-years on soil microbial community composition and metabolic activity. <b>2017</b> , 7, 178	25
1428	Differences among Soil-Inhabiting Microbial Communities in Poa annua Turf throughout the Growing Season. <b>2017</b> , 57, S-262	11
1427	Organoids, organs-on-chips and other systems, and microbiota. <b>2017</b> , 1, 385-400	21

1426	Interpreting Microbial Biosynthesis in the Genomic Age: Biological and Practical Considerations. <b>2017</b> , 15,	21
1425	Analysis of single-cell genome sequences of bacteria and archaea. <b>2017</b> , 1, 249-255	6
1424	phyloSkeleton: taxon selection, data retrieval and marker identification for phylogenomics. <b>2017</b> , 33, 1230-1232	5
1423	On Earth, there would be a number of fundamental kinds of primary cells - cellular domains - greater than or equal to four. <b>2018</b> , 443, 10-17	10
1422	Major New Microbial Groups Expand Diversity and Alter our Understanding of the Tree of Life. <b>2018</b> , 172, 1181-1197	272
1421	Growth yield and selection of nosZ clade II types in a continuous enrichment culture of N <sub>2</sub> respiring bacteria. <b>2018</b> , 10, 239-244	19
1420	Microbial community composition along a 50'000-year lacustrine sediment sequence. <b>2018</b> , 94,	20
1419	UBCG: Up-to-date bacterial core gene set and pipeline for phylogenomic tree reconstruction. <b>2018</b> , 56, 280-285	505
1418	Toxicity assessment of pharmaceutical compounds on mixed culture from activated sludge using respirometric technique: The role of microbial community structure. <b>2018</b> , 630, 809-819	55
1417	Extreme halophilic archaea derive from two distinct methanogen Class II lineages. <b>2018</b> , 127, 46-54	38
1416	Earth BioGenome Project: Sequencing life for the future of life. <b>2018</b> , 115, 4325-4333	334
1415	Deep mitochondrial origin outside the sampled alphaproteobacteria. <i>Nature</i> , <b>2018</b> , 557, 101-105	50.4 169
1414	Insights into RNA-processing pathways and associated RNA-degrading enzymes in Archaea. <b>2018</b> , 42, 579-613	26
1413	The bacterium <i>Pseudomonas aeruginosa</i> senses and gradually responds to interspecific competition for iron. <b>2018</b> , 72, 1515	23
1412	Metabolic potential and in situ transcriptomic profiles of previously uncharacterized key microbial groups involved in coupled carbon, nitrogen and sulfur cycling in anoxic marine zones. <b>2018</b> , 20, 2727-2742	13
1411	The Geographic Structure of Viruses in the Cuatro Ciénegas Basin, a Unique Oasis in Northern Mexico, Reveals a Highly Diverse Population on a Small Geographic Scale. <b>2018</b> , 84,	23
1410	Effects of triallin on the soil microbial community and functional groups involved in nitrogen cycling. <b>2018</b> , 353, 204-213	33
1409	Multilayer approach for characterization of bacterial diversity in a marginal sea: From surface to seabed. <b>2018</b> , 184, 15-27	4

1408	Exploration and exploitation of the environment for novel specialized metabolites. <b>2018</b> , 50, 206-213	24
1407	Obtaining high-quality draft genomes from uncultured microbes by cleaning and co-assembly of single-cell amplified genomes. <b>2018</b> , 8, 2059	25
1406	Discovery of novel bacterial toxins by genomics and computational biology. <b>2018</b> , 147, 2-12	35
1405	Microbial Dark Matter Investigations: How Microbial Studies Transform Biological Knowledge and Empirically Sketch a Logic of Scientific Discovery. <b>2018</b> , 10, 707-715	42
1404	Differential depth distribution of microbial function and putative symbionts through sediment-hosted aquifers in the deep terrestrial subsurface. <b>2018</b> , 3, 328-336	133
1403	Unraveling uncultivable pesticide degraders via stable isotope probing (SIP). <b>2018</b> , 38, 1025-1048	30
1402	Life on NO: deciphering the ecophysiology of NO respiring bacterial communities in a continuous culture. <b>2018</b> , 12, 1142-1153	44
1401	Phylogenetic clustering of small low nucleic acid-content bacteria across diverse freshwater ecosystems. <b>2018</b> , 12, 1344-1359	47
1400	The RNA-splicing endonuclease from the euryarchaeon <i>Methanopyrus kandleri</i> is a heterotetramer with constrained substrate specificity. <b>2018</b> , 46, 1958-1972	5
1399	Evolutionary history of carbon monoxide dehydrogenase/acetyl-CoA synthase, one of the oldest enzymatic complexes. <b>2018</b> , 115, E1166-E1173	85
1398	Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. <b>2018</b> , 200,	29
1397	A year in the life of a thrombolite: comparative metatranscriptomics reveals dynamic metabolic changes over diel and seasonal cycles. <b>2018</b> , 20, 842-861	14
1396	Potential recycling of thaumarchaeotal lipids by DPANN Archaea in seasonally hypoxic surface marine sediments. <b>2018</b> , 119, 101-109	18
1395	Retrieval of a million high-quality, full-length microbial 16S and 18S rRNA gene sequences without primer bias. <b>2018</b> , 36, 190-195	105
1394	Genomic features of bacterial adaptation to plants. <b>2017</b> , 50, 138-150	253
1393	Analyzing large scale genomic data on the cloud with Sparkhit. <b>2018</b> , 34, 1457-1465	6
1392	Genome-enabled metabolic reconstruction of dominant chemosynthetic colonizers in deep-sea massive sulfide deposits. <b>2018</b> , 20, 862-877	18
1391	How Much Do rRNA Gene Surveys Underestimate Extant Bacterial Diversity?. <b>2018</b> , 84,	34

1390	Studying microbial functionality within the gut ecosystem by systems biology. <b>2018</b> , 13, 5	25
1389	Deciphering viral presences: two novel partial giant viruses detected in marine metagenome and in a mine drainage metagenome. <b>2018</b> , 15, 66	15
1388	Early emergence of the FtsH proteases involved in photosystem II repair. <b>2018</b> , 56, 163-177	13
1387	Microfluidic Devices in the Fast-Growing Domain of Single-Cell Analysis. <b>2018</b> , 24, 15398-15420	21
1386	Metagenomic Binning. <b>2018</b> , 89-99	1
1385	Methodology challenges in studying human gut microbiota - effects of collection, storage, DNA extraction and next generation sequencing technologies. <b>2018</b> , 8, 5143	84
1384	Diversity-generating retroelements: natural variation, classification and evolution inferred from a large-scale genomic survey. <b>2018</b> , 46, 11-24	35
1383	Homologous Recombination and Transposon Propagation Shape the Population Structure of an Organism from the Deep Subsurface with Minimal Metabolism. <b>2018</b> , 10, 1115-1119	7
1382	Surface-Enhanced Raman Scattering (SERS) in Microbiology: Illumination and Enhancement of the Microbial World. <b>2018</b> , 72, 987-1000	43
1381	Predicted microbial secretomes and their target substrates in marine sediment. <b>2018</b> , 3, 32-37	57
1380	Microbial diversity from chlorophyll maximum, oxygen minimum and bottom zones in the southwestern Atlantic Ocean. <b>2018</b> , 178, 52-61	7
1379	Microbiome dynamics and adaptation of expression signatures during methane production failure and process recovery. <b>2018</b> , 247, 347-356	11
1378	Bacterial Shifts in Nutrient Solutions Flowing Through Biofilters Used in Tomato Soilless Culture. <b>2018</b> , 76, 169-181	2
1377	Metabolic versatility of small archaea Micrarchaeota and Parvarchaeota. <b>2018</b> , 12, 756-775	62
1376	The Emergency Medical Service Microbiome. <b>2018</b> , 84,	5
1375	Sequencing of Genomes from Environmental Single Cells. <b>2018</b> , 1712, 97-111	1
1374	Contrasting patterns of genome-level diversity across distinct co-occurring bacterial populations. <b>2018</b> , 12, 742-755	47
1373	Localized high abundance of Marine Group II archaea in the subtropical Pearl River Estuary: implications for their niche adaptation. <b>2018</b> , 20, 734-754	27



1372	Next Generation Sequencing. <b>2018,</b>	1
1371	Identification and Experimental Characterization of an Extremophilic Brine Pool Alcohol Dehydrogenase from Single Amplified Genomes. <b>2018, 13, 161-170</b>	13
1370	The enigmatic SAR202 cluster up close: shedding light on a globally distributed dark ocean lineage involved in sulfur cycling. <b>2018, 12, 655-668</b>	44
1369	Phylogeny and genomics of SAUL, an enigmatic bacterial lineage frequently associated with marine sponges. <b>2018, 20, 561-576</b>	18
1368	Deep ocean prokaryotic communities are remarkably malleable when facing long-term starvation. <b>2018, 20, 713-723</b>	16
1367	Free-living chemoautotrophic and particle-attached heterotrophic prokaryotes dominate microbial assemblages along a pelagic redox gradient. <b>2018, 20, 693-712</b>	24
1366	Cultivation of Peptidiphaga gingivicola from subgingival plaque: The first representative of a novel genus of Actinomycetaceae. <b>2018, 33, 105-110</b>	1
1365	Genotyping of Bartonella bacteria and their animal hosts: current status and perspectives. <b>2018, 145, 543-562</b>	33
1364	Freshwater carbon and nutrient cycles revealed through reconstructed population genomes. <b>2018, 6, e6075</b>	31
1363	Caldisericum. <b>2018, 1-4</b>	
1362	Draft Genome Sequence of " Moanabacter tarae," Representing a Novel Marine Verrucomicrobial Lineage. <b>2018, 7,</b>	1
1361	Untersuchung prozessrelevanter mikrobieller Populationen mittels RNA-SIP. <b>2018, 24, 264-266</b>	
1360	Assessment of Molecular Markers for Classification of Bacterial Phyla using Topological Dissimilarity of Phylogenetic Trees. <b>2018, 06,</b>	
1359	. <b>2018,</b>	13
1358	Metagenomics meets read clouds. <b>2018, 36, 1049-1051</b>	1
1357	Members of the Genus Are Inferred To Account for the Majority of Aerobic Methane Oxidation in Oxic Soils from a Freshwater Wetland. <b>2018, 9,</b>	32
1356	Parallel Evolution of Genome Streamlining and Cellular Bioenergetics across the Marine Radiation of a Bacterial Phylum. <b>2018, 9,</b>	16
1355	Syntrophy in Methanogenic Degradation. <b>2018, 153-192</b>	3

1354	Proteomics goes parallel. <b>2018</b> , 36, 1051-1053	9
1353	High Microbial Diversity Despite Extremely Low Biomass in a Deep Karst Aquifer. <b>2018</b> , 9, 2823	15
1352	Genome size evolution in the Archaea. <b>2018</b> , 2, 595-605	10
1351	Metatranscriptomes Reveal That All Three Domains of Life Are Active but Are Dominated by Bacteria in the Fennoscandian Crystalline Granitic Continental Deep Biosphere. <b>2018</b> , 9,	19
1350	(Endo)symbiotic Methanogenic Archaea. <b>2018</b> ,	7
1349	Evolutionary Success of Prokaryotes. <b>2018</b> , 131-240	
1348	Phylogeny and Biodiversity of Prokaryotes. <b>2018</b> , 23-55	
1347	The Evolution of Living Beings Started with Prokaryotes and in Interaction with Prokaryotes. <b>2018</b> , 241-338	1
1346	Single cell genomic and transcriptomic evidence for the use of alternative nitrogen substrates by anammox bacteria. <b>2018</b> , 12, 2706-2722	25
1345	The Microbial Diversity of Caves. <b>2018</b> , 69-90	9
1344	Technologies for Automated Single Cell Isolation. <b>2018</b> , 1-28	1
1343	Ecological Succession of Sulfur-Oxidizing - and During Colonization of a Shallow-Water Gas Vent. <b>2018</b> , 9, 2970	11
1342	Prokaryotes and Evolution. <b>2018</b> ,	2
1341	Metatranscriptomic and comparative genomic insights into resuscitation mechanisms during enrichment culturing. <b>2018</b> , 6, 230	76
1340	Genomic Insight Into the Predominance of Candidate Phylum Atribacteria JS1 Lineage in Marine Sediments. <b>2018</b> , 9, 2909	18
1339	Hunters or farmers? Microbiome characteristics help elucidate the diet composition in an aquatic carnivorous plant. <b>2018</b> , 6, 225	13
1338	Supragingival Plaque Microbiome Ecology and Functional Potential in the Context of Health and Disease. <b>2018</b> , 9,	42
1337	Metabolism and Occurrence of Methanogenic and Sulfate-Reducing Syntrophic Acetate Oxidizing Communities in Haloalkaline Environments. <b>2018</b> , 9, 3039	21

1336	Functional shifts in microbial mats recapitulate early Earth metabolic transitions. <b>2018</b> , 2, 1700-1708	21
1335	Leveraging single-cell genomics to expand the fungal tree of life. <b>2018</b> , 3, 1417-1428	60
1334	Desiccation- and Saline-Tolerant Bacteria and Archaea in Kalahari Pan Sediments. <b>2018</b> , 9, 2082	15
1333	Widespread Antibiotic, Biocide, and Metal Resistance in Microbial Communities Inhabiting a Municipal Waste Environment and Anthropogenically Impacted River. <b>2018</b> , 3,	5
1332	Genetic repertoires of anaerobic microbiomes driving generation of biogas. <b>2018</b> , 11, 255	5
1331	Clinician Guide to Microbiome Testing. <b>2018</b> , 63, 3167-3177	12
1330	Single-Cell Genomics Reveals a Diverse Metabolic Potential of Uncultivated -Related Deltaproteobacteria Widely Distributed in Marine Sediment. <b>2018</b> , 9, 2038	36
1329	Population Genomics of Archaea: Signatures of Archaeal Biology from Natural Populations. <b>2018</b> , 145-155	
1328	Genomes from uncultivated prokaryotes: a comparison of metagenome-assembled and single-amplified genomes. <b>2018</b> , 6, 173	43
1327	The biomass and biodiversity of the continental subsurface. <b>2018</b> , 11, 707-717	160
1326	A metagenomics roadmap to the uncultured genome diversity in hypersaline soda lake sediments. <b>2018</b> , 6, 168	59
1325	Phylogenetically Novel Uncultured Microbial Cells Dominate Earth Microbiomes. <b>2018</b> , 3,	167
1324	Diversity-Function Relationships in Natural, Applied, and Engineered Microbial Ecosystems. <b>2018</b> , 105, 131-189	7
1323	Discovering novel hydrolases from hot environments. <b>2018</b> , 36, 2077-2100	27
1322	Single-Cell Genomics of Microbial Dark Matter. <b>2018</b> , 1849, 99-111	3
1321	Effects of a Superabsorbent Resin with Boron on Bacterial Diversity of Peat Substrate and Maize Straw. <b>2018</b> , 2018, 6071085	3
1320	Microbial Resource Conservation. <b>2018</b> ,	3
1319	Archaea: Ecology, Application, and Conservation. <b>2018</b> , 431-451	2

1318	The Tree of Life. <b>2018</b> , 55-99	7
1317	Mayr Versus Woese: Akaryotes and Eukaryotes. <b>2018</b> , 13-54	
1316	Programmed DNA destruction by miniature CRISPR-Cas14 enzymes. <b>2018</b> , 362, 839-842	394
1315	Repertoire of the gut microbiota from stomach to colon using culturomics and next-generation sequencing. <b>2018</b> , 18, 157	37
1314	Ecologically informed microbial biomarkers and accurate classification of mixed and unmixed samples in an extensive cross-study of human body sites. <b>2018</b> , 6, 192	15
1313	Trends in Synthetic Biology Applications, Tools, Industry, and Oversight and Their Security Implications. <b>2018</b> , 16, 320-333	3
1312	Genomic Description of ' Abyssubacteria,' a Novel Subsurface Lineage Within the Candidate Phylum Hydrogenedentes. <b>2018</b> , 9, 1993	10
1311	MetaWRAP-a flexible pipeline for genome-resolved metagenomic data analysis. <b>2018</b> , 6, 158	370
1310	Dietary supplementation with <i>Rehmannia glutinosa</i> affects the composition of intestinal microorganisms in common carp. <b>2018</b> , 58, 1023-1032	6
1309	Genomic and phenotypic description of the newly isolated human species <i>Collinsella bouchesdurhonensis</i> sp. nov. <b>2018</b> , 7, e00580	2
1308	Secondary metabolites overproduction through transcriptional gene cluster refactoring. <b>2018</b> , 49, 299-315	41
1307	Dynamics of microbial populations mediating biogeochemical cycling in a freshwater lake. <b>2018</b> , 6, 165	26
1306	Dynamic Human Environmental Exposome Revealed by Longitudinal Personal Monitoring. <b>2018</b> , 175, 277-291.e31	86
1305	Single-cell genomics of co-sorted Nanoarchaeota suggests novel putative host associations and diversification of proteins involved in symbiosis. <b>2018</b> , 6, 161	24
1304	Structure and function of archaeal histones. <b>2018</b> , 14, e1007582	36
1303	Production of $\beta$ Alanine from Fumaric Acid Using a Dual-Enzyme Cascade. <b>2018</b> , 10, 4984-4991	24
1302	Diversity and antimicrobial potential in sea anemone and holothurian microbiomes. <b>2018</b> , 13, e0196178	21
1301	Biosynthetic capacity, metabolic variety and unusual biology in the CPR and DPANN radiations. <b>2018</b> , 16, 629-645	153

1300	A metagenomic window into the 2-km-deep terrestrial subsurface aquifer revealed multiple pathways of organic matter decomposition. <b>2018</b> , 94,	12
1299	Indicators of arable soils fatigue [Bacterial families and genera: A metagenomic approach. <b>2018</b> , 93, 490-500	28
1298	Raman-activated cell sorting and metagenomic sequencing revealing carbon-fixing bacteria in the ocean. <b>2018</b> , 20, 2241-2255	41
1297	Group I introns are widespread in archaea. <b>2018</b> , 46, 7970-7976	13
1296	Marsarchaeota are an aerobic archaeal lineage abundant in geothermal iron oxide microbial mats. <b>2018</b> , 3, 732-740	33
1295	Microbial ecology of deep-sea hypersaline anoxic basins. <b>2018</b> , 94,	24
1294	An Ultrahigh-throughput Microfluidic Platform for Single-cell Genome Sequencing. <b>2018</b> ,	13
1293	The unexpected diversity of microbial communities associated with black corals revealed by high-throughput Illumina sequencing. <b>2018</b> , 365,	6
1292	Ecology and evolution of seafloor and subseafloor microbial communities. <b>2018</b> , 16, 671-683	71
1291	Long-Term Cultivation and Metagenomics Reveal Ecophysiology of Previously Uncultivated Thermophiles Involved in Biogeochemical Nitrogen Cycle. <b>2018</b> , 33, 107-110	23
1290	Genomics of the Uncultivated, Periodontitis-Associated Bacterium sp. BU045 (Oral Taxon 808). <b>2018</b> , 3,	7
1289	Recent Developments in Single-Cell RNA-Seq of Microorganisms. <b>2018</b> , 115, 173-180	21
1288	Analytic Methods in Microbiome Studies. <b>2018</b> , 29-42	
1287	Culturing the human microbiota and culturomics. <b>2018</b> , 16, 540-550	303
1286	Metagenomics Sheds Light on the Ecology of Marine Microbes and Their Viruses. <b>2018</b> , 26, 955-965	30
1285	Investigation of viable taxa in the deep terrestrial biosphere suggests high rates of nutrient recycling. <b>2018</b> , 94,	16
1284	Types of tobacco consumption and the oral microbiome in the United Arab Emirates Healthy Future (UAEHFS) Pilot Study. <b>2018</b> , 8, 11327	28
1283	Complex Evolutionary History of Translation Elongation Factor 2 and Diphthamide Biosynthesis in Archaea and Parabasalids. <b>2018</b> , 10, 2380-2393	24

1282	Deep learning models for bacteria taxonomic classification of metagenomic data. <b>2018</b> , 19, 198	53
1281	Genome Reduction in Species within the Gut of an Amphipod from the Ocean's Deepest Point. <b>2018</b> , 3,	14
1280	Comparative Genomic Analysis of spp., Intranuclear Symbionts of Paramecia. <b>2018</b> , 9, 738	13
1279	Putative Promoter Motif Analyses Reinforce the Evolutionary Relationships Among Faustoviruses, Kaumobavirus, and Asfarvirus. <b>2018</b> , 9, 1041	6
1278	Distinct Microbial Assemblage Structure and Archaeal Diversity in Sediments of Arctic Thermokarst Lakes Differing in Methane Sources. <b>2018</b> , 9, 1192	11
1277	Taxonomic and Functional Compositions Impacted by the Quality of Metatranscriptomic Assemblies. <b>2018</b> , 9, 1235	10
1276	Insights into the ecology, evolution, and metabolism of the widespread Woese archaeotal lineages. <b>2018</b> , 6, 102	98
1275	Disentangling the drivers of functional complexity at the metagenomic level in Shark Bay microbial mat microbiomes. <b>2018</b> , 12, 2619-2639	46
1274	Metagenomic binning reconstruction coupled with automatic pipeline annotation and giant viruses: A potential source of mistake in annotations. <b>2018</b> , 255, 36-38	5
1273	Linking Uncultivated Microbial Populations and Benthic Carbon Turnover by Using Quantitative Stable Isotope Probing. <b>2018</b> , 84,	23
1272	Meanings, measurements, and musings on the significance of patterns in human microbiome variation. <b>2018</b> , 53, 43-52	4
1271	Insights into global planktonic diatom diversity: The importance of comparisons between phylogenetically equivalent units that account for time. <b>2018</b> , 12, 2807-2810	12
1270	Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. <b>2018</b> , 9, 2832	50
1269	ReprDB and panDB: minimalist databases with maximal microbial representation. <b>2018</b> , 6, 15	12
1268	Microbial effects of part-stream low-frequency ultrasonic pretreatment on sludge anaerobic digestion as revealed by high-throughput sequencing-based metagenomics and metatranscriptomics. <b>2018</b> , 11, 47	17
1267	Bioreactor microbial ecosystems with differentiated methanogenic phenol biodegradation and competitive metabolic pathways unraveled with genome-resolved metagenomics. <b>2018</b> , 11, 135	9
1266	The last universal common ancestor between ancient Earth chemistry and the onset of genetics. <b>2018</b> , 14, e1007518	61
1265	Soil Microorganisms. <b>2018</b> , 457-482	2

1264	Bacterial and archaeal profiling of hypersaline microbial mats and endoevaporites, under natural conditions and methanogenic microcosm experiments. <b>2018</b> , 22, 903-916	10
1263	Co-occurrence network analysis reveals thermodynamics-driven microbial interactions in methanogenic bioreactors. <b>2018</b> , 10, 673-685	12
1262	Metagenomic Approaches for Understanding New Concepts in Microbial Science. <b>2018</b> , 2018, 2312987	65
1261	A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. <b>2018</b> , 36, 996-1004	1369
1260	ezTree: an automated pipeline for identifying phylogenetic marker genes and inferring evolutionary relationships among uncultivated prokaryotic draft genomes. <b>2018</b> , 19, 921	30
1259	Benthic archaea as potential sources of tetraether membrane lipids in sediments across an oxygen minimum zone. <b>2018</b> , 15, 4047-4064	34
1258	Novel Autotrophic Organisms Contribute Significantly to the Internal Carbon Cycling Potential of a Boreal Lake. <b>2018</b> , 9,	6
1257	New Biological Insights Into How Deforestation in Amazonia Affects Soil Microbial Communities Using Metagenomics and Metagenome-Assembled Genomes. <b>2018</b> , 9, 1635	33
1256	IDTAXA: a novel approach for accurate taxonomic classification of microbiome sequences. <b>2018</b> , 6, 140	147
1255	Origin and Evolution of Flavin-Based Electron Bifurcating Enzymes. <b>2018</b> , 9, 1762	18
1254	Metagenomics of Methanogenic Communities in Anaerobic Digesters. <b>2018</b> , 1-23	3
1253	On the Origin of Isoprenoid Biosynthesis. <b>2018</b> , 35, 2185-2197	29
1252	Application of Omics Approaches to Earth and Environmental Sciences Opportunities and Challenges. <b>2018</b> , 27-39	
1251	Overview of Approaches From Whole-Community Shotgun Sequencing to Single-Cell Genomics. <b>2018</b> , 41-57	
1250	Novel prosthecate bacteria from the candidate phylum Acetothermia. <b>2018</b> , 12, 2225-2237	24
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1050	Organic biogeochemistry in the oxygen-deficient ocean: A review. <b>2020</b> , 149, 104096	9
1049	Unravelling the diversity of magnetotactic bacteria through analysis of open genomic databases. <b>2020</b> , 7, 252	13

1048	Symbiosis between nanohaloarchaeon and haloarchaeon is based on utilization of different polysaccharides. <b>2020</b> , 117, 20223-20234	14
1047	Microbial Strategies for Survival in the Glass Sponge. <b>2020</b> , 5,	7
1046	Microbial Communities in Permafrost Soils of Larsemann Hills, Eastern Antarctica: Environmental Controls and Effect of Human Impact. <b>2020</b> , 8,	4
1045	Spatial and Temporal Dynamics in Attached and Suspended Bacterial Communities in Three Drinking Water Distribution Systems with Variable Biological Stability. <b>2020</b> , 54, 14535-14546	8
1044	Atribacteria Reproducing over Millions of Years in the Atlantic Abyssal Subseafloor. <b>2020</b> , 11,	15
1043	Isolation and cultivation of candidate phyla radiation (TM7) bacteria in coculture with bacterial hosts. <b>2020</b> , 12, 1814666	16
1042	Genome Analysis of a Marine Bacterium sp. and Its Role in Nitrate Reduction under the Influence of Photoelectrons. <b>2020</b> , 8,	2
1041	High-throughput cultivation based on dilution-to-extinction with catalase supplementation and a case study of cultivating acl bacteria from Lake Soyang. <b>2020</b> , 58, 893-905	7
1040	Niche Specialization and Functional Overlap of Bamboo Leaf and Root Microbiota. <b>2020</b> , 11, 571159	2
1039	Targeted isolation based on metagenome-assembled genomes reveals a phylogenetically distinct group of thermophilic spirochetes from deep biosphere. <b>2021</b> , 23, 3585-3598	9
1038	Analytical and Computational Advances, Opportunities, and Challenges in Marine Organic Biogeochemistry in an Era of Omics <b>2020</b> , 7,	6
1037	Recent advances in understanding the ecology of the lung microbiota and deciphering the gut-lung axis. <b>2020</b> , 319, L710-L716	13
1036	Revealing the in vivo growth and division patterns of mouse gut bacteria. <b>2020</b> , 6,	9
1035	Activity-based cell sorting reveals responses of uncultured archaea and bacteria to substrate amendment. <b>2020</b> , 14, 2851-2861	21
1034	Candidatus Nanosalina. <b>2020</b> , 1-3	
1033	Candidatus Nanosalinicola. <b>2020</b> , 1-4	
1032	Candidatus Nanopetraeus. <b>2020</b> , 1-4	
1031	Microbial Processes and Microbial Communities in the Water Column of the Polar Meromictic Lake Bol'shie Khruslomeny at the White Sea Coast. <b>2020</b> , 11, 1945	3

1030	Femtoplankton: What's New?. <b>2020</b> , 12,	3
1029	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. <b>2020</b> , 11, 1848	29
1028	Hot in Cold: Microbial Life in the Hottest Springs in Permafrost. <b>2020</b> , 8,	4
1027	The Ability of Taxonomic Identification of Bifidobacteria Based on the Variable Regions of 16S rRNA Gene. <b>2020</b> , 56, 926-934	4
1026	Community, Distribution, and Ecological Roles of Estuarine Archaea. <b>2020</b> , 11, 2060	7
1025	Microbial dark matter filling the niche in hypersaline microbial mats. <b>2020</b> , 8, 135	7
1024	Catching a glimpse of the bacterial gut community of companion animals: a canine and feline perspective. <b>2020</b> , 13, 1708-1732	12
1023	Estimating the quality of eukaryotic genomes recovered from metagenomic analysis with EukCC. <b>2020</b> , 21, 244	19
1022	Dissimilatory sulfate reduction in the archaeon 'Candidatus Vulcanisaeta moutnovskia' sheds light on the evolution of sulfur metabolism. <b>2020</b> , 5, 1428-1438	6
1021	Prokaryotic community composition in a great shallow soda lake covered by large reed stands (Neusiedler See/Lake Fertő) as revealed by cultivation- and DNA-based analyses. <b>2020</b> , 96,	3
1020	Flexible comparative genomics of prokaryotic transcriptional regulatory networks. <b>2020</b> , 21, 466	2
1019	Diversity and Genomic Characterization of a Novel Parvarchaeota Family in Acid Mine Drainage Sediments. <b>2020</b> , 11, 612257	2
1018	Functional and genetic markers of niche partitioning among enigmatic members of the human oral microbiome. <b>2020</b> , 21, 292	30
1017	Dysbiosis in marine aquaculture revealed through microbiome analysis: reverse ecology for environmental sustainability. <b>2020</b> , 96,	4
1016	Weak Influence of Paleoenvironmental Conditions on the Subsurface Biosphere of Lake Ohrid over the Last 515 ka. <b>2020</b> , 8,	3
1015	Advances and challenges in single-cell RNA-seq of microbial communities. <b>2020</b> , 57, 102-110	9
1014	Diversity, ecology and evolution of Archaea. <b>2020</b> , 5, 887-900	92
1013	Identification of Metagenome-Assembled Genomes Containing Antimicrobial Resistance Genes, Isolated from an Advanced Water Treatment Facility. <b>2020</b> , 9,	3

1012	Ecological and genomic analyses of candidate phylum WPS-2 bacteria in an unvegetated soil. <b>2020</b> , 22, 3143-3157	16
1011	Epigenetic biosensors for bacteriophage detection and phage receptor discrimination. <b>2020</b> , 22, 3126-3142	3
1010	Strain-resolved microbiome sequencing reveals mobile elements that drive bacterial competition on a clinical timescale. <b>2020</b> , 12, 50	16
1009	Parallel reductive genome evolution in <i>Desulfovibrio</i> ectosymbionts independently acquired by <i>Trichonympha</i> protists in the termite gut. <b>2020</b> , 14, 2288-2301	1
1008	Dental Calculus as a Tool to Study the Evolution of the Mammalian Oral Microbiome. <b>2020</b> , 37, 3003-3022	13
1007	Microbial Ecosystems in Central Andes Extreme Environments. <b>2020</b> ,	6
1006	Novel cultivated endophytic Verrucomicrobia reveal deep-rooting traits of bacteria to associate with plants. <b>2020</b> , 10, 8692	14
1005	The hyperthermophilic partners <i>Nanoarchaeum</i> and <i>Ignicoccus</i> stabilize their tRNA T-loops via different but structurally equivalent modifications. <b>2020</b> , 48, 6906-6918	9
1004	Applications of weighted association networks applied to compositional data in biology. <b>2020</b> , 22, 3020-3038	2
1003	Cholesterol Metabolism by Uncultured Human Gut Bacteria Influences Host Cholesterol Level. <b>2020</b> , 28, 245-257.e6	56
1002	Size Matters: Ultra-small and Filterable Microorganisms in the Environment. <b>2020</b> , 35,	13
1001	Methanogenesis in the Lake Elton saline aquatic system. <b>2020</b> , 24, 657-672	6
1000	Heterotrophic Thaumarchaea with Small Genomes Are Widespread in the Dark Ocean. <b>2020</b> , 5,	24
999	Roadmap for naming uncultivated Archaea and Bacteria. <b>2020</b> , 5, 987-994	64
998	A case study of salivary microbiome in smokers and non-smokers in Hungary: analysis by shotgun metagenome sequencing. <b>2020</b> , 12, 1773067	8
997	Cellular and Structural Basis of Synthesis of the Unique Intermediate Dehydro-F-0 in Mycobacteria. <b>2020</b> , 5,	4
996	Function is what counts: how microbial community complexity affects species, proteome and pathway coverage in metaproteomics. <b>2020</b> , 17, 163-173	7
995	Accurate and complete genomes from metagenomes. <b>2020</b> , 30, 315-333	112

994	Metagenomic characterization of bacterial biofilm in four food processing plants in Colombia. <b>2020</b> , 51, 1259-1267	5
993	10 Years of Extreme Microbiology: An Interim Reflection and Future Prospects. <b>2020</b> , 11, 131	0
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991	The Ecology of Predation at the Microscale. <b>2020</b> ,	3
990	Oxygen preference of deeply-rooted mesophilic thaumarchaeota in forest soil. <b>2020</b> , 148, 107848	3
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988	N-glycosylation in Archaea-New roles for an ancient posttranslational modification. <b>2020</b> , 114, 735-741	7
987	Advantages and Limits of Metagenomic Assembly and Binning of a Giant Virus. <b>2020</b> , 5,	5
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985	Marine Hydrocarbon Seeps. <b>2020</b> ,	4
984	Core microbiomes: Characterization and identification. <b>2020</b> , 43-84	
983	Taxonomic classification and abundance estimation using 16S and WGS-A comparison using controlled reference samples. <b>2020</b> , 46, 102257	7
982	Single-Cell Genomics and the Oral Microbiome. <b>2020</b> , 99, 613-620	9
981	Complete Genome of a Member of a New Bacterial Lineage in the Microgenomates Group Reveals an Unusual Nucleotide Composition Disparity Between Two Strands of DNA and Limited Metabolic Potential. <b>2020</b> , 8,	3
980	The Link Between the Ecology of the Prokaryotic Rare Biosphere and Its Biotechnological Potential. <b>2020</b> , 11, 231	19
979	Microbiome of the deep Lake Baikal, a unique oxic bathypelagic habitat. <b>2020</b> , 65, 1471-1488	21
978	Metabolic potentials of archaeal lineages resolved from metagenomes of deep Costa Rica sediments. <b>2020</b> , 14, 1345-1358	24
977	Metabolic dependencies govern microbial syntrophies during methanogenesis in an anaerobic digestion ecosystem. <b>2020</b> , 8, 22	42

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975	Viable bacterial colonization is highly limited in the human intestine in utero. <b>2020</b> , 26, 599-607	98
974	Impact of acid mine drainage chemistry and microbiology on the development of efficient Fe removal activities. <b>2020</b> , 249, 126117	8
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972	Next-generation physiology approaches to study microbiome function at single cell level. <b>2020</b> , 18, 241-256	87
971	A new lineage of segmented RNA viruses infecting animals. <b>2020</b> , 6, vez061	17
970	Enzymes revolutionize the bioproduction of value-added compounds: From enzyme discovery to special applications. <b>2020</b> , 40, 107520	61
969	Building de novo reference genome assemblies of complex eukaryotic microorganisms from single nuclei. <b>2020</b> , 10, 1303	9
968	Single-cell genomics of uncultured bacteria reveals dietary fiber responders in the mouse gut microbiota. <b>2020</b> , 8, 5	35
967	In depth metagenomic analysis in contrasting oil wells reveals syntrophic bacterial and archaeal associations for oil biodegradation in petroleum reservoirs. <b>2020</b> , 715, 136646	13
966	Unexpected diversity of acetate degraders in anaerobic membrane bioreactor treating organic solid waste revealed by high-sensitivity stable isotope probing. <b>2020</b> , 176, 115750	8
965	Evaluation of the effects of cell-dispensing using an inkjet-based bioprinter on cell integrity by RNA-seq analysis. <b>2020</b> , 10, 7158	3
964	Hiding in Plain Sight: The Globally Distributed Bacterial Candidate Phylum PAUC34f. <b>2020</b> , 11, 376	3
963	Community Structure and Influencing Factors of Airborne Microbial Aerosols over Three Chinese Cities with Contrasting Social-Economic Levels. <b>2020</b> , 11, 317	1
962	"Ethanoperedens," a Thermophilic Genus of Mediating the Anaerobic Oxidation of Ethane. <b>2020</b> , 11,	23
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960	The influence of spaceflight on the astronaut salivary microbiome and the search for a microbiome biomarker for viral reactivation. <b>2020</b> , 8, 56	16
959	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. <b>2020</b> , 8, 51	64

958	Next Generation Sequencing Methods: Pushing the Boundaries. <b>2021</b> , 19-46	
957	Extraordinary diversity of viruses in deep-sea sediments as revealed by metagenomics without prior virion separation. <b>2021</b> , 23, 728-743	14
956	Anwendungen von Einzelzellmethoden in der mikrobiellen Naturstoffforschung. <b>2021</b> , 133, 18560-18577	
955	Opening up the Single-Cell Toolbox for Microbial Natural Products Research. <b>2021</b> , 60, 18412-18428	10
954	A genomic catalog of Earth's microbiomes. <b>2021</b> , 39, 499-509	120
953	New Microbial Biodiversity in Marine Sediments. <b>2021</b> , 13, 161-175	11
952	Innovations to culturing the uncultured microbial majority. <b>2021</b> , 19, 225-240	76
951	Ecological features and global distribution of Asgard archaea. <b>2021</b> , 758, 143581	4
950	A metagenomic assessment of microbial communities in anaerobic bioreactors and sediments: Taxonomic and functional relationships. <b>2021</b> , 68, 102296	0
949	Physical connections: prokaryotes parasitizing their kin. <b>2021</b> , 13, 54-61	8
948	Anomalous Phylogenetic Behavior of Ribosomal Proteins in Metagenome-Assembled Asgard Archaea. <b>2021</b> , 13,	9
947	The impact of the Fungus-Host-Microbiota interplay upon <i>Candida albicans</i> infections: current knowledge and new perspectives. <b>2021</b> , 45,	31
946	Synergistic interactions of <i>Desulfovibrio</i> and <i>Petrimonas</i> for sulfate-reduction coupling polycyclic aromatic hydrocarbon degradation. <b>2021</b> , 407, 124385	12
945	Seasonality of archaeal proteorhodopsin and associated Marine Group IIb ecotypes (Ca. <i>Poseidonales</i> ) in the North Western Mediterranean Sea. <b>2021</b> , 15, 1302-1316	1
944	An emerging view of the diversity, ecology and function of Archaea in alkaline hydrothermal environments. <b>2021</b> , 97,	1
943	High temperatures enhance the microbial genetic potential to recycle C and N from necromass in high-mountain soils. <b>2021</b> , 27, 1365-1386	12
942	A combined method for the source apportionment of sediment organic carbon in rivers. <b>2021</b> , 752, 141840	4
941	Application of in situ cultivation in marine microbial resource mining. <b>2021</b> , 3, 148-161	3



940	FACS-iChip: a high-efficiency iChip system for microbial dark matter mining. <b>2021</b> , 3, 162-168	4
939	From ecophysiology to cultivation methodology: filling the knowledge gap between uncultured and cultured microbes. <b>2021</b> , 3, 132-147	5
938	A network approach to elucidate and prioritize microbial dark matter in microbial communities. <b>2021</b> , 15, 228-244	19
937	Advancing and refining archaeological dental calculus research using multiomic frameworks. <b>2021</b> , 7, 13-30	1
936	Analysing Microbial Biofilm Formation at a Molecular Level: Role of Fourier Transform Infrared and Raman Spectroscopy. <b>2021</b> , 69-93	1
935	One cell at a time: droplet-based microbial cultivation, screening and sequencing. <b>2021</b> , 3, 169-188	7
934	Genome streamlining, proteorhodopsin, and organic nitrogen metabolism in freshwater nitrifiers.	0
933	Heme auxotrophy in abundant aquatic microbial lineages.	
932	Mixotrophic chemosynthesis in a deep-sea anemone from hydrothermal vents in the Pescadero Basin, Gulf of California. <b>2021</b> , 19, 8	0
931	Genome-resolved metagenomics reveals site-specific diversity of episymbiotic CPR bacteria and DPANN archaea in groundwater ecosystems. <b>2021</b> , 6, 354-365	24
930	Archaea as components of forest microbiome. <b>2021</b> , 357-370	
929	Next-generation omics technologies to explore microbial diversity. <b>2021</b> , 541-563	
928	PASV: Automatic protein partitioning and validation using conserved residues.	1
927	Classification of Sequences with Deep Artificial Neural Networks: Representation and Architectural Issues. <b>2021</b> , 27-59	
926	The prevalence of novel periodontal pathogens and bacterial complexes in Stage II generalized periodontitis based on 16S rRNA next generation sequencing. <b>2021</b> , 29, e20200787	5
925	Function-driven microbial genomics for ecofriendly agriculture. <b>2021</b> , 389-431	0
924	Rhizosphere Dynamics: An OMICS Perspective. <b>2021</b> , 73-88	0
923	Imaging the in vivo growth patterns of bacteria in human gut Microbiota. <b>2021</b> , 13, 1960134	4

922	Unraveling microbial complexities via metagenomic approach: Expanding cross-talk for environment management and prospecting. <b>2021</b> , 435-453	
921	The Ecuadorian Microbiome Project: a plea to strengthen microbial genomic research. <b>2021</b> , 7, 223-237	1
920	Organic electron donors and terminal electron acceptors structure anaerobic microbial communities and interactions in a permanently stratified sulfidic lake.	
919	Accessing previously uncultured marine microbial resources by a combination of alternative cultivation methods. <b>2021</b> , 14, 1148-1158	2
918	Halocins, Bacteriocin-Like Antimicrobials Produced by the Archaeal Domain: Occurrence and Phylogenetic Diversity in Halobacteriales.	1
917	Conducting research on diet-microbiome interactions: A review of current challenges, essential methodological principles, and recommendations for best practice in study design. <b>2021</b> , 34, 631-644	3
916	Bioprospecting of Novel Extremozymes From Prokaryotes-The Advent of Culture-Independent Methods. <b>2021</b> , 12, 630013	16
915	Recoding enhances the metabolic capabilities of two novel methylotrophic Asgardarchaeota lineages.	1
914	Giant virus-related sequences in the 5300-year-old Ezi mummy metagenome. <b>2021</b> , 57, 222-227	0
913	Emergence of nosocomial associated opportunistic pathogens in the gut microbiome after antibiotic treatment. <b>2021</b> , 10, 36	4
912	Draft Genome Sequence of Methanothermobacter thermautotrophicus WHS, a Thermophilic Hydrogenotrophic Methanogen from Washburn Hot Springs in Yellowstone National Park, USA. <b>2021</b> , 10,	2
911	The Reactobiome Unravels a New Paradigm in Human Gut Microbiome Metabolism.	0
910	Biodegradation of Lindane (Hexachlorocyclohexane) To Nontoxic End Products by Sequential Treatment with Three Mixed Anaerobic Microbial Cultures. <b>2021</b> , 55, 2968-2979	4
909	Bacterial and Archaeal Taxonomic Diversity of Mud Volcanoes (Beciu, Romania) via Metagenomic Approach. <b>2021</b> , 38, 532-539	1
908	The microbiome of the Black Sea water column analyzed by shotgun and genome centric metagenomics. <b>2021</b> , 16, 5	6
907	Rainfall Alters Permafrost Soil Redox Conditions, but Meta-Omics Show Divergent Microbial Community Responses by Tundra Type in the Arctic. <b>2021</b> , 5, 17	0
906	The cyanobacterium has divergent light-harvesting antennae and may have evolved in a low-oxygen ocean. <b>2021</b> , 118,	4
905	Genomic characterization of three novel Desulfobacterota classes expand the metabolic and phylogenetic diversity of the Phylum.	1

904	Antibiotic resistance: Global health crisis and metagenomics. <b>2021</b> , 29, e00604	15
903	Synergy of culture-dependent molecular identification and whole-community metabarcoding sequencing for characterizing the microbiota of arable crop residues.	
902	Isolation and cultivation of a novel sulfate-reducing magnetotactic bacterium belonging to the genus <i>Desulfovibrio</i> . <b>2021</b> , 16, e0248313	5
901	Recovery of high-qualified Genomes from a deep-inland Salt Lake Using BASALT.	4
900	Metagenomic Data Assembly - The Way of Decoding Unknown Microorganisms. <b>2021</b> , 12, 613791	20
899	The very early evolution of protein translocation across membranes. <b>2021</b> , 17, e1008623	6
898	Resilience of the oral microbiome. <b>2021</b> , 86, 113-122	22
897	Patterns of gene content and co-occurrence constrain the evolutionary path toward animal association in CPR bacteria.	3
896	Genome-resolved metagenomics using environmental and clinical samples. <b>2021</b> , 22,	6
895	Adaptive ecological processes and metabolic independence drive microbial colonization and resilience in the human gut.	7
894	Organic Electron Donors and Terminal Electron Acceptors Structure Anaerobic Microbial Communities and Interactions in a Permanently Stratified Sulfidic Lake. <b>2021</b> , 12, 620424	2
893	The Three Domains of Life Within the Discharge Area of a Shallow Subterranean Estuary at a High Energy Beach. <b>2021</b> , 9,	0
892	Genomic analysis of family UBA6911 (Group 18 Acidobacteria) expands the metabolic capacities of the phylum and highlights adaptations to terrestrial habitats.	1
891	Diurnal changes in bacterial communities in oxic surface and hypoxic middle seawater layers of the Changjiang River Estuary. <b>2021</b> , 40, 92-106	
890	Signatures of optimal codon usage in metabolic genes inform budding yeast ecology. <b>2021</b> , 19, e3001185	2
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887	Unraveling the critical growth factors for stable cultivation of (nano-sized) Micrarchaeota.	1

886	Genomes of Thaumarchaeota from deep sea sediments reveal specific adaptations of three independently evolved lineages. <b>2021</b> , 15, 2792-2808	6
885	A single-cell genomics pipeline for environmental microbial eukaryotes. <b>2021</b> , 24, 102290	3
884	Sequence and evolutionary analysis of bacterial ribosomal S1 proteins. <b>2021</b> , 89, 1111-1124	3
883	Ten Years of Collaborative Progress in the Quest for Orthologs. <b>2021</b> , 38, 3033-3045	2
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881	Soil, ocean, hot spring, and host-associated environments reveal unique selection pressures on genomic features of bacteria in microbial communities.	
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879	Casting Light on the Adaptation Mechanisms and Evolutionary History of the Widespread Sumerlaeota. <b>2021</b> , 12,	3
878	Imaging Commensal Microbiota and Pathogenic Bacteria in the Gut. <b>2021</b> , 54, 2076-2087	10
877	Prokaryotic taxonomy and nomenclature in the age of big sequence data. <b>2021</b> , 15, 1879-1892	24
876	Assessment of 16S rRNA Gene-Based Phylogenetic Diversity of Archaeal Communities in Halite-Crystal Salts Processed from Natural Saharan Saline Systems of Southern Tunisia. <b>2021</b> , 10,	1
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874	Sequence analysis of tyrosine recombinases allows annotation of mobile genetic elements in prokaryotic genomes. <b>2021</b> , 17, e9880	4
873	A metagenomic view of novel microbial and metabolic diversity found within the deep terrestrial biosphere.	2
872	Archaea: A Gold Mine for Topoisomerase Diversity. <b>2021</b> , 12, 661411	2
871	A human respiratory tract-associated bacterium with an extremely small genome. <b>2021</b> , 4, 628	2
870	Proteomics, Personalized Medicine and Cancer. <b>2021</b> , 13,	9
869	Genetic insights into the dark matter of the mammalian gut microbiota through targeted genome reconstruction. <b>2021</b> , 23, 3294-3305	2

868	Triggering Growth via Growth Initiation Factors in Nature: A Putative Mechanism for Cultivation of Previously Uncultivated Microorganisms. <b>2021</b> , 12, 537194	1
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866	Reconstruction of metagenome-assembled genomes from aquaria.	
865	Enlightening the taxonomy darkness of human gut microbiomes with a cultured biobank. <b>2021</b> , 9, 119	3
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863	Strategies for Natural Products Discovery from Uncultured Microorganisms. <b>2021</b> , 26,	5
862	Genomic Analysis of the Yet-Uncultured Binatota Reveals Broad Methylotrophic, Alkane-Degradation, and Pigment Production Capacities. <b>2021</b> , 12,	1
861	The Molecular Basis for Life in Extreme Environments. <b>2021</b> , 50, 343-372	9
860	Editorial: New Insights Into the Biodegradation of Organic Contaminants in Subsurface Ecosystems: Approaches and Achievements of the Multiomics Era. <b>2021</b> , 12, 650615	1
859	Archaea: An Agro-Ecological Perspective. <b>2021</b> , 78, 2510-2521	3
858	Evaluation of acidogenesis products' effect on biogas production performed with metagenomics and isotopic approaches. <b>2021</b> , 14, 125	4
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856	Wide-bound salt tolerance of the inocula from marine sediment and their specific microbial community. <b>2021</b> , 197, 111119	0
855	Integrative omics of schizophrenia: from genetic determinants to clinical classification and risk prediction. <b>2021</b> ,	5
854	A computational screen for alternative genetic codes in over 250,000 genomes.	1
853	H-dependent formate production by hyperthermophilic Thermococcales: an alternative to sulfur reduction for reducing-equivalents disposal. <b>2021</b> , 15, 3423-3436	1
852	Candidatus Nanoalobium. 1-5	
851	A standardized archaeal taxonomy for the Genome Taxonomy Database. <b>2021</b> , 6, 946-959	34

850	Protein Family Content Uncovers Lineage Relationships and Bacterial Pathway Maintenance Mechanisms in DPANN Archaea. <b>2021</b> , 12, 660052	2
849	Accurate annotation of protein coding sequences with IDTAXA. <b>2021</b> , 3, lqab080	
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847	Recoding of stop codons expands the metabolic potential of two novel Asgardarchaeota lineages. <b>2021</b> , 1,	4
846	Prokaryotic Diversity and Hydrogenotrophic Methanogenesis in an Alkaline Spring (La Crouen, New Caledonia). <b>2021</b> , 9,	2
845	GUNC: detection of chimerism and contamination in prokaryotic genomes. <b>2021</b> , 22, 178	16
844	Going to extremes - a metagenomic journey into the dark matter of life. <b>2021</b> , 368,	7
843	efam: an expanded, metaproteome-supported HMM profile database of viral protein families. <b>2021</b> ,	6
842	Prokaryotic and eukaryotic diversity in hydrothermal continental systems. <b>2021</b> , 203, 3751-3766	0
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