Citation Report

List of articles citing

The SILVA ribosomal RNA gene database project: improved data processing and web-based tools

DOI: 10.1093/nar/gks1219
Nucleic Acids Research, 2013, 41, D590-6.

Source: https://exaly.com/paper-pdf/53426068/citation-report.pdf
Version: 2024-04-25

#	Paper	IF	Citations
2221	Nontuberculous Mycobacteria in Two Drinking Water Distribution Systems and the Role of Residual Disinfection.		
2220	.		
2219	The 2013 Nucleic Acids Research Database Issue and the online molecular biology database collection. *Nucleic Acids Research*, **2013**, 41, D1-7	20.1	73
2218	Viral categorization and discovery in human circulation by transcriptome sequencing. **2013**, 436, 525-9		4
2217	Aptasensor and genosensor methods for detection of microbes in real world samples. **2013**, 64, 229-40		73
2216	Survival in hostile territory: the microbiota of the stomach. **2013**, 37, 736-61		99
2215	Molecular signatures for the phylum Aquificae and its different clades: proposal for division of the phylum Aquificae into the emended order Aquificales, containing the families Aquificaceae and Hydrogenothermaceae, and a new order Desulfurobacteriales ord. nov., containing the family Desulfurobacteriaceae. **2013**, 104, 349-68		26
2214	On the description of Tisochrysis lutea gen. nov. sp. nov. and Isochrysis nuda sp. nov. in the Isochrysidales, and the transfer of Dicrateria to the Prymnesiales (Haptophyta). **2013**, 25, 1763-1776		136
2213	Differences in fungi present in induced sputum samples from asthma patients and non-atopic controls: a community based case control study. **2013**, 13, 69		106
2212	Microeukaryote community composition assessed by pyrosequencing is associated with light availability and phytoplankton primary production along a lowland river. **2013**, 58, n/a-n/a		3
2211	The microbiome of North Sea copepods. **2013**, 67, 757-773		20
2210	Eukaryotic diversity in premise drinking water using 18S rDNA sequencing: implications for health risks. **2013**, 20, 6351-66		38
2209	Hydrocarbon-degrading bacteria enriched by the Deepwater Horizon oil spill identified by cultivation and DNA-SIP. **2013**, 7, 2091-104		198
2208	Filtering and ranking techniques for automated selection of high-quality 16S rRNA gene sequences. **2013**, 36, 549-59		4
2207	A genomic update on clostridial phylogeny: Gram-negative spore formers and other misplaced clostridia. **2013**, 15, 2631-41		362
2206	The human mycobiome in health and disease. **2013**, 5, 63		204
2205	Isosteric and nonisosteric base pairs in RNA motifs: molecular dynamics and bioinformatics study of the sarcin-ricin internal loop. **2013**, 117, 14302-19		18

2204	Intragenomic heterogeneity of 16S rRNA genes causes overestimation of prokaryotic diversity. **2013**, 79, 5962-9	193
2203	Sequencing the human microbiome in health and disease. **2013**, 22, R88-94	89
2202	Insights into the structure and metabolic function of microbes that shape pelagic iron-rich aggregates ("iron snow"). **2013**, 79, 4272-81	46
2201	Microbiota modulate behavioral and physiological abnormalities associated with neurodevelopmental disorders. **2013**, 155, 1451-63	1963
2200	Filterable microbial forms in the Rybinsk water reservoir. **2013**, 82, 728-734	4
2199	Soil microbial diversity patterns of a lowland spring environment. **2013**, 86, 172-84	25
2198	Alignment-free supervised classification of metagenomes by recursive SVM. **2013**, 14, 641	21
2197	Phylogenomics and molecular signatures for the order Neisseriales: proposal for division of the order Neisseriales into the emended family Neisseriaceae and Chromobacteriaceae fam. nov. **2013**, 104, 1-24	33
2196	Transcriptomics-based screen for genes induced by flagellin and repressed by pathogen effectors identifies a cell wall-associated kinase involved in plant immunity. **2013**, 14, R139	92
2195	Comparative genomics reveals candidate carotenoid pathway regulators of ripening watermelon fruit. **2013**, 14, 781	77
2194	Advection shapes Southern Ocean microbial assemblages independent of distance and environment effects. **2013**, 4, 2457	87
2193	A newly isolated Chlorella sp. from desert sand crusts exhibits a unique resistance to excess light intensity. **2013**, 86, 373-80	43
2192	Whole cell immunomagnetic enrichment of environmental microbial consortia using rRNA-targeted Magneto-FISH. **2013**, 531, 21-44	8
2191	Coupling FACS and genomic methods for the characterization of uncultivated symbionts. **2013**, 531, 45-60	4
2190	Advancing our understanding of the human microbiome using QIIME. **2013**, 531, 371-444	373
2189	Substrate induced emergence of different active bacterial and archaeal assemblages during biomethane production. **2013**, 148, 517-24	23
2188	Investigation of the koala (Phascolarctos cinereus) hindgut microbiome via 16S pyrosequencing. **2013**, 167, 554-64	37
2187	Linking isoprenoidal GDGT membrane lipid distributions with gene abundances of ammonia-oxidizing Thaumarchaeota and uncultured crenarchaeotal groups in the water column of a tropical lake (Lake Challa, East Africa). **2013**, 15, 2445-62	59

2186	Topographic diversity of fungal and bacterial communities in human skin. **2013**, 498, 367-70		693
2185	Ribosome profiling reveals resemblance between long non-coding RNAs and 5' leaders of coding RNAs. **2013**, 140, 2828-34		196
2184	Mobile elements in a single-filament orange Guaymas Basin Beggiatoa ("Candidatus Maribeggiatoa") sp. draft genome: evidence for genetic exchange with cyanobacteria. **2013**, 79, 3974-85		23
2183	A single betaproteobacterium dominates the microbial community of the crambescidine-containing sponge Crambe crambe. **2013**, 3, 2583		45
2182	Standard methods for research on Apis mellifera gut symbionts. **2013**, 52, 1-24		62
2181	An evolutionary conserved pattern of 18S rRNA sequence complementarity to mRNA 5' UTRs and its implications for eukaryotic gene translation regulation. *Nucleic Acids Research*, **2013**, 41, 7625-34	20.1	19
2180	Analytical tools and databases for metagenomics in the next-generation sequencing era. **2013**, 11, 102-13		98
2179	Mineralogical Study of a Biologically-Based Treatment System That Removes Arsenic, Zinc and Copper from Landfill Leachate. **2013**, 3, 427-449		9
2178	Oral bacterial community dynamics in paediatric patients with malignancies in relation to chemotherapy-related oral mucositis: a prospective study. **2013**, 19, E559-67		28
2177	Microbial diversity in The Cedars, an ultrabasic, ultrareducing, and low salinity serpentinizing ecosystem. **2013**, 110, 15336-41		72
2176	Oligotyping: Differentiating between closely related microbial taxa using 16S rRNA gene data. **2013**, 4, 1111		407
2175	Genome Diversity of Spore-Forming Firmicutes. **2013**, 1,		114
2174	The microbiology of deep-sea hydrothermal vent plumes: ecological and biogeographic linkages to seafloor and water column habitats. **2013**, 4, 124		108
2173	A phylogenomic and molecular signature based approach for characterization of the phylum Spirochaetes and its major clades: proposal for a taxonomic revision of the phylum. **2013**, 4, 217		52
2172	Assessment of viral community functional potential from viral metagenomes may be hampered by contamination with cellular sequences. **2013**, 3, 130160		97
2171	Different seasonality of pelagic and benthic Thaumarchaeota in the North Sea. **2013**, 10, 7195-7206		26
2170	Transcriptome characterisation of the ant Formica exsecta with new insights into the evolution of desaturase genes in social hymenoptera. **2013**, 8, e68200		13
2169	The effect of primer choice and short read sequences on the outcome of 16S rRNA gene based diversity studies. **2013**, 8, e71360		90

2168	Microbial communities of deep-sea methane seeps at Hikurangi continental margin (New Zealand). **2013**, 8, e72627	56
2167	Characterization of eukaryotic microbial diversity in hypersaline Lake Tyrrell, Australia. **2013**, 4, 115	40
2166	Methanogens at the top of the world: occurrence and potential activity of methanogens in newly deglaciated soils in high-altitude cold deserts in the Western Himalayas. **2013**, 4, 359	34
2165	Virus-host and CRISPR dynamics in Archaea-dominated hypersaline Lake Tyrrell, Victoria, Australia. **2013**, 2013, 370871	57
2164	Assessment of helminth biodiversity in wild rats using 18S rDNA based metagenomics. **2014**, 9, e110769	35
2163	Bacterial communities in Malagasy soils with differing levels of disturbance affecting botanical diversity. **2014**, 9, e85097	6
2162	Diversity of rumen bacteria in canadian cervids. **2014**, 9, e89682	49
2161	Optimal eukaryotic 18S and universal 16S/18S ribosomal RNA primers and their application in a study of symbiosis. **2014**, 9, e90053	64
2160	Microbiota present in cystic fibrosis lungs as revealed by whole genome sequencing. **2014**, 9, e90934	31
2159	Novel PCR primers for the archaeal phylum Thaumarchaeota designed based on the comparative analysis of 16S rRNA gene sequences. **2014**, 9, e96197	5
2158	Community shifts in the surface microbiomes of the coral Porites astreoides with unusual lesions. **2014**, 9, e100316	72
2157	MediaDB: a database of microbial growth conditions in defined media. **2014**, 9, e103548	20
2156	An unclassified microorganism: novel pathogen candidate lurking in human airways. **2014**, 9, e103646	5
2155	Exploring microRNA-like small RNAs in the filamentous fungus Fusarium oxysporum. **2014**, 9, e104956	54
2154	Phylogenetic analysis of algal symbionts associated with four North American amphibian egg masses. **2014**, 9, e108915	38
2153	Specific microbiome changes in a mouse model of parenteral nutrition associated liver injury and intestinal inflammation. **2014**, 9, e110396	51
2152	Biogeochemical typing of paddy field by a data-driven approach revealing sub-systems within a complex environment--a pipeline to filtrate, organize and frame massive dataset from multi-omics analyses. **2014**, 9, e110723	21
2151	Faecal microbiota of forage-fed horses in New Zealand and the population dynamics of microbial communities following dietary change. **2014**, 9, e112846	79

2150	Stable composition of the nano- and picoplankton community during the ocean iron fertilization experiment LOHAFEX. **2014**, 9, e113244	13
2149	Massive regime shifts and high activity of heterotrophic bacteria in an ice-covered lake. **2014**, 9, e113611	35
2148	Early canine plaque biofilms: characterization of key bacterial interactions involved in initial colonization of enamel. **2014**, 9, e113744	43
2147	Diversity, distribution and hydrocarbon biodegradation capabilities of microbial communities in oil-contaminated cyanobacterial mats from a constructed wetland. **2014**, 9, e114570	41
2146	Alkane Biosynthesis Genes in Cyanobacteria and Their Transcriptional Organization. **2014**, 2, 24	42
2145	Shotgun metagenomic data reveals significant abundance but low diversity of "Candidatus Scalindua" marine anammox bacteria in the Arabian Sea oxygen minimum zone. **2014**, 5, 31	27
2144	High frequency of phylogenetically diverse reductive dehalogenase-homologous genes in deep subseafloor sedimentary metagenomes. **2014**, 5, 80	47
2143	Spatial variations of community structures and methane cycling across a transect of Lei-Gong-Hou mud volcanoes in eastern Taiwan. **2014**, 5, 121	11
2142	The giant ciliate Zoothamnium niveum and its thiotrophic epibiont Candidatus Thiobios zoothamnicoli: a model system to study interspecies cooperation. **2014**, 5, 145	19
2141	High-Throughput Sequencing, a VersatileWeapon to Support Genome-Based Diagnosis in Infectious Diseases: Applications to Clinical Bacteriology. **2014**, 3, 258-79	19
2140	Meat Science and Muscle Biology Symposium: Escherichia coli O157:H7, diet, and fecal microbiome in beef cattle. **2014**, 92, 1345-55	12
2139	Reliability of qPCR for quantitative gut content estimation in the circumglobally abundant pelagic tunicate Dolioletta gegenbauri (Tunicata, Thaliacea). **2014**, 1, 18-24	10
2138	Diversity and abundance of "Pelagibacterales" (SAR11) in the Baltic Sea salinity gradient. **2014**, 37, 601-4	37
2137	Fastq_clean: An optimized pipeline to clean the Illumina sequencing data with quality control. **2014**,	31
2136	History and impact of RDP: a legacy from Carl Woese to microbiology. **2014**, 11, 239-43	15
2135	Rapid species-level identification of vaginal and oral lactobacilli using MALDI-TOF MS analysis and 16S rDNA sequencing. **2014**, 14, 312	45
2134	An expanded genomic representation of the phylum cyanobacteria. **2014**, 6, 1031-45	186
2133	The presence of nitrate dramatically changed the predominant microbial community in perchlorate degrading cultures under saline conditions. **2014**, 14, 225	17

2132	The genome of Cardinium cBtQ1 provides insights into genome reduction, symbiont motility, and its settlement in Bemisia tabaci. **2014**, 6, 1013-30	46
2131	LotuS: an efficient and user-friendly OTU processing pipeline. **2014**, 2, 30	186
2130	Improved HF183 quantitative real-time PCR assay for characterization of human fecal pollution in ambient surface water samples. **2014**, 80, 3086-94	163
2129	Identification and activity of acetate-assimilating bacteria in diffuse fluids venting from two deep-sea hydrothermal systems. **2014**, 90, 731-46	16
2128	Efficient CO2 fixation by surface Prochlorococcus in the Atlantic Ocean. **2014**, 8, 2280-9	25
2127	Life in an unusual intracellular niche: a bacterial symbiont infecting the nucleus of amoebae. **2014**, 8, 1634-44	32
2126	A method for de novo nucleic acid diagnostic target discovery. **2014**, 30, 3174-80	4
2125	In-depth analyses of deep subsurface sediments using 454-pyrosequencing reveals a reservoir of buried fungal communities at record-breaking depths. **2014**, 90, 908-21	36
2124	Microbial sulfur transformations in sediments from Subglacial Lake Whillans. **2014**, 5, 594	49
2123	Chemolithotrophy in the continental deep subsurface: Sanford Underground Research Facility (SURF), USA. **2014**, 5, 610	74
2122	Bayesian phylogeny of sucrose transporters: ancient origins, differential expansion and convergent evolution in monocots and dicots. **2014**, 5, 615	34
2121	Parasites in algae mass culture. **2014**, 5, 278	119
2120	Convergent bacterial microbiotas in the fungal agricultural systems of insects. **2014**, 5, e02077	68
2119	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. **2014**, 5, 231	26
2118	Aerobic methanotrophic communities at the Red Sea brine-seawater interface. **2014**, 5, 487	24
2117	Phaeocystis antarctica blooms strongly influence bacterial community structures in the Amundsen Sea polynya. **2014**, 5, 646	58
2116	Illuminating microbial dark matter in meromictic Sakinaw Lake. **2014**, 80, 6807-18	79
2115	Oxygenic photosynthesis as a protection mechanism for cyanobacteria against iron-encrustation in environments with high Fe(2+) concentrations. **2014**, 5, 459	4

2114	Ecological consistency of SSU rRNA-based operational taxonomic units at a global scale. **2014**, 10, e1003594	58
2113	Systems biology studies of adult paragonimus lung flukes facilitate the identification of immunodominant parasite antigens. **2014**, 8, e3242	20
2112	Metagenomic evidence for metabolism of trace atmospheric gases by high-elevation desert Actinobacteria. **2014**, 5, 698	47
2111	Assessing the accuracy of quantitative molecular microbial profiling. **2014**, 15, 21476-91	16
2110	PhylOPDb: a 16S rRNA oligonucleotide probe database for prokaryotic identification. **2014**, 2014, bau036	13
2109	Comparative metagenomic analysis of human gut microbiome composition using two different bioinformatic pipelines. **2014**, 2014, 325340	44
2108	Carbadox has both temporary and lasting effects on the swine gut microbiota. **2014**, 5, 276	48
2107	Molecular analysis of the microbiota in hard feces from healthy rabbits (Oryctolagus cuniculus) medicated with long term oral meloxicam. **2014**, 10, 62	22
2106	Microbial diversity in a Venezuelan orthoquartzite cave is dominated by the Chloroflexi (Class Ktedonobacterales) and Thaumarchaeota Group I.1c. **2014**, 5, 615	45
2105	Draft Genome Sequence of Acinetobacter baumannii Strain ABBL099, a Multidrug-Resistant Clinical Outbreak Isolate with a Novel Multilocus Sequence Type. **2014**, 2,	2
2104	Effect of copper treatment on the composition and function of the bacterial community in the sponge Haliclona cymaeformis. **2014**, 5, e01980	24
2103	Protocols for Investigating the Microbiology of Drilling Fluids, Hydraulic Fracturing Fluids, and Formations in Unconventional Natural Gas Reservoirs. **2014**, 133-156	1
2102	Prolonged use of a proton pump inhibitor reduces microbial diversity: implications for Clostridium difficile susceptibility. **2014**, 2, 42	100
2101	Linking geology and microbiology: inactive pockmarks affect sediment microbial community structure. **2014**, 9, e85990	9
2100	A global comparison of Bactericera cockerelli (Hemiptera: Triozidae) microbial communities. **2014**, 43, 344-52	13
2099	Characterization of bacteriophage communities and CRISPR profiles from dental plaque. **2014**, 14, 175	41
2098	Altered oral viral ecology in association with periodontal disease. **2014**, 5, e01133-14	108
2097	Evaluation of the nasal microbiota in slaughter-age pigs and the impact on nasal methicillin-resistant Staphylococcus aureus (MRSA) carriage. **2014**, 10, 69	37

2096	Small RNA profiling of Xenopus embryos reveals novel miRNAs and a new class of small RNAs derived from intronic transposable elements. **2014**, 24, 96-106	16
2095	Identification of Conserved Indels that are Useful for Classification and Evolutionary Studies. **2014**, 41, 153-182	25
2094	Droplet-based microfluidics platform for ultra-high-throughput bioprospecting of cellulolytic microorganisms. **2014**, 21, 1722-32	65
2093	Anaerobic methanotrophic community of a 5346-m-deep vesicomyid clam colony in the Japan Trench. **2014**, 12, 183-99	20
2092	The oral microbiome and oral cancer. **2014**, 34, 711-9	57
2091	Microbial community of the bottom sediments of the brackish Lake Beloe (Transbaikal region). **2014**, 83, 861-868	7
2090	Endospores of thermophilic bacteria as tracers of microbial dispersal by ocean currents. **2014**, 8, 1153-65	85
2089	Determining the culturability of the rumen bacterial microbiome. **2014**, 7, 467-79	105
2088	Productivity and salinity structuring of the microplankton revealed by comparative freshwater metagenomics. **2014**, 16, 2682-98	60
2087	Microbial consumption of zero-valence sulfur in marine benthic habitats. **2014**, 16, 3416-30	49
2086	Analysis of the factors affecting the formation of the microbiome associated with chronic osteomyelitis of the jaw. **2014**, 20, O309-17	17
2085	Anaerobic oxidation of methane by sulfate in hypersaline groundwater of the Dead Sea aquifer. **2014**, 12, 511-28	34
2084	Phylogenetic constraints on elemental stoichiometry and resource allocation in heterotrophic marine bacteria. **2014**, 16, 1398-410	50
2083	Microbial communities involved in biogas production from wheat straw as the sole substrate within a two-phase solid-state anaerobic digestion. **2014**, 37, 590-600	41
2082	Mathematical tools to optimize the design of oligonucleotide probes and primers. **2014**, 98, 9595-608	11
2081	Diversity and genomic insights into the uncultured Chloroflexi from the human microbiota. **2014**, 16, 2635-43	38
2080	In situ identification of the synthrophic protein fermentative Coprothermobacter spp. involved in the thermophilic anaerobic digestion process. **2014**, 358, 55-63	10
2079	The All-Species Living Tree Project. **2014**, 41, 45-59	3

2078	A tree of cellular life inferred from a genomic census of molecular functions. **2014**, 79, 240-62	21
2077	Complete genome sequence of producer of the glycopeptide antibiotic Aculeximycin Kutzneria albida DSM 43870T, a representative of minor genus of Pseudonocardiaceae. **2014**, 15, 885	18
2076	Interspecific and host-related gene expression patterns in nematode-trapping fungi. **2014**, 15, 968	19
2075	Molecular analysis of bacterial diversity in mudflats along the salinity gradient of an acidified tropical Bornean estuary (South East Asia). **2014**, 10, 10	13
2074	Sȃnce: reference-based phylogenetic analysis for 18S rRNA studies. **2014**, 14, 235	8
2073	Alcohol and tobacco consumption affects bacterial richness in oral cavity mucosa biofilms. **2014**, 14, 250	42
2072	Diet disparity among sympatric herbivorous cichlids in the same ecomorphs in Lake Tanganyika: amplicon pyrosequences on algal farms and stomach contents. **2014**, 12, 90	22
2071	Evaluation of the impact of refrigeration on next generation sequencing-based assessment of the canine and feline fecal microbiota. **2014**, 10, 230	12
2070	Settling down: the genome of Serratia symbiotica from the aphid Cinara tujafilina zooms in on the process of accommodation to a cooperative intracellular life. **2014**, 6, 1683-98	59
2069	Characterization of the 18S rRNA gene for designing universal eukaryote specific primers. **2014**, 9, e87624	244
2068	Peripheral benzodiazepine receptor/translocator protein global knock-out mice are viable with no effects on steroid hormone biosynthesis. **2014**, 289, 27444-54	174
2067	Nasal carriage of methicillin resistant staphylococci. **2014**, 20, 108-17	13
2066	Microbial lipids reveal carbon assimilation patterns on hydrothermal sulfide chimneys. **2014**, 16, 3515-32	24
2065	Ecology in the age of DNA barcoding: the resource, the promise and the challenges ahead. **2014**, 14, 221-32	80
2064	Aerially transmitted human fungal pathogens: what can we learn from metagenomics and comparative genomics?. **2014**, 31, 54-61	4
2063	Meta-QC-Chain: comprehensive and fast quality control method for metagenomic data. **2014**, 12, 52-6	15
2062	Biodegradation of naphthenic acids in oils sands process waters in an immobilized soil/sediment bioreactor. **2014**, 109, 164-72	46
2061	Characterization of the oral microbiota of healthy cats using next-generation sequencing. **2014**, 201, 223-9	51

2060	Community differentiation and population enrichment of Sargasso Sea bacterioplankton in the euphotic zone of a mesoscale mode-water eddy. **2014**, 16, 871-87		40
2059	Metagenomic 16S rDNA Illumina tags are a powerful alternative to amplicon sequencing to explore diversity and structure of microbial communities. **2014**, 16, 2659-71		200
2058	16S rDNA pyrosequencing analysis of bacterial community in heavy metals polluted soils. **2014**, 67, 635-47		167
2057	Primer evaluation and adaption for cost-efficient SYBR Green-based qPCR and its applicability for specific quantification of methanogens. **2014**, 30, 293-304		14
2056	Microscale evidence for a high decrease of soil bacterial density and diversity by cropping. **2014**, 34, 831-840		31
2055	Metagenomic analysis of sludge from full-scale anaerobic digesters operated in municipal wastewater treatment plants. **2014**, 98, 5709-18		147
2054	Distribution of a consortium between unicellular algae and the N2 fixing cyanobacterium UCYN-A in the North Atlantic Ocean. **2014**, 16, 3153-67		29
2053	Clinical detection of human probiotics and human pathogenic bacteria by using a novel high-throughput platform based on next generation sequencing. **2014**, 4, 1		11
2052	High-throughput DNA sequencing of the ruminal bacteria from moose (Alces alces) in Vermont, Alaska, and Norway. **2014**, 68, 185-95		37
2051	Extracellular DNA can preserve the genetic signatures of present and past viral infection events in deep hypersaline anoxic basins. **2014**, 281, 20133299		53
2050	Specific microbial attachment to root knot nematodes in suppressive soil. **2014**, 80, 2679-86		58
2049	Longitudinal study of murine microbiota activity and interactions with the host during acute inflammation and recovery. **2014**, 8, 1101-14		121
2048	POGO-DB--a database of pairwise-comparisons of genomes and conserved orthologous genes. *Nucleic Acids Research*, **2014**, 42, D625-32	20.1	19
2047	Weak phylogenetic signal in physiological traits of methane-oxidizing bacteria. **2014**, 27, 1240-7		12
2046	Archaeal diversity and the extent of iron and manganese pyritization in sediments from a tropical mangrove creek (Cardoso Island, Brazil). **2014**, 146, 1-13		12
2045	Improved group-specific primers based on the full SILVA 16S rRNA gene reference database. **2014**, 16, 2389-407		28
2044	Atmospheric N deposition increases bacterial laccase-like multicopper oxidases: implications for organic matter decay. **2014**, 80, 4460-8		37
2043	Gene expression of lactobacilli in murine forestomach biofilms. **2014**, 7, 347-59		24

2042	River organic matter shapes microbial communities in the sediment of the Rhône prodelta. **2014**, 8, 2327-38	38
2041	Cultivation-independent analysis of microbial communities on Austrian raw milk hard cheese rinds. **2014**, 180, 88-97	62
2040	Towards molecular biomarkers for biogas production from lignocellulose-rich substrates. **2014**, 29, 10-21	57
2039	Efficiency of RNA extraction from selected bacteria in the context of biogas production and metatranscriptomics. **2014**, 29, 85-90	19
2038	Host-specificity among abundant and rare taxa in the sponge microbiome. **2014**, 8, 1198-209	159
2037	The (d)evolution of methanotrophy in the Beijerinckiaceae--a comparative genomics analysis. **2014**, 8, 369-82	67
2036	A molecular gut content study of Themisto abyssorum (Amphipoda) from Arctic hydrothermal vent and cold seep systems. **2014**, 23, 3877-89	12
2035	Soil microbial community responses to a decade of warming as revealed by comparative metagenomics. **2014**, 80, 1777-86	94
2034	Evaluation of the 23S rRNA gene as target for qPCR based quantification of Frankia in soils. **2014**, 37, 229-34	10
2033	RNA-Seq analysis of the toxicant-induced transcriptome of the marine diatom, Ceratoneis closterium. **2014**, 16, 45-53	15
2032	Phreatobacter oligotrophus gen. nov., sp. nov., an alphaproteobacterium isolated from ultrapure water of the water purification system of a power plant. **2014**, 64, 839-845	26
2031	Winter-summer succession of unicellular eukaryotes in a meso-eutrophic coastal system. **2014**, 67, 13-23	31
2030	Comparison of two approaches for the classification of 16S rRNA gene sequences. **2014**, 63, 1311-1315	9
2029	Analytical tools and current challenges in the modern era of neuroepigenomics. **2014**, 17, 1476-90	75
2028	Evidence of natural Wolbachia infections in field populations of Anopheles gambiae. **2014**, 5, 3985	110
2027	Rapid succession of uncultured marine bacterial and archaeal populations in a denitrifying continuous culture. **2014**, 16, 3275-86	17
2026	Diazotrophic potential among bacterial communities associated with wild and cultivated Agave species. **2014**, 90, 844-57	43
2025	Production of polyol oils from soybean oil by bioprocess: results of microbial screening and identification of positive cultures. **2014**, 3, 155-160	2

2024	Pezizomycotina dominates the fungal communities of South China Sea sponges Theonella swinhoei and Xestospongia testudinaria. **2014**, 90, 935-45	14
2023	Comparative analysis of deep-sea bacterioplankton OMICS revealed the occurrence of habitat-specific genomic attributes. **2014**, 17, 1-8	7
2022	Internal porosity of mineral coating supports microbial activity in rapid sand filters for groundwater treatment. **2014**, 80, 7010-20	27
2021	Methanobacterium paludis sp. nov. and a novel strain of Methanobacterium lacus isolated from northern peatlands. **2014**, 64, 1473-1480	34
2020	New insights into Oculina patagonica coral diseases and their associated Vibrio spp. communities. **2014**, 8, 1794-807	36
2019	ESTIMATING BACTERIAL DIVERSITY IN (THYSANOPTERA: THRIPIDAE) VIA NEXT GENERATION SEQUENCING. **2014**, 97, 362-366	11
2018	Stimulation of growth by proteorhodopsin phototrophy involves regulation of central metabolic pathways in marine planktonic bacteria. **2014**, 111, E3650-8	67
2017	Construction of aligned database of dsrA, a gene encoding dissimilatory sulfite reductase alpha subunit, for metagenomic studies of sulfate-reducing bacteria. **2014**, 57, 419-427	0
2016	Microbial community degradation of widely used quaternary ammonium disinfectants. **2014**, 80, 5892-900	45
2015	Diversity of bacterial community and detection of nirS- and nirK-encoding denitrifying bacteria in sandy intertidal sediments along Laizhou Bay of Bohai Sea, China. **2014**, 88, 215-23	43
2014	Biogeographic patterns in below-ground diversity in New York City's Central Park are similar to those observed globally. **2014**, 281,	201
2013	High-throughput sequencing reveals neustonic and planktonic microbial eukaryote diversity in coastal waters. **2014**, 50, 960-5	21
2012	16S rRNA-targeted oligonucleotide probes for direct detection of Propionibacterium freudenreichii in presence of Lactococcus lactis with multicolour fluorescence in situ hybridization. **2014**, 59, 320-7	7
2011	Diversity and activity of marine bacterioplankton during a diatom bloom in the North Sea assessed by total RNA and pyrotag sequencing. **2014**, 18 Pt B, 185-92	58
2010	RNA G-quadruplexes cause eIF4A-dependent oncogene translation in cancer. **2014**, 513, 65-70	377
2009	Conducting a microbiome study. **2014**, 158, 250-262	428
2008	Unveiling microbial activities along the halocline of Thetis, a deep-sea hypersaline anoxic basin. **2014**, 8, 2478-89	33
2007	Long-term manure exposure increases soil bacterial community potential for plasmid uptake. **2014**, 6, 125-30	44

2006	Uniting the classification of cultured and uncultured bacteria and archaea using 16S rRNA gene sequences. **2014**, 12, 635-45	1290
2005	Handling temperature bursts reaching 464°C: different microbial strategies in the sisters peak hydrothermal chimney. **2014**, 80, 4585-98	17
2004	Diverse sulfate-reducing bacteria of the Desulfosarcina/Desulfococcus clade are the key alkane degraders at marine seeps. **2014**, 8, 2029-44	134
2003	Metatranskriptomik der Mikrobiota aus der menschlichen Achselhöhle. **2014**, 20, 494-496	
2002	FastaValidator: an open-source Java library to parse and validate FASTA formatted sequences. **2014**, 7, 365	1
2001	The nasal cavity microbiota of healthy adults. **2014**, 2, 27	103
2000	Global analysis of saliva as a source of bacterial genes for insights into human population structure and migration studies. **2014**, 14, 190	11
1999	Data analysis for 16S microbial profiling from different benchtop sequencing platforms. **2014**, 107, 30-7	168
1998	The plastid ancestor originated among one of the major cyanobacterial lineages. **2014**, 5, 4937	52
1997	Bacterial community assemblages associated with the phyllosphere, dermosphere, and rhizosphere of tree species of the Atlantic forest are host taxon dependent. **2014**, 68, 567-74	61
1996	Environmental controls on fungal community composition and abundance over 3 years in native and degraded shrublands. **2014**, 68, 807-17	13
1995	Identification and characterization of alternative splicing in parasitic nematode transcriptomes. **2014**, 7, 151	4
1994	Exploring the uncultured microeukaryote majority in the oceans: reevaluation of ribogroups within stramenopiles. **2014**, 8, 854-66	119
1993	Long-term changes in soil microbial communities during primary succession. **2014**, 69, 359-370	46
1992	Genomic differentiation among two strains of the PS1 clade isolated from geographically separated marine habitats. **2014**, 89, 181-97	12
1991	Farming behaviour of reef fishes increases the prevalence of coral disease associated microbes and black band disease. **2014**, 281, 20141032	48
1990	DegePrime, a program for degenerate primer design for broad-taxonomic-range PCR in microbial ecology studies. **2014**, 80, 5116-23	210
1989	Phylogenetic analysis and molecular signatures defining a monophyletic clade of heterocystous cyanobacteria and identifying its closest relatives. **2014**, 122, 171-85	23

1988	Atypical bacterial rRNA operon structure is prevalent within the Lachnospiraceae, and use of the 16S-23S rRNA internal transcribed spacer region for the rapid identification of ruminal Butyrivibrio and Pseudobutyrivibrio strains. **2014**, 64, 1623-1631	3
1987	Metasecretome-selective phage display approach for mining the functional potential of a rumen microbial community. **2014**, 15, 356	11
1986	The fecal microbiota of semi-free-ranging wood bison (Bison bison athabascae). **2014**, 10, 120	6
1985	Acetobacter sicerae sp. nov., isolated from cider and kefir, and identification of species of the genus Acetobacter by dnaK, groEL and rpoB sequence analysis. **2014**, 64, 2407-2415	28
1984	Vertical distribution of major sulfate-reducing bacteria in a shallow eutrophic meromictic lake. **2014**, 37, 510-9	18
1983	Polyploid evolution of the Brassicaceae during the Cenozoic era. **2014**, 26, 2777-91	122
1982	Alteration of the murine gastrointestinal microbiota by tigecycline leads to increased susceptibility to Clostridium difficile infection. **2014**, 58, 2767-74	53
1981	Abiotic stress tolerance and competition-related traits underlie phylogenetic clustering in soil bacterial communities. **2014**, 17, 1191-201	73
1980	Carbon dioxide and hydrogen sulfide associations with regional bacterial diversity patterns in microbially induced concrete corrosion. **2014**, 48, 7357-64	28
1979	The kinetoplastid parasite Azumiobodo hoyamushi, the causative agent of soft tunic syndrome of the sea squirt Halocynthia roretzi, resides in the East Sea of Korea. **2014**, 116, 36-42	12
1978	Bacterial community structure and its regulating factors in the intertidal sediment along the Liaodong Bay of Bohai Sea, China. **2014**, 169, 585-92	67
1977	"Candidatus Sonnebornia yantaiensis", a member of candidate division OD1, as intracellular bacteria of the ciliated protist Paramecium bursaria (Ciliophora, Oligohymenophorea). **2014**, 37, 35-41	71
1976	Evaluation of 16SpathDB 2.0, an automated 16S rRNA gene sequence database, using 689 complete bacterial genomes. **2014**, 78, 105-15	14
1975	Selective isolation of bacterial cells within a microfluidic device using magnetic probe-based cell fishing. **2014**, 195, 581-589	27
1974	Microbial diversities (16S and 18S rRNA gene pyrosequencing) and environmental pathogens within drinking water biofilms grown on the common premise plumbing materials unplasticized polyvinylchloride and copper. **2014**, 88, 280-95	55
1973	Role of methylotrophs in the degradation of hydrocarbons during the Deepwater Horizon oil spill. **2014**, 8, 2543-5	22
1972	A phylogenomic and molecular marker based proposal for the division of the genus Borrelia into two genera: the emended genus Borrelia containing only the members of the relapsing fever Borrelia, and the genus Borreliella gen. nov. containing the members of the Lyme disease Borrelia (Borrelia burgdorferi sensu lato complex). **2014**, 105, 1049-72	108
1971	Generation of colonic IgA-secreting cells in the caecal patch. **2014**, 5, 3704	88

1970	Unraveling the outcome of 16S rDNA-based taxonomy analysis through mock data and simulations. **2014**, 30, 1530-8	27
1969	Functional type 2 photosynthetic reaction centers found in the rare bacterial phylum Gemmatimonadetes. **2014**, 111, 7795-800	138
1968	Distinct signatures of host-microbial meta-metabolome and gut microbiome in two C57BL/6 strains under high-fat diet. **2014**, 8, 2380-96	87
1967	Indications for algae-degrading benthic microbial communities in deep-sea sediments along the Antarctic Polar Front. **2014**, 108, 6-16	41
1966	Towards an integrated understanding of gut microbiota using insects as model systems. **2014**, 69, 12-8	36
1965	Automated design of probes for rRNA-targeted fluorescence in situ hybridization reveals the advantages of using dual probes for accurate identification. **2014**, 80, 5124-33	24
1964	Revegetation as an efficient means of improving the diversity and abundance of soil eukaryotes in the Loess Plateau of China. **2014**, 70, 169-174	18
1963	Changes in the bacterial microbiota in gut, blood, and lungs following acute LPS instillation into mice lungs. **2014**, 9, e111228	97
1962	Diversity and distribution of eukaryotic microbes in and around a brine pool adjacent to the Thuwal cold seeps in the Red Sea. **2014**, 5, 37	21
1961	Antibacterial gene transfer across the tree of life. **2014**, 3,	49
1960	Pseudomonas isolation and identification: an introduction to the challenges of polyphasic taxonomy. **2014**, 15, 287-91	3
1959	Purifying the impure: sequencing metagenomes and metatranscriptomes from complex animal-associated samples. **2014**,	18
1958	Localized electron transfer rates and microelectrode-based enrichment of microbial communities within a phototrophic microbial mat. **2014**, 5, 11	25
1957	High-throughput sequencing characterizes intertidal meiofaunal communities in northern Gulf of Mexico (Dauphin Island and Mobile Bay, Alabama). **2014**, 227, 161-74	21
1956	Multiple approaches to microbial source tracking in tropical northern Australia. **2014**, 3, 860-74	31
1955	Characterization and quantification of the fungal microbiome in serial samples from individuals with cystic fibrosis. **2014**, 2, 40	103
1954	Tracking year-to-year changes in intestinal nematode communities of rufous mouse lemurs (Microcebus rufus). **2015**, 142, 1095-107	12
1953	Assessment of microbial populations within Chicago area nearshore waters and interfaces with river systems. **2015**, 5, 305-8	4

1952	Survey of microbial populations within Lake Michigan nearshore waters at two Chicago public beaches. **2015**, 5, 556-9	5
1951	Piwi proteins and piRNAs in mammalian oocytes and early embryos: From sample to sequence. **2015**, 5, 309-13	30
1950	Network construction and structure detection with metagenomic count data. **2015**, 8, 40	4
1949	Solving a Bloody Mess: B-Vitamin Independent Metabolic Convergence among Gammaproteobacterial Obligate Endosymbionts from Blood-Feeding Arthropods and the Leech Haementeria officinalis. **2015**, 7, 2871-84	35
1948	Origin and higher-level diversification of acariform mites - evidence from nuclear ribosomal genes, extensive taxon sampling, and secondary structure alignment. **2015**, 15, 178	34
1947	Rare taxa have potential to make metabolic contributions in enhanced biological phosphorus removal ecosystems. **2015**, 17, 4979-93	45
1946	Divergence thresholds and divergent biodiversity estimates: can metabarcoding reliably describe zooplankton communities?. **2015**, 5, 2234-51	80
1945	Spatial distribution of marine airborne bacterial communities. **2015**, 4, 475-90	42
1944	Accessing Chemical Diversity through Metagenomics. **2015**, 3-22	
1943	Diversity Profile of Microbes Associated with Anaerobic Sulfur Oxidation in an Upflow Anaerobic Sludge Blanket Reactor Treating Municipal Sewage. **2015**, 30, 157-63	11
1942	Sample storage conditions significantly influence faecal microbiome profiles. **2015**, 5, 16350	257
1941	Minor revision to V4 region SSU rRNA 806R gene primer greatly increases detection of SAR11 bacterioplankton. **2015**, 75, 129-137	790
1940	Probiotics modify human intestinal mucosa-associated microbiota in patients with colorectal cancer. **2015**, 12, 6119-27	63
1939	Impact of oil spills on coral reefs can be reduced by bioremediation using probiotic microbiota. **2015**, 5, 18268	59
1938	Variations of gastric corpus microbiota are associated with early esophageal squamous cell carcinoma and squamous dysplasia. **2015**, 5, 8820	61
1937	Intrinsic challenges in ancient microbiome reconstruction using 16S rRNA gene amplification. **2015**, 5, 16498	95
1936	A pyrosequencing insight into sprawling bacterial diversity and community dynamics in decaying deadwood logs of Fagus sylvatica and Picea abies. **2015**, 5, 9456	70
1935	Meat, dairy and plant proteins alter bacterial composition of rat gut bacteria. **2015**, 5, 15220	98

1934	Amplicon-based metagenomics identified candidate organisms in soils that caused yield decline in strawberry. **2015**, 2, 15022	28
1933	Metagenomic insights into communities, functions of endophytes, and their associates with infection by root-knot nematode, Meloidogyne incognita, in tomato roots. **2015**, 5, 17087	94
1932	Low urinary indoxyl sulfate levels early after transplantation reflect a disrupted microbiome and are associated with poor outcome. **2015**, 126, 1723-8	129
1931	Exometabolite niche partitioning among sympatric soil bacteria. **2015**, 6, 8289	120
1930	Marine amoebae with cytoplasmic and perinuclear symbionts deeply branching in the Gammaproteobacteria. **2015**, 5, 13381	16
1929	Using Bayesian modelling to investigate factors governing antibiotic-induced Candida albicans colonization of the GI tract. **2015**, 5, 8131	27
1928	Niche differentiation of bacterial communities at a millimeter scale in Shark Bay microbial mats. **2015**, 5, 15607	71
1927	Lactic acid is a sperm motility inactivation factor in the sperm storage tubules. **2015**, 5, 17643	30
1926	Administration of defined microbiota is protective in a murine Salmonella infection model. **2015**, 5, 16094	30
1925	A new tool for long-term studies of POM-bacteria interactions: overcoming the century-old Bottle Effect. **2015**, 5, 14706	11
1924	Microbial Community Analysis Using High-Throughput Amplicon Sequencing. **2015**, 2.4.2-1-2.4.2-26	3
1923	The impact of rearing environment on the development of gut microbiota in tilapia larvae. **2015**, 5, 18206	133
1922	De Novo Assembly and Characterization of Four Anthozoan (Phylum Cnidaria) Transcriptomes. **2015**, 5, 2441-52	41
1921	Time-scales of hydrological forcing on the geochemistry and bacterial community structure of temperate peat soils. **2015**, 5, 14612	10
1920	Back to Basics--The Influence of DNA Extraction and Primer Choice on Phylogenetic Analysis of Activated Sludge Communities. **2015**, 10, e0132783	294
1919	Microbial immigration across the Mediterranean via airborne dust. **2015**, 5, 16306	27
1918	Spatially extensive microbial biogeography of the Indian Ocean provides insights into the unique community structure of a pristine coral atoll. **2015**, 5, 15383	19
1917	Surveying the endomicrobiome and ectomicrobiome of bark beetles: The case of Dendroctonus simplex. **2015**, 5, 17190	29

1916	Biological Sulfur-Oxidizing Potential of Primary and Biological Sludge in a Tannery Wastewater Treatment Plant. **2015**, 226, 1	5
1915	Repbase Update, a database of repetitive elements in eukaryotic genomes. **2015**, 6, 11	1223
1914	Draft genome sequence of Methylibium sp. strain T29, a novel fuel oxygenate-degrading bacterial isolate from Hungary. **2015**, 10, 39	9
1913	Carbohydrate Structure Database: tools for statistical analysis of bacterial, plant and fungal glycomes. **2015**, 2015,	10
1912	METAXA2: improved identification and taxonomic classification of small and large subunit rRNA in metagenomic data. **2015**, 15, 1403-14	252
1911	Novel lineage patterns from an automated water sampler to probe marine microbial biodiversity with ships of opportunity. **2015**, 137, 409-420	14
1910	DectICO: an alignment-free supervised metagenomic classification method based on feature extraction and dynamic selection. **2015**, 16, 323	5
1909	Improved taxonomic assignment of human intestinal 16S rRNA sequences by a dedicated reference database. **2015**, 16, 1056	87
1908	Metagenome from a Spirulina digesting biogas reactor: analysis via binning of contigs and classification of short reads. **2015**, 15, 277	18
1907	A bulk segregant transcriptome analysis reveals metabolic and cellular processes associated with Orange allelic variation and fruit □carotene accumulation in melon fruit. **2015**, 15, 274	35
1906	Optimizing protocols for extraction of bacteriophages prior to metagenomic analyses of phage communities in the human gut. **2015**, 3, 64	81
1905	Microbial aerosol liberation from soiled textiles isolated during routine residuals handling in a modern health care setting. **2015**, 3, 72	24
1904	Impact of cigarette smoking on the middle meatus microbiome in health and chronic rhinosinusitis. **2015**, 5, 981-9	29
1903	Barite encrustation of benthic sulfur-oxidizing bacteria at a marine cold seep. **2015**, 13, 588-603	28
1902	Taxonomic and functional metagenomic analysis of anodic communities in two pilot-scale microbial fuel cells treating different industrial wastewaters. **2015**, 12, 1-15	6
1901	Seasonal assemblages and short-lived blooms in coastal north-west Atlantic Ocean bacterioplankton. **2015**, 17, 3642-61	30
1900	Microbial communities and nutrient dynamics in experimental microcosms are altered after the application of a high dose of Bti. **2015**, 52, 763-773	12
1899	Marine protist diversity in European coastal waters and sediments as revealed by high-throughput sequencing. **2015**, 17, 4035-49	239

1898	MiDAS: the field guide to the microbes of activated sludge. **2015**, 2015, bav062	159
1897	SymbioGenomesDB: a database for the integration and access to knowledge on host-symbiont relationships. **2015**, 2015,	6
1896	Development and application of primers for the class Dehalococcoidia (phylum Chloroflexi) enables deep insights into diversity and stratification of subgroups in the marine subsurface. **2015**, 17, 3540-56	13
1895	Bacterial community dynamics during polysaccharide degradation at contrasting sites in the Southern and Atlantic Oceans. **2015**, 17, 3822-31	54
1894	Melting glacier impacts community structure of Bacteria, Archaea and Fungi in a Chilean Patagonia fjord. **2015**, 17, 3882-97	34
1893	PhytoREF: a reference database of the plastidial 16S rRNA gene of photosynthetic eukaryotes with curated taxonomy. **2015**, 15, 1435-45	90
1892	Metabolic associations with archaea drive shifts in hydrogen isotope fractionation in sulfate-reducing bacterial lipids in cocultures and methane seeps. **2015**, 13, 462-77	23
1891	Impact of paleoclimate on the distribution of microbial communities in the subsurface sediment of the Dead Sea. **2015**, 13, 546-61	11
1890	Sinus culture poorly predicts resident microbiota. **2015**, 5, 3-9	51
1889	The unique N-terminal insert in the ribosomal protein, phosphoprotein P0, of Tetrahymena thermophila: Bioinformatic evidence for an interaction with 26S rRNA. **2015**, 83, 1078-90	1
1888	Changes in the faecal microbiota of mares precede the development of post partum colic. **2015**, 47, 641-9	77
1887	Evaluation of the Performances of Ribosomal Database Project (RDP) Classifier for Taxonomic Assignment of 16S rRNA Metabarcoding Sequences Generated from Illumina-Solexa NGS. **2015**, 3, 36-9	37
1886	Methane-related changes in prokaryotes along geochemical profiles in sediments of Lake Kinneret (Israel). **2015**, 12, 2847-2860	17
1885	Microbial metabolism alters pore water chemistry and increases consolidation of oil sands tailings. **2015**, 44, 145-53	12
1884	Tsv-N1: A Novel DNA Algal Virus that Infects Tetraselmis striata. **2015**, 7, 3937-53	15
1883	Characterization of active and total fungal communities in the atmosphere over the Amazon rainforest. **2015**, 12, 6337-6349	53
1882	The microbial community of a passive biochemical reactor treating arsenic, zinc, and sulfate-rich seepage. **2015**, 3, 27	64
1881	Emerging Perspectives on the Natural Microbiome of Fresh Produce Vegetables. **2015**, 5, 170-187	36

1880	Characterization of the Bacterial Community Naturally Present on Commercially Grown Basil Leaves: Evaluation of Sample Preparation Prior to Culture-Independent Techniques. **2015**, 12, 10171-97	12
1879	Transcriptome Survey of a Marine Food Fish: Asian Seabass (Lates calcarifer). **2015**, 3, 382-400	10
1878	Assessing the utility of trace and rare earth elements as biosignatures in microbial iron oxyhydroxides. **2015**, 3,	15
1877	riboFrame: An Improved Method for Microbial Taxonomy Profiling from Non-Targeted Metagenomics. **2015**, 6, 329	12
1876	The Road to Metagenomics: From Microbiology to DNA Sequencing Technologies and Bioinformatics. **2015**, 6, 348	168
1875	Transplant experiments uncover Baltic Sea basin-specific responses in bacterioplankton community composition and metabolic activities. **2015**, 6, 223	45
1874	A taxonomic framework for emerging groups of ecologically important marine gammaproteobacteria based on the reconstruction of evolutionary relationships using genome-scale data. **2015**, 6, 281	88
1873	Gene expression in the mixotrophic prymnesiophyte, Prymnesium parvum, responds to prey availability. **2015**, 6, 319	25
1872	Genomic and proteomic evidences unravel the UV-resistome of the poly-extremophile Acinetobacter sp. Ver3. **2015**, 6, 328	35
1871	Forest floor community metatranscriptomes identify fungal and bacterial responses to N deposition in two maple forests. **2015**, 6, 337	62
1870	Transcriptional activity of the giant barrel sponge, Xestospongia muta Holobiont: molecular evidence for metabolic interchange. **2015**, 6, 364	75
1869	Microbial responses to changes in flow status in temporary headwater streams: a cross-system comparison. **2015**, 6, 522	32
1868	Metatranscriptome analysis reveals host-microbiome interactions in traps of carnivorous Genlisea species. **2015**, 6, 526	19
1867	Anaerobic digestion of the microalga Spirulina at extreme alkaline conditions: biogas production, metagenome, and metatranscriptome. **2015**, 6, 597	42
1866	Changes in gene expression of Prymnesium parvum induced by nitrogen and phosphorus limitation. **2015**, 6, 631	36
1865	Novel molecular markers for the detection of methanogens and phylogenetic analyses of methanogenic communities. **2015**, 6, 694	23
1864	The effect of carbon subsidies on marine planktonic niche partitioning and recruitment during biofilm assembly. **2015**, 6, 703	12
1863	Primer and platform effects on 16S rRNA tag sequencing. **2015**, 6, 771	314

1862	Metagenome-based diversity analyses suggest a significant contribution of non-cyanobacterial lineages to carbonate precipitation in modern microbialites. **2015**, 6, 797	37
1861	The green impact: bacterioplankton response toward a phytoplankton spring bloom in the southern North Sea assessed by comparative metagenomic and metatranscriptomic approaches. **2015**, 6, 805	52
1860	Microbial diversity and activity in the Nematostella vectensis holobiont: insights from 16S rRNA gene sequencing, isolate genomes, and a pilot-scale survey of gene expression. **2015**, 6, 818	18
1859	Characterization of the gut microbiota of Kawasaki disease patients by metagenomic analysis. **2015** , 6, 824	30
1858	Halo(natrono)archaea isolated from hypersaline lakes utilize cellulose and chitin as growth substrates. **2015**, 6, 942	40
1857	Growth and activity of ANME clades with different sulfate and sulfide concentrations in the presence of methane. **2015**, 6, 988	23
1856	Metagenomic evidence for reciprocal particle exchange between the mainstem estuary and lateral bay sediments of the lower Columbia River. **2015**, 6, 1074	9
1855	Salt resistance genes revealed by functional metagenomics from brines and moderate-salinity rhizosphere within a hypersaline environment. **2015**, 6, 1121	31
1854	Diversity and structure of soil bacterial communities in the Fildes Region (maritime Antarctica) as revealed by 454 pyrosequencing. **2015**, 6, 1188	47
1853	Prokaryotes in Subsoil-Evidence for a Strong Spatial Separation of Different Phyla by Analysing Co-occurrence Networks. **2015**, 6, 1269	33
1852	Combined Culture-Based and Culture-Independent Approaches Provide Insights into Diversity of Jakobids, an Extremely Plesiomorphic Eukaryotic Lineage. **2015**, 6, 1288	16
1851	Impact of Lowland Rainforest Transformation on Diversity and Composition of Soil Prokaryotic Communities in Sumatra (Indonesia). **2015**, 6, 1339	62
1850	The Scion/Rootstock Genotypes and Habitats Affect Arbuscular Mycorrhizal Fungal Community in Citrus. **2015**, 6, 1372	15
1849	gbtools: Interactive Visualization of Metagenome Bins in R. **2015**, 6, 1451	32
1848	Groundwater Isolation Governs Chemistry and Microbial Community Structure along Hydrologic Flowpaths. **2015**, 6, 1457	64
1847	Prokaryotic Diversity in the Rhizosphere of Organic, Intensive, and Transitional Coffee Farms in Brazil. **2015**, 10, e0106355	21
1846	Comparative analysis of the intestinal bacterial and RNA viral communities from sentinel birds placed on selected broiler chicken farms. **2015**, 10, e0117210	30
1845	Differential assemblage of functional units in paddy soil microbiomes. **2015**, 10, e0122221	38

1844	Influence of a non-hospital medical care facility on antimicrobial resistance in wastewater. **2015**, 10, e0122635	23
1843	Response of the Rumen Microbiota of Sika Deer (Cervus nippon) Fed Different Concentrations of Tannin Rich Plants. **2015**, 10, e0123481	22
1842	Patterns in species persistence and biomass production in soil microcosms recovering from a disturbance reject a neutral hypothesis for bacterial community assembly. **2015**, 10, e0126962	6
1841	In Silico Analysis of the Metabolic Potential and Niche Specialization of Candidate Phylum "Latescibacteria" (WS3). **2015**, 10, e0127499	69
1840	Revealing microparasite diversity in aquatic environments using brute force molecular techniques and subtle microscopy. 93-116	5
1839	Oral Administration of P. gingivalis Induces Dysbiosis of Gut Microbiota and Impaired Barrier Function Leading to Dissemination of Enterobacteria to the Liver. **2015**, 10, e0134234	170
1838	A Comparison between Transcriptome Sequencing and 16S Metagenomics for Detection of Bacterial Pathogens in Wildlife. **2015**, 9, e0003929	45
1837	Comparison of Fecal Microbiota in Children with Autism Spectrum Disorders and Neurotypical Siblings in the Simons Simplex Collection. **2015**, 10, e0137725	125
1836	Urban Market Gardening and Rodent-Borne Pathogenic Leptospira in Arid Zones: A Case Study in Niamey, Niger. **2015**, 9, e0004097	20
1835	Determining Microeukaryotic Plankton Community around Xiamen Island, Southeast China, Using Illumina MiSeq and PCR-DGGE Techniques. **2015**, 10, e0127721	23
1834	Bioinformatic Amplicon Read Processing Strategies Strongly Affect Eukaryotic Diversity and the Taxonomic Composition of Communities. **2015**, 10, e0130035	48
1833	Comparative Transcriptome Analysis of Cultivated and Wild Watermelon during Fruit Development. **2015**, 10, e0130267	61
1832	Relationship between the decomposition process of coarse woody debris and fungal community structure as detected by high-throughput sequencing in a deciduous broad-leaved forest in Japan. **2015**, 10, e0131510	11
1831	The Microbiota and Abundance of the Class 1 Integron-Integrase Gene in Tropical Sewage Treatment Plant Influent and Activated Sludge. **2015**, 10, e0131532	10
1830	Perilipin-2 Modulates Lipid Absorption and Microbiome Responses in the Mouse Intestine. **2015**, 10, e0131944	33
1829	Comparative Transcriptomes Analysis of Red- and White-Fleshed Apples in an F1 Population of Malus sieversii f. niedzwetzkyana Crossed with M. domestica 'Fuji'. **2015**, 10, e0133468	22
1828	Identification of Habitat-Specific Biomes of Aquatic Fungal Communities Using a Comprehensive Nearly Full-Length 18S rRNA Dataset Enriched with Contextual Data. **2015**, 10, e0134377	40
1827	Bacterial Landscape of Bloodstream Infections in Neutropenic Patients via High Throughput Sequencing. **2015**, 10, e0135756	26

1826	Characterization of the In Situ Ecophysiology of Novel Phylotypes in Nutrient Removal Activated Sludge Treatment Plants. **2015**, 10, e0136424	5
1825	Characterization of Bacterial, Archaeal and Eukaryote Symbionts from Antarctic Sponges Reveals a High Diversity at a Three-Domain Level and a Particular Signature for This Ecosystem. **2015**, 10, e0138837	55
1824	Implementation of a Pan-Genomic Approach to Investigate Holobiont-Infecting Microbe Interaction: A Case Report of a Leukemic Patient with Invasive Mucormycosis. **2015**, 10, e0139851	42
1823	Profiling the Succession of Bacterial Communities throughout the Life Stages of a Higher Termite Nasutitermes arborum (Termitidae, Nasutitermitinae) Using 16S rRNA Gene Pyrosequencing. **2015**, 10, e0140014	20
1822	Fickle or Faithful: The Roles of Host and Environmental Context in Determining Symbiont Composition in Two Bathymodioline Mussels. **2015**, 10, e0144307	8
1821	FN-Identify: Novel Restriction Enzymes-Based Method for Bacterial Identification in Absence of Genome Sequencing. **2015**, 2015, 303605	5
1820	Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses. **2015**, 4,	435
1819	Variations of Tongue Coating Microbiota in Patients with Gastric Cancer. **2015**, 2015, 173729	34
1818	Abundant toxin-related genes in the genomes of beneficial symbionts from deep-sea hydrothermal vent mussels. **2015**, 4, e07966	39
1817	Manganese-Cycling Microbial Communities Inside Deep-Sea Manganese Nodules. **2015**, 49, 7692-700	88
1816	Navigating the labyrinth: a guide to sequence-based, community ecology of arbuscular mycorrhizal fungi. **2015**, 207, 235-247	87
1815	Distinct microbial populations are tightly linked to the profile of dissolved iron in the methanic sediments of the Helgoland mud area, North Sea. **2015**, 6, 365	51
1814	Ocean plankton. Structure and function of the global ocean microbiome. **2015**, 348, 1261359	1261
1813	Molecular analysis of single room humidifier bacteriology. **2015**, 69, 318-327	8
1812	Metagenomics: tools and insights for analyzing next-generation sequencing data derived from biodiversity studies. **2015**, 9, 75-88	222
1811	Functional guild classification predicts the enzymatic role of fungi in litter and soil biogeochemistry. **2015**, 88, 441-456	87
1810	Microbiota disbiosis is associated with colorectal cancer. **2015**, 6, 20	282
1809	Environmental selection pressures related to iron utilization are involved in the loss of the flavodoxin gene from the plant genome. **2015**, 7, 750-67	29

1808	High diversity of skin-associated bacterial communities of marine fishes is promoted by their high variability among body parts, individuals and species. **2015**, 91,	55
1807	Size-fractionated diversity of eukaryotic microbial communities in the Eastern Tropical North Pacific oxygen minimum zone. **2015**, 91,	20
1806	Pyrosequencing-Based Assessment of the Microbial Community Structure of Pastoruri Glacier Area (Huascar� National Park, Per�), a Natural Extreme Acidic Environment. **2015**, 70, 936-47	15
1805	Decreased microbiota diversity associated with urinary tract infection in a trial of bacterial interference. **2015**, 71, 358-367	54
1804	Analysis of microbial community structure and composition in leachates from a young landfill by 454 pyrosequencing. **2015**, 99, 5657-68	58
1803	Diversity of extremely halophilic cultivable prokaryotes in Mediterranean, Atlantic and Pacific solar salterns: Evidence that unexplored sites constitute sources of cultivable novelty. **2015**, 38, 266-75	35
1802	Cautionary tale of using 16S rRNA gene sequence similarity values in identification of human-associated bacterial species. **2015**, 65, 1929-1934	94
1801	Deriving accurate microbiota profiles from human samples with low bacterial content through post-sequencing processing of Illumina MiSeq data. **2015**, 3, 19	126
1800	Meiofaunal community analysis by high-throughput sequencing: comparison of extraction, quality filtering, and clustering methods. **2015**, 23, 67-75	59
1799	An Integrated Metagenomics/Metaproteomics Investigation of the Microbial Communities and Enzymes in Solid-state Fermentation of Pu-erh tea. **2015**, 5, 10117	65
1798	Herbinix hemicellulosilytica gen. nov., sp. nov., a thermophilic cellulose-degrading bacterium isolated from a thermophilic biogas reactor. **2015**, 65, 2365-2371	54
1797	Arenimonas subflava sp. nov., isolated from a drinking water network, and emended description of the genus Arenimonas. **2015**, 65, 1915-1921	12
1796	Acromyrmex Leaf-Cutting Ants Have Simple Gut Microbiota with Nitrogen-Fixing Potential. **2015**, 81, 5527-37	55
1795	Does a barcoding gap exist in prokaryotes? Evidences from species delimitation in cyanobacteria. **2014**, 5, 50-64	13
1794	Improvement of barley genome annotations by deciphering the Haruna Nijo genome. **2016**, 23, 21-8	22
1793	Toward accurate molecular identification of species in complex environmental samples: testing the performance of sequence filtering and clustering methods. **2015**, 5, 2252-66	104
1792	Meta-barcoded evaluation of the ISO standard 11063 DNA extraction procedure to characterize soil bacterial and fungal community diversity and composition. **2015**, 8, 131-42	34
1791	Horizontal gene transfer and genome evolution in Methanosarcina. **2015**, 15, 102	13

1790	Characterization of the bacterial gut microbiota of piglets suffering from new neonatal porcine diarrhoea. **2015**, 11, 139		49
1789	Invasive dreissenid mussels and benthic algae in Lake Michigan: characterizing effects on sediment bacterial communities. **2015**, 91, 1-12		15
1788	Identifying novel sequence variants of RNA 3D motifs. *Nucleic Acids Research*, **2015**, 43, 7504-20	20.1	30
1787	Metagenomic Analyses of White Sea Picoalgae: First Data. **2015**, 80, 1514-21		13
1786	Phaeobacter inhibens from the Roseobacter clade has an environmental niche as a surface colonizer in harbors. **2015**, 38, 483-93		21
1785	Texture and type of polymer fiber carrier determine bacterial colonization and biofilm properties in wastewater treatment. **2015**, 264, 824-834		38
1784	Microbial diversity in sugarcane ethanol production in a Brazilian distillery using a culture-independent method. **2015**, 42, 73-84		36
1783	Nitrotoga-like bacteria are previously unrecognized key nitrite oxidizers in full-scale wastewater treatment plants. **2015**, 9, 708-20		93
1782	Metatranscriptome of marine bacterioplankton during winter time in the North Sea assessed by total RNA sequencing. **2015**, 19, 45-6		13
1781	Growth of anaerobic methane-oxidizing archaea and sulfate-reducing bacteria in a high-pressure membrane capsule bioreactor. **2015**, 81, 1286-96		52
1780	Cyanobacterial Diversity in Biological Soil Crusts along a Precipitation Gradient, Northwest Negev Desert, Israel. **2015**, 70, 219-30		45
1779	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. **2015**, 1, 72-87		164
1778	Bombella intestini gen. nov., sp. nov., an acetic acid bacterium isolated from bumble bee crop. **2015** , 65, 267-273		31
1777	Genomic potential for polysaccharide deconstruction in bacteria. **2015**, 81, 1513-19		94
1776	Comprehensive microbial analysis of combined mesophilic anaerobic-thermophilic aerobic process treating high-strength food wastewater. **2015**, 73, 291-303		45
1775	Biodegradation of chloro- and bromobenzoic acids: effect of milieu conditions and microbial community analysis. **2015**, 287, 24-31		5
1774	Synchronous shifts in dissolved organic carbon bioavailability and bacterial community responses over the course of an upwelling-driven phytoplankton bloom. **2015**, 60, 657-677		47
1773	Comparison of Sanger and next generation sequencing performance for genotyping Cryptosporidium isolates at the 18S rRNA and actin loci. **2015**, 151-152, 21-7		29

1772	Transcriptomics in the tropics: Total RNA-based profiling of Costa Rican bromeliad-associated communities. **2015**, 13, 18-23	14
1771	Detection and decay rates of prey and prey symbionts in the gut of a predator through metagenomics. **2015**, 15, 880-92	31
1770	Microbial communities present in the lower respiratory tract of clinically healthy birds in Pakistan. **2015**, 94, 612-20	26
1769	Assessment of quality control approaches for metagenomic data analysis. **2014**, 4, 6957	31
1768	Classifying the uncultivated microbial majority: A place for metagenomic data in the Candidatus proposal. **2015**, 38, 223-30	51
1767	The effects of variable sample biomass on comparative metagenomics. **2015**, 17, 2239-53	19
1766	Soil bacterial communities are shaped by temporal and environmental filtering: evidence from a long-term chronosequence. **2015**, 17, 3208-18	71
1765	Different bacterial populations associated with the roots and rhizosphere of rice incorporate plant-derived carbon. **2015**, 81, 2244-53	92
1764	New mode of energy metabolism in the seventh order of methanogens as revealed by comparative genome analysis of Candidatus methanoplasma termitum**2015**, 81, 1338-52	154
1763	Dynamic hydrologic and biogeochemical processes drive microbially enhanced iron and sulfur cycling within the intertidal mixing zone of a beach aquifer. **2015**, 60, 329-345	63
1762	A Winogradsky-based culture system shows an association between microbial fermentation and cystic fibrosis exacerbation. **2015**, 9, 1024-38	43
1761	Antibiotics in ingested human blood affect the mosquito microbiota and capacity to transmit malaria. **2015**, 6, 5921	106
1760	Using carbon dioxide to maintain an elevated oleaginous microalga concentration in mixed-culture photo-bioreactors. **2015**, 185, 178-84	7
1759	Bacterial diversity in the South Adriatic Sea during a strong, deep winter convection year. **2015**, 81, 1715-26	28
1758	Single stage treatment of saline wastewater with marine bacterial-microalgae consortia in a fixed-bed photobioreactor. **2015**, 292, 155-63	29
1757	Environmental genes and genomes: understanding the differences and challenges in the approaches and software for their analyses. **2015**, 16, 745-58	44
1756	Profiling microbial communities in manganese remediation systems treating coal mine drainage. **2015**, 81, 2189-98	30
1755	Bacterial and archaeal communities in bleached mottles of tropical podzols. **2015**, 69, 372-82	4

1754	Changing bacterial profile of Sundarbans, the world heritage mangrove: impact of anthropogenic interventions. **2015**, 31, 593-610		27
1753	Effects of light and autochthonous carbon additions on microbial turnover of allochthonous organic carbon and community composition. **2015**, 69, 361-71		14
1752	Minimum entropy decomposition: unsupervised oligotyping for sensitive partitioning of high-throughput marker gene sequences. **2015**, 9, 968-79		355
1751	A new era in palaeomicrobiology: prospects for ancient dental calculus as a long-term record of the human oral microbiome. **2015**, 370, 20130376		136
1750	Deep-branching novel lineages and high diversity of haptophytes in the Skagerrak (Norway) uncovered by 454 pyrosequencing. **2015**, 62, 121-40		34
1749	High-throughput sequencing of nematode communities from total soil DNA extractions. **2015**, 15, 3		38
1748	Bacterial and archaeal community structures in the Arctic deep-sea sediment. **2015**, 34, 93-113		9
1747	Comparative Metagenomics of Eight Geographically Remote Terrestrial Hot Springs. **2015**, 70, 411-24		79
1746	Diverse protist grazers select for virulence-related traits in Legionella. **2015**, 9, 1607-18		36
1745	Effects of tigecycline and vancomycin administration on established Clostridium difficile infection. **2015**, 59, 1596-604		10
1744	Type material in the NCBI Taxonomy Database. *Nucleic Acids Research*, **2015**, 43, D1086-98	20.1	107
1743	Hydrogen sulfide can inhibit and enhance oxygenic photosynthesis in a cyanobacterium from sulfidic springs. **2015**, 17, 3301-13		27
1742	Past and future species definitions for Bacteria and Archaea. **2015**, 38, 209-16		312
1741	Seagrass biofilm communities at a naturally CO2 -rich vent. **2015**, 7, 516-25		19
1740	Non-invasive analysis of intestinal development in preterm and term infants using RNA-Sequencing. **2014**, 4, 5453		29
1739	A comparison of DNA extraction methods for biodiversity studies of eukaryotes in marine sediments. **2015**, 75, 15-25		16
1738	Activity and phylogenetic diversity of sulfate-reducing microorganisms in low-temperature subsurface fluids within the upper oceanic crust. **2014**, 5, 748		30
1737	Identification, Functional Characterization, and Evolution of Terpene Synthases from a Basal Dicot. **2015**, 169, 1683-97		31

1736	The immunotranscriptome of the Caribbean reef-building coral Pseudodiploria strigosa. **2015**, 67, 515-30	19
1735	Successive bioanode regenerations to maintain efficient current production from biowaste. **2015**, 106, 133-40	12
1734	Crohn associated microbial communities associated to colonic mucosal biopsies in patients of the western Mediterranean. **2015**, 38, 442-52	21
1733	Murine model of chemotherapy-induced extraintestinal pathogenic Escherichia coli translocation. **2015**, 83, 3243-56	17
1732	Uncultivated thermophiles: current status and spotlight on 'Aigarchaeota'. **2015**, 25, 136-45	32
1731	Influence of seawater intrusion on microbial communities in groundwater. **2015**, 532, 337-43	28
1730	Pyrosequencing analysis of bacterial diversity in dental unit waterlines. **2015**, 81, 223-31	26
1729	Dominance of rumen microorganisms during cheese whey acidification: acidogenesis can be governed by a rare Selenomonas lacticifex-type fermentation. **2015**, 99, 9309-18	6
1728	The Hidden World within Plants: Ecological and Evolutionary Considerations for Defining Functioning of Microbial Endophytes. **2015**, 79, 293-320	1229
1727	Rhizosphere bacteria and fungi associated with plant growth in soils of three replanted apple orchards. **2015**, 395, 317-333	134
1726	Transcriptome analyses to investigate symbiotic relationships between marine protists. **2015**, 6, 98	18
1725	Combining metagenomics, metatranscriptomics and viromics to explore novel microbial interactions: towards a systems-level understanding of human microbiome. **2015**, 13, 390-401	133
1724	Earthworms modify microbial community structure and accelerate maize stover decomposition during vermicomposting. **2015**, 22, 17161-70	18
1723	Vitamin B12 modulates the transcriptome of the skin microbiota in acne pathogenesis. **2015**, 7, 293ra103	87
1722	Shotgun metagenomes and multiple primer pair-barcode combinations of amplicons reveal biases in metabarcoding analyses of fungi. **2015**, 10, 1-43	275
1721	Sedimenticola thiotaurini sp. nov., a sulfur-oxidizing bacterium isolated from salt marsh sediments, and emended descriptions of the genus Sedimenticola and Sedimenticola selenatireducens. **2015**, 65, 2522-2530	35
1720	Marine sediments microbes capable of electrode oxidation as a surrogate for lithotrophic insoluble substrate metabolism. **2014**, 5, 784	59
1719	Alterations in Intestinal Microbiota Correlate With Susceptibility to Type 1 Diabetes. **2015**, 64, 3510-20	170

1718	Chemoautotrophic growth of ammonia-oxidizing Thaumarchaeota enriched from a pelagic redox gradient in the Baltic Sea. **2014**, 5, 786	27
1717	Rhizobiales as functional and endosymbiontic members in the lichen symbiosis of Lobaria pulmonaria L. **2015**, 6, 53	89
1716	Colonization of plant substrates at hydrothermal vents and cold seeps in the northeast Atlantic and Mediterranean and occurrence of symbiont-related bacteria. **2015**, 6, 162	7
1715	Changes in fibrolytic enzyme activity during vermicomposting of maize stover by an anecic earthworm Amynthas hupeiensis. **2015**, 120, 169-177	9
1714	The spatial organization and microbial community structure of an epilithic biofilm. **2015**, 91,	18
1713	Temporal evolution of bacterial communities associated with the in situ wetland-based remediation of a marine shore porphyry copper tailings deposit. **2015**, 533, 110-21	16
1712	DEEP BIOSPHERE. Exploring deep microbial life in coal-bearing sediment down to ~2.5 km below the ocean floor. **2015**, 349, 420-4	253
1711	Abundant Trimethylornithine Lipids and Specific Gene Sequences Are Indicative of Planctomycete Importance at the Oxic/Anoxic Interface in Sphagnum-Dominated Northern Wetlands. **2015**, 81, 6333-44	33
1710	Bacillus stamsii sp. nov., a facultatively anaerobic sugar degrader that is numerically dominant in freshwater lake sediment. **2015**, 38, 379-89	11
1709	Genomic Applications in the Clinical Management of Infectious Diseases. **2015**, 581-604	
1708	Changing composition of microbial communities indicates seepage fluid difference of the Thuwal Seeps in the Red Sea. **2015**, 108, 461-71	2
1707	Electrochemical and microbial monitoring of multi-generational electroactive biofilms formed from mangrove sediment. **2015**, 106, 125-32	8
1706	Unusual biology across a group comprising more than 15% of domain Bacteria. **2015**, 523, 208-11	688
1705	Dynamic microbe and molecule networks in a mouse model of colitis-associated colorectal cancer. **2014**, 4, 4985	41
1704	Alteromonas gracilis sp. nov., a marine polysaccharide-producing bacterium. **2015**, 65, 1498-1503	19
1703	Bacterial community composition and diversity in an ancestral ant fungus symbiosis. **2015**, 91,	36
1702	RNA shotgun metagenomic sequencing of northern California (USA) mosquitoes uncovers viruses, bacteria, and fungi. **2015**, 6, 185	92
1701	Biogeographic patterns of bacterial microdiversity in Arctic deep-sea sediments (HAUSGARTEN, Fram Strait). **2014**, 5, 660	14

1700	A comprehensive analysis of the microbial communities of healthy and diseased marine macroalgae and the detection of known and potential bacterial pathogens. **2015**, 6, 146	47
1699	Isolation of diverse members of the Aquificales from geothermal springs in Tengchong, China. **2015** , 6, 157	20
1698	Contrasting taxonomic stratification of microbial communities in two hypersaline meromictic lakes. **2015**, 9, 2642-56	55
1697	Isolation of a significant fraction of non-phototroph diversity from a desert Biological Soil Crust. **2015**, 6, 277	37
1696	Characterization of mucosa-associated bacterial communities in abomasal ulcers by pyrosequencing. **2015**, 177, 132-41	12
1695	Evaluation of composition and individual variability of rumen microbiota in yaks by 16S rRNA high-throughput sequencing technology. **2015**, 34, 74-9	37
1694	Characterization and comparison of the bacterial microbiota in different gastrointestinal tract compartments in horses. **2015**, 205, 74-80	111
1693	Bacterial diversity and fatty acid composition of hypersaline cyanobacterial mats from an inland desert wadi. **2015**, 115, 81-89	11
1692	Multilocus sequence analysis (MLSA) in prokaryotic taxonomy. **2015**, 38, 237-45	205
1691	Method optimization for fecal sample collection and fecal DNA extraction. **2015**, 13, 79-93	28
1690	Analysis of swine fecal´microbiota at various growth stages. **2015**, 197, 753-9	41
1689	The Gut Microbiota of Workers of the Litter-Feeding Termite Syntermes wheeleri (Termitidae: Syntermitinae): Archaeal, Bacterial, and Fungal Communities. **2015**, 70, 545-56	23
1688	Clostridium cluster I and their pathogenic members in a full-scale operating biogas plant. **2015**, 99, 3585-98	9
1687	Diversity of Actinobacteria Associated with the Marine Ascidian Eudistoma toealensis. **2015**, 17, 377-85	23
1686	The biotransformation of ibuprofen to trihydroxyibuprofen in activated sludge and by Variovorax Ibu-1. **2015**, 26, 105-13	48
1685	Pyrosequencing analysis of microbial communities reveals dominant cosmopolitan phylotypes in deep-sea sediments of the eastern Mediterranean Sea. **2015**, 166, 448-457	12
1684	Phylogenetic placement of metagenomic reads using the minimum evolution principle. **2015**, 16 Suppl 1, S13	9
1683	NoDe: a fast error-correction algorithm for pyrosequencing amplicon reads. **2015**, 16, 88	13

1682	Highly diversified fungi are associated with the achlorophyllous orchid Gastrodia flavilabella. **2015**, 16, 185	12
1681	Prokaryotic assemblages and metagenomes in pelagic zones of the South China Sea. **2015**, 16, 219	25
1680	Transcriptome characterization of three wild Chinese Vitis uncovers a large number of distinct disease related genes. **2015**, 16, 223	15
1679	Babela massiliensis, a representative of a widespread bacterial phylum with unusual adaptations to parasitism in amoebae. **2015**, 10, 13	31
1678	Deciphering chicken gut microbial dynamics based on high-throughput 16S rRNA metagenomics analyses. **2015**, 7, 4	155
1677	The oral and conjunctival microbiotas in cats with and without feline immunodeficiency virus infection. **2015**, 46, 21	20
1676	Perturbation and restoration of the fathead minnow gut microbiome after low-level triclosan exposure. **2015**, 3, 6	96
1675	Comparison of synthetic medium and wastewater used as dilution medium to design scalable microbial anodes: Application to food waste treatment. **2015**, 185, 106-15	30
1674	The effect of oil spills on the bacterial diversity and catabolic function in coastal sediments: a case study on the Prestige oil spill. **2015**, 22, 15200-14	52
1673	Stable-Isotope Probing Identifies Uncultured Planctomycetes as Primary Degraders of a Complex Heteropolysaccharide in Soil. **2015**, 81, 4607-15	64
1672	Comparison of Archaeal and Bacterial Diversity in Methane Seep Carbonate Nodules and Host Sediments, Eel River Basin and Hydrate Ridge, USA. **2015**, 70, 766-84	28
1671	The integration of sequencing and bioinformatics in metagenomics. **2015**, 14, 357-383	10
1670	Phylogenetic structure of soil bacterial communities predicts ecosystem functioning. **2015**, 91,	27
1669	Calcite-accumulating large sulfur bacteria of the genus Achromatium in Sippewissett Salt Marsh. **2015**, 9, 2503-14	23
1668	Comparison of the gut microbiota of people in France and Saudi Arabia. **2015**, 5, e153	57
1667	Adaptation of soil microbial community structure and function to chronic metal contamination at an abandoned Pb-Zn mine. **2015**, 91, 1-11	85
1666	Biogeography and ecology of the rare and abundant microbial lineages in deep-sea hydrothermal vents. **2015**, 91, 1-11	43
1665	Global dispersion and local diversification of the methane seep microbiome. **2015**, 112, 4015-20	168

1664	The response of root-associated bacterial community to the grafting of watermelon. **2015**, 391, 253-264	19
1663	Rhizosphere microbial community manipulated by 2 years of consecutive biofertilizer application associated with banana Fusarium wilt disease suppression. **2015**, 51, 553-562	119
1662	The ribosome challenge to the RNA world. **2015**, 80, 143-61	57
1661	Thermophilic microbial cellulose decomposition and methanogenesis pathways recharacterized by metatranscriptomic and metagenomic analysis. **2014**, 4, 6708	37
1660	High-resolution microbial community succession of microbially induced concrete corrosion in working sanitary manholes. **2015**, 10, e0116400	25
1659	Contrasting spatial patterns and ecological attributes of soil bacterial and archaeal taxa across a landscape. **2015**, 4, 518-31	30
1658	pH influences the importance of niche-related and neutral processes in lacustrine bacterioplankton assembly. **2015**, 81, 3104-14	46
1657	Gut microbiome and innate immune response patterns in IgE-associated eczema. **2015**, 45, 1419-29	84
1656	Tax4Fun: predicting functional profiles from metagenomic 16S rRNA data. **2015**, 31, 2882-4	745
1655	Microbial community composition and diversity via 16S rRNA gene amplicons: evaluating the illumina platform. **2015**, 10, e0116955	205
1654	Complex archaea that bridge the gap between prokaryotes and eukaryotes. **2015**, 521, 173-179	726
1653	Sinus microbiota varies among chronic rhinosinusitis phenotypes and predicts surgical outcome. **2015**, 136, 334-42.e1	115
1652	Berberine blocks the relapse of Clostridium difficile infection in C57BL/6 mice after standard vancomycin treatment. **2015**, 59, 3726-35	31
1651	Microbial diversity and community respiration in freshwater sediments influenced by artificial light at night. **2015**, 370,	84
1650	Elements of metacommunity structure and community-environment relationships in stream organisms. **2015**, 60, 973-988	46
1649	Short communication: Evaluation of the microbiota of kefir samples using metagenetic analysis targeting the 16S and 26S ribosomal DNA fragments. **2015**, 98, 3684-9	52
1648	Predicting the origin of soil evidence: High throughput eukaryote sequencing and MIR spectroscopy applied to a crime scene scenario. **2015**, 251, 22-31	29
1647	Le mycobiome humain : actualitš et perspectives. **2015**, 2015, 67-73	

1646	Biogeography of Planktonic and Benthic Archaeal Communities in a Subtropical Eutrophic Estuary of China. **2015**, 70, 322-35	27
1645	Cataloguing the bacterial diversity of the Sundarbans mangrove, India in the light of metagenomics. **2015**, 4, 90-2	19
1644	Single-cell genomics of a rare environmental alphaproteobacterium provides unique insights into Rickettsiaceae evolution. **2015**, 9, 2373-85	33
1643	Effect of monochloramine treatment on the microbial ecology of Legionella and associated bacterial populations in a hospital hot water system. **2015**, 38, 198-205	13
1642	Concordance of bacterial communities of two tick species and blood of their shared rodent host. **2015**, 24, 2566-79	73
1641	Identification of a recently active mammalian SINE derived from ribosomal RNA. **2015**, 7, 775-88	10
1640	Cyanobacterial distributions along a physico-chemical gradient in the Northeastern Pacific Ocean. **2015**, 17, 3692-707	20
1639	Physicochemical control of bacterial and protist community composition and diversity in Antarctic sea ice. **2015**, 17, 3869-81	36
1638	Diversity of Iron Oxidizing and Reducing Bacteria in Flow Reactors in the ▯sp▯Hard Rock Laboratory. **2015**, 32, 207-220	17
1637	Cyanobacteria and Diatoms in Biofilms of Two Karstic Streams in Germany and Changes of Their Communities Along Calcite Saturation Gradients. **2015**, 32, 255-274	17
1636	Decrease of the level of extractable polychlorinated biphenyls in soil microcosms: Influence of granular activated carbon and inoculation by natural microbial consortia. **2015**, 105, 127-136	8
1635	Next-Generation Sequencing for Infectious Disease Diagnosis and Management: A Report of the Association for Molecular Pathology. **2015**, 17, 623-34	107
1634	Persistent U(IV) and U(VI) following in-situ recovery (ISR) mining of a sandstone uranium deposit, Wyoming, USA. **2015**, 63, 222-234	17
1633	Dietary Capsicum and Curcuma longa oleoresins increase intestinal microbiome and necrotic enteritis in three commercial broiler breeds. **2015**, 102, 150-8	38
1632	Functionally Structured Genomes in Lactobacillus kunkeei Colonizing the Honey Crop and Food Products of Honeybees and Stingless Bees. **2015**, 7, 1455-73	32
1631	Cilantro microbiome before and after nonselective pre-enrichment for Salmonella using 16S rRNA and metagenomic sequencing. **2015**, 15, 160	38
1630	Developmental succession of the microbiome of Culex mosquitoes. **2015**, 15, 140	72
1629	Comparison of Rock Varnish Bacterial Communities with Surrounding Non-Varnished Rock Surfaces: Taxon-Specific Analysis and Morphological Description. **2015**, 70, 741-50	23

1628	Fast Algorithms for Inferring Gene-Species Associations. **2015**, 36-47		5
1627	Seasonal patterns of bacterial communities in the coastal brackish sediments of the Gulf of Finland, Baltic Sea. **2015**, 165, 86-96		14
1626	Wastewater treatment and microbial communities in an integrated photo-bioelectrochemical system affected by different wastewater algal inocula. **2015**, 12, 446-454		25
1625	Genome-wide redistribution of H3K27me3 is linked to genotoxic stress and defective growth. **2015** , 112, E6339-48		57
1624	Transcriptome analysis of an apple (Malus domestica) yellow fruit somatic mutation identifies a gene network module highly associated with anthocyanin and epigenetic regulation. **2015**, 66, 7359-76		133
1623	Changes in the equine fecal microbiota associated with the use of systemic antimicrobial drugs. **2015**, 11, 19		81
1622	Evolutionary insights from de novo transcriptome assembly and SNP discovery in California white oaks. **2015**, 16, 552		26
1621	MHC variation sculpts individualized microbial communities that control susceptibility to enteric infection. **2015**, 6, 8642		94
1620	Skin-to-Skin Care and the Development of the Preterm Infant Oral Microbiome. **2015**, 32, 1205-16		33
1619	Microbiome profiling in fresh-cut products. **2015**, 46, 295-301		18
1618	A Kelch Domain-Containing F-Box Coding Gene Negatively Regulates Flavonoid Accumulation in Muskmelon. **2015**, 169, 1714-26		57
1617	Dietary analysis on the shallow-water hydrothermal vent crab Xenograpsus testudinatus using Illumina sequencing. **2015**, 162, 1787-1798		14
1616	The Food Web of Boiling Springs Lake Appears Dominated by the Heterolobosean Tetramitus thermacidophilus Strain BSL. **2015**, 62, 374-90		5
1615	Cable Bacteria in Freshwater Sediments. **2015**, 81, 6003-11		68
1614	Diversity of Rhodopirellula and related planctomycetes in a North Sea coastal sediment employing carB as molecular marker. **2015**, 362, fnv127		5
1613	Metagenome Skimming of Insect Specimen Pools: Potential for Comparative Genomics. **2015**, 7, 1474-89		26
1612	rrnDB: improved tools for interpreting rRNA gene abundance in bacteria and archaea and a new foundation for future development. *Nucleic Acids Research*, **2015**, 43, D593-8	20.1	466
1611	Bacteriocin production augments niche competition by enterococci in the mammalian gastrointestinal tract. **2015**, 526, 719-22		254

1610	Predation of nitritation-anammox biofilms used for nitrogen removal from wastewater. **2015**, 91,	13
1609	Uncovering co-expression gene network modules regulating fruit acidity in diverse apples. **2015**, 16, 612	39
1608	Systems approach for exploring the intricate associations between sweetness, color and aroma in melon fruits. **2015**, 15, 71	28
1607	Insights into the evolution of enzyme substrate promiscuity after the discovery of ()□isomerase evolutionary intermediates from a diverse metagenome. **2015**, 15, 107	15
1606	Comprehensive analysis of Panax ginseng root transcriptomes. **2015**, 15, 138	44
1605	Dynamic changes in the subgingival microbiome and their potential for diagnosis and prognosis of periodontitis. **2015**, 6, e01926-14	95
1604	Universal and domain-specific sequences in 23S-28S ribosomal RNA identified by computational phylogenetics. **2015**, 21, 1719-30	17
1603	Endosymbionts escape dead hydrothermal vent tubeworms to enrich the free-living population. **2015**, 112, 11300-5	39
1602	Consistent responses of soil microbial communities to elevated nutrient inputs in grasslands across the globe. **2015**, 112, 10967-72	649
1601	Sex differences in gut fermentation and immune parameters in rats fed an oligofructose-supplemented diet. **2015**, 6, 13	55
1600	Comprehensive Tissue-Specific Transcriptome Analysis Reveals Distinct Regulatory Programs during Early Tomato Fruit Development. **2015**, 168, 1684-701	86
1599	Annual dynamics of North Sea bacterioplankton: seasonal variability superimposes short-term variation. **2015**, 91, fiv099	26
1598	Climate change and physical disturbance manipulations result in distinct biological soil crust communities. **2015**, 81, 7448-59	45
1597	Selective elimination of bacterial faecal indicators in the Schmutzdecke of slow sand filtration columns. **2015**, 99, 10323-32	17
1596	The female urinary microbiome in urgency urinary incontinence. **2015**, 213, 347.e1-11	166
1595	Combined Flux Chamber and Genomics Approach Links Nitrous Acid Emissions to Ammonia Oxidizing Bacteria and Archaea in Urban and Agricultural Soil. **2015**, 49, 13825-34	42
1594	Patterns of Endemism and Habitat Selection in Coalbed Microbial Communities. **2015**, 81, 7924-37	22
1593	Impacts of Initial Fertilizers and Irrigation Systems on Paddy Methanogens and Methane Emission. **2015**, 226, 1	9

1592	Dynamics of an experimental microbial invasion. **2015**, 112, 11594-9	35
1591	Rumen Metagenomics. **2015**, 223-245	4
1590	Impact of pyrolysis and hydrothermal biochar on gas-emitting activity of soil microorganisms and bacterial and archaeal community composition. **2015**, 96, 225-239	35
1589	Microbial diversity in deep-sea sediments from the Menez Gwen hydrothermal vent system of the Mid-Atlantic Ridge. **2015**, 24 Pt 3, 343-55	25
1588	Synthesis of phylogeny and taxonomy into a comprehensive tree of life. **2015**, 112, 12764-9	400
1587	Sulfur Reduction in Acid Rock Drainage Environments. **2015**, 49, 11746-55	39
1586	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. **2015**, 528, 262-266	1107
1585	Temporal and spatial dynamics of phytoplankton diversity in the East China Sea near Jeju Island (Korea): A pyrosequencing-based study. **2015**, 63, 143-152	6
1584	The rectal microbiota of cats infected with feline immunodeficiency virus infection and uninfected controls. **2015**, 180, 96-102	8
1583	Marine metagenomics as a source for bioprospecting. **2015**, 24 Pt 1, 21-30	36
1582	Iron Modulates Butyrate Production by a Child Gut Microbiota In Vitro. **2015**, 6, e01453-15	58
1581	454 Pyrosequencing-based assessment of bacterial diversity and community structure in termite guts, mounds and surrounding soils. **2015**, 4, 471	31
1580	Complete nitrification by a single microorganism. **2015**, 528, 555-9	857
1579	Messenger RNA exchange between scions and rootstocks in grafted grapevines. **2015**, 15, 251	89
1578	Prokaryotic Metatranscriptomics. **2015**, 69-98	1
1577	PTPN2 controls differentiation of CD4+ T cells and limits intestinal inflammation and intestinal dysbiosis. **2015**, 8, 918-29	60
1576	Community shift from phototrophic to chemotrophic sulfide oxidation following anoxic holomixis in a stratified seawater lake. **2015**, 81, 298-308	35
1575	CATCh, an ensemble classifier for chimera detection in 16S rRNA sequencing studies. **2015**, 81, 1573-84	35

1574	Biotransformation of coal linked to nitrification. **2015**, 137, 136-141	4
1573	Seasonal and interannual variability of the marine bacterioplankton community throughout the water column over ten years. **2015**, 9, 563-80	118
1572	The current provided by oxygen-reducing microbial cathodes is related to the composition of their bacterial community. **2015**, 102, 42-9	35
1571	Phylogenomic analyses and molecular signatures for the class Halobacteria and its two major clades: a proposal for division of the class Halobacteria into an emended order Halobacteriales and two new orders, Haloferacales ord. nov. and Natrialbales ord. nov., containing the novel families Haloferacaceae fam. nov. and Natrialbaceae fam. nov. **2015**, 65, 1050-1069	192
1570	Deciphering the human microbiome using next-generation sequencing data and bioinformatics approaches. **2015**, 79-80, 52-9	35
1569	Case study: using sequence homology to identify putative phosphorylation sites in an evolutionarily distant species (honeybee). **2015**, 16, 820-9	5
1568	Association of obesity with serum leptin, adiponectin, and serotonin and gut microflora in beagle dogs. **2015**, 29, 43-50	52
1567	Microbial diversity and dynamics of a groundwater and a still bottled natural mineral water. **2015**, 17, 577-93	32
1566	Methyloprofundus sedimenti gen. nov., sp. nov., an obligate methanotroph from ocean sediment belonging to the 'deep sea-1' clade of marine methanotrophs. **2015**, 65, 251-259	56
1565	Origin and ecological selection of core and food-specific bacterial communities associated with meat and seafood spoilage. **2015**, 9, 1105-18	179
1564	Assessing the global phylum level diversity within the bacterial domain: A review. **2015**, 6, 269-82	41
1563	Community transcriptomics reveals unexpected high microbial diversity in acidophilic biofilm communities. **2015**, 9, 1014-23	46
1562	Cable bacteria associated with long-distance electron transport in New England salt marsh sediment. **2015**, 7, 175-9	44
1561	Desulfoprunum benzoelyticum gen. nov., sp. nov., a Gram-stain-negative, benzoate-degrading, sulfate-reducing bacterium isolated from a wastewater treatment plant. **2015**, 65, 77-84	21
1560	Long-term phenotypic evolution of bacteria. **2015**, 517, 369-72	54
1559	Tepidisphaera mucosa gen. nov., sp. nov., a moderately thermophilic member of the class Phycisphaerae in the phylum Planctomycetes, and proposal of a new family, Tepidisphaeraceae fam. nov., and a new order, Tepidisphaerales ord. nov. **2015**, 65, 549-555	51
1558	Metagenomics for Bacteriology. **2015**, 113-134	1
1557	Impact of long-term fertilizer treatment on the microeukaryotic community structure of a rice field soil. **2015**, 80, 237-243	29

1556	Diversity and potential sources of microbiota associated with snow on western portions of the Greenland Ice Sheet. **2015**, 17, 594-609	39
1555	Norwegian deep-water coral reefs: cultivation and molecular analysis of planktonic microbial communities. **2015**, 17, 3597-609	10
1554	Comparison of bacterial communities on limnic versus coastal marine particles reveals profound differences in colonization. **2015**, 17, 3500-14	84
1553	Phylogenetics and the human microbiome. **2015**, 64, e26-41	24
1552	Diverse alkane hydroxylase genes in microorganisms and environments. **2014**, 4, 4968	148
1551	Validation of a new catalysed reporter deposition-fluorescence in situ hybridization probe for the accurate quantification of marine Bacteroidetes populations. **2015**, 17, 3557-69	8
1550	Genome-wide identification of transcription factors and transcription-factor binding sites in oleaginous microalgae Nannochloropsis. **2014**, 4, 5454	61
1549	Comparing the effect of digestate and chemical fertiliser on soil bacteria. **2015**, 86, 1-9	54
1548	Investigating bacterial populations in styrene-degrading biofilters by 16S rDNA tag pyrosequencing. **2015**, 99, 3-18	24
1547	Application of Identification of Bacteria by DNA Target Sequencing in a Clinical Microbiology Laboratory. **2016**, 19-31	0
1546	Genome Diversity of Spore-Forming Firmicutes. **2016**, 1-18	2
1545	Enrichment of Fusobacteria in Sea Surface Oil Slicks from the Deepwater Horizon Oil Spill. **2016**, 4,	15
1544	Effects of wastewater treatment plant effluent inputs on planktonic metabolic rates and microbial community composition in the Baltic Sea. **2016**, 13, 4751-4765	12
1543	Probing the diversity of healthy oral microbiome with bioinformatics approaches. **2016**, 49, 662-670	27
1542	Seasonal changes in the D / H ratio of fatty acids of pelagic microorganisms in the coastal North Sea. **2016**, 13, 5527-5539	8
1541	Decline in Performance of Biochemical Reactors for Sulphate Removal from Mine-Influenced Water is Accompanied by Changes in Organic Matter Characteristics and Microbial Population Composition. **2016**, 8, 124	10
1540	Simultaneous DNA-based diet analysis of breeding, non-breeding and chick Adľie penguins. **2016**, 3, 150443	25
1539	Diversity of fungi in sediments and water sampled from the hot springs of Lake Magadi and Little Magadi in Kenya. **2016**, 10, 330-338	13

1538	Metagenomic analysis of nitrogen and methane cycling in the Arabian Sea oxygen minimum zone. **2016**, 4, e1924	60
1537	Mechanisms of <i>Trichodesmium</i> demise within the New Caledonian lagoon during the VAHINE mesocosm experiment. **2016**, 13, 4187-4203	20
1536	Archive of bacterial community in anhydrite crystals from a deep-sea basin provides evidence of past oil-spilling in a benthic environment in the Red Sea. **2016**, 13, 6405-6417	1
1535	Marine Subsurface Microbial Community Shifts Across a Hydrothermal Gradient in Okinawa Trough Sediments. **2016**, 2016, 2690329	11
1534	Using Small RNA Deep Sequencing Data to Detect Human Viruses. **2016**, 2016, 2596782	18
1533	Assessing the Gene Content of the Megagenome: Sugar Pine (Pinus lambertiana). **2016**, 6, 3787-3802	30
1532	A Metagenomic Insight Into the Human Microbiome. **2016**, 107-119	12
1531	Controls on microalgal community structures in cryoconite holes upon high-Arctic glaciers, Svalbard. **2016**, 13, 659-674	25
1530	Succession within the prokaryotic communities during the VAHINE mesocosms experiment in the New Caledonia lagoon. **2016**, 13, 2319-2337	14
1529	Lactobacillus fermentum CRL1446 Ameliorates Oxidative and Metabolic Parameters by Increasing Intestinal Feruloyl Esterase Activity and Modulating Microbiota in Caloric-Restricted Mice. **2016**, 8,	22
1528	Recurring patterns in bacterioplankton dynamics during coastal spring algae blooms. **2016**, 5, e11888	193
1527	Does the Urinary Microbiome Play a Role in Urgency Urinary Incontinence and Its Severity?. **2016**, 6, 78	138
1526	Diversity, Specificity, and Phylogenetic Relationships of Endohyphal Bacteria in Fungi That Inhabit Tropical Seeds and Leaves. **2016**, 4,	31
1525	Selective Pressure of Temperature on Competition and Cross-Feeding within Denitrifying and Fermentative Microbial Communities. **2015**, 6, 1461	13
1524	A Phylogenomic Analysis of the Bacterial Phylum Fibrobacteres. **2015**, 6, 1469	48
1523	Structural Iron (II) of Basaltic Glass as an Energy Source for Zetaproteobacteria in an Abyssal Plain Environment, Off the Mid Atlantic Ridge. **2015**, 6, 1518	19
1522	Expanding the World of Marine Bacterial and Archaeal Clades. **2015**, 6, 1524	83
1521	Spatial Interaction of Archaeal Ammonia-Oxidizers and Nitrite-Oxidizing Bacteria in an Unfertilized Grassland Soil. **2015**, 6, 1567	32

1520	Microbial Communities in Methane- and Short Chain Alkane-Rich Hydrothermal Sediments of Guaymas Basin. **2016**, 7, 17	43
1519	Metabolic Capabilities of Microorganisms Involved in and Associated with the Anaerobic Oxidation of Methane. **2016**, 7, 46	81
1518	Diversity and Dynamics of Active Small Microbial Eukaryotes in the Anoxic Zone of a Freshwater Meromictic Lake (Pavin, France). **2016**, 7, 130	23
1517	Bacterial Community Succession in Pine-Wood Decomposition. **2016**, 7, 231	72
1516	Biogeochemical and Microbial Variation across 5500 km of Antarctic Surface Sediment Implicates Organic Matter as a Driver of Benthic Community Structure. **2016**, 7, 284	31
1515	Short-Term Dynamics of North Sea Bacterioplankton-Dissolved Organic Matter Coherence on Molecular Level. **2016**, 7, 321	34
1514	Composition and Interactions among Bacterial, Microeukaryotic, and T4-like Viral Assemblages in Lakes from Both Polar Zones. **2016**, 7, 337	6
1513	Methane Seep in Shallow-Water Permeable Sediment Harbors High Diversity of Anaerobic Methanotrophic Communities, Elba, Italy. **2016**, 7, 374	25
1512	Phenotypic and Genomic Properties of Chitinispirillum alkaliphilum gen. nov., sp. nov., A Haloalkaliphilic Anaerobic Chitinolytic Bacterium Representing a Novel Class in the Phylum Fibrobacteres. **2016**, 7, 407	20
1511	In Search of Alternative Antibiotic Drugs: Quorum-Quenching Activity in Sponges and their Bacterial Isolates. **2016**, 7, 416	46
1510	Mycobacterium avium Subspecies paratuberculosis Infection Modifies Gut Microbiota under Different Dietary Conditions in a Rabbit Model. **2016**, 7, 446	29
1509	Temporal and Spatial Dynamics of Archaeal Communities in Two Freshwater Lakes at Different Trophic Status. **2016**, 7, 451	28
1508	Characterization of the Gut Microbiome Using 16S or Shotgun Metagenomics. **2016**, 7, 459	436
1507	Sample Processing Impacts the Viability and Cultivability of the Sponge Microbiome. **2016**, 7, 499	36
1506	A Novel Extracellular Gut Symbiont in the Marine Worm Priapulus caudatus (Priapulida) Reveals an Alphaproteobacterial Symbiont Clade of the Ecdysozoa. **2016**, 7, 539	5
1505	Host and Environmental Specificity in Bacterial Communities Associated to Two Highly Invasive Marine Species (Genus Asparagopsis). **2016**, 7, 559	36
1504	Chitin Mixed in Potting Soil Alters Lettuce Growth, the Survival of Zoonotic Bacteria on the Leaves and Associated Rhizosphere Microbiology. **2016**, 7, 565	44
1503	Metagenomics Reveals Pervasive Bacterial Populations and Reduced Community Diversity across the Alaska Tundra Ecosystem. **2016**, 7, 579	45

1502	Single-Cell (Meta-)Genomics of a Dimorphic Candidatus Thiomargarita nelsonii Reveals Genomic Plasticity. **2016**, 7, 603	18
1501	Seasonal Succession Leads to Habitat-Dependent Differentiation in Ribosomal RNA:DNA Ratios among Freshwater Lake Bacteria. **2016**, 7, 606	20
1500	Performance of 16s rDNA Primer Pairs in the Study of Rhizosphere and Endosphere Bacterial Microbiomes in Metabarcoding Studies. **2016**, 7, 650	120
1499	Deep Subsurface Life from North Pond: Enrichment, Isolation, Characterization and Genomes of Heterotrophic Bacteria. **2016**, 7, 678	15
1498	Diversity of Pico- to Mesoplankton along the 2000 km Salinity Gradient of the Baltic Sea. **2016**, 7, 679	56
1497	Unearthing the Ecology of Soil Microorganisms Using a High Resolution DNA-SIP Approach to Explore Cellulose and Xylose Metabolism in Soil. **2016**, 7, 703	99
1496	The Common Gut Microbe Eubacterium hallii also Contributes to Intestinal Propionate Formation. **2016**, 7, 713	135
1495	Capturing One of the Human Gut Microbiome's Most Wanted: Reconstructing the Genome of a Novel Butyrate-Producing, Clostridial Scavenger from Metagenomic Sequence Data. **2016**, 7, 783	20
1494	The Architecture of Iron Microbial Mats Reflects the Adaptation of Chemolithotrophic Iron Oxidation in Freshwater and Marine Environments. **2016**, 7, 796	61
1493	HoloVir: A Workflow for Investigating the Diversity and Function of Viruses in Invertebrate Holobionts. **2016**, 7, 822	31
1492	Fungal and Prokaryotic Activities in the Marine Subsurface Biosphere at Peru Margin and Canterbury Basin Inferred from RNA-Based Analyses and Microscopy. **2016**, 7, 846	34
1491	Microbiomes of Muricea californica and M. fruticosa: Comparative Analyses of Two Co-occurring Eastern Pacific Octocorals. **2016**, 7, 917	26
1490	Single-cell Sequencing of Thiomargarita Reveals Genomic Flexibility for Adaptation to Dynamic Redox Conditions. **2016**, 7, 964	24
1489	A Modified SDS-Based DNA Extraction Method for High Quality Environmental DNA from Seafloor Environments. **2016**, 7, 986	37
1488	Taxonomic Assessment of Rumen Microbiota Using Total RNA and Targeted Amplicon Sequencing Approaches. **2016**, 7, 987	42
1487	"Candidatus Propionivibrio aalborgensis": A Novel Glycogen Accumulating Organism Abundant in Full-Scale Enhanced Biological Phosphorus Removal Plants. **2016**, 7, 1033	53
1486	Unanticipated Geochemical and Microbial Community Structure under Seasonal Ice Cover in a Dilute, Dimictic Arctic Lake. **2016**, 7, 1035	14
1485	Endozoicomonas Are Specific, Facultative Symbionts of Sea Squirts. **2016**, 7, 1042	22

1484	Populations of Stored Product Mite Tyrophagus putrescentiae Differ in Their Bacterial Communities. **2016**, 7, 1046	25
1483	Genomic and Transcriptomic Resolution of Organic Matter Utilization Among Deep-Sea Bacteria in Guaymas Basin Hydrothermal Plumes. **2016**, 7, 1125	29
1482	How Clonal Is Clonal? Genome Plasticity across Multicellular Segments of a "Candidatus Marithrix sp." Filament from Sulfidic, Briny Seafloor Sediments in the Gulf of Mexico. **2016**, 7, 1173	11
1481	Lichen-Associated Fungal Community in Hypogymnia hypotrypa (Parmeliaceae, Ascomycota) Affected by Geographic Distribution and Altitude. **2016**, 7, 1231	17
1480	Phylogeography, Salinity Adaptations and Metabolic Potential of the Candidate Division KB1 Bacteria Based on a Partial Single Cell Genome. **2016**, 7, 1266	19
1479	Chronic Polyaromatic Hydrocarbon (PAH) Contamination Is a Marginal Driver for Community Diversity and Prokaryotic Predicted Functioning in Coastal Sediments. **2016**, 7, 1303	23
1478	Mineral vs. Organic Amendments: Microbial Community Structure, Activity and Abundance of Agriculturally Relevant Microbes Are Driven by Long-Term Fertilization Strategies. **2016**, 7, 1446	266
1477	Modulation of the Bifidobacterial Communities of the Dog Microbiota by Zeolite. **2016**, 7, 1491	9
1476	Differences in the Composition of Archaeal Communities in Sediments from Contrasting Zones of Lake Taihu. **2016**, 7, 1510	21
1475	Metagenomics of Thermophiles with a Focus on Discovery of Novel Thermozymes. **2016**, 7, 1521	74
1474	High Ozone (O) Affects the Fitness Associated with the Microbial Composition and Abundance of Q Biotype. **2016**, 7, 1593	4
1473	Response of Core Microbial Consortia to Chronic Hydrocarbon Contaminations in Coastal Sediment Habitats. **2016**, 7, 1637	44
1472	Community Composition and Abundance of Bacterial, Archaeal and Nitrifying Populations in Savanna Soils on Contrasting Bedrock Material in Kruger National Park, South Africa. **2016**, 7, 1638	25
1471	Abundance and Diversity of Denitrifying and Anammox Bacteria in Seasonally Hypoxic and Sulfidic Sediments of the Saline Lake Grevelingen. **2016**, 7, 1661	22
1470	Physical Factors Correlate to Microbial Community Structure and Nitrogen Cycling Gene Abundance in a Nitrate Fed Eutrophic Lagoon. **2016**, 7, 1691	11
1469	" Gortzia shahrazadis", a Novel Endosymbiont of and a Revision of the Biogeographical Distribution of -Like Bacteria. **2016**, 7, 1704	29
1468	Bacterial Active Community Cycling in Response to Solar Radiation and Their Influence on Nutrient Changes in a High-Altitude Wetland. **2016**, 7, 1823	23
1467	Phylogenetic Signals of Salinity and Season in Bacterial Community Composition Across the Salinity Gradient of the Baltic Sea. **2016**, 7, 1883	42

1466	Intraclade Heterogeneity in Nitrogen Utilization by Marine Prokaryotes Revealed Using Stable Isotope Probing Coupled with Tag Sequencing (Tag-SIP). **2016**, 7, 1932	14
1465	Local and Regional Diversity Reveals Dispersal Limitation and Drift as Drivers for Groundwater Bacterial Communities from a Fractured Granite Formation. **2016**, 7, 1933	13
1464	Trace Elements Induce Predominance among Methanogenic Activity in Anaerobic Digestion. **2016**, 7, 2034	48
1463	Dynamics in the Strawberry Rhizosphere Microbiome in Response to Biochar and Leaf Infection. **2016**, 7, 2062	31
1462	High Diversity of in Soils of Two Lichen-Dominated Sub-Arctic Ecosystems of Northwestern Siberia. **2016**, 7, 2065	41
1461	Local Environmental Conditions Shape Generalist But Not Specialist Components of Microbial Metacommunities in the Baltic Sea. **2016**, 7, 2078	16
1460	Reconstruction of the Metabolic Potential of Acidophilic Strains from the Metagenome of an Microaerophilic Enrichment Culture of Acidophilic Iron-Oxidizing Bacteria from a Pilot Plant for the Treatment of Acid Mine Drainage Reveals Metabolic Versatility and Adaptation to Life at Low pH. **2016**, 7, 2082	15
1459	Effect of Different Lignocellulosic Diets on Bacterial Microbiota and Hydrolytic Enzyme Activities in the Gut of the Cotton Boll Weevil (). **2016**, 7, 2093	13
1458	Considerations For Optimizing Microbiome Analysis Using a Marker Gene. **2016**, 3, 26	18
1457	Effect of Silver or Copper Nanoparticles-Dispersed Silane Coatings on Biofilm Formation in Cooling Water Systems. **2016**, 9,	11
1456	Remote transient Lactobacillus animalis bacteremia causing prosthetic hip joint infection: a case report. **2016**, 16, 634	5
1455	Conservation and diversification of the transcriptomes of adult Paragonimus westermani and P. skrjabini. **2016**, 9, 497	8
1454	On the reversibility of parasitism: adaptation to a free-living lifestyle via gene acquisitions in the diplomonad Trepomonas sp. PC1. **2016**, 14, 62	23
1453	Trophic and Non-Trophic Interactions in a Biodiversity Experiment Assessed by Next-Generation Sequencing. **2016**, 11, e0148781	16
1452	Rare Freshwater Ciliate Paramecium chlorelligerum Kahl, 1935 and Its Macronuclear Symbiotic Bacterium "Candidatus Holospora parva". **2016**, 11, e0167928	29
1451	Bacterial Communities of Three Saline Meromictic Lakes in Central Asia. **2016**, 11, e0150847	35
1450	Dynamics of the Fouling Layer Microbial Community in a Membrane Bioreactor. **2016**, 11, e0158811	34
1449	Microbiome and Exudates of the Root and Rhizosphere of Brachypodium distachyon, a Model for Wheat. **2016**, 11, e0164533	123

1448	Influences of Plant Species, Season and Location on Leaf Endophytic Bacterial Communities of Non-Cultivated Plants. **2016**, 11, e0150895	50
1447	Oral Samples as Non-Invasive Proxies for Assessing the Composition of the Rumen Microbial Community. **2016**, 11, e0151220	41
1446	SeqFeatR for the Discovery of Feature-Sequence Associations. **2016**, 11, e0146409	8
1445	Assessing Bacterial Diversity in the Rhizosphere of Thymus zygis Growing in the Sierra Nevada National Park (Spain) through Culture-Dependent and Independent Approaches. **2016**, 11, e0146558	40
1444	Characterization of Bacterial Communities in Selected Smokeless Tobacco Products Using 16S rDNA Analysis. **2016**, 11, e0146939	37
1443	Comparative Genomic Analysis of Sulfurospirillum cavolei MES Reconstructed from the Metagenome of an Electrosynthetic Microbiome. **2016**, 11, e0151214	16
1442	Gut Bacterial Community of the Xylophagous Cockroaches Cryptocercus punctulatus and Parasphaeria boleiriana. **2016**, 11, e0152400	19
1441	Molecular Evolution of the Oxygen-Binding Hemerythrin Domain. **2016**, 11, e0157904	17
1440	Factors Influencing Bacterial Diversity and Community Composition in Municipal Drinking Waters in the Ohio River Basin, USA. **2016**, 11, e0157966	42
1439	Microbes on a Bottle: Substrate, Season and Geography Influence Community Composition of Microbes Colonizing Marine Plastic Debris. **2016**, 11, e0159289	225
1438	Uncovering Trophic Interactions in Arthropod Predators through DNA Shotgun-Sequencing of Gut Contents. **2016**, 11, e0161841	34
1437	MetaStorm: A Public Resource for Customizable Metagenomics Annotation. **2016**, 11, e0162442	42
1436	A Novel Colonial Ciliate Zoothamnium ignavum sp. nov. (Ciliophora, Oligohymenophorea) and Its Ectosymbiont Candidatus Navis piranensis gen. nov., sp. nov. from Shallow-Water Wood Falls. **2016**, 11, e0162834	12
1435	Piphillin: Improved Prediction of Metagenomic Content by Direct Inference from Human Microbiomes. **2016**, 11, e0166104	203
1434	Environmental and Geographical Factors Structure Soil Microbial Diversity in New Caledonian Ultramafic Substrates: A Metagenomic Approach. **2016**, 11, e0167405	35
1433	Airway Microbiota in Bronchoalveolar Lavage Fluid from Clinically Well Infants with Cystic Fibrosis. **2016**, 11, e0167649	39
1432	Host-Microbiome Interaction and Cancer: Potential Application in Precision Medicine. **2016**, 7, 606	24
1431	Comprehensive Transcriptome Profiling Reveals Long Noncoding RNA Expression and Alternative Splicing Regulation during Fruit Development and Ripening in Kiwifruit (Actinidia chinensis). **2016**, 7, 335	54

1430	Transcriptome Profiling of Petal Abscission Zone and Functional Analysis of an Aux/IAA Family Gene Involved in Petal Shedding in Rose. **2016**, 7, 1375	24
1429	Identification of a Chromosome 4 Fruit Flavor and Nutritional Quality-Associated Metabolite QTL. **2016**, 7, 1671	19
1428	Understanding Marine Microbes, the Driving Engines of the Ocean. **2016**, 4,	2
1427	Prophylactic Administration of Vector-Encoded Porcine Granulocyte-Colony Stimulating Factor Reduces Salmonella Shedding, Tonsil Colonization, and Microbiota Alterations of the Gastrointestinal Tract in Salmonella-Challenged Swine. **2016**, 3, 66	13
1426	Gene silencing pathways found in the green alga Volvox carteri reveal insights into evolution and origins of small RNA systems in plants. **2016**, 17, 853	9
1425	Novel Strategies for Applied Metagenomics. **2016**, 22, 709-18	13
1424	Effect of Vitamin E With Therapeutic Iron Supplementation on Iron Repletion and Gut Microbiome in US Iron Deficient Infants and Toddlers. **2016**, 63, 379-85	24
1423	Thiosulfate oxidation by Thiomicrospira thermophila: metabolic flexibility in response to ambient geochemistry. **2016**, 18, 3057-72	21
1422	Mucosa-attached bacterial community in Crohn's disease coheres with the clinical disease activity index. **2016**, 8, 614-621	24
1421	Bacterial communities in Arctic first-year drift ice during the winter/spring transition. **2016**, 8, 527-35	8
1420	Influences of plant type on bacterial and archaeal communities in constructed wetland treating polluted river water. **2016**, 23, 19570-9	28
1419	Metabarcoding reveals environmental factors influencing spatio-temporal variation in pelagic micro-eukaryotes. **2016**, 25, 3593-604	29
1418	Diversity and Activity of Communities Inhabiting Plastic Debris in the North Pacific Gyre. **2016**, 1,	191
1417	Bacteria and Archaea diversity within the hot springs of Lake Magadi and Little Magadi in Kenya. **2016**, 16, 136	66
1416	Genomic characterization of the uncultured Bacteroidales family S24-7 inhabiting the guts of homeothermic animals. **2016**, 4, 36	322
1415	Lessons from genome skimming of arthropod-preserving ethanol. **2016**, 16, 1365-1377	42
1414	metaBIT, an integrative and automated metagenomic pipeline for analysing microbial profiles from high-throughput sequencing shotgun data. **2016**, 16, 1415-1427	30
1413	Effects of polyhydroxyalkanoate degradation on soil microbial community. **2016**, 131, 9-19	23

1412	Dysbiosis Contributes to Arthritis Development via Activation of Autoreactive T Cells in the Intestine. **2016**, 68, 2646-2661	303
1411	Microbiome of the paranasal sinuses: Update and literature review. **2016**, 30, 3-16	46
1410	Plasmids from the gut microbiome of cabbage root fly larvae encode SaxA that catalyses the conversion of the plant toxin 2-phenylethyl isothiocyanate. **2016**, 18, 1379-90	51
1409	Diversity and fluctuation in ciliate protozoan population in the rumen of cattle. **2016**, 87, 1188-92	4
1408	Invasive willows drive instream community structure. **2016**, 61, 1379-1391	11
1407	Rickettsial endosymbiont in the "early-diverging" streptophyte green alga Mesostigma viride. **2016**, 52, 219-29	11
1406	Ligature-induced periodontitis in mice induces elevated levels of circulating interleukin-6 but shows only weak effects on adipose and liver tissues. **2016**, 51, 639-46	29
1405	Dual RNA-seq reveals Meloidogyne graminicola transcriptome and candidate effectors during the interaction with rice plants. **2016**, 17, 860-74	39
1404	Development, diet and dynamism: longitudinal and cross-sectional predictors of gut microbial communities in wild baboons. **2016**, 18, 1312-25	41
1403	Every base matters: assessing small subunit rRNA primers for marine microbiomes with mock communities, time series and global field samples. **2016**, 18, 1403-14	1190
1402	Chytrids dominate arctic marine fungal communities. **2016**, 18, 2001-9	93
1401	Differences in soil micro-eukaryotic communities over soil pH gradients are strongly driven by parasites and saprotrophs. **2016**, 18, 2010-24	58
1400	Effects of dispersal limitation in the face of intense selection via dietary intervention on the faecal microbiota of rats. **2016**, 8, 187-95	6
1399	High occurrence of Pacearchaeota and Woesearchaeota (Archaea superphylum DPANN) in the surface waters of oligotrophic high-altitude lakes. **2016**, 8, 210-7	75
1398	Evolution and adaptation of SAR11 and Cyanobium in a saline Tibetan lake. **2016**, 8, 595-604	3
1397	Carbon content and climate variability drive global soil bacterial diversity patterns. **2016**, 86, 373-390	97
1396	Modulatory effects of condensed tannin fractions of different molecular weights from a Leucaena leucocephala hybrid on the bovine rumen bacterial community in vitro. **2016**, 96, 4565-74	12
1395	Effects of transport, fasting and anaesthesia on the faecal microbiota of healthy adult horses. **2016** , 48, 595-602	40

1394	Development of the faecal microbiota in foals. **2016**, 48, 681-688	47
1393	The microbiome of the leaf surface of Arabidopsis protects against a fungal pathogen. **2016**, 210, 1033-43	177
1392	Insights into the biodiversity of the gut microbiota of broiler chickens. **2016**, 18, 4727-4738	89
1391	Visualizing in situ translational activity for identifying and sorting slow-growing archaeal-bacterial consortia. **2016**, 113, E4069-78	119
1390	Isolation of Marine Paracoccus sp. Ss63 from the Sponge Sarcotragus sp. and Characterization of its Quorum-Sensing Chemical-Signaling Molecules by LC-MS/MS Analysis. **2016**, 56, 330-340	12
1389	Yeast culture collections in the twenty-first century: new opportunities and challenges. **2016**, 33, 243-60	30
1388	Unexpectedly high bacteriochlorophyll a concentrations in neotropical tank bromeliads. **2016**, 8, 689-698	7
1387	Subalpine conifers in different geographical locations host highly similar foliar bacterial endophyte communities. **2016**, 92,	17
1386	Long-term changes of bacterial and viral compositions in the intestine of a recovered Clostridium difficile patient after fecal microbiota transplantation. **2016**, 2, a000448	37
1385	Evaluation of bacterial transmission to the paranasal sinuses through sinus irrigation. **2016**, 6, 800-6	4
1384	Microbial diversity and community structure along a lake elevation gradient in Yosemite National Park, California, USA. **2016**, 18, 1782-91	47
1383	The role of tissue-specific microbiota in initial establishment success of Pacific oysters. **2016**, 18, 970-87	67
1382	Candidatus Desulfofervidus auxilii, a hydrogenotrophic sulfate-reducing bacterium involved in the thermophilic anaerobic oxidation of methane. **2016**, 18, 3073-91	72
1381	Next-Generation Sequencing of the Bacterial 16S rRNA Gene for Forensic Soil Comparison: A Feasibility Study. **2016**, 61, 607-17	30
1380	MicroRNA signatures characterizing caste-independent ovarian activity in queen and worker honeybees (Apis mellifera L.). **2016**, 25, 216-26	25
1379	R-Syst::diatom: an open-access and curated barcode database for diatoms and freshwater monitoring. **2016**, 2016,	51
1378	Gut microbes in correlation with mood: case study in a closed experimental human life support system. **2016**, 28, 1233-40	54
1377	OEZY: Optimising EnZYme selection for best performing terminal restriction fragment length polymorphism analysis using ARB. **2016**, 7, 242-248	

1376	mdRNA-Seq analysis of marine microbial communities from the northern Red Sea. **2016**, 6, 35470	11
1375	Transcriptome analyses of seed development in grape hybrids reveals a possible mechanism influencing seed size. **2016**, 17, 898	23
1374	De novo and comparative transcriptome analysis of cultivated and wild spinach. **2015**, 5, 17706	34
1373	Halorhabdus. **2016**, 1-9	0
1372	Cellular adhesiveness and cellulolytic capacity in Anaerolineae revealed by omics-based genome interpretation. **2016**, 9, 111	104
1371	Plant Proteins Are Smaller Because They Are Encoded by Fewer Exons than Animal Proteins. **2016**, 14, 357-370	26
1370	Unraveling the microbiome of a thermophilic biogas plant by metagenome and metatranscriptome analysis complemented by characterization of bacterial and archaeal isolates. **2016**, 9, 171	102
1369	Phylogenetic and functional potential links pH and NO emissions in pasture soils. **2016**, 6, 35990	42
1368	MeFiT: merging and filtering tool for illumina paired-end reads for 16S rRNA amplicon sequencing. **2016**, 17, 491	50
1367	Glycans affect DNA extraction and induce substantial differences in gut metagenomic studies. **2016** , 6, 26276	34
1366	Widespread Distribution of Dehalococcoides mccartyi in the Houston Ship Channel and Galveston Bay, Texas, Sediments and the Potential for Reductive Dechlorination of PCDD/F in an Estuarine Environment. **2016**, 18, 630-644	16
1365	Abundance of sulfur-degrading bacteria in a benthic bacterial community of shallow sea sediment in the off-Terengganu coast of the South China Sea. **2016**, 5, 967-978	6
1364	Microbial Communities in Globodera pallida Females Raised in Potato Monoculture Soil. **2016**, 106, 581-90	9
1363	Determination of fungal community diversity in fresh and traditional Chinese fermented pepper by pyrosequencing. **2016**, 363,	14
1362	Influence of the Po River runoff on the bacterioplankton community along trophic and salinity gradients in the Northern Adriatic Sea. **2016**, 37, 1386-1397	4
1361	Comparative metagenomics reveals taxonomically idiosyncratic yet functionally congruent communities in periodontitis. **2016**, 6, 38993	60
1360	The draft genome of whitefly Bemisia tabaci MEAM1, a global crop pest, provides novel insights into virus transmission, host adaptation, and insecticide resistance. **2016**, 14, 110	178
1359	Complete genome sequence of Desulfurivibrio alkaliphilus strain AHT2(T), a haloalkaliphilic sulfidogen from Egyptian hypersaline alkaline lakes. **2016**, 11, 67	22

1358	Ecosystem function decays by fungal outbreaks in Antarctic microbial mats. **2016**, 6, 22954	11
1357	The effects of Bt Cry1Ie toxin on bacterial diversity in the midgut of Apis mellifera ligustica (Hymenoptera: Apidae). **2016**, 6, 24664	36
1356	Metagenomic profiling of historic Colorado Front Range flood impact on distribution of riverine antibiotic resistance genes. **2016**, 6, 38432	41
1355	Long term repeated fire disturbance alters soil bacterial diversity but not the abundance in an Australian wet sclerophyll forest. **2016**, 6, 19639	26
1354	A distinct and active bacterial community in cold oxygenated fluids circulating beneath the western flank of the Mid-Atlantic ridge. **2016**, 6, 22541	46
1353	Genetic Drift, Not Life History or RNAi, Determine Long-Term Evolution of Transposable Elements. **2016**, 8, 2964-2978	37
1352	Effect of metal concentration on the microbial community in acid mine drainage of a polysulfide ore deposit. **2016**, 85, 745-751	14
1351	Resilient microorganisms in dust samples of the International Space Station-survival of the adaptation specialists. **2016**, 4, 65	43
1350	Metagenomic Profiling, Interaction of Genomics with Meta-genomics. **2016**, 241-267	
1349	Bioremediation of polychlorinated-p-dioxins/dibenzofurans contaminated soil using simulated compost-amended landfill reactors under hypoxic conditions. **2016**, 312, 159-168	23
1348	Effects of temperature and nutrients on changes in genetic diversity of bacterioplankton communities in a semi-closed bay, South Korea. **2016**, 106, 139-48	10
1347	Paratransgenesis to control malaria vectors: a semi-field pilot study. **2016**, 9, 140	46
1346	Biological, physicochemical and plant health responses in lettuce and strawberry in soil or peat amended with biochar. **2016**, 107, 1-12	87
1345	Ionic Strength Is a Barrier to the Habitability of Mars. **2016**, 16, 427-42	76
1344	The POU/Oct Transcription Factor Pdm1/nub Is Necessary for a Beneficial Gut Microbiota and Normal Lifespan of Drosophila. **2016**, 8, 412-26	21
1343	MIC of carbon steel in Amazonian environment: Electrochemical, biological and surface analyses. **2016**, 112, 98-107	11
1342	Anaerobic oxidation of methane associated with sulfate reduction in a natural freshwater gas source. **2016**, 10, 1400-12	68
1341	Biogeography of planktonic and coral-associated microorganisms across the Hawaiian Archipelago. **2016**, 92,	7

1340	First report of Wautersiella falsenii genomovar 2 isolated from the respiratory tract of an immunosuppressed man. **2016**, 4, 27-9	7
1339	Genomic insights into members of the candidate phylum Hyd24-12 common in mesophilic anaerobic digesters. **2016**, 10, 2352-64	31
1338	Detection of foodborne bacterial zoonoses by fluorescence in situ hybridization. **2016**, 69, 297-305	9
1337	Revised phylogeny of Bacteroidetes and proposal of sixteen new taxa and two new combinations including Rhodothermaeota phyl. nov. **2016**, 39, 281-96	95
1336	Long-term natural remediation process in textile dye-polluted river sediment driven by bacterial community changes. **2016**, 100, 458-465	97
1335	A systematic computational analysis of the rRNA-3' UTR sequence complementarity suggests a regulatory mechanism influencing post-termination events in metazoan translation. **2016**, 22, 957-67	3
1334	Biocathodes reducing oxygen at high potential select biofilms dominated by Ectothiorhodospiraceae populations harboring a specific association of genes. **2016**, 214, 55-62	17
1333	Subaerial biofilms on granitic historic buildings: microbial diversity and development of phototrophic multi-species cultures. **2016**, 32, 657-69	39
1332	Gene expression characterizes different nutritional strategies among three mixotrophic protists. **2016**, 92,	27
1331	A clinical Acanthamoeba isolate harboring two distinct bacterial endosymbionts. **2016**, 56, 21-25	9
1330	Multiple evidence for methylotrophic methanogenesis as the dominant methanogenic pathway in hypersaline sediments from the Orca Basin, Gulf of Mexico. **2016**, 187, 1-20	53
1329	Dietary nucleotides protect against alcoholic liver injury by attenuating inflammation and regulating gut microbiota in rats. **2016**, 7, 2898-908	17
1328	Two Bacterial Genera, Sodalis and Rickettsia, Associated with the Seal Louse Proechinophthirus fluctus (Phthiraptera: Anoplura). **2016**, 82, 3185-97	38
1327	Multicenter quality assessment of 16S ribosomal DNA-sequencing for microbiome analyses reveals high inter-center variability. **2016**, 306, 334-342	97
1326	Unique sequence characteristics account for good DGGE separation of almost full-length 18S rDNAs. **2016**, 32, 48	2
1325	Comparison of Fecal Microbiota between German Holstein Dairy Cows with and without Left-Sided Displacement of the Abomasum. **2016**, 54, 1140-3	2
1324	Genome-Resolved Metagenomic Analysis Reveals Roles for Candidate Phyla and Other Microbial Community Members in Biogeochemical Transformations in Oil Reservoirs. **2016**, 7, e01669-15	100
1323	Oceanic fronts: transition zones for bacterioplankton community composition. **2016**, 8, 132-8	31

1322	Exploring soil microbial 16S rRNA sequence data to increase carbon yield and nitrogen efficiency of a bioenergy crop. **2016**, 8, 867-879	50
1321	Selection of fungi by candidate cover crops. **2016**, 103, 72-82	27
1320	Amplicon-based metabarcoding reveals temporal response of soil microbial community to fumigation-derived products. **2016**, 103, 83-92	15
1319	Metabarcoding of marine zooplankton: prospects, progress and pitfalls. **2016**, 38, 393-400	96
1318	Ordinary stoichiometry of extraordinary microorganisms. **2016**, 14, 33-53	6
1317	Multi-primer qPCR assay capable of highly efficient and specific detection of the vast majority of all known Mycoplasma. **2016**, 44, 129-38	7
1316	Differential Effects of Azithromycin, Doxycycline, and Cotrimoxazole in Ingested Blood on the Vectorial Capacity of Malaria Mosquitoes. **2016**, 3, ofw074	18
1315	Phylogenetic diversity and ecophysiology of Candidate phylum Saccharibacteria in activated sludge. **2016**, 92, fiw078	112
1314	The Identification of Discriminating Patterns from 16S rRNA Gene to Generate Signature for Bacillus Genus. **2016**, 23, 651-61	6
1313	Batch enrichment of anammox bacteria and study of the underlying microbial community dynamics. **2016**, 297, 217-228	40
1312	Respiratory syncytial virus and rhinovirus severe bronchiolitis are associated with distinct nasopharyngeal microbiota. **2016**, 137, 1909-1913.e4	67
1311	Comparison of Varroa destructor and Worker Honeybee Microbiota Within Hives Indicates Shared Bacteria. **2016**, 72, 448-59	17
1310	Electricity generation from an inorganic sulfur compound containing mining wastewater by acidophilic microorganisms. **2016**, 167, 568-75	40
1309	Microbiome sequencing: challenges and opportunities for molecular medicine. **2016**, 16, 795-805	25
1308	Assessment of Bacterial Communities in Thirteen Species of Laboratory-Cultured Domestic Mites (Acari: Acaridida). **2016**, 109, 1887-96	24
1307	RubisCO of a nucleoside pathway known from Archaea is found in diverse uncultivated phyla in bacteria. **2016**, 10, 2702-2714	65
1306	Changes in snoRNA and snRNA Abundance in the Human, Chimpanzee, Macaque, and Mouse Brain. **2016**, 8, 840-50	7
1305	Alterations in human milk leptin and insulin are associated with early changes in the infant intestinal microbiome. **2016**, 103, 1291-300	94

1304	Microbial-Derived Metabolites Reflect an Altered Intestinal Microbiota during Catch-Up Growth in Undernourished Neonatal Mice. **2016**, 146, 940-8		13
1303	Reducing Salt in Raw Pork Sausages Increases Spoilage and Correlates with Reduced Bacterial Diversity. **2016**, 82, 3928-3939		53
1302	Variation in coastal Antarctic microbial community composition at sub-mesoscale: spatial distance or environmental filtering?. **2016**, 92,		21
1301	A Novel Pathway for Triacylglycerol Biosynthesis Is Responsible for the Accumulation of Massive Quantities of Glycerolipids in the Surface Wax of Bayberry (Myrica pensylvanica) Fruit. **2016**, 28, 248-64		24
1300	Phylogeny-aware identification and correction of taxonomically mislabeled sequences. *Nucleic Acids Research*, **2016**, 44, 5022-33	20.1	67
1299	Unusual Butane- and Pentanetriol-Based Tetraether Lipids in Methanomassiliicoccus luminyensis, a Representative of the Seventh Order of Methanogens. **2016**, 82, 4505-4516		47
1298	Genetic assessment of meiobenthic community composition and spatial distribution in coastal sediments along northern Gulf of Mexico. **2016**, 119, 166-75		8
1297	Evaluation of Enrichment Protocols for Bacterial Endosymbionts of Ciliates by Real-Time PCR. **2016**, 72, 723-32		2
1296	Bacteriocin from epidemic Listeria strains alters the host intestinal microbiota to favor infection. **2016**, 113, 5706-11		113
1295	Studying the Human Microbiota. **2016**, 902, 5-32		14
1294	Analysis of microbial diversity and dynamics during wine fermentation of Grenache grape variety by high-throughput barcoding sequencing. **2016**, 72, 317-321		75
1293	Oligotrophic lagoons of the South Pacific Ocean are home to a surprising number of novel eukaryotic microorganisms. **2016**, 18, 4549-4563		15
1292	The Core Gut Microbiome of the American Cockroach, Periplaneta americana, Is Stable and Resilient to Dietary Shifts. **2016**, 82, 6603-6610		65
1291	16S rRNA Amplicon Sequencing for Epidemiological Surveys of Bacteria in Wildlife. **2016**, 1,		66
1290	High-throughput sequencing of 16S rRNA Gene Reveals Substantial Bacterial Diversity on the Municipal Dumpsite. **2016**, 16, 145		25
1289	Influence of soil contamination with PAH on microbial community dynamics and expression level of genes responsible for biodegradation of PAH and production of rhamnolipids. **2016**, 23, 23043-23056		28
1288	Elucidating the gut microbiome of ulcerative colitis: bifidobacteria as novel microbial biomarkers. **2016**, 92,		75
1287	Where are the polyps? Molecular identification, distribution and population differentiation of jellyfish polyps in the southern North Sea area. **2016**, 163, 172		16

1286	Efficiency of different solarization-based ecological soil treatments on the control of Fusarium wilt and their impacts on the soil microbial community. **2016**, 108, 341-351		19
1285	Behavioural and neurochemical consequences of chronic gut microbiota depletion during adulthood in the rat. **2016**, 339, 463-477		129
1284	A systematic study of the whole genome sequence of strain 239 provides an insight into its physiological and taxonomic properties which correlate with its position in the genus. **2016**, 1, 169-186		14
1283	Organic farming induces changes in soil microbiota that affect agro-ecosystem functions. **2016**, 103, 327-336		80
1282	Deep metagenome and metatranscriptome analyses of microbial communities affiliated with an industrial biogas fermenter, a cow rumen, and elephant feces reveal major differences in carbohydrate hydrolysis strategies. **2016**, 9, 121		82
1281	Autonomous Marine Robotic Technology Reveals an Expansive Benthic Bacterial Community Relevant to Regional Nitrogen Biogeochemistry. **2016**, 50, 11057-11065		11
1280	Design of the MCAW compute service for food safety bioinformatics. **2016**, 60, 2:1-2:12		4
1279	Sexual variation of bacterial microbiota of Dendroctonus valens guts and frass in relation to verbenone production. **2016**, 95, 110-117		25
1278	16S rRNA gene profiling of planktonic and biofilm microbial populations in the Gulf of Guinea using Illumina NGS. **2016**, 122, 105-112		28
1277	The structure and diversity of human, animal and environmental resistomes. **2016**, 4, 54		239
1276	Identification of candidate soil microbes responsible for small-scale heterogeneity in strawberry plant vigour. **2016**, 15, 2049-2058		6
1275	Long-term grazing exclusion effects on vegetation characteristics, soil properties and bacterial communities in the semi-arid grasslands of China. **2016**, 97, 170-178		80
1274	JAR3D Webserver: Scoring and aligning RNA loop sequences to known 3D motifs. *Nucleic Acids Research*, **2016**, 44, W320-7	20.1	12
1273	Ohmic resistance affects microbial community and electrochemical kinetics in a multi-anode microbial electrochemical cell. **2016**, 331, 315-321		29
1272	Gene transfers from diverse bacteria compensate for reductive genome evolution in the chromatophore of Paulinella chromatophora. **2016**, 113, 12214-12219		96
1271	Microbial Succession and Flavor Production in the Fermented Dairy Beverage Kefir. **2016**, 1,		132
1270	Short communication: Presence of Lactococcus and lactococcal exopolysaccharide operons on the leaves of Pinguicula vulgaris supports the traditional source of bacteria present in Scandinavian ropy fermented milk. **2016**, 99, 7049-7052		2
1269	Lettuce and rhizosphere microbiome responses to growth promoting Pseudomonas species under field conditions. **2016**, 92,		43

1268	Metabarcoding and metabolome analyses of copepod grazing reveal feeding preference and linkage to metabolite classes in dynamic microbial plankton communities. **2016**, 25, 5585-5602	25
1267	Impact of poplar-based phytomanagement on soil properties and microbial communities in a metal-contaminated site. **2016**, 92,	25
1266	Structure of bacterial communities in soil following cover crop and organic fertilizer incorporation. **2016**, 100, 9331-9341	50
1265	Molecular Diagnostic Solutions in Algal Cultivation Systems. **2016**, 183-204	2
1264	Assessment of artificial substrates for evaluating groundwater microbial quality. **2016**, 71, 577-586	11
1263	Intact polar diacylglycerol biomarker lipids isolated from suspended particulate organic matter accumulating in an ultraoligotrophic water column. **2016**, 100, 29-41	14
1262	Vancomycin-Resistant Enterococci and Bacterial Community Structure following a Sewage Spill into an Aquatic Environment. **2016**, 82, 5653-60	20
1261	An overview of major metagenomic studies on human microbiomes in health and disease. **2016**, 4, 192-206	8
1260	Strain diversity and host specificity in a specialized gut symbiont of honeybees and bumblebees. **2016**, 25, 4461-71	47
1259	Crossing the Freshwater/Saline Barrier: A Phylogenetic Analysis of Bacteria Inhabiting Both Freshwater and Marine Ecosystems. **2016**, 35-44	2
1258	Comparative analysis of the fecal bacterial community of five harbor seals (Phoca vitulina). **2016**, 5, 782-792	18
1257	Biochar decreased microbial metabolic quotient and shifted community composition four years after a single incorporation in a slightly acid rice paddy from southwest China. **2016**, 571, 206-17	166
1256	Investigation of bacterial repopulation after sinus surgery and perioperative antibiotics. **2016**, 6, 34-40	35
1255	Analysis of the distal gut bacterial community by 454-pyrosequencing in captive giraffes (Giraffa camelopardalis). **2016**, 35, 42-50	9
1254	Metagenomic signatures of a tropical mining-impacted stream reveal complex microbial and metabolic networks. **2016**, 161, 266-273	27
1253	A taxonomic framework for cable bacteria and proposal of the candidate genera Electrothrix and Electronema. **2016**, 39, 297-306	68
1252	Laminarin favorably modulates gut microbiota in mice fed a high-fat diet. **2016**, 7, 4193-4201	47
1251	Distribution and activity of the anaerobic methanotrophic community in a nitrogen-fertilized Italian paddy soil. **2016**, 92,	53

1250	Response of diatom-associated bacteria to host growth state, nutrient concentrations, and viral host infection in a model system. **2016**, 8, 917-927	9
1249	Bacterial dynamics and functional analysis of microbial metagenomes during ripening of Dutch-type cheese. **2016**, 61, 182-188	27
1248	Propionibacterium acnes overabundance and natural killer group 2 member D system activation in corpus-dominant lymphocytic gastritis. **2016**, 240, 425-436	30
1247	Censusing marine eukaryotic diversity in the twenty-first century. **2016**, 371,	111
1246	Resolvin E1 Reverses Experimental Periodontitis and Dysbiosis. **2016**, 197, 2796-806	91
1245	The Nearctic Nedubini: The Most Basal Lineage of Katydids Is Resolved Among the Paraphyletic Tettigoniinae (Orthoptera: Tettigoniidae). **2016**, 109, 652-662	4
1244	Identification of microbial populations driving biopolymer degradation in acidic peatlands by metatranscriptomic analysis. **2016**, 25, 4818-35	43
1243	Gut Microbiome Associates With Lifetime Cardiovascular Disease Risk Profile Among Bogalusa Heart Study Participants. **2016**, 119, 956-64	170
1242	Free-living amoebae and their associated bacteria in Austrian cooling towers: a 1-year routine screening. **2016**, 115, 3365-74	15
1241	Reflection on Molecular Approaches Influencing State-of-the-Art Bioremediation Design: Culturing to Microbial Community Fingerprinting to Omics. **2016**, 142,	18
1240	Landscape-scale spatial abundance distributions discriminate core from random components of boreal lake bacterioplankton. **2016**, 19, 1506-1515	25
1239	Diversity, structure and convergent evolution of the global sponge microbiome. **2016**, 7, 11870	318
1238	Habitat generalists and specialists in microbial communities across a terrestrial-freshwater gradient. **2016**, 6, 37719	58
1237	Microbiome analysis reveals the abundance of bacterial pathogens in Rousettus leschenaultii guano. **2016**, 6, 36948	34
1236	An oligotrophic deep-subsurface community dependent on syntrophy is dominated by sulfur-driven autotrophic denitrifiers. **2016**, 113, E7927-E7936	108
1235	Colonization with the enteric protozoa Blastocystis is associated with increased diversity of human gut bacterial microbiota. **2016**, 6, 25255	144
1234	Gut microbiome and dietary patterns in different Saudi populations and monkeys. **2016**, 6, 32191	39
1233	Pipeline for amplifying and analyzing amplicons of the V1-V3 region of the 16S rRNA gene. **2016**, 9, 380	38

1232	Influence of Thawing Methods and Storage Temperatures on Bacterial Diversity, Growth Kinetics, and Biogenic Amine Development in Atlantic Mackerel. **2016**, 79, 1929-1937	4
1231	Lesion recovery and the bacterial microbiome in two Caribbean gorgonian corals. **2016**, 163, 1	14
1230	Diversity and bioactive potentials of culturable heterotrophic bacteria from the surficial sediments of the Arabian Sea. **2016**, 6, 238	8
1229	Alterations in the airborne bacterial community during Asian dust events occurring between February and March 2015 in South Korea. **2016**, 6, 37271	16
1228	Metagenomics and Bioinformatics in Microbial Ecology: Current Status and Beyond. **2016**, 31, 204-12	56
1227	Spatiotemporal distribution of bacterioplankton functional groups along a freshwater estuary to pelagic gradient in Lake Michigan. **2016**, 42, 1036-1048	17
1226	Occurrence and diversity of both bacterial and fungal communities in dental unit waterlines subjected to disinfectants. **2016**, 74,	3
1225	Water management impacts rice methylmercury and the soil microbiome. **2016**, 572, 608-617	42
1224	COMAN: a web server for comprehensive metatranscriptomics analysis. **2016**, 17, 622	26
1223	Bacterial community dynamics in a rumen fluid bioreactor during in-vitro cultivation. **2016**, 234, 43-49	9
1222	On the origin and evolutionary consequences of gene body DNA methylation. **2016**, 113, 9111-6	189
1221	Bacterial diversity across a highly stratified ecosystem: A salt-wedge Mediterranean estuary. **2016**, 39, 398-408	10
1220	After All, Only Millions?. **2016**, 7,	31
1219	The Non-Coding RNA Ncr0700/PmgR1 is Required for Photomixotrophic Growth and the Regulation of Glycogen Accumulation in the Cyanobacterium Synechocystis sp. PCC 6803. **2016**, 57, 2091-2103	21
1218	Mobile genes in the human microbiome are structured from global to individual scales. **2016**, 535, 435-439	148
1217	Global biogeography of microbial nitrogen-cycling traits in soil. **2016**, 113, 8033-40	186
1216	Planktic Tychonema (Cyanobacteria) in the large lakes south of the Alps: phylogenetic assessment and toxigenic potential. **2016**, 92,	28
1215	A specific and widespread association between deep-sea Bathymodiolus mussels and a novel family of Epsilonproteobacteria. **2016**, 8, 805-813	27

1214	Thermophilic archaea activate butane via alkyl-coenzyme M formation. **2016**, 539, 396-401	170
1213	High-affinity monoclonal IgA regulates gut microbiota and prevents colitis in mice. **2016**, 1, 16103	96
1212	Exploiting rRNA operon copy number to investigate bacterial reproductive strategies. **2016**, 1, 16160	183
1211	Species-function relationships shape ecological properties of the human gut microbiome. **2016**, 1, 16088	145
1210	Characterization of the microbiome of nipple aspirate fluid of breast cancer survivors. **2016**, 6, 28061	103
1209	Characterization of bacterial communities associating with larval development of Yesso Scallop (Patinopecten yessoensisis Jay, 1857) by high-throughput sequencing. **2016**, 15, 1067-1072	3
1208	High Biofilm Conductivity Maintained Despite Anode Potential Changes in a Geobacter-Enriched Biofilm. **2016**, 9, 3485-3491	26
1207	Fluid chemistry in the Solitaire and Dodo hydrothermal fields of the Central Indian Ridge. **2016**, 16, 988-1005	17
1206	Selection and Application of Sulfide Oxidizing Microorganisms Able to Withstand Thiols in Gas Biodesulfurization Systems. **2016**, 50, 12808-12815	15
1205	Bacterial associations with the hydromedusa Nemopsis bachei and scyphomedusa Aurelia aurita from the North Atlantic Ocean. **2016**, 12, 1088-1100	16
1204	Pectin enhances the effect of fecal microbiota transplantation in ulcerative colitis by delaying the loss of diversity of gut flora. **2016**, 16, 255	43
1203	Probiotic legacy effects on gut microbial assembly in tilapia larvae. **2016**, 6, 33965	36
1202	Acidification and warming affect prominent bacteria in two seasonal phytoplankton bloom mesocosms. **2016**, 18, 4579-4595	22
1201	A new primer set for DNA metabarcoding of soil Metazoa. **2016**, 77, 53-59	11
1200	Evaluation of a membrane bioreactor system as post-treatment in waste water treatment for better removal of micropollutants. **2016**, 107, 37-46	32
1199	Land-use choices follow profitability at the expense of ecological functions in Indonesian smallholder landscapes. **2016**, 7, 13137	116
1198	Microbial metabolisms in a 2.5-km-deep ecosystem created by hydraulic fracturing in shales. **2016**, 1, 16146	144
1197	Endemic hydrothermal vent species identified in the open ocean seed bank. **2016**, 1, 16086	32

1196	Intensive cryptic microbial iron cycling in the low iron water column of the meromictic Lake Cadagno. **2016**, 18, 5288-5302	39
1195	Dispersal of Bacillus subtilis and its effect on strawberry phyllosphere microbiota under open field and protection conditions. **2016**, 6, 22611	39
1194	Soil bacterial and fungal community dynamics in relation to Panax notoginseng death rate in a continuous cropping system. **2016**, 6, 31802	79
1193	The endotracheal tube microbiome associated with Pseudomonas aeruginosa or Staphylococcus epidermidis. **2016**, 6, 36507	30
1192	The Roles of Biofilm Conductivity and Donor Substrate Kinetics in a Mixed-Culture Biofilm Anode. **2016**, 50, 12799-12807	39
1191	Disentangling the Taxonomy of Rickettsiales and Description of Two Novel Symbionts ("Candidatus Bealeia paramacronuclearis" and "Candidatus Fokinia cryptica") Sharing the Cytoplasm of the Ciliate Protist Paramecium biaurelia. **2016**, 82, 7236-7247	53
1190	Metagenomics: Probing pollutant fate in natural and engineered ecosystems. **2016**, 34, 1413-1426	34
1189	Polystyrene influences bacterial assemblages in Arenicola marina-populated aquatic environments in´vitro. **2016**, 219, 219-227	27
1188	Plant and soil fungal but not soil bacterial communities are linked in long-term fertilized grassland. **2016**, 6, 23680	74
1187	Summer holidays as break-point in shaping a tannery sludge microbial community around a stable core microbiota. **2016**, 6, 30376	6
1186	Pronounced daily succession of phytoplankton, archaea and bacteria following a spring bloom. **2016**, 1, 16005	197
1185	Nitrate- and nitrite-dependent anaerobic oxidation of methane. **2016**, 8, 941-955	109
1184	Microbial community structure of a freshwater system receiving wastewater effluent. **2016**, 188, 626	7
1183	The small unicellular diazotrophic symbiont, UCYN-A, is a key player in the marine nitrogen cycle. **2016**, 1, 16163	112
1182	Trade-off between taxon diversity and functional diversity in European lake ecosystems. **2016**, 25, 5876-5888	22
1181	The effect of helminth infection on the microbial composition and structure of the caprine abomasal microbiome. **2016**, 6, 20606	74
1180	Bacterial succession and metabolite changes during flax (Linum usitatissimum L.) retting with Bacillus cereus HDYM-02. **2016**, 6, 31812	11
1179	IMNGS: A comprehensive open resource of processed 16S rRNA microbial profiles for ecology and diversity studies. **2016**, 6, 33721	192

1178	Surveys, simulation and single-cell assays relate function and phylogeny in a lake ecosystem. **2016**, 1, 16130	24
1177	A distinct microbiota composition is associated with protection from food allergy in an oral mouse immunization model. **2016**, 173, 10-18	42
1176	Correlations of Fecal Metabonomic and Microbiomic Changes Induced by High-fat Diet in the Pre-Obesity State. **2016**, 6, 21618	87
1175	Driving forces of soil bacterial community structure, diversity, and function in temperate grasslands and forests. **2016**, 6, 33696	188
1174	Association of nasopharyngeal microbiota profiles with bronchiolitis severity in infants hospitalised for bronchiolitis. **2016**, 48, 1329-1339	99
1173	Assessing the Airway Microbiota in Cystic Fibrosis. **2016**, 38, 179-184	0
1172	Next generation sequencing data of a defined microbial mock community. **2016**, 3, 160081	55
1171	Mining gut microbiome oligopeptides by functional metaproteome display. **2016**, 6, 34337	11
1170	Adjusting microbiome profiles for differences in microbial load by spike-in bacteria. **2016**, 4, 28	113
1169	Microbial Communities Are Well Adapted to Disturbances in Energy Input. **2016**, 1,	15
1168	Gut microbiota associated with HIV infection is significantly enriched in bacteria tolerant to oxygen. **2016**, 3, e000080	42
1167	Spirochaetes dominate the microbial community associated with the red coral Corallium rubrum on a broad geographic scale. **2016**, 6, 27277	44
1166	Identity of major sulfur-cycle prokaryotes in freshwater lake ecosystems revealed by a comprehensive phylogenetic study of the dissimilatory adenylylsulfate reductase. **2016**, 6, 36262	19
1165	Low abundance of Archaeorhizomycetes among fungi in soil metatranscriptomes. **2016**, 6, 38455	24
1164	Distinguishing between Microbial Habitats Unravels Ecological Complexity in Coral Microbiomes. **2016**, 1,	53
1163	TACO: Taxonomic prediction of unknown OTUs through OTU co-abundance networks. **2016**, 4, 149-158	3
1162	Phylogenetic distribution of plant snoRNA families. **2016**, 17, 969	11
1161	A novel real-time PCR assay for quantitative detection of Campylobacter fetus based on ribosomal sequences. **2016**, 12, 286	10

1160	Triatomine bugs, their microbiota and Trypanosoma cruzi: asymmetric responses of bacteria to an infected blood meal. **2016**, 9, 636	39
1159	Alterations of the gut microbiome in Chinese patients with systemic lupus erythematosus. **2016**, 8, 64	120
1158	INC-Seq: accurate single molecule reads using nanopore sequencing. **2016**, 5, 34	98
1157	Illumina sequencing-based community analysis of bacteria associated with different bryophytes collected from Tibet, China. **2016**, 16, 276	13
1156	A method for automated pathogenic content estimation with application to rheumatoid arthritis. **2016**, 10, 107	8
1155	Influence of GABA and GABA-producing Lactobacillus brevis DPC 6108 on the development of diabetes in a streptozotocin rat model. **2016**, 7, 409-20	37
1154	The role of the gastrointestinal microbiome in infectious complications during induction chemotherapy for acute myeloid leukemia. **2016**, 122, 2186-96	85
1153	Identification of subannual patterns in microbial community signatures from individual sedimentary laminae using a freeze-coring approach. **2016**, 61, 735-747	3
1152	Dead or alive: Deoxyribonuclease I sensitive bacteria and implications for the sinus microbiome. **2016**, 30, 94-8	15
1151	Heterotrophic Proteobacteria in the vicinity of diffuse hydrothermal venting. **2016**, 18, 4348-4368	26
1150	Gypsum amendment to rice paddy soil stimulated bacteria involved in sulfur cycling but largely preserved the phylogenetic composition of the total bacterial community. **2016**, 8, 413-23	19
1149	Distribution patterns of microbial communities in ultramafic landscape: a metagenetic approach highlights the strong relationships between diversity and environmental traits. **2016**, 25, 2258-72	22
1148	Proteomic Stable Isotope Probing Reveals Taxonomically Distinct Patterns in Amino Acid Assimilation by Coastal Marine Bacterioplankton. **2016**, 1,	22
1147	Nitrogen and Oxygen Isotope Effects of Ammonia Oxidation by Thermophilic Thaumarchaeota from a Geothermal Water Stream. **2016**, 82, 4492-504	19
1146	Exploring the Microbiology of the Deep Sea. **2016**, 227-249	
1145	Shared and divergent pathways for flower abscission are triggered by gibberellic acid and carbon starvation in seedless Vitis vinifera L. **2016**, 16, 38	22
1144	Dynamics of the fecal microbiome in patients with recurrent and nonrecurrent Clostridium difficile infection. **2016**, 8, 47	75
1143	Characterization of microbial communities in wetland mesocosms receiving caffeine-enriched wastewater. **2016**, 23, 14526-39	11

1142	A New Perspective on Microbes Formerly Known as Nitrite-Oxidizing Bacteria. **2016**, 24, 699-712	362
1141	Sensitivity and correlation of hypervariable regions in 16S rRNA genes in phylogenetic analysis. **2016**, 17, 135	246
1140	MDSINE: Microbial Dynamical Systems INference Engine for microbiome time-series analyses. **2016**, 17, 121	122
1139	Adaption of microbial community during the start-up stage of a thermophilic anaerobic digester treating food waste. **2016**, 80, 2025-32	15
1138	Microbial Reconstitution Reverses Maternal Diet-Induced Social and Synaptic Deficits in Offspring. **2016**, 165, 1762-1775	583
1137	Mode of Delivery Determines Neonatal Pharyngeal Bacterial Composition and Early Intestinal Colonization. **2016**, 63, 320-8	36
1136	Investigation of bacterial and archaeal communities: novel protocols using modern sequencing by Illumina MiSeq and traditional DGGE-cloning. **2016**, 20, 795-808	14
1135	Biological characterization of the hygrobafilomycin antibiotic JBIR-100 and bioinformatic insights into the hygrolide family of natural products. **2016**, 24, 6276-6290	11
1134	Relationship between chemical characteristics and bacterial community of a Korean salted-fermented anchovy sauce, Myeolchi-Aekjeot. **2016**, 73, 251-258	18
1133	Environmental Sequencing Provides Reasonable Estimates of the Relative Abundance of Specific Picoeukaryotes. **2016**, 82, 4757-4766	80
1132	Antibiotic-Induced Alterations of the Gut Microbiota Alter Secondary Bile Acid Production and Allow for Clostridium difficile Spore Germination and Outgrowth in the Large Intestine. **2016**, 1,	216
1131	Acclimation strategy to increase phenol tolerance of an anaerobic microbiota. **2016**, 216, 77-86	51
1130	Influence of oligomeric herbicidal ionic liquids with MCPA and Dicamba anions on the community structure of autochthonic bacteria present in agricultural soil. **2016**, 563-564, 247-55	39
1129	Co-occurrence of methanogenesis and N2 fixation in oil sands tailings. **2016**, 565, 306-312	18
1128	Modeling the integration of bacterial rRNA fragments into the human cancer genome. **2016**, 17, 134	4
1127	Characterization of an extensive rainbow trout miRNA transcriptome by next generation sequencing. **2016**, 17, 164	52
1126	A metabarcoding framework for facilitated survey of endolithic phototrophs with tufA. **2016**, 16, 8	42
1125	Enhancement of HIV-1 infection and intestinal CD4+ T cell depletion ex vivo by gut microbes altered during chronic HIV-1 infection. **2016**, 13, 5	49

1124	The microbiome associated with equine periodontitis and oral health. **2016**, 47, 49	36
1123	Species-level resolution of 16S rRNA gene amplicons sequenced through the MinION portable nanopore sequencer. **2016**, 5, 4	123
1122	Interpreting Prevotella and Bacteroides as biomarkers of diet and lifestyle. **2016**, 4, 15	210
1121	Marker genes that are less conserved in their sequences are useful for predicting genome-wide similarity levels between closely related prokaryotic strains. **2016**, 4, 18	42
1120	Bioinformatics for agriculture in the Next-Generation sequencing era. **2016**, 3,	23
1119	Contribution of Vegetation to the Microbial Composition of Nearby Outdoor Air. **2016**, 82, 3822-33	88
1118	Microbial community variation in cryoconite granules on Qaanaaq Glacier, NW Greenland. **2016**, 92,	33
1117	Impacts of human activities on distribution of sulfate-reducing prokaryotes and antibiotic resistance genes in marine coastal sediments of Hong Kong. **2016**, 92,	20
1116	Microbial community structure of Arctic seawater as revealed by pyrosequencing. **2016**, 35, 78-84	6
1115	The Role of Microbial Electron Transfer in the Coevolution of the Biosphere and Geosphere. **2016**, 70, 45-62	51
1114	Gut microbiota community adaption during young children fecal microbiota transplantation by 16s rDNA sequencing. **2016**, 206, 66-72	2
1113	Acute Appendicitis in Children Is Associated With a Local Expansion of Fusobacteria. **2016**, 63, 71-78	35
1112	Detection, identification and typing of Acidithiobacillus species and strains: a review. **2016**, 167, 555-67	15
1111	Associations between soil bacterial community structure and nutrient cycling functions in long-term organic farm soils following cover crop and organic fertilizer amendment. **2016**, 566-567, 949-959	69
1110	Description of Endozoicomonas ascidiicola sp. nov., isolated from Scandinavian ascidians. **2016**, 39, 313-8	12
1109	The native microbiome of the nematode Caenorhabditis elegans: gateway to a new host-microbiome model. **2016**, 14, 38	189
1108	Learning Ecological Networks from Next-Generation Sequencing Data. **2016**, 1-39	49
1107	Is metabarcoding suitable for estuarine plankton monitoring? A comparative study with microscopy. **2016**, 163, 1	63

1106	Characterization of the first cultured representative of Verrucomicrobia subdivision 5 indicates the proposal of a novel phylum. **2016**, 10, 2801-2816	98
1105	Metabarcoding improves detection of eukaryotes from early biofouling communities: implications for pest monitoring and pathway management. **2016**, 32, 671-84	40
1104	Limited sinking of Phaeocystis during a 12´days sediment trap study. **2016**, 25, 3428-35	4
1103	Variability of the Sheep Lung Microbiota. **2016**, 82, 3225-3238	30
1102	The Fecal Microbiota Profile and Bronchiolitis in Infants. **2016**, 138,	40
1101	Response of the bacterial community associated with a cosmopolitan marine diatom to crude oil shows a preference for the biodegradation of aromatic hydrocarbons. **2016**, 18, 1817-33	44
1100	Chlamydial seasonal dynamics and isolation of 'Candidatus Neptunochlamydia vexilliferae' from a Tyrrhenian coastal lake. **2016**, 18, 2405-17	9
1099	The detection of magnetotactic bacteria in deep sea sediments from the east Pacific Manganese Nodule Province. **2016**, 8, 239-49	18
1098	The longitudinal effect of a multi-strain probiotic on the intestinal bacterial microbiota of neonatal foals. **2016**, 48, 689-696	21
1097	Microbial community dynamics during the early stages of plant polymer breakdown in paddy soil. **2016**, 18, 2825-42	48
1096	Geographic patterns of co-occurrence network topological features for soil microbiota at continental scale in eastern China. **2016**, 10, 1891-901	403
1095	Redefining Healthy Urine: A Cross-Sectional Exploratory Metagenomic Study of People With and Without Bladder Dysfunction. **2016**, 196, 579-87	41
1094	Bottom-Up Proteomics Methods for Strain-Level Typing and Identification of Bacteria. **2016**, 83-146	2
1093	FT-IR spectroscopy: A powerful tool for studying the inter- and intraspecific biodiversity of cultivable non-Saccharomyces yeasts isolated from grape must. **2016**, 121, 50-8	8
1092	Quantitative metabolome, proteome and transcriptome analysis of midgut and fat body tissues in the mountain pine beetle, Dendroctonus ponderosae Hopkins, and insights into pheromone biosynthesis. **2016**, 70, 170-83	26
1091	A novel method to assess the biodiversity of parasites using 18S rDNA Illumina sequencing; parasitome analysis method. **2016**, 65, 572-575	23
1090	Salinity is the major factor influencing the sediment bacterial communities in a Mediterranean lagoonal complex (Amvrakikos Gulf, Ionian Sea). **2016**, 28, 71-81	17
1089	Response of marine bacterioplankton pH homeostasis gene expression to elevated CO2. **2016**, 6, 483-487	52

1088	Elevated nutrients change bacterial community composition and connectivity: high throughput sequencing of young marine biofilms. **2016**, 32, 57-69	37
1087	Can closed artificial ecosystem have an impact on insect microbial community? A case study of yellow mealworm (Tenebrio molitor L.). **2016**, 86, 183-189	20
1086	The role of gut microbiota in fetal methylmercury exposure: Insights from a pilot study. **2016**, 242, 60-67	45
1085	A New N-Acyl Homoserine Lactone Synthase in an Uncultured Symbiont of the Red Sea Sponge Theonella swinhoei. **2016**, 82, 1274-1285	19
1084	Molecular diversity of microbial eukaryotes in sea water from Fildes Peninsula, King George Island, Antarctica. **2016**, 39, 605-616	18
1083	metaModules identifies key functional subnetworks in microbiome-related disease. **2016**, 32, 1678-85	14
1082	Single-Cell-Genomics-Facilitated Read Binning of Candidate Phylum EM19 Genomes from Geothermal Spring Metagenomes. **2016**, 82, 992-1003	16
1081	Utility of combining morphological characters, nuclear and mitochondrial genes: An attempt to resolve the conflicts of species identification for ciliated protists. **2016**, 94, 718-729	45
1080	Bacterial communities of an agricultural soil amended with solid pig and dairy manures, and urea fertilizer. **2016**, 103, 61-71	41
1079	Genome-Based Microbial Taxonomy Coming of Age. **2016**, 8,	50
1078	Application of cryopreservation to genetic analyses of a photosynthetic picoeukaryote community. **2016**, 576, 708-16	4
1077	NSimScan: DNA comparison tool with increased speed, sensitivity and accuracy. **2016**, 32, 2380-1	7
1076	Host origin and tissue microhabitat shaping the microbiota of the terrestrial isopod Armadillidium vulgare. **2016**, 92, fiw063	31
1075	Phylogenetic distribution and evolutionary pattern of an ⍰proteobacterial small RNA gene that controls polyhydroxybutyrate accumulation in Sinorhizobium meliloti. **2016**, 99, 182-193	11
1074	Consortia of low-abundance bacteria drive sulfate reduction-dependent degradation of fermentation products in peat soil microcosms. **2016**, 10, 2365-75	87
1073	Diversity and productivity of photosynthetic picoeukaryotes in biogeochemically distinct regions of the South East Pacific Ocean. **2016**, 61, 806-824	45
1072	MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. **2016**, 33, 1870-4	25146
1071	Probiotics modulated gut microbiota suppresses hepatocellular carcinoma growth in mice. **2016**, 113, E1306-15	288

1070	Variation in soil microbial communities associated with critically endangered Wollemi pine affects fungal, but not bacterial, assembly within seedling roots. **2016**, 59, 61-71		8
1069	The utility of diversity profiling using Illumina 18S rRNA gene amplicon deep sequencing to detect and discriminate Toxoplasma gondii among the cyst-forming coccidia. **2016**, 216, 38-45		12
1068	Nitrogen removal by granular nitritation-anammox in an upflow membrane-aerated biofilm reactor. **2016**, 94, 23-31		120
1067	Complementary Microorganisms in Highly Corrosive Biofilms from an Offshore Oil Production Facility. **2016**, 82, 2545-2554		95
1066	Artificial electron acceptors decouple archaeal methane oxidation from sulfate reduction. **2016**, 351, 703-7		236
1065	Microbiological mechanism of the improved nitrogen and phosphorus removal by embedding microbial fuel cell in Anaerobic-Anoxic-Oxic wastewater treatment process. **2016**, 207, 109-17		45
1064	Ubiquitous Gammaproteobacteria dominate dark carbon fixation in coastal sediments. **2016**, 10, 1939-53		124
1063	probeBase--an online resource for rRNA-targeted oligonucleotide probes and primers: new features 2016. *Nucleic Acids Research*, **2016**, 44, D586-9	20.1	119
1062	High-resolution phylogenetic microbial community profiling. **2016**, 10, 2020-32		161
1061	rRNA and rDNA based assessment of sea ice protist biodiversity from the central Arctic Ocean. **2016**, 51, 31-46		26
1060	Characterization of bacterial communities in wetland mesocosms receiving pharmaceutical-enriched wastewater. **2016**, 90, 215-224		28
1059	Opposing phylogenetic diversity gradients of plant and soil bacterial communities. **2016**, 283, 20153003		11
1058	Improved Bacterial 16S rRNA Gene (V4 and V4-5) and Fungal Internal Transcribed Spacer Marker Gene Primers for Microbial Community Surveys. **2016**, 1,		703
1057	High mycobacterial diversity in recreational lakes. **2016**, 109, 619-31		13
1056	Changes of soil microbial community under different degraded gradients of alpine meadow. **2016**, 222, 213-222		66
1055	Ecological and evolutionary significance of novel protist lineages. **2016**, 55, 4-11		17
1054	Genomic and in situ investigations of the novel uncultured Chloroflexi associated with 0092 morphotype filamentous bulking in activated sludge. **2016**, 10, 2223-34		34
1053	The effect of temperature change on the microbial diversity and community structure along the chronosequence of the sub-arctic glacier forefield of Styggedalsbreen (Norway). **2016**, 92, fnw038		22

1052	The Colonic Microbiome and Epithelial Transcriptome Are Altered in Rats Fed a High-Protein Diet Compared with a Normal-Protein Diet. **2016**, 146, 474-83		71
1051	Plankton networks driving carbon export in the oligotrophic ocean. **2016**, 532, 465-470		392
1050	High Bacterial Diversity and Phylogenetic Novelty in Dark Euxinic Freshwaters Analyzed by 16S Tag Community Profiling. **2016**, 71, 566-74		5
1049	Short-term effects of mechanical drainage on fungal and bacterial community structure in a managed grassland soil. **2016**, 101, 93-100		6
1048	Identification, enumeration and diversity of nitrifying planktonic archaea and bacteria in trophic end members of the Laurentian Great Lakes. **2016**, 42, 39-49		19
1047	A novel conceptual approach to read-filtering in high-throughput amplicon sequencing studies. *Nucleic Acids Research*, **2016**, 44, e40	20.1	26
1046	Microbial, host and xenobiotic diversity in the cystic fibrosis sputum metabolome. **2016**, 10, 1483-98		68
1045	Marine mammals harbor unique microbiotas shaped by and yet distinct from the sea. **2016**, 7, 10516		129
1044	Rare actinomycetes Nocardia caishijiensis and Pseudonocardia carboxydivorans as endophytes, their bioactivity and metabolites evaluation. **2016**, 185, 22-35		29
1043	Archaeal community in a human-disturbed watershed in southeast China: diversity, distribution, and responses to environmental changes. **2016**, 100, 4685-98		19
1042	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. **2016**, 7, 10476		90
1041	Expansion of Microbial Forensics. **2016**, 54, 1964-74		49
1040	Characterization of biofilm formation in natural water subjected to low-frequency electromagnetic fields. **2016**, 32, 287-99		8
1039	Tracing the production and fate of individual archaeal intact polar lipids using stable isotope probing. **2016**, 95, 13-20		22
1038	StreptomeDB 2.0--an extended resource of natural products produced by streptomycetes. *Nucleic Acids Research*, **2016**, 44, D509-14	20.1	60
1037	Stochastic neutral modelling of the Gut Microbiota's relative species abundance from next generation sequencing data. **2016**, 17 Suppl 2, 16		14
1036	Anaerobic digestion of biowaste under extreme ammonia concentration: Identification of key microbial phylotypes. **2016**, 207, 92-101		108
1035	Chasing the elusive Euryarchaeota class WSA2: genomes reveal a uniquely fastidious methyl-reducing methanogen. **2016**, 10, 2478-87		146

1034	Metagenomic Signatures of Bacterial Adaptation to Life in the Phyllosphere of a Salt-Secreting Desert Tree. **2016**, 82, 2854-2861	31
1033	In hospite Symbiodinium photophysiology and antioxidant responses in Acropora muricata on a coast-reef scale: implications for variable bleaching patterns. **2016**, 68, 61-72	14
1032	Species-Level Identification of Actinomyces Isolates Causing Invasive Infections: Multiyear Comparison of Vitek MS (Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry) to Partial Sequencing of the 16S rRNA Gene. **2016**, 54, 712-7	11
1031	Seasonal variation in nifH abundance and expression of cyanobacterial communities associated with boreal feather mosses. **2016**, 10, 2198-208	45
1030	Protistan diversity and activity inferred from RNA and DNA at a coastal ocean site in the eastern North Pacific. **2016**, 92, fiw050	48
1029	Unexpected prevalence of parasite 18S rDNA sequences in winter among Antarctic marine protists. **2016**, 38, 401-417	21
1028	Dominance of Oscillospira and Bacteroides in the bacterial community associated with the degradation of high-concentration dimethyl sulfide under iron-reducing condition. **2016**, 66, 1199-1206	13
1027	Capturing the most wanted taxa through cross-sample correlations. **2016**, 10, 2459-67	7
1026	Comparative Genomics of Candidate Phylum TM6 Suggests That Parasitism Is Widespread and Ancestral in This Lineage. **2016**, 33, 915-27	50
1025	"Candidatus Finniella" (Rickettsiales, Alphaproteobacteria), Novel Endosymbionts of Viridiraptorid Amoeboflagellates (Cercozoa, Rhizaria). **2016**, 82, 659-70	31
1024	Chloroflexi CL500-11 Populations That Predominate Deep-Lake Hypolimnion Bacterioplankton Rely on Nitrogen-Rich Dissolved Organic Matter Metabolism and C1 Compound Oxidation. **2015**, 82, 1423-32	39
1023	Kombucha tea fermentation: Microbial and biochemical dynamics. **2016**, 220, 63-72	156
1022	Investigation of microbial structure and composition involved in membrane fouling in the forward osmosis membrane bioreactor treating anaerobic bioreactor effluent. **2016**, 286, 198-207	46
1021	Ibuprofen removal in horizontal subsurface flow constructed wetlands: treatment performance and fungal community dynamics. **2016**, 37, 1467-79	7
1020	Identification of Specialists and Abundance-Occupancy Relationships among Intestinal Bacteria of Aves, Mammalia, and Actinopterygii. **2015**, 82, 1496-1503	3
1019	Getting ready for host invasion: elevated expression and action of xyloglucan endotransglucosylases/hydrolases in developing haustoria of the holoparasitic angiosperm Cuscuta. **2016**, 67, 695-708	23
1018	The 5300-year-old Helicobacter pylori genome of the Iceman. **2016**, 351, 162-165	152
1017	Global biogeography of marine fungi is shaped by the environment. **2016**, 19, 39-46	90

1016	Fungal identification using a Bayesian classifier and the Warcup training set of internal transcribed spacer sequences. **2016**, 108, 1-5	128
1015	Phylogenetic and genomic analysis of Methanomassiliicoccales in wetlands and animal intestinal tracts reveals clade-specific habitat preferences. **2016**, 92,	78
1014	Corticosteroid therapy and airflow obstruction influence the bronchial microbiome, which is distinct from that of bronchoalveolar lavage in asthmatic airways. **2016**, 137, 1398-1405.e3	89
1013	Stable and sporadic symbiotic communities of coral and algal holobionts. **2016**, 10, 1157-69	89
1012	Microbial Mat Communities along an Oxygen Gradient in a Perennially Ice-Covered Antarctic Lake. **2016**, 82, 620-30	38
1011	Fungal Community Assembly in the Amazonian Dark Earth. **2016**, 71, 962-73	24
1010	Role of aeration intensity on performance and microbial community profiles in a sequencing batch reaction kettle (SBRK) for wastewater nutrients rapid removal. **2016**, 201, 140-7	32
1009	MetaQUAST: evaluation of metagenome assemblies. **2016**, 32, 1088-90	253
1008	Activity and interactions of methane seep microorganisms assessed by parallel transcription and FISH-NanoSIMS analyses. **2016**, 10, 678-92	39
1007	Databases of the marine metagenomics. **2016**, 576, 724-8	14
1006	Divergent Viruses Discovered in Arthropods and Vertebrates Revise the Evolutionary History of the Flaviviridae and Related Viruses. **2016**, 90, 659-69	162
1005	Unresolved diversity and monthly dynamics of eukaryotic phytoplankton in a temperate freshwater reservoir explored by pyrosequencing. **2016**, 67, 1680	5
1004	Anthropogenic activities drive the microbial community and its function in urban river sediment. **2016**, 16, 716-725	25
1003	Massively parallel sequencing of single cells by epicPCR links functional genes with phylogenetic markers. **2016**, 10, 427-36	125
1002	Influences of diurnal sampling bias on fixed-point monitoring of plankton biodiversity determined using a massively parallel sequencing-based technique. **2016**, 576, 667-75	8
1001	Predicting microbial traits with phylogenies. **2016**, 10, 959-67	88
1000	Activity and community structures of sulfate-reducing microorganisms in polar, temperate and tropical marine sediments. **2016**, 10, 796-809	41
999	Biological control of biofilms on membranes by metazoans. **2016**, 88, 20-29	58

998	Thiosulphate conversion in a methane and acetate fed membrane bioreactor. **2016**, 23, 2467-78	8
997	Microbial Community Analysis with Ribosomal Gene Fragments from Shotgun Metagenomes. **2016**, 82, 157-66	41
996	Effects of high doses of vitamin D3 on mucosa-associated gut microbiome vary between regions of the human gastrointestinal tract. **2016**, 55, 1479-89	138
995	Large variability of bathypelagic microbial eukaryotic communities across the world's oceans. **2016**, 10, 945-58	103
994	Assessment of a 16S rRNA amplicon Illumina sequencing procedure for studying the microbiome of a symbiont-rich aphid genus. **2016**, 16, 628-40	40
993	Experimental insights into the importance of aquatic bacterial community composition to the degradation of dissolved organic matter. **2016**, 10, 533-45	197
992	Long-term effects of timber harvesting on hemicellulolytic microbial populations in coniferous forest soils. **2016**, 10, 363-75	29
991	Gut dendritic cell activation links an altered colonic microbiome to mucosal and systemic T-cell activation in untreated HIV-1 infection. **2016**, 9, 24-37	127
990	Diverse, rare microbial taxa responded to the Deepwater Horizon deep-sea hydrocarbon plume. **2016**, 10, 400-15	96
989	Carcass mass has little influence on the structure of gravesoil microbial communities. **2016**, 130, 253-63	34
988	Unravelling the drivers of aquatic communities using disparate organismal groups and different taxonomic levels. **2016**, 60, 108-118	44
987	Abundance and Relative Distribution of Frankia Host Infection Groups Under Actinorhizal Alnus glutinosa and Non-actinorhizal Betula nigra Trees. **2016**, 71, 473-81	14
986	Taxon-specific responses of soil microbial communities to different soil priming effects induced by addition of plant residues and their biochars. **2017**, 17, 674-684	42
985	Phages rarely encode antibiotic resistance genes: a cautionary tale for virome analyses. **2017**, 11, 237-247	189
984	Spatial distribution of aquatic marine fungi across the western Arctic and sub-arctic. **2017**, 19, 475-484	48
983	Long-term effect of plastic film mulching and fertilization on bacterial communities in a brown soil revealed by high through-put sequencing. **2017**, 63, 230-241	51
982	Bacterial community structure in intertidal sediments of Fildes Peninsula, maritime Antarctica. **2017**, 40, 339-349	18
981	Ecological succession of the microbial communities of an air-conditioning cooling coil in the tropics. **2017**, 27, 345-353	15

980	Reference Tree and Environmental Sequence Diversity of Labyrinthulomycetes. **2017**, 64, 88-96	26
979	The Composition of Human Milk and Infant Faecal Microbiota Over the First Three Months of Life: A Pilot Study. **2017**, 7, 40597	180
978	Effects of daidzein on performance, serum metabolites, nutrient digestibility, and fecal bacterial community in bull calves. **2017**, 225, 87-96	29
977	Anaerobic hydrocarbon biodegradation and biocorrosion of carbon steel in marine environments: The impact of different ultra low sulfur diesels and bioaugmentation. **2017**, 118, 45-56	16
976	Bacterial endophyte communities of three agricultural important grass species differ in their response towards management regimes. **2017**, 7, 40914	59
975	Molecular and carbon isotopic characterization of an anaerobic stable enrichment culture containing Dehalobacterium sp. during dichloromethane fermentation. **2017**, 581-582, 640-648	19
974	Horizontal gene transfer drives the evolution of Rh50 permeases in prokaryotes. **2017**, 17, 2	9
973	Genomic repertoire of the Woeseiaceae/JTB255, cosmopolitan and abundant core members of microbial communities in marine sediments. **2017**, 11, 1276-1281	89
972	Invasions Toolkit. **2017**, 85-182	32
971	Taxonomic and functional diversity of a coastal planktonic bacterial community in a river-influenced marine area. **2017**, 32, 61-69	11
970	Epilithic and endolithic microorganisms and deterioration on stone church facades subject to urban pollution in a sub-tropical climate. **2017**, 33, 113-127	37
969	DNA metabarcoding reveals that 200-□m-size-fractionated filtering is unable to discriminate between planktonic microbial and large eukaryotes. **2017**, 17, 991-1002	35
968	THESES db: the algae 18S rDNA sequence□tructure database for inferring phylogenies. **2017**, 56, 186-192	4
967	McrA primers for the detection and quantification of the anaerobic archaeal methanotroph 'Candidatus Methanoperedens nitroreducens'. **2017**, 101, 1631-1641	38
966	Studying Vertical Microbiome Transmission from Mothers to Infants by Strain-Level Metagenomic Profiling. **2017**, 2,	207
965	Bacterial Diversity in Ships' Ballast Water, Ballast-Water Exchange, and Implications for Ship-Mediated Dispersal of Microorganisms. **2017**, 51, 1962-1972	29
964	Loss-of-function mutation of the calcium sensor CBL1 increases aluminum sensitivity in Arabidopsis. **2017**, 214, 830-841	28
963	Sediment Microbial Diversity of Three Deep-Sea Hydrothermal Vents Southwest of the Azores. **2017**, 74, 332-349	18

962	Chemical characterization of the glycated myofibrillar proteins from grass carp (Ctenopharyngodon idella) and their impacts on the human gut microbiota in vitro fermentation. **2017**, 8, 1184-1194	18
961	A Culture-Independent Approach to Enrich Endophytic Bacterial Cells from Sugarcane Stems for Community Characterization. **2017**, 74, 453-465	13
960	A quantitative SMRT cell sequencing method for ribosomal amplicons. **2017**, 135, 77-84	5
959	Priming of soil organic matter: Chemical structure of added compounds is more important than the energy content. **2017**, 108, 41-54	61
958	Defective ATG16L1-mediated removal of IRE1□drives Crohn’s disease-like ileitis. **2017**, 214, 401-422	109
957	Polymetallic nodules, sediments, and deep waters in the equatorial North Pacific exhibit highly diverse and distinct bacterial, archaeal, and microeukaryotic communities. **2017**, 6, e00428	49
956	Efficient Low-pH Iron Removal by a Microbial Iron Oxide Mound Ecosystem at Scalp Level Run. **2017** , 83,	15
955	New roles in hemicellulosic sugar fermentation for the uncultivated Bacteroidetes family BS11. **2017**, 11, 691-703	72
954	Soil microbial communities and elk foraging intensity: implications for soil biogeochemical cycling in the sagebrush steppe. **2017**, 20, 202-211	14
953	A metaproteomic approach dissecting major bacterial functions in the rhizosphere of plants living in serpentine soil. **2017**, 409, 2327-2339	34
952	Anaerobic Dechlorination of Tetrachlorobisphenol A in River Sediment and Associated Changes in Bacterial Communities. **2017**, 228, 1	8
951	Effects of the Dietary Protein and Carbohydrate Ratio on Gut Microbiomes in Dogs of Different Body Conditions. **2017**, 8,	75
950	Arbuscular mycorrhizal fungi inoculation mediated changes in rhizosphere bacterial community structure while promoting revegetation in a semiarid ecosystem. **2017**, 584-585, 838-848	42
949	Permeability shapes bacterial communities in sublittoral surface sediments. **2017**, 19, 1584-1599	51
948	Changes in rumen microbiota composition and in situ degradation kinetics during the dry period and early lactation as affected by rate of increase of concentrate allowance. **2017**, 100, 2695-2710	17
947	The effect of the source of microorganisms on adaptation of hydrolytic consortia dedicated to anaerobic digestion of maize silage. **2017**, 46, 46-55	17
946	Transcriptomic analysis of common carp anterior kidney during Cyprinid herpesvirus 3 infection: Immunoglobulin repertoire and homologue functional divergence. **2017**, 7, 41531	18
945	Randomised clinical trial: faecal microbiota transplantation for recurrent Clostridum difficile infection - fresh, or frozen, or lyophilised microbiota from a small pool of healthy donors delivered by colonoscopy. **2017**, 45, 899-908	116

944	Effect of salinity on the microbial community and performance on anaerobic digestion of marine macroalgae. **2017**, 92, 2392-2399		29
943	Metataxonomics reveal vultures as a reservoir for Clostridium perfringens. **2017**, 6, e9		17
942	Optimization of DNA extraction for advancing coral microbiota investigations. **2017**, 5, 18		21
941	Organic nitrogen rearranges both structure and activity of the soil-borne microbial seedbank. **2017**, 7, 42634		29
940	Attached and Suspended Denitrifier Communities in Pristine Limestone Aquifers Harbor High Fractions of Potential Autotrophs Oxidizing Reduced Iron and Sulfur Compounds. **2017**, 74, 264-277		32
939	High-resolution sequencing reveals unexplored archaeal diversity in freshwater wetland soils. **2017**, 19, 2192-2209		34
938	Plant Community and Nitrogen Deposition as Drivers of Alpha and Beta Diversities of Prokaryotes in Reconstructed Oil Sand Soils and Natural Boreal Forest Soils. **2017**, 83,		16
937	Microbiota composition of simultaneously colonized mice housed under either a gnotobiotic isolator or individually ventilated cage regime. **2017**, 7, 42245		28
936	Succession and dynamics of Pristionchus nematodes and their microbiome during decomposition of Oryctes borbonicus on La Rûnion Island. **2017**, 19, 1476-1489		25
935	Microbial diversity of the hypersaline and lithium-rich Salar de Uyuni, Bolivia. **2017**, 199, 19-28		27
934	How Can We Understand the Genomic Basis of Nematode Parasitism?. **2017**, 33, 444-452		13
933	Microbial community changes during different empty bed residence times and operational fluctuations in an air diffusion reactor for odor abatement. **2017**, 590-591, 352-360		13
932	CD40-signalling abrogates induction of ROR▯ Treg cells by intestinal CD103 DCs and causes fatal colitis. **2017**, 8, 14715		24
931	Low-dose penicillin exposure in early life decreases Th17 and the susceptibility to DSS colitis in mice through gut microbiota modification. **2017**, 7, 43662		40
930	Microbial potential for carbon and nutrient cycling in a geogenic supercritical carbon dioxide reservoir. **2017**, 19, 2228-2245		15
929	Fungal diversity in soils across a gradient of preserved Brazilian Cerrado. **2017**, 55, 273-279		13
928	No effect of Bt Cry1Ie toxin on bacterial diversity in the midgut of the Chinese honey bees, Apis cerana cerana (Hymenoptera, Apidae). **2017**, 7, 41688		11
927	MEGARes: an antimicrobial resistance database for high throughput sequencing. *Nucleic Acids Research*, **2017**, 45, D574-D580	20.1	190

926	Differential effects of monensin and a blend of essential oils on rumen microbiota composition of transition dairy cows. **2017**, 100, 2765-2783	55
925	The MiiA motif is a common marker present in polytopic surface proteins of oral and urinary tract invasive bacteria. **2017**, 49, 283-292	2
924	Retrospective analysis of phytoplankton assemblages on the Iwate coast before and after the 2011 tsunami using cryopreserved DNA samples. **2017**, 26, 234-250	3
923	Global Molecular Epidemiology of IMP-Producing Enterobacteriaceae. **2017**, 61,	31
922	Wells provide a distorted view of life in the aquifer: implications for sampling, monitoring and assessment of groundwater ecosystems. **2017**, 7, 40702	49
921	Towards long-read metagenomics: complete assembly of three novel genomes from bacteria dependent on a diazotrophic cyanobacterium in a freshwater lake co-culture. **2017**, 12, 9	38
920	Metatranscriptomic Evidence for Direct Interspecies Electron Transfer between Geobacter and Methanothrix Species in Methanogenic Rice Paddy Soils. **2017**, 83,	161
919	SAG-QC: quality control of single amplified genome information by subtracting non-target sequences based on sequence compositions. **2017**, 18, 152	4
918	The microbiome of the ant-built home: the microbial communities of a tropical arboreal ant and its nest. **2017**, 8, e01639	20
917	Divergent Relationships between Fecal Microbiota and Metabolome following Distinct Antibiotic-Induced Disruptions. **2017**, 2,	18
916	New natural products identified by combined genomics-metabolomics profiling of marine Streptomyces sp. MP131-18. **2017**, 7, 42382	49
915	Use of Endophytic and Rhizosphere Bacteria To Improve Phytoremediation of Arsenic-Contaminated Industrial Soils by Autochthonous Betula celtiberica. **2017**, 83,	77
914	Unique Bacteria Community Composition and Co-occurrence in the Milk of Different Ruminants. **2017**, 7, 40950	21
913	Deciphering composition and function of the root microbiome of a legume plant. **2017**, 5, 2	100
912	Ovarian cycling and reproductive state shape the vaginal microbiota in wild baboons. **2017**, 5, 8	29
911	Soil bacteria as trace evidence. **2017**, 339-357	1
910	An introduction to metagenomic data generation, analysis, visualization, and interpretation. **2017**, 94-126	2
909	Microbial Endoliths on East Adriatic Limestone Coast: Morphological vs. Molecular Diversity. **2017**, 34, 903-915	4

908	Soda pans of the Pannonian steppe harbor unique bacterial communities adapted to multiple extreme conditions. **2017**, 21, 639-649	28
907	Influences of dissolved oxygen concentration on biocathodic microbial communities in microbial fuel cells. **2017**, 116, 39-51	70
906	Non-Random Inversion Landscapes in Prokaryotic Genomes Are Shaped by Heterogeneous Selection Pressures. **2017**, 34, 1902-1911	14
905	Potentially Active Iron, Sulfur, and Sulfate Reducing Bacteria in Skagerrak and Bothnian Bay Sediments. **2017**, 34, 840-850	17
904	The microbiome in respiratory medicine: current challenges and future perspectives. **2017**, 49,	124
903	Metazoan mitochondrial gene sequence reference datasets for taxonomic assignment of environmental samples. **2017**, 4, 170027	90
902	Origin-Dependent Variations in the Atmospheric Microbiome Community in Eastern Mediterranean Dust Storms. **2017**, 51, 6709-6718	68
901	Association of Maternal Gestational Weight Gain With the Infant Fecal Microbiota. **2017**, 65, 509-515	12
900	Fecal microbiota signatures of adult patients with different types of short bowel syndrome. **2017**, 32, 1949-1957	27
899	The effect of reconstruction works on planktonic bacterial diversity of a unique thermal lake revealed by cultivation, molecular cloning and next generation sequencing. **2017**, 199, 1077-1089	11
898	Smokeless tobacco products harbor diverse bacterial microbiota that differ across products and brands. **2017**, 101, 5391-5403	22
897	Eukaryotic diversity in late Pleistocene marine sediments around a shallow methane hydrate deposit in the Japan Sea. **2017**, 15, 715-727	4
896	The Influence of Energy Harvesting Strategies on Performance and Microbial Community for Sediment Microbial Fuel Cells. **2017**, 164, H3109-H3114	15
895	Shifts among Eukaryota, Bacteria, and Archaea define the vertical organization of a lake sediment. **2017**, 5, 41	37
894	Revealing the bacterial profile of an anoxic-aerobic moving-bed biofilm reactor system treating a chemical industry wastewater. **2017**, 120, 152-160	26
893	Microbial community structure and biodiversity of size-fractionated granules in a partial nitritation-anammox process. **2017**, 93,	32
892	Microbial communities associated with the anthropogenic, highly alkaline environment of a saline soda lime, Poland. **2017**, 110, 945-962	18
891	Reconstructed ancestral enzymes suggest long-term cooling of Earth’s photic zone since the Archean. **2017**, 114, 4619-4624	30

890	Intestinal alkaline phosphatase deficiency leads to dysbiosis and bacterial translocation in the newborn intestine. **2017**, 218, 35-42	15
889	Variation of Bacterial Communities with Water Quality in an Urban Tropical Catchment. **2017**, 51, 5591-5601	9
888	Molecular characterisation of protistan species and communities in ships' ballast water across three U.S. coasts. **2017**, 23, 680-691	13
887	Viruses in the Oceanic Basement. **2017**, 8,	33
886	Cultured microbes represent a substantial fraction of the human and mouse gut microbiota. **2017**, 8, 493-503	57
885	Effect of cadexomer iodine on the microbial load and diversity of chronic non-healing diabetic foot ulcers complicated by biofilm in vivo. **2017**, 72, 2093-2101	34
884	The low diverse gastric microbiome of the jellyfish Cotylorhiza tuberculata is dominated by four novel taxa. **2017**, 19, 3039-3058	32
883	The novel bacterial phylum Calditrichaeota is diverse, widespread and abundant in marine sediments and has the capacity to degrade detrital proteins. **2017**, 9, 397-403	27
882	Differential responses of soil bacteria, fungi, archaea and protists to plant species richness and plant functional group identity. **2017**, 26, 4085-4098	99
881	Unveiling microbial interactions in stratified mat communities from a warm saline shallow pond. **2017**, 19, 2405-2421	22
880	Enrichment and Physiological Characterization of a Cold-Adapted Nitrite-Oxidizing Nitrotoga sp. from an Eelgrass Sediment. **2017**, 83,	26
879	Using systems biology approaches to elucidate cause and effect in host–microbiome interactions. **2017**, 3, 141-146	10
878	Effect of fumigation with chloropicrin on soil bacterial communities and genes encoding key enzymes involved in nitrogen cycling. **2017**, 227, 534-542	52
877	Bifidobacterium CECT 7765 modulates early stress-induced immune, neuroendocrine and behavioral alterations in mice. **2017**, 65, 43-56	87
876	DNA-based study of the diet of the marine calanoid copepod Calanus sinicus. **2017**, 494, 1-9	14
875	Unraveling microbial ecology of industrial-scale Kombucha fermentations by metabarcoding and culture-based methods. **2017**, 93,	100
874	Vertical distribution of microbial communities in soils contaminated by chromium and perfluoroalkyl substances. **2017**, 599-600, 156-164	60
873	Oral microbiome in HIV-associated periodontitis. **2017**, 96, e5821	34

872	Comparison of bacterial microbiota of the predatory mite Neoseiulus cucumeris (Acari: Phytoseiidae) and its factitious prey Tyrophagus putrescentiae (Acari: Acaridae). **2017**, 7, 2		77
871	Soil Bacterial and Fungal Communities Show Distinct Recovery Patterns during Forest Ecosystem Restoration. **2017**, 83,		95
870	Bioinformatics tools for quantitative and functional metagenome and metatranscriptome data analysis in microbes. **2018**, 19, 1415-1429		22
869	Subspecies Influences Proinflammatory Cytokine Expression and Monocyte Activation in Human Colorectal Tumors. **2017**, 10, 398-409		74
868	Single Delivery of High-Diversity Fecal Microbiota Preparation by Colonoscopy Is Safe and Effective in Increasing Microbial Diversity in Active Ulcerative Colitis. **2017**, 23, 903-911		60
867	Chemical and pathogen-induced inflammation disrupt the murine intestinal microbiome. **2017**, 5, 47		64
866	Actual measurement, hygrothermal response experiment and growth prediction analysis of microbial contamination of central air conditioning system in Dalian, China. **2017**, 7, 44190		2
865	A Robust Framework for Microbial Archaeology. **2017**, 18, 321-356		92
864	Compositional differences among female-associated and embryo-associated microbiota of the viviparous Pacific Beetle cockroach, Diploptera punctata. **2017**, 93,		5
863	Interactive microbial distribution analysis using BioAtlas. *Nucleic Acids Research*, **2017**, 45, W509-W513	20.1	8
862	Nasal Airway Microbiota Profile and Severe Bronchiolitis in Infants: A Case-control Study. **2017**, 36, 1044-1051		38
861	Microbial community function in the bleaching disease of the marine macroalgae Delisea pulchra. **2017**, 19, 3012-3024		23
860	Resilience of the prokaryotic microbial community of Acropora digitifera to elevated temperature. **2017**, 6, e00478		19
859	Impact of wet aerobic pretreatments on cellulose accessibility and bacterial communities in rape straw. **2017**, 237, 31-38		11
858	Hexavalent chromium bioreduction and chemical precipitation of sulphate as a treatment of site-specific fly ash leachates. **2017**, 33, 88		5
857	Microbial community structure and diversity in a municipal solid waste landfill. **2017**, 66, 79-87		52
856	Size-variable zone in V3 region of 16S rRNA. **2017**, 14, 1514-1521		5
855	Changes in rumen protozoal community by condensed tannin fractions of different molecular weights from a Leucaena leucocephala hybrid in vitro. **2017**, 123, 41-53		7

854	Mentholation affects the cigarette microbiota by selecting for bacteria resistant to harsh environmental conditions and selecting against potential bacterial pathogens. **2017**, 5, 22	24
853	Effect of humic acid on anaerobic digestion of cellulose and xylan in completely stirred tank reactors: inhibitory effect, mitigation of the inhibition and the dynamics of the microbial communities. **2017**, 101, 889-901	53
852	Microbiome and metabolic disease: revisiting the bacterial phylum Bacteroidetes. **2017**, 95, 1-8	159
851	Analysis of dark crusts on the church of Nossa Senhora do Carmo in Rio de Janeiro, Brazil, using chemical, microscope and metabarcoding microbial identification techniques. **2017**, 117, 60-67	21
850	Assessing Bacterial and Fungal Diversity in the Plant Endosphere. **2017**, 1539, 75-84	12
849	Dechlorination of three tetrachlorobenzene isomers by contaminated harbor sludge-derived enrichment cultures follows thermodynamically favorable reactions. **2017**, 101, 2589-2601	11
848	Distinct Anaerobic Bacterial Consumers of Cellobiose-Derived Carbon in Boreal Fens with Different CO2/CH4 Production Ratios. **2017**, 83,	21
847	In vitro and in vivo evaluation of the probiotic attributes of Lactobacillus kefiranofaciens XL10 isolated from Tibetan kefir grain. **2017**, 101, 2467-2477	21
846	Summer microbial community composition governed by upper-ocean stratification and nutrient availability in northern Marguerite Bay, Antarctica. **2017**, 139, 151-166	15
845	The microbiome of the octocoral Lobophytum pauciflorum: minor differences between sexes and resilience to short-term stress. **2017**, 93,	17
844	Green alder (Alnus viridis) encroachment shapes microbial communities in subalpine soils and impacts its bacterial or fungal symbionts differently. **2017**, 19, 3235-3250	12
843	Mobilization and integration of bacterial phenotypic data-Enabling next generation biodiversity analysis through the BacDive metadatabase. **2017**, 261, 187-193	7
842	Genomic epidemiology of global VIM-producing Enterobacteriaceae. **2017**, 72, 2249-2258	33
841	Inter-individual differences determine the outcome of wheat bran colonization by the human gut microbiome. **2017**, 19, 3251-3267	55
840	Analysis of phytoplankton assemblage structure in the Mediterranean Sea based on high-throughput sequencing of partial 18S rRNA sequences. **2017**, 36, 49-55	16
839	Strain-Level Metagenomic Analysis of the Fermented Dairy Beverage Nunu Highlights Potential Food Safety Risks. **2017**, 83,	55
838	Microbial population profile during ripening of Protected Designation of Origin (PDO) Silter cheese, produced with and without autochthonous starter culture. **2017**, 84, 821-831	21
837	Bacterioplankton assemblages in coastal ponds reflect the influence of hydrology and geomorphological setting. **2017**, 93,	4

836	Abundance and Co-Distribution of Widespread Marine Archaeal Lineages in Surface Sediments of Freshwater Water Bodies across the Iberian Peninsula. **2017**, 74, 776-787	11
835	Millions of Boreal Shield Lakes can be used to Probe Archaean Ocean Biogeochemistry. **2017**, 7, 46708	21
834	Microbial community dynamics in a pilot-scale MFC-AA/O system treating domestic sewage. **2017**, 241, 439-447	34
833	The heterogeneity of composition and assembly processes of the microbial community between different nutrient loading lake zones in Taihu Lake. **2017**, 101, 5913-5923	29
832	Succession in the petroleum reservoir microbiome through an oil field production lifecycle. **2017**, 11, 2141-2154	86
831	Comparison of biofilm ecology supporting growth of individual Naegleria species in a drinking water distribution system. **2017**, 93,	13
830	Different Amplicon Targets for Sequencing-Based Studies of Fungal Diversity. **2017**, 83,	67
829	Temperature-responsive miRNAs in orchestrate adaptation to different ambient temperatures. **2017**, 23, 1352-1364	13
828	Microbiota Analysis Using an Illumina MiSeq Platform to Sequence 16S rRNA Genes. **2017**, 7, 100-129	22
827	Novel in vivo experimental viability assays with high sensitivity and throughput capacity using a bdelloid rotifer. **2017**, 144, 115-122	10
826	Effect of post-harvest starvation and rinsing on the microbial numbers and the bacterial community composition of mealworm larvae (Tenebrio molitor). **2017**, 42, 8-15	55
825	Genome-wide profiling and differential expression of microRNA in rat pluripotent stem cells. **2017**, 7, 2787	12
824	Preferential suppression of Anopheles gambiae host sequences allows detection of the mosquito eukaryotic microbiome. **2017**, 7, 3241	25
823	Dysbiosis in chronic periodontitis: Key microbial players and interactions with the human host. **2017** , 7, 3703	102
822	Complex interactions between potentially pathogenic, opportunistic, and resident bacteria emerge during infection on a reef-building coral. **2017**, 93,	29
821	Identification of Pelomyxa palustris Endosymbionts. **2017**, 168, 408-424	11
820	Energy and carbon metabolisms in a deep terrestrial subsurface fluid microbial community. **2017**, 11, 2319-2333	59
819	Unexpected genomic features in widespread intracellular bacteria: evidence for motility of marine chlamydiae. **2017**, 11, 2334-2344	16

818	Microbial network, phylogenetic diversity and community membership in the active layer across a permafrost thaw gradient. **2017**, 19, 3201-3218	52
817	Benzene degradation in a denitrifying biofilm reactor: activity and microbial community composition. **2017**, 101, 5175-5188	26
816	Low temperature, autotrophic microbial denitrification using thiosulfate or thiocyanate as electron donor. **2017**, 28, 287-301	27
815	Bacterial community dynamics in a cooling tower with emphasis on pathogenic bacteria and Legionella species using universal and genus-specific deep sequencing. **2017**, 122, 363-376	33
814	Crenothrix are major methane consumers in stratified lakes. **2017**, 11, 2124-2140	87
813	Decreased plant productivity resulting from plant group removal experiment constrains soil microbial functional diversity. **2017**, 23, 4318-4332	24
812	Lateral Gene Transfer Dynamics in the Ancient Bacterial Genus. **2017**, 8,	63
811	Eukaryotic microbial richness increases with latitude and decreasing temperature in the Pacific Subarctic domain in late winter. **2017**, 40, 2161-2169	
810	Microbes influence the biogeochemical and optical properties of maritime Antarctic snow. **2017**, 122, 1456-1470	16
809	An 18S rRNA Workflow for Characterizing Protists in Sewage, with a Focus on Zoonotic Trichomonads. **2017**, 74, 923-936	18
808	Characterization of Phormidium lacuna strains from the North Sea and the Mediterranean Sea for biotechnological applications. **2017**, 59, 194-206	5
807	Cultivable gut bacteria provide a pathway for adaptation of Chrysolina herbacea to Mentha aquatica volatiles. **2017**, 17, 30	10
806	Inhibition Effect of Sodium Concentrations on the Anaerobic Digestion Performance of Sargassum Species. **2017**, 31, 7101-7109	23
805	PipeCraft: Flexible open-source toolkit for bioinformatics analysis of custom high-throughput amplicon sequencing data. **2017**, 17, e234-e240	72
804	Effects of ecological restoration on soil microbial diversity in a temperate grassy woodland. **2017**, 117-118, 117-128	21
803	Metagenomic potential for and diversity of N-cycle driving microorganisms in the Bothnian Sea sediment. **2017**, 6, e00475	34
802	Effects of replacing Leymus chinensis with whole-crop wheat hay on Holstein bull apparent digestibility, plasma parameters, rumen fermentation, and microbiota. **2017**, 7, 2114	11
801	Bioaerosol sampling and detection methods based on molecular approaches: No pain no gain. **2017** , 599-600, 2095-2104	33

800	Probiotic yogurt and acidified milk similarly reduce postprandial inflammation and both alter the gut microbiota of healthy, young men. **2017**, 117, 1312-1322	61
799	Genetic Characterization of Periphyton Communities Associated with Selenium Bioconcentration and Trophic Transfer in a Simple Food Chain. **2017**, 51, 7532-7541	6
798	Biogenic non-crystalline U revealed as major component in uranium ore deposits. **2017**, 8, 15538	44
797	Meta-analysis To Define a Core Microbiota in the Swine Gut. **2017**, 2,	125
796	Temporal Dynamics of Bacterial and Fungal Colonization on Plastic Debris in the North Sea. **2017**, 51, 7350-7360	118
795	Detection of Helicobacter pylori in the Gastric Mucosa by Fluorescence In Vivo Hybridization. **2017**, 1616, 137-146	4
794	A phylogenetic framework for the kingdom Fungi based on 18S rRNA gene sequences. **2017**, 36, 33-39	29
793	Ubiquity and quantitative significance of bacterioplankton lineages inhabiting the oxygenated hypolimnion of deep freshwater lakes. **2017**, 11, 2279-2293	37
792	Characterization of Sinus Microbiota by 16S Sequencing from Swabs. **2017**, 1616, 23-38	4
791	Characterization of a combined batch-continuous procedure for the culture of anammox biomass. **2017**, 106, 231-241	12
790	Evaluation of method bias for determining bacterial populations in bacterial community analyses. **2017**, 124, 476-486	7
789	Multi-locus and long amplicon sequencing approach to study microbial diversity at species level using the MinION portable nanopore sequencer. **2017**, 6, 1-12	48
788	Enhancement of IFN Production by Distinct Commensals Ameliorates Salmonella-Induced Disease. **2017**, 21, 682-694.e5	64
787	Comparison of the fecal bacterial microbiota of healthy and diarrheic foals at two and four weeks of life. **2017**, 13, 144	24
786	Agricultural management practices influence AMF diversity and community composition with cascading effects on plant productivity. **2017**, 115, 53-59	41
785	Coral hybridization or phenotypic variation? Genomic data reveal gene flow between Porites lobata and P. Compressa. **2017**, 111, 132-148	44
784	Patterns in the skin microbiota differ in children and teenagers between rural and urban environments. **2017**, 7, 45651	63
783	Symbiosis and microbiome flexibility in calcifying benthic foraminifera of the Great Barrier Reef. **2017**, 5, 38	23

782	Identification of microbial communities, with a focus on foodborne pathogens, during kimchi manufacturing process using culture-independent and -dependent analyses. **2017**, 81, 153-159	23
781	Niche partitioning of diverse sulfur-oxidizing bacteria at hydrothermal vents. **2017**, 11, 1545-1558	81
780	Methods for Microbiome Analysis. **2017**, 269-298	1
779	Cataloguing the bacterial community of the Great Salt Plains, Oklahoma using 16S rRNA based metagenomics pyrosequencing. **2017**, 12, 54-57	
778	UniEuk: Time to Speak a Common Language in Protistology!. **2017**, 64, 407-411	39
777	Comprehensive Transcriptome Analyses Reveal that Potato Spindle Tuber Viroid Triggers Genome-Wide Changes in Alternative Splicing, Inducible -Acting Activity of Phased Secondary Small Interfering RNAs, and Immune Responses. **2017**, 91,	73
776	Metagenomic analyses of bacterial endophytes associated with the phyllosphere of a Bt maize cultivar and its isogenic parental line from South Africa. **2017**, 33, 80	37
775	Assessment of the metabarcoding approach for community analysis of benthic-epiphytic dinoflagellates using mock communities. **2017**, 51, 555-576	37
774	Multiple stressors in sediments impact adjacent hard substrate habitats and across biological domains. **2017**, 592, 295-305	17
773	Giant viruses with an expanded complement of translation system components. **2017**, 356, 82-85	148
772	Simulated rRNA/DNA Ratios Show Potential To Misclassify Active Populations as Dormant. **2017**, 83,	37
771	Factors influencing ruminal bacterial community diversity and composition and microbial fibrolytic enzyme abundance in lactating dairy cows with a focus on the role of active dry yeast. **2017**, 100, 4377-4393	39
770	Methylphosphonate metabolism by Pseudomonas sp. populations contributes to the methane oversaturation paradox in an oxic freshwater lake. **2017**, 19, 2366-2378	34
769	Cassava foliage affects the microbial diversity of Chinese indigenous geese caecum using 16S rRNA sequencing. **2017**, 7, 45697	20
768	Microbial community response to hydration-desiccation cycles in desert soil. **2017**, 7, 45735	53
767	A Review of Research-Grade Human Induced Pluripotent Stem Cells Qualification and Biobanking Processes. **2017**, 15, 384-392	10
766	Contamination-induced transformation of bacterial and fungal communities in spruce-fir and birch forest litter. **2017**, 114, 111-122	10
765	Characterization of the Fecal Bacterial Microbiota of Healthy and Diarrheic Dairy Calves. **2017**, 31, 928-939	58

764	The nasopharyngeal microbiota of beef cattle before and after transport to a feedlot. **2017**, 17, 70	46
763	Health and Disease Imprinted in the Time Variability of the Human Microbiome. **2017**, 2,	30
762	Comammox in drinking water systems. **2017**, 116, 332-341	106
761	Dynamic microbiome evolution in social bees. **2017**, 3, e1600513	183
760	Translational Bioinformatics and Its Application. **2017**,	5
759	Biodegradation of chlortetracycline by acclimated microbiota. **2017**, 109, 11-17	32
758	Next-Generation Sequencing Combined with Specific PCR Assays To Determine the Bacterial 16S rRNA Gene Profiles of Middle Ear Fluid Collected from Children with Acute Otitis Media. **2017**, 2,	27
757	Longitudinal and Source-to-Tap New Orleans, LA, U.S.A. Drinking Water Microbiology. **2017**, 51, 4220-4229	28
756	Bacterial diversity of the rhizosphere and nearby surface soil of rice (Oryza sativa) growing in the Camargue (France). **2017**, 3, 112-122	15
755	Exploring the under-investigated "microbial dark matter" of drinking water treatment plants. **2017**, 7, 44350	25
754	RNA virus receptor Rig-I monitors gut microbiota and inhibits colitis-associated colorectal cancer. **2017**, 36, 2	28
753	Variability of airborne bacteria in an urban Mediterranean area (Thessaloniki, Greece). **2017**, 157, 101-110	39
752	Striking alterations in the soil bacterial community structure and functioning of the biological N cycle induced by Pennisetum setaceum invasion in a semiarid environment. **2017**, 109, 176-187	32
751	Whole-Community Metagenomics in Two Different Anammox Configurations: Process Performance and Community Structure. **2017**, 51, 4317-4327	68
750	Impact of Seasonal Hypoxia on Activity and Community Structure of Chemolithoautotrophic Bacteria in a Coastal Sediment. **2017**, 83,	17
749	Metagenomic discovery of polybrominated diphenyl ether biosynthesis by marine sponges. **2017**, 13, 537-543	95
748	Microbial communities of aquatic environments on Heard Island characterized by pyrotag sequencing and environmental data. **2017**, 7, 44480	8
747	Characterization of oral and gut microbiome temporal variability in hospitalized cancer patients. **2017**, 9, 21	51

746	Recurrent rewiring and emergence of RNA regulatory networks. **2017**, 114, E2816-E2825	17
745	Happens in the best of subfamilies: establishment and repeated replacements of co-obligate secondary endosymbionts within Lachninae aphids. **2017**, 19, 393-408	43
744	Analysis of 16S rRNA Gene Amplicon Sequences Using the QIIME Software Package. **2017**, 1537, 153-163	38
743	Ex-situ biogas upgrading and enhancement in different reactor systems. **2017**, 225, 429-437	176
742	A metagenomic study of the preventive effect of Lactobacillus rhamnosus GG on intestinal polyp formation in Apc mice. **2017**, 122, 770-784	14
741	Cyanobacterial harmful algal blooms are a biological disturbance to Western Lake Erie bacterial communities. **2017**, 19, 1149-1162	110
740	Metapopulation theory identifies biogeographical patterns among core and satellite marine bacteria scaling from tens to thousands of kilometers. **2017**, 19, 1222-1236	20
739	Microbial diversity and autotrophic activity in Kamchatka hot springs. **2017**, 21, 307-317	51
738	Strengths and Biases of High-Throughput Sequencing Data in the Characterization of Freshwater Ciliate Microbiomes. **2017**, 73, 865-875	9
737	Ericoid Roots and Mycospheres Govern Plant-Specific Bacterial Communities in Boreal Forest Humus. **2017**, 73, 939-953	24
736	Draft genome and description of Orrella dioscoreae gen. nov. sp. nov., a new species of Alcaligenaceae isolated from leaf acumens of Dioscorea sansibarensis. **2017**, 40, 11-21	13
735	Optimised scat collection protocols for dietary DNA metabarcoding in vertebrates. **2017**, 8, 192-202	55
734	Pristine but metal-rich Río Sucio (Dirty River) is dominated by Gallionella and other iron-sulfur oxidizing microbes. **2017**, 21, 235-243	7
733	Warming and nutrient enrichment in combination increase stochasticity and beta diversity of bacterioplankton assemblages across freshwater mesocosms. **2017**, 11, 613-625	36
732	Characterization of the first cultured representative of a Bacteroidetes clade specialized on the scavenging of cyanobacteria. **2017**, 19, 1134-1148	24
731	Comparative analysis of the gut microbiota of black bears in China using high-throughput sequencing. **2017**, 292, 407-414	38
730	Expression of eukaryotic-like protein in the microbiome of sponges. **2017**, 26, 1432-1451	29
729	The Enrichment of Microbial Community for Accumulating Polyhydroxyalkanoates Using Propionate-Rich Waste. **2017**, 182, 755-768	6

728	Distinct Microbiome-Neuroimmune Signatures Correlate With ́Functional Abdominal Pain in Children With Autism Spectrum Disorder. **2017**, 3, 218-230	157
727	Bacterial community collapse: a meta-analysis of the sinonasal microbiota in chronic rhinosinusitis. **2017**, 19, 381-392	104
726	A metabarcoding comparison of windward and leeward airborne algal diversity across the Ko'olau mountain range on the island of O'ahu, Hawai'i. **2017**, 53, 437-445	22
725	Imbalance of bacteriome profiles within the Finnish Diabetes Prediction and Prevention study: Parallel use of 16S profiling and virome sequencing in stool samples from children with islet autoimmunity and matched controls. **2017**, 18, 588-598	30
724	A long-term hybrid poplar plantation on cropland reduces soil organic carbon mineralization and shifts microbial community abundance and composition. **2017**, 111, 94-104	43
723	Experimental warming reveals positive feedbacks to climate change in the Eurasian Steppe. **2017**, 11, 885-895	37
722	Effects of Actinomycete Secondary Metabolites on Sediment Microbial Communities. **2017**, 83,	23
721	Prairie strips remove swine manure associated antimicrobial resistance genes and bacteria from runoff. **2023**, 349, 108469	0
720	Combined melatonin and UV-C treatment maintains the quality of fresh-cut bamboo shoots during storage by altering microbial diversity and metabolites. **2023**, 200, 112327	0
719	Nicotinamide riboside and dietary restriction effects on gut microbiota and liver inflammatory and morphologic markers in cafeteria dietnduced obesity in rats. **2023**, 110, 112019	0
718	Study on characteristic and mechanism involved in the formation of N-nitrosodimethylamine precursors during microbial metabolism of amino acids. **2023**, 874, 162469	0
717	The characteristics and metabolic potentials of the soil bacterial community of two typical military demolition ranges in China. **2023**, 874, 162562	0
716	The effects of long-term hexabromocyclododecanes contamination on microbial communities in the microcosms. **2023**, 325, 138412	0
715	The structural and functional shift in the soil rhizosphere and raspberry shoot microbiomes underlies changes caused by phytopathogens contamination and naturalization strategies implementation. **2023**, 186, 104810	0
714	Poly-glutamic acid-producing Bacillus velezensis fermentation can improve the feed properties of soybean meal. **2023**, 53, 102503	0
713	Decreasing hydraulic retention time of anaerobic membrane bioreactor: Effect on core genera and microbial contaminants removal. **2023**, 22, 101389	0
712	Lebanese fermented goat milk products: From tradition to meta-omics. **2023**, 168, 112762	0
711	Coupling microbial and abiotic amendments accelerates in situ remediation of bauxite residue at field scale. **2023**, 877, 162699	0

710	Response of soil microbial Communities, inorganic and organic soil carbon pools in arid saline soils to alternative land use practices. **2023**, 150, 110227	0
709	Depth-dependent effects of tree species identity on soil microbial community characteristics and multifunctionality. **2023**, 878, 162972	0
708	A meta-analysis of the effect of Eimeria spp. and/or Clostridium perfringens infection on the microbiota of broiler chickens. **2023**, 102, 102652	0
707	Unravelling diversity, drivers, and indicators of soil microbiome of Trillium govanianum, an endangered plant species of the Himalaya. **2023**, 227, 115819	0
706	Exogenous-organic-matter-driven mobilization of groundwater arsenic. **2023**, 15, 100243	0
705	Soil substrate source drives the microbes involved in the degradation of gelatin used as a biostimulant. **2023**, 189, 104906	0
704	Tracing recent outdoor geolocation by analyzing microbiota from shoe soles and shoeprints even after indoor walking. **2023**, 65, 102869	0
703	Identification and synergetic mechanism of TCE, H2 and O2 metabolic microorganisms in the joint H2/O2 system. **2023**, 879, 163026	0
702	Microbes drive metabolism, community diversity, and interactions in response to microplastic-induced nutrient imbalance. **2023**, 877, 162885	0
701	Delving into the study of lactic acid bacteria and yeasts distribution in table olive biofilms using a non-destructive procedure. **2023**, 113, 104250	0
700	Targeted microbiome metabolomics reveals flaxseed oil supplementation regulated the gut microbiota and farnesoid X receptor pathway in high-fat diet mice. **2023**, 12, 2324-2335	0
699	Components of N-fixation system response to glyphosate are un-coupled in agroecosystems. **2023**, 188, 104859	0
698	Short-term prescribed fire-induced changes in soil microbial communities and nutrients in native rangelands of Florida. **2023**, 189, 104914	0
697	Effects of thermal treatments on the extraction and in vitro fermentation patterns of pectins from pomelo (Citrus grandis). **2023**, 141, 108755	0
696	Shifts of soil archaeal nitrification and methanogenesis with elevation in water level fluctuation zone of the three Gorges Reservoir, China. **2023**, 339, 117871	0
695	Clinical NEC prevention practices drive different microbiome profiles and functional responses in the preterm intestine. **2023**, 14,	0
694	Consumer feces impact coral health in guild-specific ways. 10,	0
693	Innova 2020: A Follow-Up Study of the Fecal Microbiota of Infants Using a Novel Infant Formula between 6 Months and 12 Months of Age. **2023**, 24, 7392	0

692	Development of a novel definitive scoring system for an enteral feed-only model of necrotizing enterocolitis in piglets. 11,	o
691	Identification of microbial communities and their removal efficiency of multiple pharmaceutical micropollutants combined in Membrane-Bioreactors.	o
690	Enriching the endophytic bacterial microbiota of Ginkgo roots. 14,	o
689	Effects of dietary synbiotics and biofloc meal on the growth, tissue histomorphology, whole-body composition and intestinal microbiota profile of Nile tilapia (Oreochromis niloticus) cultured at different salinities. **2023**, 570, 739391	o
688	Sediment prokaryotic microbial community and potential biogeochemical cycle from saline lakes shaped by habitat. **2023**, 270, 127342	o
687	Dissolved storage glycans shaped the community composition of abundant bacterioplankton clades during a North Sea spring phytoplankton bloom. **2023**, 11,	o
686	Long-term integrated rice-crayfish culture disrupts the microbial communities in paddy soil. **2023**, 29, 101515	o
685	Nitrogen application influences the effect of bacteria on the belowground allocation of photosynthesized carbon under elevated CO2. **2023**, 180, 109021	o
684	Surfactant-enhanced bioremediation of petroleum-contaminated soil and microbial community response: A field study. **2023**, 322, 138225	o
683	Energy-related wastewater contamination alters microbial communities of sediment, water, and amphibian skin. **2023**, 880, 163160	o
682	Bacterial benz(a)anthracene catabolic networks in contaminated soils and their modulation by other co-occurring HMW-PAHs. **2023**, 328, 121624	o
681	Plastic litter changes the rhizosphere bacterial community of coastal dune plants. **2023**, 880, 163293	o
680	Bacillus amyloliquefaciens FG14 as a potential biocontrol strain against rusty root rot of Panax ginseng, and its impact on the rhizosphere microbial community. **2023**, 182, 105221	o
679	Impacts of microplastics and the associated plastisphere on physiological, biochemical, genetic expression and gut microbiota of the filter-feeder amphioxus. **2023**, 172, 107750	o
678	Dynamics of gut microbiome upon pollination in bumblebee (Bombus terrestris). **2023**, 26, 102042	o
677	Yellow mealworms (Tenebrio molitor) as an alternative animal feed source: A comprehensive characterization of nutritional values and the larval gut microbiome. **2023**, 389, 136104	o
676	Divergence in the soil and rhizosphere microbial communities of monoculture and silvopastoral traditional C. dodecandra agroforestry systems in Yucatan, Mexico.	o
675	(Meta)genomics -assisted screening of novel antibacterial lactic acid bacteria strains from traditional fermented milk from Western China and their bioprotective effects on cheese. **2023**, 175, 114507	o

674	Pasture management intensification shifts the soil microbiome composition and ecosystem functions. **2023**, 346, 108355	0
673	Continuous operation of fungal wheel reactor based on solid-state fermentation for the removal of pharmaceutical and personal care products. **2023**, 331, 117316	0
672	A novel insight into energy conservation and efficiency enhancement in wastewater treatment process: Low-frequency mechanical vibration induced. **2023**, 52, 103492	0
671	Assessing the impacts of light synthetic crude oil on microbial communities within Laurentian Great Lakes sediment habitats. **2023**, 49, 440-452	0
670	Biofilm characteristics for providing resilient denitrification in a hydrogen-based membrane biofilm reactor. **2023**, 231, 119654	0
669	Assessing siliceous sinter matrices for long-term preservation of lipid biomarkers in opaline sinter deposits analogous to Mars in El Tatio (Chile). **2023**, 870, 161765	1
668	Role of Agricultural Management in the Provision of Ecosystem Services in Warm Climate Vineyards: Functional Prediction of Genes Involved in Nutrient Cycling and Carbon Sequestration. **2023**, 12, 527	0
667	Closed genomes uncover a saltwater species of Candidatus Electronema and shed new light on the boundary between marine and freshwater cable bacteria. **2023**, 17, 561-569	0
666	Sodium butyrate ameliorates gut dysfunction and motor deficits in a mouse model of Parkinson's disease by regulating gut microbiota. 15,	0
665	Soil bacterial community response to continuous cropping of cotton. 14,	0
664	Effects of Continuous Straw Returning on Soil Functional Microorganisms and Microbial Communities. **2023**, 61, 49-62	0
663	Time-dependent microbial shifts during crayfish decomposition in freshwater and sediment under different environmental conditions. **2023**, 13,	0
662	Gallionellaceae pangenomic analysis reveals insight into phylogeny, metabolic flexibility, and iron oxidation mechanisms.	0
661	LC / MS analysis of mushrooms provided new insights into dietary management of diabetes mellitus in rats.	1
660	Maternal and host effects mediate the adaptive expansion and contraction of the microbiome during ontogeny in a holometabolous, polyphagous insect. **2023**, 37, 929-946	0
659	Deciphering the interactions between lipids and red wine polyphenols through the gastrointestinal tract. **2023**, 165, 112524	0
658	Comparison of network connectivity and environmental driving factors of root-associated fungal communities of desert ephemeral plants in two habitat soils. **2023**, 332, 117375	0
657	Mechanistic and microbial ecological insights into the impacts of micro- and nano-´plastics on microbial reductive dehalogenation of organohalide pollutants. **2023**, 448, 130895	0

656	Linking soil microbial community to the chemical composition of dissolved organic matter in a boreal forest during freeze–thaw cycles. **2023**, 431, 116359	0
655	Gut microbiota-derived metabolites mediate the neuroprotective effect of melatonin in cognitive impairment induced by sleep deprivation. **2023**, 11,	0
654	High abundance of hydrocarbon-degrading Alcanivorax in plumes of hydrothermally active volcanoes in the South Pacific Ocean. **2023**, 17, 600-610	0
653	Prevalence of Viral Frequency-Dependent Infection in Coastal Marine Prokaryotes Revealed Using Monthly Time Series Virome Analysis. **2023**, 8,	1
652	Dredged sediments contain potentially beneficial microorganisms for agriculture and little harmful cyanobacteria. **2023**, 2, 45-57	0
651	Dynamic of the Soil Microbiota in Short-Term Crop Rotation. **2023**, 13, 400	0
650	Immune priming prior to pathogen exposure sheds light on the relationship between host, microbiome and pathogen in disease. **2023**, 10,	1
649	Microbial iron cycling is prevalent in water-logged Alaskan Arctic tundra habitats, but sensitive to disturbance. **2023**, 99,	0
648	Soil water extract and bacteriome determine N2O emission potential in soils. **2023**, 59, 217-232	0
647	Dynamic network modeling of gut microbiota during Alzheimer's disease progression in mice. **2023**, 15,	0
646	Gut microbiota variation between climatic zones and due to migration strategy in passerine birds. 14,	0
645	The belowground of the resurrection plant Myrothamnus flabellifolia: Exploring the desiccation-tolerant root-associated microbiome.	0
644	Salp blooms drive strong increases in passive carbon export in the Southern Ocean. **2023**, 14,	0
643	Analysis of strain, sex, and diet-dependent modulation of gut microbiota reveals candidate keystone organisms driving microbial diversity in response to American and ketogenic diets.	0
642	Occurrence and diversity of bacterioplankton in drinking water tropical reservoirs of contrasting trophic state.	0
641	A dark matter in sake brewing: Origin of microbes producing a Kimoto-style fermentation starter. 14,	0
640	Maturational patterns of the infant gut mycobiome are associated with early-life body mass index. **2023**, 4, 100928	0
639	The ecology of bacterial communities in groundwater of industrial areas: Diversity, composition, network, and assembly. **2023**, 322, 121207	0

638	Influence of root cortical aerenchyma on the rhizosphere microbiome of field-grown maize.	0
637	Natural variation of Macrocystis pyrifera gametophyte germplasm culture microbiomes and applications for improving yield in offshore farms. **2023**, 59, 402-417	0
636	Microbiological quality and safety of vacuum-packaged white-tailed deer meat stored at 4°C. **2023**, 390, 110110	0
635	Overview of microbial profiles in human hepatocellular carcinoma and adjacent nontumor tissues. **2023**, 21,	0
634	Winter mulching practice alters soil bacterial communities and networks in lei bamboo (Phyllostachys praecox) forests.	0
633	Implications of a short carbon pulse on biofilm formation on mica schist in microcosms with deep crystalline bedrock groundwater. 14,	0
632	Mining Chromodoris quadricolor symbionts for biosynthesis of novel secondary metabolites. **2023**, 68, 101017	0
631	Comparative analysis of bacterial diversity in clouds and aerosols. **2023**, 298, 119635	0
630	Diversity and Regional Variation of Endosymbionts in the Green Peach Aphid, Myzus persicae (Sulzer). **2023**, 15, 206	0
629	Taxonomic difference in marine bloom-forming phytoplanktonic species affects dynamics of both bloom-responding prokaryotes and prokaryotic viruses.	0
628	Phylogeny analysis of whole protein-coding genes in metagenomic data detected an environmental gradient for the microbiota. **2023**, 18, e0281288	0
627	Effects of adding different carbon sources on the microbial behavior of sulfate-reducing bacteria in sulfate-containing wastewater. **2023**, 392, 136332	0
626	Functionality of methane cycling microbiome during methane flux hot moments from riparian buffer systems. **2023**, 870, 161921	0
625	Genomics discovery of giant fungal viruses from subsurface oceanic crustal fluids. **2023**, 3,	0
624	Non-additive effects of bamboo-derived biochar and dicyandiamide on soil greenhouse gas emissions, enzyme activity and bacterial community. **2023**, 194, 116385	1
623	Functional Prediction of Microbial Communities in Sediment Microbial Fuel Cells. **2023**, 10, 199	0
622	Gut microbial signature in lung cancer patients highlights specific taxa as predictors for durable clinical benefit. **2023**, 13,	0
621	Anaerobic membrane bioreactor-based treatment of poultry slaughterhouse wastewater: Microbial community adaptation and antibiotic resistance gene profiles. **2023**, 192, 108847	1

620	Large-scale impact of the 2016 Marine Heatwave on the plankton-associated microbial communities of the Great Barrier Reef (Australia). **2023**, 188, 114685	1
619	Fecal virome transplantation is sufficient to alter fecal microbiota and drive lean and obese body phenotypes in mice.	0
618	The First Domestic Experience of Detecting the Association of Anaerobic Bacteria <i>Filifactor Alocis</i> and <i>Porphyromonas Gingivalis</i> by Molecular Biological Methods in Periodontal Diseases and Comorbid Pathology (Comparative Research). **2023**, 77, 437-446	0
617	Novel diversity of polar Cyanobacteria revealed by genome-resolved metagenomics.	0
616	Host phylogeny and functional traits differentiate gut microbiomes in a diverse natural community of small mammals.	0
615	The mystery of the ice cold rose□Microbiome of an Arctic winter frost flower. **2023**, 12,	0
614	Chondroitin sulfate alleviates osteoporosis caused by calcium deficiency by regulating lipid metabolism. **2023**, 20,	0
613	The skin microbiome enhances disease through IL-1b and delays healing in cutaneous leishmaniasis patients.	0
612	Antarctic Ardley Island terrace □An ideal place to study the marine to terrestrial succession of microbial communities. 14,	0
611	Microbiological Changes during Long-Storage of Beef Meat under Different Temperature and Vacuum-Packaging Conditions. **2023**, 12, 694	1
610	Effects of Salinity on Assembly Characteristics and Function of Microbial Communities in the Phyllosphere and Rhizosphere of Salt-Tolerant Avicennia marina Mangrove Species. **2023**, 11,	0
609	Microbiota-derived acetate enhances host antiviral response via NLRP3. **2023**, 14,	1
608	Muc2-dependent microbial colonization of the jejunal mucus layer is diet sensitive and confers local resistance to enteric pathogen infection. **2023**, 42, 112084	0
607	Effects of a Novel Infant Formula on the Fecal Microbiota in the First Six Months of Life: The INNOVA 2020 Study. **2023**, 24, 3034	1
606	Growth Stages and Inter-Species Gut Microbiota Composition and Function in Captive Red Deer (Cervus elaphus alxaicus) and Blue Sheep (Pseudois nayaur). **2023**, 13, 553	0
605	Structure, anti-fatigue activity and regulation on gut microflora in vivo of ethanol-fractional polysaccharides from Dendrobium officinale. **2023**, 234, 123572	0
604	Changes to Soil Microbiome Resulting from Synergetic Effects of Fungistatic Compounds Pyrimethanil and Fluopyram in Lowbush Blueberry Agriculture, with Nine Fungicide Products Tested. **2023**, 11, 410	0
603	Geographic variation in bacterial assemblages on cane toad skin is influenced more by local environments than by evolved changes in host traits. **2023**, 12,	0

602	The utility of dust for forensic intelligence: Exploring collection methods and detection limits for environmental DNA, elemental and mineralogical analyses of dust samples. **2023**, 344, 111599	0
601	Marine Picoplankton Metagenomes from Eleven Vertical Profiles Obtained by the Malaspina Expedition in the Tropical and Subtropical Oceans.	0
600	Aminithiophilus ramosus gen. nov., sp. nov., a sulphur-reducing bacterium isolated from a pyrite-forming enrichment culture, and taxonomic revision of the family Synergistaceae. **2023**, 73,	0
599	The Soil Microbiome Reduces Striga Infection of Sorghum by Modulation of Host-Derived Signaling Molecules and Root Development.	0
598	Inputs of seabird guano alter microbial growth, community composition and the phytoplankton□bacterial interactions in a coastal system.	0
597	Identification and characterization of the causative agents of Focal Ulcerative Dermatitis in commercial laying hens. 10,	0
596	SLAMseq resolves the kinetics of maternal and zygotic gene expression during early zebrafish embryogenesis. **2023**, 42, 112070	0
595	Structural stability of the oyster gut microbiome contributes to the hosts□ physiological tolerance to temperature fluctuations on tropical rocky shores.	0
594	Symbioses of alvinocaridid shrimps from the South West Pacific: No chemosymbiotic diets but partially conserved gut microbiomes.	0
593	Associations of Microbial Diversity with Age and Other Clinical Variables among Pediatric Chronic Rhinosinusitis (CRS) Patients. **2023**, 11, 422	0
592	Microbial Dynamics in Mixed-Culture Biofilms of Salmonella Typhimurium and Escherichia coli O157:H7 and Bacteria Surviving Sanitation of Conveyor Belts of Meat Processing Plants. **2023**, 11, 421	0
591	Limosilactobacillus reuteri administration alters the gut-brain-behavior axis in a sex-dependent manner in socially monogamous prairie voles. 14,	0
590	Convergent dysbiosis of upper aerodigestive microbiota between patients with esophageal and oral cavity squamous cell carcinoma. **2023**, 152, 1903-1915	0
589	Patterns of free-living and particle-attached bacteria along environmental gradients in Lake Taihu.	0
588	Combined Omics Approach Reveals Key Differences between Aerobic and Microaerobic Xylene-Degrading Enrichment Bacterial Communities: Rhodoferax-A Hitherto Unknown Player Emerges from the Microbial Dark Matter. **2023**, 57, 2846-2855	0
587	Fecal identification markers impact the feline fecal microbiota. 10,	0
586	Porcine fungal mock community analyses: Implications for mycobiome investigations. 13,	0
585	Detection and identification of fungi in the lower airway of children with and without cystic fibrosis. 14,	0

584	Microbial community structural response to variations in physicochemical features of different aquifers. 14,	0
583	Leveraging Scheme for Cross-Study Microbiome Machine Learning Prediction and Feature Evaluations. **2023**, 10, 231	0
582	Root associated bacterial communities and root metabolite composition are linked to nitrogen use efficiency in sorghum.	0
581	Environmental factors contributing to the convergence of bacterial community structure during indigo reduction. 14,	0
580	TRAF3 Suppression Encourages B Cell Recruitment and Prolongs Survival of Microbiome-Intact Mice with Ovarian Cancer.	0
579	The cecal ecosystem is a great contributor to intramuscular fat deposition in broilers. **2023**, 102, 102568	0
578	Microbiota changes in a stranding simulation of the holopelagic macroalgae Sargassum natans and Sargassum fluitans.	0
577	Microbial Communities of Peaty Permafrost Tundra Soils along the Gradient of Environmental Conditions and Anthropogenic Disturbance in Pechora River Delta in the Eastern European Arctic. **2023**, 15, 251	0
576	Effect of Clindamycin on Intestinal Microbiome and Miltefosine Pharmacology in Hamsters Infected with Leishmania infantum. **2023**, 12, 362	0
575	Temporal variability of microbial response to crude oil exposure in the northern Gulf of Mexico. 11,	0
574	Salinity determines performance, functional populations, and microbial ecology in consortia attenuating organohalide pollutants. **2023**, 17, 660-670	0
573	The mechanism´of promoting rhizosphere nutrient turnover for arbuscular mycorrhizal fungi attributes to recruited functional bacterial assembly.	0
572	Uncovering bacterial hosts of class 1 integrons in an urban coastal aquatic environment with a single-cell fusion-polymerase chain reaction technology.	0
571	Acquiring Iron-Reducing Enrichment Cultures: Environments, Methods and Quality Assessments. **2023**, 11, 448	1
570	The gut microbiomeDoes stool represent right?. **2023**, 9, e13602	0
569	On the Oral Microbiome of Oral Potentially Malignant and Malignant Disorders: Dysbiosis, Loss of Diversity, and Pathogens Enrichment. **2023**, 24, 3466	0
568	Exposure at low tide leads to a different microbial abundance of intertidal coral Acropora pulchra. **2022**, 18, 520-530	0
567	Taxonomic Diversity of the Microbial Biofilms Collected along the Thermal Streams on Kunashir Island. **2023**, 4, 106-123	0

566	Turnover of the extracellular polymeric matrix of granules performing biological phosphate removal. **2023**, 107, 1997-2009	1
565	Identification of bacterial communities related to handling in commercial white-leg shrimp (Litopenaeus vannamei) using metagenomic analysis. **2023**, 1137, 012035	0
564	Recycled Household Ash in Rice Paddies of Bangladesh for Sustainable Production of Rice Without Altering Grain Arsenic and Cadmium.	0
563	Diversity of enterobacterales in sediments of lagoons with fish farming activity and analysis of antibiotic resistance. **2023**, 10, 235-244	0
562	The diet rapidly and differentially affects the gut microbiota and host lipid mediators in a healthy population. **2023**, 11,	0
561	Colonization of axenic beet by rhizosphere bacteria takes place in discreet phases regardless of bioinculation with next generation bioinoculant.	0
560	Simulated heat waves promote the growth but suppress the N2 fixation rates of Dolichospermum spp. and cyanobacterial communities in temperate lakes. **2023**, 147, 109983	0
559	Cloacal microbiota are biogeographically structured in larks from desert, tropical and temperate areas. **2023**, 23,	0
558	Seed coat treatment by plant-growth-promoting rhizobacteria Lysobacter antibioticus 136□ enhances maize yield and changes rhizosphere bacterial communities. **2023**, 59, 317-331	0
557	Ophthalmic viscoelastics commonly used in cataract surgery: A microbiota investigation.	0
556	Effects of dietary supplementation with prebiotics and Pediococcus acidilactici on gut health, transcriptome, microbiota, and metabolome in Atlantic salmon (Salmo salar L.) after seawater transfer. **2023**, 5,	0
555	Bioremediation of coastal aquaculture effluents spiked with florfenicol using microalgae-based granular sludge □a promising solution for recirculating aquaculture systems. **2023**, 233, 119733	0
554	Compositional and functional diversities of core microbial communities in wild and artificial Ophiocordyceps sinensis.	0
553	Microbiome Composition and Microbial Community Structure in Mosquito Vectors Aedes aegypti and Aedes albopictus in Northeastern Thailand, a Dengue-Endemic Area. **2023**, 14, 184	0
552	Dark Fermentation of Arundo donax: Characterization of the Anaerobic Microbial Consortium. **2023**, 16, 1813	0
551	Complementary effects of above- and belowground biodiversity on ecosystem functions across global grasslands.	0
550	Analysis of the cervical microbiome in women from the German national cervical cancer screening program.	0
549	Intestinal homeostasis disruption in mice chronically exposed to arsenite-contaminated drinking water. **2023**, 373, 110404	0

548	Variation of butyrate production in the gut microbiome in type 2 diabetes patients.	1
547	Diversity and Community Composition of Labyrinthulomycetes Protists in the Coastal Zone of Hainan Island, South China Sea. **2023**, 15, 738	0
546	Impact of aging on the immunological and microbial landscape of the lung during non-tuberculous mycobacterial infection.	0
545	Marine Fungi Select and Transport Aerobic and Anaerobic Bacterial Populations from Polycyclic Aromatic Hydrocarbon-Contaminated Sediments.	0
544	Environmental Selection and Biogeography Shape the Microbiome of Subsurface Petroleum Reservoirs.	0
543	Microbiome dynamics in resistant and susceptible colonies throughout thermal bleaching and recovery support host specificity, phenotypic variability, but common microbial consortia modulating stress responses in different coral species in Hawaii	0
542	Exosome-derived Small RNAs in mouse Sertoli cells inhibit spermatogonial apoptosis. **2023**, 200, 155-167	0
541	Geographical variability of bacterial communities of cryoconite holes of Andean glaciers. **2023**, 13,	0
540	TRAF3 Suppression Encourages B Cell Recruitment and Prolongs Survival of Microbiome-Intact Mice with Ovarian Cancer.	0
539	Metagenomic data of bacterial communities associated with Acropora species from Phu Quoc Islands, Vietnam. **2023**, 47, 108977	0
538	Two dimensions of chemical variation of the human microbiome across body sites and in COVID-19 patients.	0
537	Sputum Microbiome and Chronic Obstructive Pulmonary Disease in a Rural Ugandan Cohort of Well-Controlled HIV Infection. **2023**, 11,	0
536	Revealing the Differences in Ulnaria acus and Fragilaria radians Distribution in Lake Baikal via Analysis of Existing Metabarcoding Data. **2023**, 15, 280	1
535	Carbon Emission and Biodiversity of Arctic Soil Microbial Communities of the Novaya Zemlya and Franz Josef Land Archipelagos. **2023**, 11, 482	0
534	kakapo: Easy extraction and annotation of genes from raw RNA-seq reads.	0
533	Metabolic turnover rate, digestive enzyme activities, and bacterial communities in the white shrimp Litopenaeus vannamei under compensatory growth. 11, e14747	0
532	Immobilization of metribuzin-degrading bacteria on biochar: Enhanced soil remediation and bacterial community restoration. 13,	0
531	Infants gut microbiome data: A Bayesian Marginal Zero-inflated Negative Binomial regression model for multivariate analyses of count data. **2023**, 21, 1621-1629	0

530	Nearly (?) sterile avian egg in a passerine bird.	0
529	Geraniol-a potential alternative to antibiotics for bovine mastitis treatment without disturbing the host microbial community or causing drug residues and resistance. 13,	1
528	Multidisciplinary evaluation of plant growth promoting rhizobacteria on soil microbiome and strawberry quality. **2023**, 13,	0
527	Standardized Complex Gut Microbiomes Influence Fetal Growth, Food Intake, and Adult Body Weight in Outbred Mice. **2023**, 11, 484	0
526	The rotation of primary starter culture mixtures results in batch-to-batch variations during Gouda cheese production. 14,	0
525	Genetic analysis of the frozen microbiome at 7900 m a.s.l., on the South Col of Sagarmatha (Mount Everest). **2023**, 55,	0
524	Using fecal immmunochemical cartridges for gut microbiome analysis within a colorectal cancer screening program. **2023**, 15,	0
523	Universal Dynamics of Microbial Communities in Full-Scale Textile Wastewater Treatment Plants and System Prediction by Machine Learning. **2023**, 57, 3345-3356	0
522	Golgi fragmentation One of the earliest organelle phenotypes in Alzheimer disease neurons. 17,	0
521	A Bacillaceae consortium positively impacts arbuscular mycorrhizal fungus colonisation, plant phosphate nutrition, and tuber yield in Solanum tuberosum cv. Jazzy. **2023**, 89, 235-250	0
520	Interleukin-23 receptor signaling impairs the stability and function of colonic regulatory T´cells. **2023**, 42, 112128	0
519	Dynamic changes of the gut microbial colonization in preterm infants with different time points after birth. 14,	0
518	Effects of field inoculation of potato tubers with the arbuscular mycorrhizal fungus Rhizophagus irregularis DAOM 197198 are cultivar dependent. **2023**, 89, 213-226	0
517	An open label, non-randomized study assessing a prebiotic fiber intervention in a small cohort of Parkinson disease participants. **2023**, 14,	0
516	Moss and Liverwort Covers Structure Soil Bacterial and Fungal Communities Differently in the Icelandic Highlands.	0
515	Stochasticity causes high diversity and functional divergence of bacterial assemblages in closed systems. **2023**, 104,	0
514	Molecular Accounting and Profiling of Human Respiratory Microbial Communities: Toward Precision Medicine by Targeting the Respiratory Microbiome for Disease Diagnosis and Treatment. **2023**, 24, 4086	2
513	Core root-associated prokaryotic community and its relationship to host traits across wheat varieties. **2023**, 74, 2740-2753	0

512	Sputum bacterial load and bacterial composition correlate with lung function and are altered by long-term azithromycin treatment in children with HIV-associated chronic lung disease. **2023**, 11,	o
511	Water column dynamics control nitrite-dependent anaerobic methane oxidation by Candidatus Methylomirabilis in stratified lake basins. **2023**, 17, 693-702	o
510	Subgingival microbiome at different levels of cognition. **2023**, 15,	o
509	Characteristics of Microbiota in Different Segments of the Digestive Tract of Lycodon rufozonatus. **2023**, 13, 731	o
508	Daylily intercropping: Effects on soil nutrients, enzyme activities, and microbial community structure. 14,	o
507	Microbial Diversity, Community Turnover, and Putative Functions in Submarine Canyon Sediments under the Action of Sedimentary Geology. **2023**, 11,	o
506	Earthworms shape prokaryotic communities and affect extracellular enzyme activities in agricultural soil. **2023**, 115, 103474	o
505	Full-Length 16S rRNA Gene Analysis Using Long-Read Nanopore Sequencing for Rapid Identification of Bacteria from Clinical Specimens. **2023**, 193-213	o
504	Design of the Building Research in CRC prevention (BRIDGE-CRC) trial: a 6-month, parallel group Mediterranean diet and weight loss randomized controlled lifestyle intervention targeting the bile acid-gut microbiome axis to reduce colorectal cancer risk among African American/Black adults with obesity. **2023**, 24,	o
503	Saliva microbiome alterations in dental fluorosis population. **2023**, 15,	o
502	Elevated atmospheric CO2 concentrations caused a shift of the metabolically active microbiome in vineyard soil. **2023**, 23,	o
501	A Guide to Gene-Centric Analysis Using TreeSAPP. **2023**, 3,	o
500	Reliability of pathophysiological markers reflective of exercise-induced gastrointestinal syndrome (EIGS) in response to 2-h high-intensity interval exercise: A comprehensive methodological efficacy exploration. 14,	o
499	Changes of In Situ Prokaryotic and Eukaryotic Communities in the Upper Sanya River to the Sea over a Nine-Hour Period. **2023**, 11, 536	o
498	Impacts of dietary supplementation of bamboo vinegar and charcoal powder on growth performance, intestinal morphology, and gut microflora of large-scale loach Paramisgurnus dabryanus.	o
497	Shift of Feeding Strategies from Grazing to Different Forage Feeds Reshapes the Rumen Microbiota To Improve the Ability of Tibetan Sheep (Ovis aries) To Adapt to the Cold Season. **2023**, 11,	o
496	The Gut Commensal Escherichia coli Aggravates High-Fat-Diet-Induced Obesity and Insulin Resistance in Mice. **2023**, 89,	o
495	Warming affects herbaceous germination, early survival, and growth by shifting plant-soil microbe interactions in an alpine ecosystem.	o

494	HIV, asymptomatic STI, and the rectal mucosal immune environment among young men who have sex with men.	0
493	Bacterial community structure in the alcyoniid Lobophytum pauciflorum.	0
492	The Impact of Sewage-Sludge- and Olive-Mill-Waste-Derived Biochar Amendments to Tomato Cultivation. **2023**, 15, 3879	0
491	Life stage and vaccination shape the gut microbiome of hatchery-reared Atlantic salmon (Salmo salar).	0
490	The use of different 16S rRNA gene variable regions in biogeographical studies.	0
489	Classifying asthma control using salivary and fecal bacterial microbiome in children with moderate-to-severe asthma. **2023**, 34,	0
488	Fecal Microbiota, Forage Nutrients, and Metabolic Responses of Horses Grazing Warm- and Cool-Season Grass Pastures. **2023**, 13, 790	0
487	Machado Joseph disease severity is linked with gut microbiota alterations in transgenic mice. **2023**, 179, 106051	0
486	Effect of composted pig manure, biochar, and their combination on antibiotic resistome dissipation in swine wastewater-treated soil. **2023**, 323, 121323	0
485	Composition and biodiversity of soil and root-associated microbiome in Vitis vinifera cultivar Lambrusco distinguish the microbial terroir of the Lambrusco DOC protected designation of origin area on a local scale. 14,	0
484	Phagotrophic Protists Modulate Copper Resistance of the Bacterial Community in Soil. **2023**, 57, 3590-3601	0
483	Host Species and Environment Shape the Gut Microbiota of Cohabiting Marine Bivalves.	0
482	Impact of local iron enrichment on the small benthic biota in the deep Arctic Ocean. 10,	0
481	Carbon metabolism and biogeography of candidate phylum Candidatus Bipolaricaulota in geothermal environments of Biga Peninsula, Turkey. 14,	0
480	Persistence and Potential Atmospheric Ramifications of Ice-Nucleating Particles Released from Thawing Permafrost. **2023**, 57, 3505-3515	0
479	Short- and long-term effects of continuous compost amendment on soil microbiome community.	0
478	Comparing the transmission of carbapenemase-producing and extended-spectrum beta-lactamase-producingEscherichia colibetween broiler chickens.	0
477	The geographical and seasonal effects on the composition of marine microplastic and its microbial communities: The case study of Israel and Portugal. 14,	0

476	Gut microbiota composition during hospitalization is associated with 60-day mortality after severe COVID-19. **2023**, 27,	0
475	Thermal and alkaline pre-treatments of inoculum halt methanogenesis and enables cheese whey valorization by batch acidogenic fermentation.	0
474	Bacterial community composition of the sediment in Sayram Lake, an alpine lake in the arid northwest of China. **2023**, 23,	0
473	A novel and diverse group of Candidatus Patescibacteria from bathypelagic Lake Baikal revealed through long-read metagenomics. **2023**, 18,	0
472	Key soil physicochemical properties regulating microbial community structure under vegetation restoration in a karst region.	0
471	Fine-scale evaluation of two standard 16S rRNA gene amplicon primer pairs for analysis of total prokaryotes and archaeal nitrifiers in differently managed soils. 14,	0
470	Persistent flocks of diverse motile bacteria in long-term incubations of electron-conducting cable bacteria, Candidatus Electronema aureum. 14,	0
469	Rapid and Comprehensive Identification of Nontuberculous Mycobacteria. **2023**, 247-255	0
468	Network analysis of 16S rRNA sequences suggests microbial keystone taxa contribute to marine N2O cycling. **2023**, 6,	0
467	Tail fell syndrome impacts intestinal microbiota in porcupinefish (Diodon hystrix). 10,	0
466	Metabolic and inflammatory linkage of the chicken cecal microbiome to growth performance. 14,	0
465	Data on lung and intestinal microbiome after air pollution exposure in ageing rats. **2023**, 47, 109004	0
464	Diversity and Distribution of Harmful Algal Bloom Species from Seamount to Coastal Waters in the South China Sea. **2023**, 11,	0
463	The Acute Impact of Arsenic As(III) on the Prokaryotic Community Composition and Selected Bacterial Strains Based on Microcosm Experiments. 1-14	0
462	A Distinct Nasal Microbiota Signature in Peritoneal Dialysis Patients.	0
461	Composition and Patterns of Taxa Assemblages in the Western Channel Assessed by 18S Sequencing, Microscopy and Flow Cytometry. **2023**, 11, 480	0
460	Concentrations of dissolved dimethyl sulfide (DMS), methanethiol and other trace gases in context of microbial communities from the temperate Atlantic to the Arctic Ocean. **2023**, 20, 851-867	1
459	Seasons Influence the Native Gut Microbiome of Lake Trout Salvelinus namaycush. **2023**, 3, 276-287	0

458	Environmental changes associated with drying climate are expected to affect functional groups of pro- and microeukaryotes differently in temporary saline waters. **2023**, 13,	0
457	Reprogramming of the gut microbiota following feralization in Sus scrofa. **2023**, 5,	0
456	Effects of altitude on the gut microbiome and metabolomics of Sanhe heifers. 14,	0
455	Anthropogenic Nitrate Contamination Impacts Nitrous Oxide Emissions and Microbial Communities in the Marchica Lagoon (Morocco). **2023**, 15, 4077	0
454	Prebiotic Consumption Alters Microbiota but Not Biological Markers of Stress and Inflammation or Mental Health Symptoms in Healthy Adults: A Randomized, Controlled, Crossover Trial. **2023**, 153, 1283-1296	0
453	Identifying Eukaryotes and Factors Influencing Their Biogeography in Drinking Water Metagenomes. **2023**, 57, 3645-3660	0
452	Biostimulation ofSalicornia europaeaL. crops with plant growth-promoting bacteria in laboratory and field conditions: effects on growth and metabolite profile. **2023**, 134,	0
451	A longitudinal survey in the wild reveals major shifts in fish host microbiota after parasite infection.	0
450	An insight into gut microbiota and metabolites in the mice with adenomyosis. 13,	0
449	Thermal Selection of Microbial Communities and Preservation of Microbial Function in Guaymas Basin Hydrothermal Sediments. **2023**, 89,	0
448	Homogeneous Environmental Selection Structures the Bacterial Communities of Benthic Biofilms in Proglacial Floodplain Streams. **2023**, 89,	0
447	High Loading Start-Up and Rapid Loading Increase of an Anammox UASB Reactor Generate Superior Anammox Granules. **2023**, 234,	0
446	Candidatus Scalindua, a Biological Solution to Treat Saline Recirculating Aquaculture System Wastewater. **2023**, 11, 690	0
445	Compositional Alteration of Gut Microbiota in Psoriasis Treated with IL-23 and IL-17 Inhibitors. **2023**, 24, 4568	0
444	Short-Term Impact of Oxytetracycline Administration on the Fecal Microbiome, Resistome and Virulome of Grazing Cattle. **2023**, 12, 470	0
443	Longitudinal study of the short- and long-term effects of hospitalisation and oral trimethoprim-sulfadiazine administration on the equine faecal microbiome and resistome. **2023**, 11,	0
442	Diversity of Microbial Communities Associated with Epilithic Macroalgae in Different Coral Reef Conditions and Damselfish Territories of the Gulf of Thailand. **2023**, 11, 514	0
441	Modern Rivularia Freshwater Stromatolites as Models for Formation of Laminated Stromatolitic Crusts. **2023**, 40, 382-398	0

440	The Relationship and Influencing Factors between Endangered Plant Tetraena mongolica and Soil Microorganisms in West Ordos Desert Ecosystem, Northern China. **2023**, 12, 1048	0
439	The Extract of Perilla frutescens Seed Residue Attenuated the Progression of Aberrant Crypt Foci in Rat Colon by Reducing Inflammatory Processes and Altered Gut Microbiota. **2023**, 12, 988	0
438	The Colorectal Cancer Gut Environment Regulates Activity of the Microbiome and Promotes the Multidrug Resistant Phenotype of ESKAPE and Other Pathogens. **2023**, 8,	1
437	Particle Size Matters: Distribution, Source, and Seasonality Characteristics of Airborne and Pathogenic Bacteria in Wastewater Treatment Plants. **2023**, 14, 465	0
436	Nutrients strengthen density dependence of per-capita growth and mortality rates in the soil bacterial community. **2023**, 201, 771-782	0
435	From the Sunlit to the Aphotic Zone: Assembly Mechanisms and Co-Occurrence Patterns of Protistan-Bacterial Microbiotas in the Western Pacific Ocean.	0
434	New microbiological insights from the Bowland shale highlight heterogeneity of the hydraulically fractured shale microbiome. **2023**, 18,	0
433	Freeze-thaw cycles alter the growth sprouting strategy of wetland plants by promoting denitrification. **2023**, 4,	0
432	Comparison of Fecal Microbiota Communities between Primiparous and Multiparous Cows during Non-Pregnancy and Pregnancy. **2023**, 13, 869	0
431	Secretory IgM (sIgM) is an ancient master regulator of microbiota homeostasis and metabolism.	0
430	Microbial community shift on artificial biological reef structures (ABRs) deployed in the South China Sea. **2023**, 13,	0
429	Associations of soil bacterial diversity and function with plant diversity in Carex tussock wetland. 14,	0
428	Effects of Coumarin on Rhizosphere Microbiome and Metabolome of Lolium multiflorum. **2023**, 12, 1096	0
427	Zearalenone and Its Emerging Metabolites Promptly Affect the Rumen Microbiota in Holstein Cows Fed a Forage-Rich Diet. **2023**, 15, 185	0
426	Variable preterm oral microbiome stabilizes and reflects a full-term infant profile within three months.	0
425	Responses of the gastrointestinal microbiota to the protein metabolism of pond-cultured Japanese flounder (Paralichthys olivaceus). 10,	0
424	Global Meta-analysis of Urine Microbiome: Colonization of Polycyclic Aromatic Hydrocarbon□degrading Bacteria Among Bladder Cancer Patients. **2023**, 6, 190-203	0
423	Amplicons, Metagenomes, and Metatranscriptomes from Sediment and Water. **2023**, 12,	0

422	Leaf Microbiome Data for European Cultivated Grapevine (Vitis vinifera) During Downy Mildew (Plasmopara viticola) Epidemics in Three Wine-Producing Regions in France.	0
421	The endometrial microbiota of women with or without a live birth within 12´months after a first failed IVF/ICSI cycle. **2023**, 13,	0
420	Diversity and function of soybean rhizosphere microbiome under nature farming. 14,	0
419	The Microbiome of Complicated Diverticulitis: An Imbalance of Sulfur-Metabolizing Bacteria. **2023**, 66, 707-715	0
418	Metagenomics Analysis of Breast Microbiome Highlights the Abundance of Rothia Genus in Tumor Tissues. **2023**, 13, 450	0
417	Disentangling the mixed effects of soil management on microbial diversity and soil functions: A case study in vineyards. **2023**, 13,	0
416	Composition, structure, and functional shifts of prokaryotic communities in response to co-composting of various nitrogenous green feedstocks. **2023**, 23,	0
415	Neighboring plant community attributes drive rhizobiome assemblages of a focal plant in a Kobresia meadow. **2023**, 432, 116409	0
414	Different assembly mechanisms of leaf epiphytic and endophytic bacterial communities underlie their higher diversity in more diverse forests.	0
413	Changes in upper airways microbiota in ventilator-associated pneumonia. **2023**, 11,	0
412	Astragalus-cultivated soil was a suitable bed soil for nurturing Angelica sinensis seedlings from the rhizosphere microbiome perspective. **2023**, 13,	0
411	Fine-scale spatial variation shape fecal microbiome diversity and composition in black-tailed prairie dogs (Cynomys ludovicianus). **2023**, 23,	0
410	The koala gut microbiome is largely unaffected by host translocation but rather influences host diet. 14,	0
409	Loss of soil carbon and nitrogen indicates climate change-induced alterations in a temperate forest ecosystem. **2023**, 148, 110055	0
408	Australian soil microbiome: A first sightseeing regional prediction driven by cycles of soil temperature and pedogenic variations.	0
407	Winners and Losers of Atlantification: The Degree of Ocean Warming Affects the Structure of Arctic Microbial Communities. **2023**, 14, 623	0
406	Temporal dynamics of the cecal and litter microbiome of chickens raised in two separate broiler houses. 14,	0
405	Variety of rumen microbial populations involved in biohydrogenation related to individual milk fat percentage of dairy cows. 10,	0

404	Fine Resolution Analysis of bacterial communities associated with Neochloris oleoabundans culture and insights into terpenes as contamination control agents.	0
403	From defaults to databases: parameter and database choice dramatically impact the performance of metagenomic taxonomic classification tools. **2023**, 9,	0
402	Microbiome analysis revealed distinct microbial communities occupying different sized nodules in field-grown peanut. 14,	0
401	Mechanical weeding enhances ecosystem multifunctionality and profit in industrial oil palm.	0
400	Prokaryotic community dynamics and nitrogen-cycling genes in an oxygen-deficient upwelling system during La Ni▯a and El Ni▯o conditions.	0
399	Polybacterial shift in benthic river biofilms attributed to organic pollution ▯a prospect of a new biosentinel?. **2023**, 54, 348-359	0
398	Abiotic factors and endophytes co-regulate flavone and terpenoid glycoside metabolism in Glycyrrhiza uralensis. **2023**, 107, 2671-2688	0
397	Fluorescence activated cell sorting and fermentation analysis to study rumen microbiome responses to administered live microbials and yeast cell wall derived prebiotics. 13,	0
396	Bacterial Communities in Lanna Fermented Soybeans from Three Different Ethnolinguistic Groups in Northern Thailand. **2023**, 11, 649	0
395	Experimentally Induced Dieback Conditions Limit Phragmites australis Growth. **2023**, 11, 639	0
394	Decoupling Fe0 Application and Bioaugmentation in Space and Time Enables Microbial Reductive Dechlorination of Trichloroethene to Ethene: Evidence from Soil Columns. **2023**, 57, 4167-4179	0
393	Dopamine Inhibits Arabidopsis Growth through Increased Oxidative Stress and Auxin Activity. **2023**, 3, 351-371	0
392	Omics and imaging combinatorial approach reveals butyrate-induced inflammatory effects in the zebrafish gut. **2023**, 5,	0
391	Disparate population and holobiont structure of pocilloporid corals across the Red Sea gradient demonstrate species-specific evolutionary trajectories.	0
390	[Translated article] Pilot study to determine the association between gut microbiota and fragility hip fracture. **2023**,	0
389	Experimental community coalescence sheds light on microbial interactions in soil and restores impaired functions. **2023**, 11,	0
388	Local environment drives rapid shifts in composition and phylogenetic clustering of seagrass microbiomes. **2023**, 13,	0
387	Cold Exposure▯nduced Alterations in the Brain Peptidome and Gut Microbiome Are Linked to Energy Homeostasis in Mice. **2023**, 22, 100525	0

386	Macroecological patterns in coarse-grained microbial communities.	0
385	Community differentiation of rhizosphere microorganisms and their responses to environmental factors at different development stages of medicinal plant Glehnia littoralis. 11, e14988	0
384	Laser capture microdissection as a method for investigating the human hair follicle microbiome reveals region-specific differences in the bacteriome profile. **2023**, 16,	0
383	Microbiome Structure and Mucosal Morphology of Jejunum Appendix and Colon of Rats in Health and Dysbiosis. **2023**, 80,	0
382	Iodidimonas, a bacterium unable to degrade hydrocarbons, thrives in a bioreactor treating oil and gas produced water.	0
381	High Variation in Protist Diversity and Community Composition in Surface Sediment of Hot Springs in Himalayan Geothermal Belt, China. **2023**, 11, 674	0
380	Effects of metal contamination with physicochemical properties on the sediment microbial communities in a tropical eutrophic-hypereutrophic urban reservoir in Brazil. **2023**, 30, 54961-54978	0
379	Effects of topical fluoride application on oral microbiota in young children with severe dental caries. 13,	0
378	Effects of rice blast biocontrol strain Pseudomonas alcaliphila Ej2 on the endophytic microbiome and proteome of rice under salt stress. 14,	0
377	Association of intestinal microbiota and its metabolite markers with excess weight in Chinese children and adolescents.	0
376	The commensal protistTritrichomonas musculusexhibits a dynamic life cycle that induces B cell-modulated remodeling of the gut microbiota.	0
375	Roles of microbiota in autoimmunity in Arabidopsis.	0
374	Moss and underlying soil bacterial community structures are linked to moss functional traits. **2023**, 14,	0
373	Positive response of host root-associated bacterial community and soil nutrients to inhibitory parasitism of dodder.	0
372	Productive and physiological implications of top-dress addition of branched-chain amino acids and arginine on lactating sows and offspring. **2023**, 14,	0
371	Abundance and composition of particles and their attached microbiomes along an Atlantic Meridional Transect. 10,	0
370	The terrestrial isopod symbiont Candidatus Hepatincola porcellionum is a potential nutrient scavenger related to Holosporales symbionts of protists. **2023**, 3,	0
369	Stay in the loop: lessons learned about the microbial water quality in pipe loops transitioned from conventional to direct potable reuse water.	0

368	Nasal Bacteriomes of Patients with Asthma and Allergic Rhinitis Show Unique Composition, Structure, Function and Interactions. **2023**, 11, 683	0
367	Bovine Colostrum Supplementation Modulates the Intestinal Microbial Community in Rabbits. **2023** , 13, 976	0
366	Phosphorus mining activities alter endophytic bacterial communities and metabolic functions of surrounding vegetables and crops.	0
365	Effects of grazing and fire management on rangeland soil and biocrust microbiomes. **2023**, 148, 110094	0
364	Mother-to-infant microbiota transmission and infant microbiota development across multiple body sites. **2023**, 31, 447-460.e6	0
363	Litter Matters: The Importance of Decomposition Products for Soil Bacterial Diversity and abundance of key groups of the N cycle in Tropical Areas.	0
362	Metal-driven bacterial community variation in urban and suburban park soils of Shanghai, China. **2023**, 115, 103475	0
361	A broadly distributed predicted helicase/nuclease confers phage resistance via abortive infection. **2023**, 31, 343-355.e5	0
360	Sample Collection, DNA Extraction, and Library Construction Protocols of the Human Microbiome Studies in the International Human Phenome Project.	0
359	Captive and urban environments are associated with distinct gut microbiota in deer mice (Peromyscus maniculatus). **2023**, 19,	0
358	External and internal microbiomes of Antarctic nematodes are distinct, but more similar to each other than the surrounding environment. **2023**, 55,	0
357	Leaf microbiome data for European beech (Fagus sylvatica) at the leaf and canopy scales collected in a gallery forest in South-West France. **2023**, 80,	0
356	Comparison of four DNA extraction kits efficiency for 16SrDNA microbiota profiling of diverse human samples. **2023**, 9,	0
355	A hydrogenotrophic Sulfurimonas is globally abundant in deep-sea oxygen-saturated hydrothermal plumes. **2023**, 8, 651-665	0
354	Response of microbial community of surface and deep chlorophyll maximum to nutrients and light in South China Sea. 10,	0
353	Surface Bacterioplankton Community Structure Crossing the Antarctic Circumpolar Current Fronts. **2023**, 11, 702	0
352	Biotic interactions contribute more than environmental factors and geographic distance to biogeographic patterns of soil prokaryotic and fungal communities. 14,	0
351	Water chlorination increases the relative abundance of an antibiotic resistance marker in developing sourdough starters.	0

350	Reciprocal influence of soil, phyllosphere and aphid microbiomes.	0
349	Host plant affects the larval gut microbial communities of the generalist herbivoresHelicoverpa armigeraandSpodoptera frugiperda.	0
348	Exploring the growing forest musk deer (Moschus berezovskii) dietary protein requirement based on gut microbiome. 14,	0
347	Characterization of the Lower Airways and Oral Microbiota in Healthy Young Persons in the Community. **2023**, 11, 841	0
346	Deterministic processes dominate microbial community assembly in artificially bred Schizothorax wangchiachii juveniles after being released into wild.	0
345	A parasitic nematode induces dysbiosis in susceptible but not resistant gastropod hosts. **2023**, 12,	0
344	Algal amendment enhances biogenic methane production from coals of different thermal maturity. 14,	0
343	Dysbiotic lung microbial communities of neonates from allergic mothers confer neonate responsiveness to suboptimal allergen. 4,	0
342	Microbiota and functional analyses of nitrogen-fixing bacteria in root-knot nematode parasitism of plants. **2023**, 11,	0
341	Basal Diet Fed to Recipient Mice Was the Driving Factor for Colitis and Colon Tumorigenesis, despite Fecal Microbiota Transfer from Mice with Severe or Mild Disease. **2023**, 15, 1338	0
340	Analysis of Microbial Diversity and Metabolites in Sauerkraut Products with and without Microorganism Addition. **2023**, 12, 1164	0
339	Quantitative 16S rRNA Gene Amplicon Sequencing for Comprehensive Pathogenic Bacterial Tracking in a Municipal Wastewater Treatment Plant. **2023**, 3, 923-933	0
338	Uncovering the link between gut microbiome, highly processed food consumption and diet quality through bioinformatics methods.	0
337	Tillage homogenizes soil bacterial communities in microaggregate fractions by facilitating dispersal.	0
336	Individual variation in the avian gut microbiota: The influence of host state and environmental heterogeneity.	0
335	Bacterial diversity and co-occurrence patterns differ across a world-wide spatial distribution of habitats in glacier ecosystems.	0
334	Spinach (Spinacia oleracea) as green manure modifies the soil nutrients and microbiota structure for enhanced pepper productivity. **2023**, 13,	0
333	16S Amplicon Metabarcoding of the Nest Materials of Native Australian Stingless Bees. **2023**, 12,	0

332	Disentangling the Functional Role of Fungi in Cold Seep Sediment. **2023**, 11,	○
331	Responses of bacterial communities along vertical soil profile to the chromium-contamination stress. **2023**, 179, 105584	○
330	Integrated multiomic wastewater-based epidemiology can elucidate population-level dietary behaviour and inform public health nutrition assessments. **2023**, 4, 257-266	○
329	Water Quality, Toxicity and Diversity of Planktonic and Benthic Cyanobacteria in Pristine Ancient Lake Khubsugul (H□sg□), Mongolia. **2023**, 15, 213	○
328	Microbial Composition on Abandoned and Reclaimed Mining Sites in the Komi Republic (North Russia). **2023**, 11, 720	○
327	Thrive or survive: prokaryotic life in hypersaline soils. **2023**, 18,	○
326	Tumor bacterial markers diagnose the initiation and four stages of colorectal cancer. 13,	○
325	The Endometrial Microbiota□6S rRNA Gene Sequence Signatures in Healthy, Pregnant and Endometritis Dairy Cows. **2023**, 10, 215	○
324	The Middle Ear Microbiota in Healthy Dogs Is Similar to That of the External Ear Canal. **2023**, 10, 216	○
323	Soil microbes support Janzen□ mountain passes hypothesis: The role of local-scale climate variability along a tropical montane gradient. 14,	○
322	The Oral Microbiome as Mediator between Oral Hygiene and Its Impact on Nasopharyngeal Carcinoma. **2023**, 11, 719	○
321	Uncovering Bacterial Hosts of Class 1 Integrons in an Urban Coastal Aquatic Environment with a Single-Cell Fusion-Polymerase Chain Reaction Technology. **2023**, 57, 4870-4879	○
320	From a cell model to a fish trial: Immunomodulatory effects of heat-killed Lactiplantibacillus plantarum as a functional ingredient in aquafeeds for salmonids. 14,	○
319	Characterization of SARS-CoV-2 Distribution and Microbial Succession in a Clinical Microbiology Testing Facility during the SARS-CoV-2 Pandemic. **2023**, 11,	○
318	Acetoclastic archaea adaptation under increasing temperature in lake sediments and wetland soils from Alaska.	○
317	Transition of an estuarine benthic meiofauna assemblage 1.7 and 2.8 years after a mining disaster. 11, e14992	○
316	Extensive identification of serum metabolites related to microbes in different gut locations and evaluating their associations with porcine fatness.	○
315	A Longitudinal Characterization of the Seminal Microbiota and Antibiotic Resistance in Yearling Beef Bulls Subjected to Different Rates of Gain. **2023**, 11,	○

314	Impact of Infection with Flavobacterium psychrophilum and Antimicrobial Treatment on the Intestinal Microbiota of Rainbow Trout. **2023**, 12, 454	0
313	Trade-Offs between Competitive Ability and Resistance to Top-Down Control in Marine Microbes.	0
312	Ubiquitous, B12-dependent virioplankton utilizing ribonucleotide triphosphate reductase demonstrate interseasonal dynamics and associate with a diverse range of bacterial hosts in the pelagic ocean.	0
311	Archaeal and Extremophilic Bacteria from Different Archaeological Excavation Sites. **2023**, 24, 5519	0
310	Molecular signature of domestication in the arboviral vectorAedes aegypti.	0
309	Effects of Consuming Fermented Fish (Surströmming) on the Fecal Microflora in Healthy Individuals. **2023**, 26, 185-192	0
308	Microbial and Viral Genome and Proteome Nitrogen Demand Varies across Multiple Spatial Scales within a Marine Oxygen Minimum Zone.	0
307	Effects of supplementation of Bacillus amyloliquefaciens on performance, systemic immunity, and intestinal microbiota of weaned pigs experimentally infected with a pathogenic enterotoxigenic E. coli F18. 14,	0
306	NEMoE: a nutrition aware regularized mixture of experts model to identify heterogeneous diet-microbiome-host health interactions. **2023**, 11,	0
305	A phytobiotic extract, in an aqueous or in a cyclodextrin encapsulated form, added in diet affects meat oxidation, cellular responses and intestinal morphometry and microbiota of broilers. 4,	0
304	Nutrient availability of roughages in isocaloric and îsonitrogenous diets alters the bacterial networks in the whole gastrointestinal tract of Hu sheep. **2023**, 23,	0
303	Does biochar addition improve soil physicochemical properties, bacterial community and alfalfa growth for saline soils?.	0
302	Temporal dynamics of geothermal microbial communities in Aotearoa-New Zealand. 14,	0
301	Spatially-resolved metabolomic identifies colibactin-specific principles of reprogrammed lipid metabolism to promote cancer progression.	0
300	Diseased-induced multifaceted variations in community assembly and functions of plant-associated microbiomes. 14,	0
299	Neoadjuvant chemotherapy plus nivolumab with or without ipilimumab in operable non-small cell lung cancer: the phase 2 platform NEOSTAR trial. **2023**, 29, 593-604	0
298	Influence of mental health medication on microbiota in the elderly population in the Valencian region. 14,	0
297	Gut microbiome signatures of Yorkshire Terrier enteropathy during disease and remission. **2023**, 13,	0

296	Changes of intestinal microbiota in the giant salamander (Andrias davidianus) during growth based on high-throughput sequencing. 14,	o
295	Electrokinetic-Enhanced Bioremediation of Trichloroethylene-Contaminated Low-Permeability Soils: Mechanistic Insight from Spatio-Temporal Variations of Indigenous Microbial Community and Biodehalogenation Activity. **2023**, 57, 5046-5055	o
294	Transcriptome analysis ofAurantiochytrium limacinumunder low salt conditions. **2023**, 134,	o
293	From the Mountain to the Valley: Drivers of Groundwater Prokaryotic Communities along an Alpine River Corridor. **2023**, 11, 779	o
292	Insights into the mechanisms underlying the biodegradation of phenanthrene in biochar-amended soil: from bioavailability to soil microbial communities. **2023**, 5,	o
291	Spatial variation of the gut microbiome in response to long-term metformin treatment in high-fat diet-induced type 2 diabetes mouse model of both sexes. **2023**, 15,	o
290	Chlorine Dioxide Reprograms Rhizosphere Microbial Communities to Enrich Interactions with Tobacco (Nicotiana tabacum). **2023**, 72, 47-60	o
289	Seasonal variation in near-surface seasonally thawed active layer and permafrost soil microbial communities. **2023**, 18, 055001	o
288	Using simulated wildland fire to assess microbial survival at multiple depths from biocrust and bare soils. 14,	o
287	Differences in Soil Microbiota of Continuous Cultivation of Ganoderma leucocontextum. **2023**, 13, 888	o
286	Association between Non-Alcoholic Steatohepatitis-Related Hepatocellular Carcinoma and Periodontopathic Bacteria: A Cross-Sectional Pilot Study. **2023**, 13, 3893	o
285	Effects of Eimeria acervulina infection on the luminal and mucosal microbiota of the duodenum and jejunum in broiler chickens. 14,	o
284	Mucosa-Associated Oscillospira sp. Is Related to Intestinal Stricture and Post-Operative Disease Course in Crohn's Disease. **2023**, 11, 794	o
283	Snow Microorganisms Colonise Arctic Soils Following Snow Melt.	o
282	Interspecific plant interaction via root exudates structures the disease suppressiveness of´rhizosphere microbiomes. **2023**,	o
281	Core species and interactions prominent in fish-associated microbiome dynamics. **2023**, 11,	o
280	Microbial response to warming and cellulose addition in a maritime Antarctic soil.	o
279	Broad-Spectrum Antifungal, Biosurfactants and Bioemulsifier Activity of Bacillus subtilis subsp. spizizenii A Potential Biocontrol and Bioremediation Agent in Agriculture. **2023**, 12, 1374	o

278	Occurrence of mycotoxins and microbial communities in artisanal infant flours marketed in Côte d'Ivoire. **2023**, 39,	0
277	Lower respiratory tract microbiome composition and community interactions in smokers. **2023**, 5,	0
276	Microbial Drivers of Plant Performance during Drought Depend upon Community Composition and the Greater Soil Environment. **2023**, 11,	0
275	Comprehensive characterization of maternal, fetal, and neonatal microbiomes supports prenatal colonization of the gastrointestinal tract. **2023**, 13,	0
274	Characterization of the Bacterial Microbiome in Natural Populations of Barley Stem Gall Midge, Mayetiola hordei, in Morocco. **2023**, 11, 797	0
273	HIV Tat Expression and Cocaine Exposure Lead to Sex- and Age-Specific Changes of the Microbiota Composition in the Gut. **2023**, 11, 799	0
272	The gut microbiota of tropical marine fish is largely uncultured and distinct from surrounding water microbiota.	0
271	Significant antimicrobial-producing vegetation uniquely shapes the stormwater biofilter microbiome with implications for enhanced faecal pathogen inactivation. **2023**, 2, e0000094	0
270	Extensive Cryptic Diversity and Ecological Associations Uncovered among Mexican and Global Collections of Naegleria and Vermamoeba Species by 18S Ribosomal DNA, Internal Transcribed Spacer, and Cytochrome Oxidase Subunit I Sequence Analysis. **2023**, 11,	0
269	The Effect of a Diet Enriched with Jerusalem artichoke, Inulin, and Fluoxetine on Cognitive Functions, Neurogenesis, and the Composition of the Intestinal Microbiota in Mice. **2023**, 45, 2561-2579	0
268	Colonization order of bacterial isolates on treefrog embryos impacts microbiome structure in tadpoles. **2023**, 290,	0
267	Genome-resolved metagenomics of milk microbiomes reveals the influence of maternal dietary fiber on neonatal inheritance of immunoregulatory traits.	0
266	Metabolic syndrome and the urinary microbiome of patients undergoing percutaneous nephrolithotomy. **2023**,	0
265	Whole-body Microbiota of Newborn Calves and Their Response to Prenatal Vitamin and Mineral Supplementation.	0
264	Increased Leaf Bacterial Network Complexity along the Native Plant Diversity Gradient Facilitates Plant Invasion?. **2023**, 12, 1406	0
263	16S-rRNA-Based Metagenomic Profiling of the Bacterial Communities in Traditional Bulgarian Sourdoughs. **2023**, 11, 803	0
262	Nanopore Is Preferable over Illumina for 16S Amplicon Sequencing of the Gut Microbiota When Species-Level Taxonomic Classification, Accurate Estimation of Richness, or Focus on Rare Taxa Is Required. **2023**, 11, 804	0
261	Diversity and function of methyl-coenzyme M reductase-encoding archaea in Yellowstone hot springs revealed by metagenomics and mesocosm experiments. **2023**, 3,	0

260	Uncovering plant microbiomes using long-read metagenomic sequencing.	0
259	Spatial Distribution of airborne bacterial communities in caged poultry houses.	0
258	First insights into nasal microbiome in wine tasters.	0
257	Bacterial Community Structure of Two Cold Sulfur Springs in Slovakia (Central Europe). **2023**, 80,	0
256	The Impact of Mineral and Energy Supplementation and Phytogenic Compounds on Rumen Microbial Diversity and Nitrogen Utilization in Grazing Beef Cattle. **2023**, 11, 810	0
255	Fine-scale mapping of physicochemical and microbial landscapes of the coral skeleton.	0
254	The potential to produce tropodithietic acid by Phaeobacter inhibens affects the assembly of microbial biofilm communities in natural seawater. **2023**, 9,	0
253	Heavy Metal Pollution Impacts Soil Bacterial Community Structure and Antimicrobial Resistance at the Birmingham 35th Avenue Superfund Site. **2023**, 11,	0
252	Microbe-mineral interactions in the Plastisphere: Coastal biogeochemistry and consequences for degradation of plastics. 10,	0
251	The Impact of Early Life Experiences and Gut Microbiota on Neurobehavioral Development in Preterm Infants: A Longitudinal Cohort Study. **2023**, 11, 814	0
250	Effects of recurrent summer droughts on arbuscular mycorrhizal and total fungal communities in experimental grasslands differing in plant diversity and community composition.	0
249	Longitudinal changes in subgingival biofilm composition following periodontal treatment.	0
248	Alterations of gut microbes and their correlation with clinical features in middle and end-stages chronic kidney disease. 13,	0
247	Exogenous and Endophytic Fungal Communities of Dendrobium nobile Lindl. across Different Habitats and Their Enhancement of Host Plants’ Dendrobine Content and Biomass Accumulation. **2023**, 8, 12489-12500	0
246	Nasal microbiota profiles in shelter dogs with dermatological conditions carrying methicillin-resistant and methicillin-sensitive Staphylococcus species. **2023**, 13,	0
245	Multi-omic analysis of coral development elucidates the metabolic transitions from parental provisioning to endosymbiotic nutritional exchange.	0
244	Microbially-derived indole-3-acetate alleviates diet induced steatosis and inflammation in mice.	0
243	Contributions of carbon source, crop cultivation, and chemical property on microbial community assemblage in soil subjected to reductive disinfestation. 14,	0

242	Microbiomes of blood feeding triatomines in the context of their predatory relatives and the environment.	0
241	Infant gut microbiome composition correlated with type 1 diabetes acquisition in the general population: the ABIS study.	0
240	Intestinal bacteria diversity of suckermouth catfish (Pterygoplichthys pardalis) in the Cd, Hg, and Pb contaminated Ciliwung River, Indonesia. **2023**, 9, e14842	0
239	Fe/S oxidation-coupled arsenic speciation transformation mediated by AMD enrichment culture under different pH conditions. **2024**, 137, 681-700	0
238	No evidence for associations between brood size, gut microbiome diversity and survival in great tit (Parus major) nestlings. **2023**, 5,	0
237	Three Species of Axenic Mosquito Larvae Recruit a Shared Core of Bacteria in a Common Garden Experiment.	0
236	Bacillus subtilis KM0 Impacts gut Microbiota Profile and Transcription of Genes Related to Transcellular Transport in Zebrafish (Danio rerio). **2023**, 80,	0
235	Construction of hybrid constructed wetlands for phosphorus chemical industry tailwater treatment in the middle Yangtze river basin: Responses of plant growth and root-associated microbial communities. **2023**, 100144	0
234	Microbial Diversity of Deep-sea Sediments from Three Newly Discovered Hydrothermal Vent Fields in the Central Indian Ridge. **2023**, 58,	0
233	Potato root-associated microbiomes adapt to combined water and nutrient limitation and have a plant genotype-specific role for plant stress mitigation. **2023**, 18,	0
232	Phylogeny-guided genome mining of roseocin family lantibiotics to generate improved variants of roseocin. **2023**, 13,	0
231	Dectin-1 signaling on colonic □T cells promotes psychosocial stress responses. **2023**, 24, 625-636	0
230	The microbiome of the marine flatworm Macrostomum lignano provides fitness advantages and exhibits circadian rhythmicity. **2023**, 6,	0
229	Effects of Thymbra capitata essential oil on in vitro fermentation end-products and ruminal bacterial communities. **2023**, 13,	0
228	Responses of bacterial and three sub-microeukaryote communities in the water of white shrimp Penaeus vannamei aquaculture ponds in two polyculture models.	0
227	Sulfur disproportionating microbial communities in a dynamic, microoxic-sulfidic karst system.	0
226	Effects of plants and soil microorganisms on organic carbon and the relationship between carbon and nitrogen in constructed wetlands.	0
225	Emerging investigator series: differential effects of carbon nanotubes and graphene on the tomato rhizosphere microbiome.	0

224	Microbiota diversity, composition and drivers in waxy proso millet sourdoughs of Niandoubao, a traditional fermented cereal food in northeast China. **2023**, 180, 114699	o
223	Effective Biocorrosive Control in Oil Industry Facilities: 16S rRNA Gene Metabarcoding for Monitoring Microbial Communities in Produced Water. **2023**, 11, 846	o
222	High Microeukaryotic Diversity in the Cold-Seep Sediment.	o
221	Current levels of microplastic pollution impact wild seabird gut microbiomes.	o
220	High-resolution single-molecule long-fragment rRNA gene amplicon sequencing of bacterial and eukaryotic microbial communities. **2023**, 3, 100437	o
219	Impact of testosterone use on the vaginal microbiota of transgender men, including susceptibility to bacterial vaginosis: study protocol for a prospective, observational study. **2023**, 13, e073068	o
218	Lethal and sublethal effects on stingless bee (Partamona helleri) larvae caused by chronic exposure to three agrochemicals.	o
217	Cultivation of SAR202 Bacteria from the Ocean.	o
216	Effect of Rice Straw and Stubble Burning on Soil Physicochemical Properties and Bacterial Communities in Central Thailand. **2023**, 12, 501	o
215	Vaginal Microbiome Metagenome Inference Accuracy: Differential Measurement Error according to Community Composition.	o
214	The Succession of the Cellulolytic Microbial Community from the Soil during Oat Straw Decomposition. **2023**, 24, 6342	o
213	Amplicon sequencing allows differential quantification of closely related parasite species: an example from rodent coccidia (Eimeria).	o
212	Intestinal microbiota of Nearctic-Neotropical migratory birds vary more over seasons and years than between host species.	o
211	Biological Methanation in an Anaerobic Biofilm Reactor▯Trace Element and Mineral Requirements for Stable Operation. **2023**, 11, 1013	o
210	Inhibition of Methylmercury and Methane Formation by Nitrous Oxide in Arctic Tundra Soil Microcosms. **2023**, 57, 5655-5665	o
209	The microbial dark matter and ▯wanted list▯in worldwide wastewater treatment plants. **2023**, 11,	o
208	Evaluation of Physicochemical and Microbial Properties of Extracts from Wine Lees Waste of Matelica▯ Verdicchio and Their Applications in Novel Cosmetic Products. **2023**, 12, 816	o
207	Scaling deep phylogenetic embedding to ultra-large reference trees: a tree-aware ensemble approach.	o

206	Klebsiella quasipneumoniae in intestine damages bile acid metabolism in hematopoietic stem cell transplantation patients with bloodstream infection. **2023**, 21,	0
205	Niche Modification by Sulfate-Reducing Bacteria Drives Microbial Community Assembly in Anoxic Marine Sediments.	0
204	Bacteria, yeasts, and fungi associated with larval food of Brazilian native stingless bees. **2023**, 13,	0
203	Diverticulosis is not associated with altered gut microbiota nor is it predictive of future diverticulitis: a population-based colonoscopy study. 1-8	0
202	Microbial Diversity Using a Metataxonomic Approach, Associated with Coffee Fermentation Processes in the Department of Quind�, Colombia. **2023**, 9, 343	0
201	Alternative stable states, nonlinear behavior, and predictability of microbiome dynamics. **2023**, 11,	0
200	Effects of Inbreeding on Microbial Community Diversity of Zea mays. **2023**, 11, 879	0
199	Genome-resolved analyses of oligotrophic groundwater microbial communities along phenol pollution in a continuous-flow biodegradation model system. 14,	0
198	Molecular Evidence of Internal Carbon-Driven Partial Denitrification Annamox (PdNA) in a mainstream Pilot A-B System Coupled with Side-stream EBPR treating municipal wastewater.	0
197	Exploiting a targeted resistome sequencing approach in assessing antimicrobial resistance in retail foods. **2023**, 18,	0
196	The Gut Microbiota of Broilers Reared with and without Antibiotic Treatment. **2023**, 11, 876	0
195	Microbial interaction between human skin and Nukadoko, a fermented rice bran bed for pickling vegetables.	0
194	Biochar improves soil organic carbon stability by shaping the microbial community structures at different soil depths four years after an incorporation in a farmland soil. **2023**, 5, 100214	0
193	Microbiome differences in sugarcane and metabolically engineered oilcane accessions and their implications for bioenergy production. **2023**, 16,	0
192	Anaerobic Microbial Degradation of Polypropylene and Polyvinyl Chloride Samples. **2023**, 92, 83-93	0
191	Temperate bacteriophages infecting the mucin-degrading bacterium Ruminococcus gnavus from the human gut. **2023**, 15,	0
190	Rumen microbial composition associated with the non-glucogenic to glucogenic short-chain fatty acids ratio in Holstein cows. **2023**, 94,	0
189	Regulation of bacterial behavior to mitigate membrane fouling in gravity-driven membrane system: The beneficial effects of gravity-driven up-flow slow biofilter. **2023**, 53, 103669	0

188	The inhibition of high ammonia to in vitro rumen fermentation is pH dependent. 10,	0
187	Organic fertilization drives shifts in microbiome complexity and keystone taxa increase the resistance of microbial mediated functions to biodiversity loss. **2023**, 59, 441-458	0
186	Trophic interrelationships of bacteria are important for shaping soil protist communities.	0
185	The core fungal microbiome of banana (Musa spp.). 14,	0
184	Short Term Impact of Recycling-Derived Fertilizers on Their P Supply for Perennial Ryegrass (Lolium perenne).	0
183	Actinobacteria from Arctic and Atlantic deep-sea sediments—Biodiversity and bioactive potential. 14,	0
182	Taxonomical and functional responses of microbial communities from forest soils of differing tree species diversity to drying-rewetting cycles. **2023**, 150875	0
181	Dominant bacterial taxa drive microbiome differences of juvenile Pacific oysters of the same age and variable sizes. 2,	0
180	Reducing bias in microbiome research: Comparing methods from sample collection to sequencing. 14,	0
179	Compact and automated eDNA sampler for in situ monitoring of marine environments. **2023**, 13,	0
178	Metagenomic analyses of a microbial assemblage in a subglacial lake beneath the Vatnajökull ice cap, Iceland. 14,	0
177	Maternal diet modulates the infant microbiome and intestinal Flt3L necessary for dendritic cell development and immunity to respiratory infection. **2023**,	0
176	Oral microbiome changes associated with the menstrual cycle in healthy young adult females. 13,	0
175	Microbial diversity and community composition of fecal microbiota in dual-purpose and egg type ducks. 14,	0
174	Diversity and assembly of root-associated microbiomes of rubber trees. 14,	0
173	Characterization of the Root-Associated Microbiome Provides Insights into Endemism ofThymusSpecies Growing in the Kazdagi National Park.	0
172	Antibacterial plant combinations prevent postweaning diarrhea in organically raised piglets challenged with enterotoxigenic Escherichia coli F18. 10,	0
171	Deciphering the rhizosphere bacteriome associated with biological control of tobacco black shank disease. 14,	0

170	16S rRNA Gene Amplicon Sequencing of the Gut Microbiota of Chimaera phantasma (Silver Chimaera) Captured off Koshimoda in Suruga Bay, Japan.	0
169	A Novel E3 Probiotics Formula Restored Gut Dysbiosis and Remodelled Gut Microbial Network and Microbiome Dysbiosis Index (MDI) in Southern Chinese Adult Psoriasis Patients. **2023**, 24, 6571	0
168	Vaginal Microbiome Dysbiosis is Associated with the Different Cervical Disease Status.	0
167	Virus-Host Dynamics in Archaeal Groundwater Biofilms and the Associated Bacterial Community Composition. **2023**, 15, 910	0
166	Successional dynamics of the cultivated kelp microbiome.	0
165	Gut Microbiota in Children with Hand Foot and Mouth Disease on 16S rRNA Gene Sequencing. **2023** , 80,	0
164	The impact of culture systems on the gut microbiota and gut metabolome of bighead carp (Hypophthalmichthys nobilis). **2023**, 5,	0
163	Comparative analysis of macroalgae supplementation on the rumen microbial community: Asparagopsis taxiformis inhibits major ruminal methanogenic, fibrolytic, and volatile fatty acid-producing microbes in vitro. 14,	0
162	Subclinical doses of dietary fumonisins and deoxynivalenol cause cecal microbiota dysbiosis in broiler chickens challenged with Clostridium perfringens. 14,	0
161	Concatenated 16S rRNA sequence analysis improves bacterial taxonomy. 11, 1530	0
160	Soil Suppressiveness Against Pythium ultimum and Rhizoctonia solani in Two Land Management Systems and Eleven Soil Health Treatments.	0
159	Microbial and Biochemical Profile of Different Types of Greek Table Olives. **2023**, 12, 1527	0
158	Annotation-free discovery of functional groups in microbial communities.	0
157	Investigating the effects of Brachiaria (Syn. Urochloa) varieties on soil properties and microbiome.	0
156	Microbial mat compositions and localization patterns explain the virulence of black band disease in corals. **2023**, 9,	0
155	The Association between Caffeine Intake and the Colonic Mucosa-Associated Gut Microbiota in HumansA Preliminary Investigation. **2023**, 15, 1747	0
154	Fauna-microbe diversity coupling lost in agricultural soils: Implications from the bacteria hidden in earthworm gut. **2023**,	0
153	Gluconic acid improves performance of newly weaned piglets associated with alterations in gut microbiome and fermentation. **2023**, 9,	0

152	Deterministic and stochastic processes generating alternative states of microbiomes.	0
151	Isha yoga practices, vegan diet, and participation in Samyama meditation retreat: impact on the gut microbiome & metabolome – a non-randomized trial. **2023**, 23,	0
150	Bee breweries: The unusually fermentative, lactobacilli-dominated brood cell microbiomes of cellophane bees. 14,	0
149	Ecological divergence of a mesocosm in an eastern boundary upwelling system assessed with multi-marker environmental DNA metabarcoding. **2023**, 20, 1277-1298	0
148	Unveiling the role of emerging metagenomics for the examination of hypersaline environments. 1-39	0
147	A cryopreservation method to recover laboratory- and field-derived bacterial communities from mosquito larval habitats. **2023**, 17, e0011234	0
146	Characterization of the Blood Microbiome and Comparison with the Fecal Microbiome in Healthy Dogs and Dogs with Gastrointestinal Disease. **2023**, 10, 277	0
145	Big Data for a Small World: A Review on Databases and Resources for Studying Microbiomes.	0
144	Quantification of diversity sampling bias resulting from rice root bacterial isolation on popular and nitrogen-free culture media using 16S amplicon barcoding. **2023**, 18, e0279049	0
143	Selecting 16S rRNA Primers for Microbiome Analysis in a Host–Microbe System: The Case of the Jellyfish Rhopilema nomadica. **2023**, 11, 955	0
142	Land use modification causes slow, but predictable, change in soil microbial community composition and functional potential. **2023**, 18,	0
141	Freshwater transfer affected intestinal microbiota with correlation to cytokine gene expression in Asian sea bass. 14,	0
140	Gut Bacterial Communities in HIV-Infected Individuals with Metabolic Syndrome: Effects of the Therapy with Integrase Strand Transfer Inhibitor-Based and Protease Inhibitor-Based Regimens. **2023**, 11, 951	0
139	Exploring the short-term in-field performance of Recovered Nitrogen from Manure (RENURE) materials to substitute synthetic nitrogen fertilisers. **2023**, 5, 100043	0
138	Continuous single-stage elemental sulfur reduction and copper sulfide precipitation under thermoacidophilic conditions. **2023**, 119948	0
137	Biotechnological potential of Bacillus sp. S26 for alleviation of abiotic and biotic stresses in vine. **2023**, 39,	0
136	Mesophilic and thermophilic viruses are associated with nutrient cycling during hyperthermophilic composting.	0
135	Bacterial diversity and function shift of strawberry root in different cultivation substrates. **2023**, 100696	0

134	Evidence for a Parabasalian Gut Symbiote in Egg-Feeding Poison Frog Tadpoles in Peru.	0
133	Experimental Factors Influence Diversity Metrics of the Gut Microbiome in Laboratory Mice.	0
132	Global Marine Cold Seep Metagenomes Reveal Diversity of Taxonomy, Metabolic Function, and Natural Products.	0
131	Aquafeed fermentation improves dietary nutritional quality and benefits feeding behavior, meat flavor, and intestinal microbiota of Chinese mitten crab (Eriocheir sinensis). **2023**,	0
130	A metabarcoding analysis of the wrackbed microbiome indicates a phylogeographic break along the North SeaBaltic Sea transition zone.	0
129	Comparative analysis of bacterial diversity in two hot springs in Hefei, China. **2023**, 13,	0
128	Maternal Psychosocial Stress Is Associated with Reduced Diversity in the Early Infant Gut Microbiome. **2023**, 11, 975	0
127	Mechanism of Metabolic Response to Hepatectomy by Integrated Analysis of Gut Microbiota, Metabolomics, and Proteomics.	0
126	Integrated Microbiota and Metabolite Changes following Rice Bran Intake during Murine Inflammatory Colitis-Associated Colon Cancer and in Colorectal Cancer Survivors. **2023**, 15, 2231	0
125	Exploration of Soil Microbial Diversity and Community Structure along Mid-Subtropical Elevation Gradients in Southeast China. **2023**, 14, 769	0
124	Antibiotic treatment using amoxicillin-clavulanic acid impairs gut mycobiota development through modification of the bacterial ecosystem. **2023**, 11,	0
123	Dark-zone alterations expand throughout Paleolithic Lascaux Cave despite spatial heterogeneity of the cave microbiome. **2023**, 18,	0
122	O2 partitioning of sulfur oxidizing bacteria drives acidity and thiosulfate distributions in mining waters. **2023**, 14,	0
121	Chemical Characterization and Metagenomic Identification of Endophytic Microbiome from South African Sunflower (Helianthus annus) Seeds. **2023**, 11, 988	0
120	Ecology of food waste chain-elongating microbiome. 11,	0
119	Effects of whole-grain cereals on fecal microbiota and short-chain fatty acids in dogs - A comparison of rye, oats and wheat.	0
118	Profiles of oral microbiome associated with nasogastric tube feeding. **2023**, 15,	0
117	Comprehensive Microbiome and Metabolome Analyses Reveal the Medicinal Components of Paeonia lactiflora. **2023**, 12, 1612	0

116	The Local Tumor Microbiome Is Associated with Survival in Late-Stage Colorectal Cancer Patients.	0
115	High methane flux in a tropical peatland post-fire is linked to homogenous selection of diverse methanogenic archaea.	0
114	In sickness and in health: the dynamics of the fruit bat gut microbiota under a bacterial antigen challenge and its association with the immune response. 14,	0
113	Comparing the bacterial composition, succession and assembly patterns in plastisphere and kitchen waste composting with PLA/PBAT blends. **2023**, 131405	0
112	Research Note: Therapeutic effect of a Salmonella phage combination on chicks infected with Salmonella Typhimurium. **2023**, 102715	0
111	First Study on profiling of gut microbiome in wild and captive Sumatran orangutans (Pongo abelii). **2023**, 717-727	0
110	Syncytiotrophoblast 5′tRNA fragments are placental endocrine signals contributing to sterile inflammation in preeclampsia.	0
109	The effect of Andrographis paniculata water extract on palliative management of metastatic esophageal squamous cell carcinoma A phase II clinical trial.	0
108	Nitrogen dynamics and fixation control cyanobacterial abundance, diversity, and toxicity in Lake of the Woods (USA, Canada).	0
107	The impact of urine collection method on canine urinary microbiota detection: a cross-sectional study. **2023**, 23,	0
106	Plant chemical variation mediates soil bacterial community composition. **2023**, 13,	0
105	Dynamic Development of Viral and Bacterial Diversity during Grass Silage Preservation. **2023**, 15, 951	0
104	Dissemination of antibiotic resistance genes from the Pearl River Estuary to adjacent coastal areas. **2023**, 188, 105978	0
103	Graphene oxide exposure alters gut microbial community composition and metabolism in an in vitro human model. **2023**, 100463	0
102	A comparison between Greengenes, SILVA, RDP, and NCBI reference databases in four published microbiota datasets.	0
101	The Potential Roles of Free and Attached Microbial Community in Decreasing Cadmium Level from Cadmium-Contaminated Soils by Mixotrophic Acidophiles of Different Scale-Up Cultivation Stages. **2023**, 13, 546	0
100	Bringing Antarctica to the lab: a polar desert environmental chamber to study the response of Antarctic microbial communities to climate change.	0
99	CDBN-YGXZ, a Novel Small-Molecule Drug, Shows Efficacy against Clostridioides difficile Infection and Recurrence in Mouse and Hamster Infection Models.	0

98	Sugarcane leaves-derived polyphenols alleviate metabolic syndrome and modulate gut microbiota of ob/ob mice. **2023**, 1-24	0
97	Using Inflammatory Biological Age To Evaluate the Preventing Aging Effect of a Polyphenol-Probiotic-Enhanced Dietary Pattern in Adults Aged 50 Years and Older.	0
96	Feeding ecology of the obligate urchin symbiont Dactylopleustes yoshimurai (Crustacea: Amphipoda: Pleustidae) revealed by DNA metabarcoding analysis..	0
95	Aircraft surveys for air eDNA: probing biodiversity in the sky. 11, e15171	0
94	The nasal microbiome in patients suffering from non-steroidal anti-inflammatory drugs-exacerbated respiratory disease in absence of corticosteroids. 14,	0
93	Short-term soil amendment by sewage sludge anaerobic digestate in a tomato monoculture suppresses Fusarium vascular wilt disease by changing the taxonomic characteristics of soil microbiota. **2023**, 189, 104915	0
92	The structure of microbial communities in redoximorphic microsites of Gleysol.	0
91	Organic amendments alter microbiota assembly to stimulate soil metabolism for improving soil quality in wheat-maize rotation system. **2023**, 339, 117927	0
90	Characterization of the lung microbiome and inflammatory cytokine levels in women exposed to environmental risk factors: A pilot study. **2023**, 11,	0
89	A westernized diet changed the colonic bacterial composition and metabolite concentration in a dextran sulfate sodium pig model for ulcerative colitis. 14,	0
88	Screening and Identification of the Strain Pediococcus acidilactici and Its Application in Fermentation of Corn–Soybean Meal Uncooked Materials. **2023**, 9, 383	0
87	Evaluation of DNA extraction methods and direct PCR in metabarcoding of mock and marine bacterial communities. 14,	0
86	Gut Microbiome in Post-COVID-19 Patients Is Linked to Immune and Cardiovascular Health Status but Not COVID-19 Severity. **2023**, 11, 1036	0
85	Diversity of endosymbionts in camellia spiny whitefly, Aleurocanthus camelliae (Hemiptera: Aleyrodidae), estimated by 16S rRNA analysis and their biological implications. 14,	0
84	Effects of cadmium and diethylhexyl phthalate on skin microbiota of Rana chinensis tadpoles.	0
83	Alterations in vaginal microbiota in uterine fibroids patients with ultrasound-guided high-intensity focused ultrasound ablation. 14,	0
82	Diversity and functions of soil microbial communities in the Trans-Himalayan grazing ecosystem: influence of herbivores and abiotic factors.	0
81	Elevated temperature alters microbial communities, but not decomposition rates, during three years of in-situ peat decomposition.	0

80	Uterine Tissue Metabonomics Combined with 16S rRNA Gene Sequencing To Analyze the Changes of Gut Microbiota in Mice with Endometritis and the Intervention Effect of Tau Interferon.	0
79	Information storage across a microbial community using universal RNA memory.	0
78	Microbial succession and its effect on the formation of umami peptides during sufu fermentation. 14,	0
77	Oral intake of Lactiplantibacillus pentosus LPG1 Produces a Beneficial Regulation of Gut Microbiota in Healthy Persons: A Randomised, Placebo-Controlled, Single-Blind Trial. **2023**, 15, 1931	0
76	Differences in the luminal and mucosal gut microbiomes and metabolomes of oriental rat snake (Ptyas mucosus).	0
75	Development of the gut microbiota in the first 14´years of life and its relations to internalizing and externalizing difficulties and social anxiety during puberty.	0
74	Identification of gut dysbiosis in axial spondyloarthritis patients and improvement of experimental ankylosing spondyloarthritis by microbiome-derived butyrate with immune-modulating function. 14,	0
73	Dachaihu decoction ameliorates septic intestinal injury via modulating the gut microbiota and glutathione metabolism as revealed by multi-omics. **2023**, 312, 116505	0
72	Isolation and identification of ligninolytic bacterium (Bacillus cereus) from buffalo (Bubalus bubalis) rumen and its effects on the fermentation quality, nutrient composition, and bacterial community of rape silage. 14,	0
71	Microbiome variability of mosquito lines is consistent over time and across environments.	0
70	Effects of non-protein nitrogen on buffel grass fiber and ruminal bacterial composition in sheep. **2023**, 105237	0
69	Expression of Microcystis Biosynthetic Gene Clusters in Natural Populations Suggests Temporally Dynamic Synthesis of Novel and Known Secondary Metabolites in Western Lake Erie.	0
68	Rapid differentiation of soil and root microbiomes in response to plant composition and biodiversity in the field. **2023**, 3,	0
67	Multi-factorial examination of amplicon sequencing workflows from sample preparation to bioinformatic analysis. **2023**, 23,	0
66	Bacterial community responses to planktonic and terrestrial substrates in coastal northern Baltic Sea. 10,	0
65	Diversity Analysis of Tick-Borne Viruses from Hedgehogs and Hares in Qingdao, China.	0
64	Maternal Bacterial Engraftment in Multiple Body Sites of Cesarean Section Born Neonates after Vaginal Seeding Randomized Controlled Trial.	0
63	A scuticociliate causes mass mortality of Diadema antillarum in the Caribbean Sea. **2023**, 9,	1

62	Genetic determinants of switchgrass-root-associated microbiota in field sites spanning its natural range. **2023**,	0
61	Timing of root barriers controls soil-to-shoot integration of rhizosphere status.	0
60	Effect of Antibiotics and Gut Microbiota on the Development of Sepsis in Children with Hematopoietic Stem Cell Transplants.	0
59	Unraveling the Dysbiosis of Vaginal Microbiome to Understand Cervical Cancer Disease Etiology An Explainable AI Approach. **2023**, 14, 936	0
58	Associations among Milk Microbiota, Milk Fatty Acids, Milk Glycans, and Inflammation from Lactating Holstein Cows.	0
57	Integrating Multi-Omics Data to Construct Reliable Interconnected Models of Signaling, Gene Regulatory, and Metabolic Pathways. **2023**, 139-151	0
56	Specific host metabolite and gut microbiome alterations are associated with bone loss during spaceflight. **2023**, 112299	0
55	Organohalide respiration by aDesulforhopalus-dominated community.	0
54	DNA extraction protocol impacts ocular surface microbiome profile. 14,	0
53	Surfaces of gymnastic equipment as reservoirs of microbial pathogens with potential for transmission of bacterial infection and antimicrobial resistance. 14,	0
52	SituSeq: an offline protocol for rapid and remote Nanopore 16S rRNA amplicon sequence analysis. **2023**, 3,	0
51	Interactions between rootstocks and compost influence the active rhizosphere bacterial communities in citrus. **2023**, 11,	0
50	Human microbiome transfer in the built environment differs based on occupants, objects, and buildings. **2023**, 13,	0
49	Gut Microbiota and Serum Metabolites in Individuals with Class III Obesity Without Type 2 Diabetes Mellitus: Pilot Analysis.	0
48	Fungal Diversity and Dynamics during Long-Term Immersion of Conventional and Biodegradable Plastics in the Marine Environment. **2023**, 15, 579	0
47	Effects of biochar addition on aeolian soil microbial community assembly and structure.	0
46	Methane Cycle in a Littoral Site of a Temperate Freshwater Lake. **2023**, 92, 153-170	0
45	Application of Wheat Straw Compost Mixed with Chemical Fertilizer Regulates Soil Bacterial Community Diversity in Tea (Camellia sinensis) Plantation. **2023**, 15, 580	0

44	Gut microbiome responds compositionally and functionally to the seasonal diet variations in wild gibbons. **2023**, 9,	0
43	Cuticle supplementation and nitrogen recycling by a dual bacterial symbiosis in a family of xylophagous beetles.	0
42	Structure and Seasonal Variability of Microbial Communities of Groundwater in the City of Moscow. **2023**, 92, 192-203	0
41	Field scale biodegradation of total petroleum hydrocarbons and soil restoration by Ecopiles: microbiological analysis of the process. 14,	0
40	Lung-gut axis of microbiome alterations following co-exposure to ultrafine carbon black and ozone. **2023**, 20,	0
39	Disentangling temporal associations in marine microbial networks. **2023**, 11,	0
38	Microbial communities in freshwater used for hydraulic fracturing are unable to withstand the high temperatures and pressures characteristic of fractured shales. **2023**, 5,	0
37	Diet replacement with whole insect larvae affects intestinal morphology and microbial ecosystem of broiler chickens.	0
36	Effects of recurrent summer droughts on arbuscular mycorrhizal and total fungal communities in experimental grasslands differing in plant diversity and community composition. 3,	0
35	18S-NemaBase: Curated 18S rRNA Database of Nematode Sequences. **2023**, 55,	0
34	From waste to feed: Microbial fermented abalone waste improves the digestibility, gut health, and immunity in marron, Cherax cainii. **2023**, 108748	0
33	IN SITU GROWTH OF MODERN ONCOIDS FROM SALADO RIVER, SALAR DE LA LAGUNA VERDE COMPLEX, ARGENTINA. **2023**, 106396	0
32	Sex-specific effects of voluntary wheel running on behavior and the gut microbiota-immune-brain axis in mice. **2023**, 100628	0
31	Assembly processes of eukaryotic plankton communities in the world's largest drinking water diversion project. **2023**, 163665	0
30	mRNA Location and Translation Rate Determine Protein Targeting to Dual Destinations.	0
29	Distinct healthy and atopic canine gut microbiota is influenced by diet and antibiotics. **2023**, 10,	0
28	Paenibacillus melissococcoides sp. nov., isolated from a honey bee colony affected by European foulbrood disease. **2023**, 73,	0
27	Bacterial inoculation of Quercus pyrenaica trees alters co-occurrence patterns but not the composition of the rhizosphere bacteriome in wild conditions.	0

26	Cecal Microbiota Development and Physiological Responses of Broilers Following Early Life Microbial Inoculation Using Different Delivery Methods and Microbial Sources.	0
25	Metatranscriptomic analysis of the gut microbiome of black soldier fly larvae reared on lignocellulose-rich fiber diets unveils key lignocellulolytic enzymes. 14,	0
24	Biogeographical and Biodiversity Patterns of Marine Planktonic Bacteria Spanning from the South China Sea across the Gulf of Bengal to the Northern Arabian Sea.	0
23	Sociality does not predict oral microbiome composition or diversity in free-living prairie voles. **2023**, 200, 167-182	0
22	Predicting feed efficiency traits in growing lambs from their ruminal microbiota. **2023**, 17, 100824	0
21	Longitudinal Analysis of the Impacts of Urogenital Schistosomiasis on the Gut microbiota of Adolescents in Nigeria.	0
20	Exploring Microbial Diversity and Functional Potential along the Bay of Bengal Coastline in Bangladesh: Insights from Amplicon Sequencing and Shotgun Metagenomics.	0
19	Characterization of the Bacterial Communities Inhabiting Tropical Propolis of Puerto Rico. **2023**, 11, 1130	0
18	Bact-to-Batch: A Microbiota-Based Tool to Determine Optimal Animal Allocation in Experimental Designs. **2023**, 24, 7912	0
17	Prokaryotic Responses to Estuarine Coalescence Contribute to Planktonic Community Assembly in a Mediterranean Nutrient-Rich Estuary. **2023**, 11, 933	0
16	Rhizosphere-induced shift in the composition of bacterial community favors mineralization of crop residue nitrogen.	0
15	Intestinal microbiota analyses of five economic fishery resources in the South China Sea. **2023**, 46, 101085	0
14	Unraveling microbial community by next-generation sequencing in living membrane bioreactors for wastewater treatment. **2023**, 886, 163965	0
13	Plastisphere and microorganisms involved in polyurethane biodegradation. **2023**, 886, 163932	0
12	The bacterial community of the European spruce bark beetle in space and time.	0
11	Boosting resilience of microbial electrolysis cell-assisted anaerobic digestion of blackwater with granular activated carbon amendment. **2023**, 381, 129136	0
10	Role of soil organic matter composition and microbial communities on SOC stability: Insights from particle-size aggregates.	0
9	The effect of southwest monsoon on the meso-scale biogeographic patterns of the bacteria in the northeast of South China Sea. **2023**, 59, 01021	0

8	Metataxonomic characterization of the microbial community involved in the production of biogas with microcrystalline cellulose in pilot and laboratory scale. **2023**, 39,	0
7	Deep sea treasures - insights from museum archives shed light on coral microbial diversity and functioning within deepest ocean ecosystems.	0
6	A reduced but stable core microbiome found in seeds of hyperaccumulators. **2023**, 887, 164131	0
5	Biodegradation of polyvinyl chloride by Citrobacter koseri isolated from superworms (Zophobas atratus larvae). 14,	0
4	Permanent cover crop as a strategy to promote soil health and vineyard performance.	0
3	Geography, not lifestyle, explains the population structure of free-living and host-associated deep-sea hydrothermal vent snail symbionts. **2023**, 11,	0
2	N/S element transformation modulating lithospheric microbial communities by single-species manipulation. **2023**, 11,	0
1	Disruption of fish gut microbiota composition and holobionts metabolome during a simulated Microcystis aeruginosa (Cyanobacteria) bloom. **2023**, 11,	0