

CITATION REPORT

List of articles citing

Greengenes, a chimera-checked 16S rRNA gene database and workbench compatible with ARB

DOI: 10.1128/aem.03006-05

Applied and Environmental Microbiology, 2006, 72, 5069-72.

Source: <https://exaly.com/paper-pdf/39833274/citation-report.pdf>

Version: 2024-04-27

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
2282	In Vitro Metabolic Labeling of Intestinal Microbiota for Quantitative Metaproteomics.		
2281	Natural Attenuation in Streambed Sediment Receiving Chlorinated Solvents from Underlying Fracture Networks.		
2280	Degradation of Crude 4MCHM (4-Methylcyclohexanemethanol) in Sediments from Elk River, West Virginia.		
2279	Biological Bromate Reduction Driven by Methane in a Membrane Biofilm Reactor.		
2278	Structure Variation, and Co-occurrence of Soil Microbial Communities in Abandoned Sites of a Rare Earth Elements Mine.		
2277	The Prevalence of Integrons as the Carrier of Antibiotic Resistance Genes in Natural and Man-Made Environments.		0
2276	Bacterial Survival Strategies in an Alkaline Tailing Site and the Physiological Mechanisms of Dominant Phylotypes As Revealed by Metagenomic Analyses.		
2275	Protection Mechanisms of Periphytic Biofilm to Photocatalytic Nanoparticle Exposure.		
2274	Inhibition of Microbial Methylation via <i>arsM</i> in the Rhizosphere: Arsenic Speciation in the Soil to Plant Continuum.		
2273	.		
2272	Effects of triclosan on bacterial community composition and <i>Vibrio</i> populations in natural seawater microcosms. 2017 , 5,		
2271	Effects of triclosan on bacterial community composition and <i>Vibrio</i> populations in natural seawater microcosms. 2017 , 5,		
2270	Multiple sequence alignment for phylogenetic purposes. 2006 , 19, 479		113
2269	NASt: a multiple sequence alignment server for comparative analysis of 16S rRNA genes. 2006 , 34, W394-9		810
2268	Identification and isolation of a <i>Castellaniella</i> species important during biostimulation of an acidic nitrate- and uranium-contaminated aquifer. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 4892-904 ^{4.8}		48
2267	The Genomes On Line Database (GOLD) in 2007: status of genomic and metagenomic projects and their associated metadata. 2008 , 36, D475-9		276
2266	Molecular-phylogenetic characterization of microbial community imbalances in human inflammatory bowel diseases. 2007 , 104, 13780-5		3103

2265	Microbial community biofabrics in a geothermal mine adit. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 6172-80	4.8	66
2264	Urban aerosols harbor diverse and dynamic bacterial populations. 2007 , 104, 299-304		512
2263	Large-scale maximum likelihood-based phylogenetic analysis on the IBM BlueGene/L. 2007 ,		64
2262	probeBase--an online resource for rRNA-targeted oligonucleotide probes: new features 2007. 2007 , 35, D800-4		373
2261	Dynamic multigrain parallelization on the cell broadband engine. 2007 ,		22
2260	"Candidatus Bacilloplasma," a novel lineage of Mollicutes associated with the hindgut wall of the terrestrial isopod <i>Porcellio scaber</i> (Crustacea: Isopoda). <i>Applied and Environmental Microbiology</i> , 2007 , 73, 5566-73	4.8	55
2259	Ecology of the microbial community removing phosphate from wastewater under continuously aerobic conditions in a sequencing batch reactor. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 2257-70	4.8	100
2258	Geographical Distribution and Diversity of Moderately Thermophilic Members of the Thermoplasmatales. 2007 , 20-21, 405-408		
2257	The termite group I phylum is highly diverse and widespread in the environment. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 6682-5	4.8	38
2256	An Initial Inventory of Bacteria Found within the Soils and Waters of Great Smoky Mountains National Park. 2007 , 6, 57-72		1
2255	PhylArray: phylogenetic probe design algorithm for microarray. 2007 , 23, 2550-7		29
2254	Isolation of polymer-degrading bacteria and characterization of the hindgut bacterial community from the detritus-feeding larvae of <i>Tipula abdominalis</i> (Diptera: Tipulidae). <i>Applied and Environmental Microbiology</i> , 2007 , 73, 5683-6	4.8	18
2253	Microbial diversity in natural asphalts of the Rancho La Brea Tar Pits. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 4579-91	4.8	93
2252	Targeted access to the genomes of low-abundance organisms in complex microbial communities. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 3205-14	4.8	190
2251	What's in the mix: phylogenetic classification of metagenome sequence samples. 2007 , 10, 499-503		85
2250	Improved 16S rRNA-targeted probe set for analysis of sulfate-reducing bacteria by fluorescence in situ hybridization. 2007 , 69, 523-8		87
2249	Short pyrosequencing reads suffice for accurate microbial community analysis. 2007 , 35, e120		510
2248	SILVA: a comprehensive online resource for quality checked and aligned ribosomal RNA sequence data compatible with ARB. 2007 , 35, 7188-96		4492

2247	Comparative genomics and site-directed mutagenesis support the existence of only one input channel for protons in the C-family (cbb3 oxidase) of heme-copper oxygen reductases. 2007 , 46, 9963-72	66
2246	RAxML-Cell: Parallel Phylogenetic Tree Inference on the Cell Broadband Engine. 2007 ,	21
2245	Loss of bacterial diversity during antibiotic treatment of intubated patients colonized with <i>Pseudomonas aeruginosa</i> . 2007 , 45, 1954-62	143
2244	Environmental controls on the landscape-scale biogeography of stream bacterial communities. 2007 , 88, 2162-73	157
2243	Phylogenetic systematics of microorganisms inhabiting thermal environments. 2007 , 72, 1299-312	22
2242	Pyrosequencing enumerates and contrasts soil microbial diversity. 2007 , 1, 283-90	1338
2241	An ecological and evolutionary perspective on human-microbe mutualism and disease. 2007 , 449, 811-8	1172
2240	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. 2007 , 450, 560-5	990
2239	Distribution of candidate division JS1 and other Bacteria in tidal sediments of the German Wadden Sea using targeted 16S rRNA gene PCR-DGGE. 2007 , 62, 78-89	50
2238	Automated group assignment in large phylogenetic trees using GRUNT: GRouping, Ungrouping, Naming Tool. 2007 , 8, 402	9
2237	AxPcoords & parallel AxParafit: statistical co-phylogenetic analyses on thousands of taxa. 2007 , 8, 405	37
2236	The phylogeny of fluorescent pseudomonads in an unflooded rice paddy soil. 2007 , 57, 299-306	5
2235	High-density universal 16S rRNA microarray analysis reveals broader diversity than typical clone library when sampling the environment. 2007 , 53, 371-83	387
2234	Unravelling microbial communities with DNA-microarrays: challenges and future directions. 2007 , 53, 498-506	86
2233	The most conserved genome segments for life detection on Earth and other planets. 2008 , 38, 517-33	59
2232	Microarray analysis of bacterial diversity and distribution in aggregates from a desert agricultural soil. 2008 , 44, 1003-1011	16
2231	Effects of seed sludge on fermentative characteristics and microbial community structures in thermophilic hydrogen fermentation of starch. 2008 , 33, 6541-6548	58
2230	Evolution of mammals and their gut microbes. 2008 , 320, 1647-51	2355

2229	Diversity of the heme-copper superfamily in archaea: insights from genomics and structural modeling. 2008 , 45, 1-31		108
2228	Bacteria subsisting on antibiotics. 2008 , 320, 100-3		398
2227	Novelty and uniqueness patterns of rare members of the soil biosphere. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 5422-8	4.8	170
2226	The influence of sex, handedness, and washing on the diversity of hand surface bacteria. 2008 , 105, 17994-9		795
2225	Physiology, ecology, phylogeny, and genomics of microorganisms capable of syntrophic metabolism. 2008 , 1125, 58-72		265
2224	FACS enrichment and identification of floc-associated alphaproteobacterial tetrad-forming organisms in an activated sludge community. 2008 , 285, 130-5		10
2223	High archaeal richness in the water column of a freshwater sulfurous karstic lake along an interannual study. 2008 , 66, 331-42		78
2222	A novel ecological role of the Firmicutes identified in thermophilic microbial fuel cells. 2008 , 2, 1146-56		266
2221	A salinity and sulfate manipulation of hypersaline microbial mats reveals stasis in the cyanobacterial community structure. 2008 , 2, 457-70		43
2220	Functional metagenomic profiling of nine biomes. 2008 , 452, 629-32		726
2219	Worlds within worlds: evolution of the vertebrate gut microbiota. 2008 , 6, 776-88		1042
2218	Lipid biomarker and phylogenetic analyses to reveal archaeal biodiversity and distribution in hypersaline microbial mat and underlying sediment. 2008 , 6, 394-410		57
2217	Elevated atmospheric CO ₂ affects soil microbial diversity associated with trembling aspen. 2008 , 10, 926-41		199
2216	Diversity of microbes associated with the marine sponge, <i>Haliclona simulans</i> , isolated from Irish waters and identification of polyketide synthase genes from the sponge metagenome. 2008 , 10, 1888-902		75
2215	Active bacterial community structure along vertical redox gradients in Baltic Sea sediment. 2008 , 10, 2051-63		65
2214	Discovery and characterization of a new bacterial candidate division by an anaerobic sludge digester metagenomic approach. 2008 , 10, 2111-23		22
2213	probeCheck--a central resource for evaluating oligonucleotide probe coverage and specificity. 2008 , 10, 2894-8		154
2212	The effects of chronic nitrogen fertilization on alpine tundra soil microbial communities: implications for carbon and nitrogen cycling. 2008 , 10, 3093-105		209

2211	The genome of <i>Rhodobacter sphaeroides</i> strain 2.4.1 encodes functional cobinamide salvaging systems of archaeal and bacterial origins. 2008 , 70, 824-36	20
2210	The metagenomics RAST server - a public resource for the automatic phylogenetic and functional analysis of metagenomes. 2008 , 9, 386	2527
2209	Insights and inferences about integron evolution from genomic data. 2008 , 9, 261	40
2208	Use of pyrosequencing and DNA barcodes to monitor variations in Firmicutes and Bacteroidetes communities in the gut microbiota of obese humans. 2008 , 9, 576	66
2207	The influence of soil properties on the structure of bacterial and fungal communities across land-use types. 2008 , 40, 2407-2415	1270
2206	Tag-encoded pyrosequencing analysis of bacterial diversity in a single soil type as affected by management and land use. 2008 , 40, 2762-2770	369
2205	Relative impacts of land-use, management intensity and fertilization upon soil microbial community structure in agricultural systems. 2008 , 40, 2843-2853	368
2204	Proceedings of the international workshop on Ribosomal RNA technology, April 7-9, 2008, Bremen, Germany. 2008 , 31, 258-68	9
2203	A case study for microbial biodegradation: anaerobic bacterial reductive dechlorination of polychlorinated biphenyls from sediment to defined medium. 2008 , 62, 253-70	103
2202	Exploring microbial diversity and taxonomy using SSU rRNA hypervariable tag sequencing. 2008 , 4, e1000255	666
2201	The pervasive effects of an antibiotic on the human gut microbiota, as revealed by deep 16S rRNA sequencing. 2008 , 6, e280	1660
2200	Culture-independent characterization of a novel microbial community at a hydrothermal vent at Brothers volcano, Kermadec arc, New Zealand. 2008 , 113,	16
2199	Bioenergetics. 2008 ,	4
2198	A bioinformatician's guide to metagenomics. 2008 , 72, 557-78, Table of Contents	292
2197	A renaissance for the pioneering 16S rRNA gene. 2008 , 11, 442-6	337
2196	Species richness in soil bacterial communities: a proposed approach to overcome sample size bias. 2008 , 75, 86-91	30
2195	Supplemental programs for enhanced recovery of data from the DOTUR application. 2008 , 75, 572-5	4
2194	Culture-independent characterization of the bacterial populations associated with cod (<i>Gadus morhua</i> L.) and live feed at an experimental hatchery facility using denaturing gradient gel electrophoresis. 2008 , 275, 42-50	71

2193	A rapid bootstrap algorithm for the RAxML Web servers. 2008 , 57, 758-71		5512
2192	Metagenomic approaches for defining the pathogenesis of inflammatory bowel diseases. 2008 , 3, 417-27		368
2191	Niche differentiation among sulfur-oxidizing bacterial populations in cave waters. 2008 , 2, 590-601		130
2190	Relating Microbial Community and Physicochemical Parameters of a Hot Spring: Champagne Pool, Wai-o-tapu, New Zealand. 2008 , 25, 441-453		21
2189	High-throughput diversity and functionality analysis of the gastrointestinal tract microbiota. 2008 , 57, 1605-15		463
2188	Identifying and Characterizing Bacteria in an Era of Genomics and Proteomics. 2008 , 58, 925-936		64
2187	Characterization of a bacterial community in an abandoned semiarid lead-zinc mine tailing site. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 3899-907	4.8	135
2186	Short-term temporal variability in airborne bacterial and fungal populations. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 200-7	4.8	211
2185	Habitat-Lite: a GSC case study based on free text terms for environmental metadata. 2008 , 12, 129-36		34
2184	Accurate taxonomy assignments from 16S rRNA sequences produced by highly parallel pyrosequencers. 2008 , 36, e120		423
2183	Diversity of human vaginal bacterial communities and associations with clinically defined bacterial vaginosis. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 4898-909	4.8	198
2182	Metagenomics: read length matters. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 1453-63	4.8	243
2181	A standard MIGS/MIMS compliant XML Schema: toward the development of the Genomic Contextual Data Markup Language (GCDML). 2008 , 12, 115-21		52
2180	Characterization of the microbial community and polyketide biosynthetic potential in the palmerolide-producing tunicate <i>Synoicum adareanum</i> . 2008 , 71, 1812-8		45
2179	A diversity profile of the human skin microbiota. 2008 , 18, 1043-50		665
2178	Colloquium paper: microbes on mountainsides: contrasting elevational patterns of bacterial and plant diversity. 2008 , 105 Suppl 1, 11505-11		584
2177	"Candidatus Cloacamonas acidaminovorans": genome sequence reconstruction provides a first glimpse of a new bacterial division. 2008 , 190, 2572-9		268
2176	Distribution of Crenarchaeota representatives in terrestrial hot springs of Russia and Iceland. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 7620-8	4.8	50

2175	Accumulation of trans C18:1 fatty acids in the rumen after dietary algal supplementation is associated with changes in the <i>Butyrivibrio</i> community. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 6923-30	4.8	102
2174	Miniprimer PCR, a new lens for viewing the microbial world. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 840-9	4.8	85
2173	Molecular signatures of ribosomal evolution. 2008 , 105, 13953-8		85
2172	<i>Spirochaeta cellobiosiphila</i> sp. nov., a facultatively anaerobic, marine spirochaete. 2008 , 58, 2762-8		21
2171	Influence of particle size on bacterial community structure in aquatic sediments as revealed by 16S rRNA gene sequence analysis. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 5237-40	4.8	42
2170	Cross-kingdom amplification using bacteria-specific primers: complications for studies of coral microbial ecology. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 7828-31	4.8	110
2169	Comparative characterization of the microbial diversities of an artificial microbialite model and a natural stromatolite. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 7410-21	4.8	55
2168	Subsurface microbial diversity in deep-granitic-fracture water in Colorado. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 143-52	4.8	102
2167	Photoferrotrophs thrive in an Archean Ocean analogue. 2008 , 105, 15938-43		171
2166	Microalgae and cyanobacteria of the Dead Sea and its surrounding springs. 2008 , 56, 1-13		8
2165	The smallest cells pose the biggest problems: high-performance computing and the analysis of metagenome sequence data. 2008 , 125, 012050		
2164	Bacterial communities associated with retail alfalfa sprouts. 2008 , 71, 200-4		17
2163	The airborne metagenome in an indoor urban environment. 2008 , 3, e1862		158
2162	Large-Scale Phylogenetic Analysis on Current HPC Architectures. 2008 , 16, 255-270		13
2161	The human vaginal bacterial biota and bacterial vaginosis. 2008 , 2008, 750479		148
2160	Environmental and Microbial Ecology in Sulfur Mats Responsible for the Biological Removal of Hydrogen Sulfide from Biogas. 2009 , 38, 642-651		1
2159	A high-throughput DNA sequence aligner for microbial ecology studies. 2009 , 4, e8230		229
2158	Insect symbioses: a case study of past, present, and future fungus-growing ant research. 2009 , 38, 78-92		59

2157	Effects of experimental choices and analysis noise on surveys of the "rare biosphere". <i>Applied and Environmental Microbiology</i> , 2009 , 75, 3263-70	4.8	41
2156	Filamentous bacterium Eikelboom type 0092 in activated sludge plants in Australia is a member of the phylum Chloroflexi. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 2446-52	4.8	42
2155	Potentially pathogenic bacteria in shower water and air of a stem cell transplant unit. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 5363-72	4.8	50
2154	FastTree: computing large minimum evolution trees with profiles instead of a distance matrix. 2009 , 26, 1641-50		2608
2153	Photolysis of iron-siderophore chelates promotes bacterial-algal mutualism. 2009 , 106, 17071-6		328
2152	RAMI: a tool for identification and characterization of phylogenetic clusters in microbial communities. 2009 , 25, 736-42		48
2151	Single Cell Whole Genome Amplification of Uncultivated Organisms. 2009 , 241-256		2
2150	rrnDB: documenting the number of rRNA and tRNA genes in bacteria and archaea. 2009 , 37, D489-93		333
2149	Effect of biowaste sludge maturation on the diversity of thermophilic bacteria and archaea in an anaerobic reactor. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 2566-72	4.8	96
2148	ATGC: a database of orthologous genes from closely related prokaryotic genomes and a research platform for microevolution of prokaryotes. 2009 , 37, D448-54		45
2147	Uncultivated Microorganisms. 2009 ,		6
2146	Microbial diversity in endostromatolites (cf. Fissure Calcretes) and in the surrounding permafrost landscape, Haughton impact structure region, Devon Island, Canada. 2009 , 9, 807-22		15
2145	Recent advances in molecular approaches to gut microbiota in inflammatory bowel disease. 2009 , 15, 2066-73		33
2144	Statistical methods for detecting differentially abundant features in clinical metagenomic samples. 2009 , 5, e1000352		1041
2143	Fast statistical alignment. 2009 , 5, e1000392		252
2142	Distribution and phylogeny of light-oxygen-voltage-blue-light-signaling proteins in the three kingdoms of life. 2009 , 191, 7234-42		79
2141	Phylogenetic signals in DNA composition: limitations and prospects. 2009 , 26, 1163-9		40
2140	Assessment of the diversity, abundance, and ecological distribution of members of candidate division SR1 reveals a high level of phylogenetic diversity but limited morphotypic diversity. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 4139-48	4.8	37

2139	Extensive phylogenetic analysis of a soil bacterial community illustrates extreme taxon evenness and the effects of amplicon length, degree of coverage, and DNA fractionation on classification and ecological parameters. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 668-75	4.8	45
2138	Evaluation of swine-specific PCR assays used for fecal source tracking and analysis of molecular diversity of swine-specific "bacteroidales" populations. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 5787-96	4.8	40
2137	Description of 'Synergistetes' phyl. nov. and emended description of the phylum 'Deferribacteres' and of the family Syntrophomonadaceae, phylum 'Firmicutes'. 2009 , 59, 1028-35		114
2136	Molecular biological detection and quantification of novel Fibrobacter populations in freshwater lakes. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 5148-52	4.8	18
2135	Methanosphaerula palustris gen. nov., sp. nov., a hydrogenotrophic methanogen isolated from a minerotrophic fen peatland. 2009 , 59, 928-35		80
2134	Antibiotic treatment of clostridium difficile carrier mice triggers a supershedder state, spore-mediated transmission, and severe disease in immunocompromised hosts. 2009 , 77, 3661-9		265
2133	GenGIS: A geospatial information system for genomic data. 2009 , 19, 1896-904		91
2132	Molecular diversity of Bacteroides spp. in human fecal microbiota as determined by group-specific 16S rRNA gene clone library analysis. 2009 , 32, 193-200		18
2131	Effects of seawater ozonation on biofilm development in aquaculture tanks. 2009 , 32, 266-77		46
2130	Candidatus Monilibacter spp., common bulking filaments in activated sludge, are members of Cluster III Defluviicoccus. 2009 , 32, 480-9		34
2129	Stratification of co-evolving genomic groups using ranked phylogenetic profiles. 2009 , 10, 355		6
2128	The oligonucleotide frequency derived error gradient and its application to the binning of metagenome fragments. 2009 , 10 Suppl 3, S10		12
2127	Microbial activity and diversity during extreme freeze-thaw cycles in periglacial soils, 5400 m elevation, Cordillera Vilcanota, Per". 2009 , 13, 807-16		61
2126	Characterisation of the effect of a simulated hydrocarbon spill on diazotrophs in mangrove sediment mesocosm. 2009 , 96, 343-54		28
2125	The characterization and composition of bacterial communities in soils blended with spent foundry sand. 2009 , 59, 239-246		5
2124	¹³ C-Isotopomer-based metabolomics of microbial groups isolated from two forest soils. 2009 , 5, 108-122		23
2123	Diverse archaeal community of a bat guano pile in Domica Cave (Slovak Karst, Slovakia). 2009 , 54, 436-46		15
2122	Functional shifts in unvegetated, perhumid, recently-deglaciated soils do not correlate with shifts in soil bacterial community composition. 2009 , 47, 673-81		64

21121	The diverse bacterial community in intertidal, anaerobic sediments at Sapelo Island, Georgia. 2009 , 58, 244-61	23
21120	Bacterial succession on the leaf surface: a novel system for studying successional dynamics. 2009 , 58, 189-98	169
21119	Achievements and new knowledge unraveled by metagenomic approaches. 2009 , 85, 265-76	148
21118	Litter quality is in the eye of the beholder: initial decomposition rates as a function of inoculum characteristics. 2009 , 23, 627-636	219
21117	The structure of the bacterial and archaeal community in a biogas digester as revealed by denaturing gradient gel electrophoresis and 16S rDNA sequencing analysis. 2009 , 106, 952-66	117
21116	Selective progressive response of soil microbial community to wild oat roots. 2009 , 3, 168-78	251
21115	Diversity rankings among bacterial lineages in soil. 2009 , 3, 305-13	89
21114	Environmental microarray analyses of Antarctic soil microbial communities. 2009 , 3, 340-51	130
21113	Determining the specific microbial populations and their spatial distribution within the stromatolite ecosystem of Shark Bay. 2009 , 3, 383-96	95
21112	Bacterial diversity and White Plague Disease-associated community changes in the Caribbean coral <i>Montastraea faveolata</i> . 2009 , 3, 512-21	287
21111	Phenology of high-elevation pelagic bacteria: the roles of meteorologic variability, catchment inputs and thermal stratification in structuring communities. 2009 , 3, 13-30	83
21110	Prokaryotic diversity, distribution, and insights into their role in biogeochemical cycling in marine basalts. 2009 , 3, 231-42	118
21109	Towards the definition of a core of microorganisms involved in anaerobic digestion of sludge. 2009 , 3, 700-14	584
21108	A novel symbiosis between chemoautotrophic bacteria and a freshwater cave amphipod. 2009 , 3, 935-43	81
21107	Abundance, composition, diversity and novelty of soil Proteobacteria. 2009 , 3, 992-1000	245
21106	Matriptase-deficient mice exhibit ichthyotic skin with a selective shift in skin microbiota. 2009 , 129, 2435-42	49
21105	A core gut microbiome in obese and lean twins. 2009 , 457, 480-4	5429
21104	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. 2009 , 462, 1056-60	803

2103	Microbial diversity in sediments associated with a shallow methane seep in the tropical Timor Sea of Australia reveals a novel aerobic methanotroph diversity. 2009 , 68, 142-51	32
2102	Diversity of bacteria associated with grassland soil nematodes of different feeding groups. 2009 , 69, 53-61	20
2101	Availability of glucose and light modulates the structure and function of a microbial biofilm. 2009 , 69, 27-42	59
2100	Effect of carbon addition and predation on acetate-assimilating bacterial cells in groundwater. 2009 , 70, 456-70	8
2099	Soil CO ₂ flux and photoautotrophic community composition in high-elevation, 'barren' soil. 2009 , 11, 674-86	65
2098	Microbial biodiversity of thermophilic communities in hot mineral soils of Tramway Ridge, Mount Erebus, Antarctica. 2009 , 11, 715-28	80
2097	A changing of the guard. 2009 , 11, 551-3	23
2096	Viability and potential for immigration of airborne bacteria from Africa that reach high mountain lakes in Europe. 2009 , 11, 1612-23	124
2095	Focus: Synergistetes. 2009 , 11, 1327-9	55
2094	Bacterial, archaeal and eukaryal community structures throughout soil horizons of harvested and naturally disturbed forest stands. 2009 , 11, 3045-62	143
2093	Characterization of marine isoprene-degrading communities. 2009 , 11, 3280-91	95
2092	Bacterial, archaeal and eukaryotic diversity of smooth and pustular microbial mat communities in the hypersaline lagoon of Shark Bay. 2009 , 7, 82-96	125
2091	Rhizosphere bacterial communities associated with disease suppressiveness stages of take-all decline in wheat monoculture. 2009 , 184, 694-707	115
2090	Isolation and characterization of different plant associated bacteria and their potential to degrade polychlorinated biphenyls. 2009 , 63, 667-672	51
2089	Characterization of microbial pathogens by DNA microarrays. 2009 , 9, 987-95	18
2088	Hydrolysis of fenamiphos and its toxic oxidation products by <i>Microbacterium</i> sp. in pure culture and groundwater. 2009 , 100, 2732-6	25
2087	Dominance of a clonal green sulfur bacterial population in a stratified lake. 2009 , 70, 30-41	42
2086	Fumarole-supported islands of biodiversity within a hyperarid, high-elevation landscape on Socoma Volcano, Puna de Atacama, Andes. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 735-47	4.8 120

2085	Culture-independent characterization of bacterial communities associated with the cold-water coral <i>Lophelia pertusa</i> in the northeastern Gulf of Mexico. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 2294-303	4.8	76
2084	Mapping the tree of life: progress and prospects. 2009 , 73, 565-76		174
2083	Diversity and stratification of archaea in a hypersaline microbial mat. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 1801-10	4.8	82
2082	The role of biofilms in the sedimentology of actively forming gypsum deposits at Guerrero Negro, Mexico. 2009 , 9, 875-93		25
2081	Biocorrosive thermophilic microbial communities in Alaskan North Slope oil facilities. 2009 , 43, 7977-84		162
2080	Biogeochemistry of iron oxidation in a circumneutral freshwater habitat. 2009 , 260, 149-158		73
2079	Degradation of 1,2-dichloroethane by microbial communities from river sediment at various redox conditions. 2009 , 43, 3207-16		36
2078	Characterization of microbial trophic structures of two anaerobic bioreactors processing sulfate-rich waste streams. 2009 , 43, 4451-60		25
2077	Assessment of phylogenetic diversity of bacterial microflora in drinking water using serial analysis of ribosomal sequence tags. 2009 , 43, 4197-206		53
2076	Metagenomic study of the oral microbiota by Illumina high-throughput sequencing. 2009 , 79, 266-71		248
2075	Characterization of airborne microbial communities at a high-elevation site and their potential to act as atmospheric ice nuclei. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 5121-30	4.8	231
2074	Testing the functional significance of microbial community composition. 2009 , 90, 441-51		505
2073	Microbial community profiling for human microbiome projects: Tools, techniques, and challenges. 2009 , 19, 1141-52		648
2072	Metagenomic pyrosequencing and microbial identification. 2009 , 55, 856-66		394
2071	Metagenomic approaches to natural products from free-living and symbiotic organisms. 2009 , 26, 1488-503		97
2070	Microbial processes in oil fields: culprits, problems, and opportunities. 2009 , 66, 141-251		241
2069	Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 7537-41	4.8	13777
2068	Prokaryotic genomes and diversity in surface ocean waters: interrogating the global ocean sampling metagenome. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 2221-9	4.8	144

2067	Comparison of species richness estimates obtained using nearly complete fragments and simulated pyrosequencing-generated fragments in 16S rRNA gene-based environmental surveys. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 5227-36	4.8	287
2066	Identification of phytodetritus-degrading microbial communities in sublittoral Gulf of Mexico sands. 2009 , 54, 1073-1083		40
2065	Role of the protozoan <i>Isotricha prostoma</i> , liquid-, and solid-associated bacteria in rumen biohydrogenation of linoleic acid. 2009 , 3, 961-71		20
2064	Approaches to analyse dynamic microbial communities such as those seen in cystic fibrosis lung. 2009 , 3, 246-56		10
2063	Studies on monitoring and tracking genetic resources: an executive summary. 2009 , 1, 78-86		6
2062	Bacterial Diversity in <i>Amblyomma americanum</i> (Acari: Ixodidae) With a Focus on Members of the Genus <i>Rickettsia</i> . 2010 , 47, 258-268		70
2061	Non-contiguous finished genome sequence of <i>Aminomonas paucivorans</i> type strain (GLU-3). 2010 , 3, 285-93		8
2060	Complete genome sequence of <i>Ilyobacter polytropus</i> type strain (CuHbu1). 2010 , 3, 304-14		7
2059	Complete genome sequence of <i>Nocardiopsis dassonvillei</i> type strain (IMRU 509). 2010 , 3, 325-36		27
2058	Complete genome sequence of <i>Arcanobacterium haemolyticum</i> type strain (11018). 2010 , 3, 126-35		7
2057	Complete genome sequence of <i>Spirochaeta smaragdinae</i> type strain (SEBR 4228). 2010 , 3, 136-44		15
2056	Complete genome sequence of 'Thermobaculum terrenum' type strain (YNP1). 2010 , 3, 153-62		9
2055	Complete genome sequence of <i>Syntrophothermus lipocalidus</i> type strain (TGB-C1). 2010 , 3, 268-75		10
2054	Complete genome sequence of <i>Desulfarculus baarsii</i> type strain (2st14). 2010 , 3, 276-84		27
2053	Complete genome sequence of <i>Intrasporangium calvum</i> type strain (7 KIP). 2010 , 3, 294-303		4
2052	Complete genome sequence of <i>Methanothermus fervidus</i> type strain (V24S). 2010 , 3, 315-24		14
2051	Complete genome sequence of <i>Thermaerobacter marianensis</i> type strain (7p75a). 2010 , 3, 337-45		7
2050	Microbial Ecology of Activated Sludge. 2010 , 9,		76

2049	The bacteriology of pouchitis: a molecular phylogenetic analysis using 16S rRNA gene cloning and sequencing. 2010 , 252, 90-8	85
2048	Altitudinal changes in a bacterial community on Gulkana Glacier in Alaska. 2010 , 25, 171-82	28
2047	Factors promoting microbial diversity in the McMurdo Dry Valleys, Antarctica. 221-257	16
2046	Vegetation affects the relative abundances of dominant soil bacterial taxa and soil respiration rates in an upland grassland soil. 2010 , 59, 335-43	84
2045	Robustness of the bacterial community in the cabbage white butterfly larval midgut. 2010 , 59, 199-211	96
2044	Microbial diversity in uranium mining-impacted soils as revealed by high-density 16S microarray and clone library. 2010 , 59, 94-108	89
2043	Microbial population and activity in wetland microcosms constructed for improving treated municipal wastewater. 2010 , 59, 700-9	47
2042	The influence of different land uses on the structure of archaeal communities in Amazonian anthrosols based on 16S rRNA and amoA genes. 2010 , 59, 734-43	49
2041	Discovery of commonly existing anode biofilm microbes in two different wastewater treatment MFCs using FLX Titanium pyrosequencing. 2010 , 87, 2335-43	66
2040	Structure and dynamics of the microbial communities underlying the carboxylate platform for biofuel production. 2010 , 88, 389-99	28
2039	Biodiversity of air-borne microorganisms at Halley Station, Antarctica. 2010 , 14, 145-59	51
2038	Diversity and identification of methanogenic archaea and sulphate-reducing bacteria in sediments from a pristine tropical mangrove. 2010 , 97, 401-11	57
2037	Microbial community response to a simulated hydrocarbon spill in mangrove sediments. 2010 , 48, 7-15	58
2036	Sea-land transitions in isopods: pattern of symbiont distribution in two species of intertidal isopods <i>Ligia pallasii</i> and <i>Ligia occidentalis</i> in the Eastern Pacific. 2010 , 51, 107-116	9
2035	Biocidal Activities of Cationic Surface Active Starch and Its Transition Metal Complexes Against Different Bacterial Strains. 2010 , 13, 255-260	4
2034	Microbial consumption and production of volatile organic compounds at the soil-litter interface. 2010 , 99, 97-107	78
2033	Microbial communities of arboreal and ground soils in the Esquinas rainforest, Costa Rica. 2010 , 329, 65-74	19
2032	Bacterial community of very wet and acidic subalpine forest and fire-induced grassland soils. 2010 , 332, 417-427	9

2031	Development of soil microbial communities during tallgrass prairie restoration. 2010 , 42, 302-312	73
2030	Effect of the nitrification inhibitor dicyandiamide (DCD) on microbial communities in a pasture soil amended with bovine urine. 2010 , 42, 1425-1436	112
2029	Molecular characterization of chromium (VI) reducing potential in Gram positive bacteria isolated from contaminated sites. 2010 , 42, 1857-1863	70
2028	Bacterioplankton diversity and community composition in the Southern Lagoon of Venice. 2010 , 33, 128-38	27
2027	En route to a genome-based classification of Archaea and Bacteria?. 2010 , 33, 175-82	251
2026	Alignment and clustering of phylogenetic markers--implications for microbial diversity studies. 2010 , 11, 152	53
2025	Introducing W.A.T.E.R.S.: a workflow for the alignment, taxonomy, and ecology of ribosomal sequences. 2010 , 11, 317	26
2024	VITCOMIC: visualization tool for taxonomic compositions of microbial communities based on 16S rRNA gene sequences. 2010 , 11, 332	22
2023	Phylometrics: a pipeline for inferring phylogenetic trees from a sequence relationship network perspective. 2010 , 11 Suppl 6, S18	0
2022	Planctomycetes dominate biofilms on surfaces of the kelp <i>Laminaria hyperborea</i> . 2010 , 10, 261	151
2021	Selection of candidate probionts by two different screening strategies from Atlantic cod (<i>Gadus morhua</i> L.) larvae. 2010 , 144, 153-9	81
2020	16S rRNA GENE HETEROGENEITY IN THE FILAMENTOUS MARINE CYANOBACTERIAL GENUS LYNGBYA1. 2010 , 46, 591-601	54
2019	Prevalence and diversity of microbes in the amniotic fluid, the fetal inflammatory response, and pregnancy outcome in women with preterm pre-labor rupture of membranes. 2010 , 64, 38-57	209
2018	Novel strains isolated from a coastal aquifer suggest a predatory role for flavobacteria. 2010 , 73, 254-70	26
2017	Molecular profiling and identification of methanogenic archaeal species from rabbit caecum. 2010 , 74, 623-30	30
2016	Effect of storage conditions on the assessment of bacterial community structure in soil and human-associated samples. 2010 , 307, 80-6	274
2015	Material-dependent growth of human skin bacteria on textiles investigated using challenge tests and DNA genotyping. 2010 , 108, 450-61	43
2014	Characterization of an enrichment culture debrominating tetrabromobisphenol A and optimization of its activity under anaerobic conditions. 2010 , 109, 707-715	25

2013	Taxonomic and functional diversity of atrazine-degrading bacterial communities enriched from agrochemical factory soil. 2010 , 109, 355-67	31
2012	Subsurface ecosystem resilience: long-term attenuation of subsurface contaminants supports a dynamic microbial community. 2010 , 4, 131-43	61
2011	Successional changes in bacterial communities during the development of black band disease on the reef coral, <i>Montipora hispida</i> . 2010 , 4, 203-14	82
2010	Global ecological patterns in uncultured Archaea. 2010 , 4, 182-90	312
2009	Diversity and abundance of Korarchaeota in terrestrial hot springs of Iceland and Kamchatka. 2010 , 4, 346-56	50
2008	Distinct flavobacterial communities in contrasting water masses of the north Atlantic Ocean. 2010 , 4, 472-87	119
2007	Developmental microbial ecology of the crop of the folivorous hoatzin. 2010 , 4, 611-20	47
2006	Experimental factors affecting PCR-based estimates of microbial species richness and evenness. 2010 , 4, 642-7	438
2005	Microbial community genomics in eastern Mediterranean Sea surface waters. 2010 , 4, 78-87	55
2004	Fast UniFrac: facilitating high-throughput phylogenetic analyses of microbial communities including analysis of pyrosequencing and PhyloChip data. 2010 , 4, 17-27	869
2003	Viral and microbial community dynamics in four aquatic environments. 2010 , 4, 739-51	305
2002	Bacterial diversity in the oral cavity of 10 healthy individuals. 2010 , 4, 962-74	428
2001	Postprandial remodeling of the gut microbiota in Burmese pythons. 2010 , 4, 1375-85	181
2000	Functional genomic signatures of sponge bacteria reveal unique and shared features of symbiosis. 2010 , 4, 1557-67	206
1999	Microbial community dynamics in a seasonally anoxic fjord: Saanich Inlet, British Columbia. 2010 , 12, 172-91	157
1998	Bacterial community shifts in taxa and diversity in response to localized organic loading in the deep sea. 2010 , 12, 344-63	56
1997	Microclimate and limits to photosynthesis in a diverse community of hypolithic cyanobacteria in northern Australia. 2010 , 12, 592-607	59
1996	Relationship between cystic fibrosis respiratory tract bacterial communities and age, genotype, antibiotics and <i>Pseudomonas aeruginosa</i> . 2010 , 12, 1293-303	183

1995	The effect of nutrient deposition on bacterial communities in Arctic tundra soil. 2010 , 12, 1842-54		231
1994	Halophilic archaea in the human intestinal mucosa. 2010 , 12, 2398-410		84
1993	The genome of <i>Syntrophomonas wolfei</i> : new insights into syntrophic metabolism and biohydrogen production. 2010 , 12, 2289-301		120
1992	Methanogenesis, sulfate reduction and crude oil biodegradation in hot Alaskan oilfields. 2010 , 12, 3074-86		135
1991	Thermoanaerobacteriaceae oxidize acetate in methanogenic rice field soil at 50°C. 2010 , 12, 2341-54		49
1990	454-pyrosequencing: a molecular batterscope for freshwater viral ecology. 2010 , 1, 210-26		11
1989	Identification of carbohydrate metabolism genes in the metagenome of a marine biofilm community shown to be dominated by gammaproteobacteria and bacteroidetes. 2010 , 1, 371-84		62
1988	An insect herbivore microbiome with high plant biomass-degrading capacity. 2010 , 6, e1001129		172
1987	Threatened corals provide underexplored microbial habitats. 2010 , 5, e9554		219
1986	Robust computational analysis of rRNA hypervariable tag datasets. 2010 , 5, e15220		14
1985	Archaeal and bacterial communities respond differently to environmental gradients in anoxic sediments of a California hypersaline lake, the Salton Sea. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 757-68	4.8	93
1984	Infrequent transitions between saline and fresh waters in one of the most abundant microbial lineages (SAR11). 2010 , 27, 347-57		55
1983	Forensic identification using skin bacterial communities. 2010 , 107, 6477-81		414
1982	Reclassification of the polyphyletic genus <i>Prosthecomicrobium</i> to form two novel genera, <i>Vasilyevaea</i> gen. nov. and <i>Bauldia</i> gen. nov. with four new combinations: <i>Vasilyevaea enhydra</i> comb. nov., <i>Vasilyevaea mishustinii</i> comb. nov., <i>Bauldia consociata</i> comb. nov. and <i>Bauldia litoralis</i> comb. nov. 2010 , 60, 2968-2966		21
1981	The bacterial microbiota in the oral mucosa of rural Amerindians. 2010 , 156, 3282-3287		56
1980	Reshaping the gut microbiome with bacterial transplantation and antibiotic intake. 2010 , 20, 1411-9		235
1979	Community structure of subsurface biofilms in the thermal sulfidic caves of Acquasanta Terme, Italy. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 5902-10	4.8	46
1978	Exploring the role of microorganisms in the disease-like syndrome affecting the sponge <i>Ianthella basta</i> . <i>Applied and Environmental Microbiology</i> , 2010 , 76, 5736-44	4.8	48

1977	Characterization of bacterial community structure in a drinking water distribution system during an occurrence of red water. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 7171-80	4.8	90
1976	Adaptation to herbivory by the Tammar wallaby includes bacterial and glycoside hydrolase profiles different from other herbivores. 2010 , 107, 14793-8		163
1975	Ribosomal RNA diversity predicts genome diversity in gut bacteria and their relatives. 2010 , 38, 3869-79		74
1974	Advanced computational algorithms for microbial community analysis using massive 16S rRNA sequence data. 2010 , 38, e205		37
1973	TaxCollector: Modifying Current 16S rRNA Databases for the Rapid Classification at Six Taxonomic Levels. 2010 , 2, 1015-1025		49
1972	PlutoFBI Web Based Workbench for Ecological and Taxonomic Research, with an Online Implementation for Fungal ITS Sequences. 2010 , 6, EBO.S6271		144
1971	<i>Streptococcus gallolyticus</i> subspecies <i>pasteurianus</i> (biotype II/2), a newly reported cause of adult meningitis. 2010 , 48, 2247-9		28
1970	Sequence transformation to a complex signature form for consistent phylogenetic tree using Extensible Markov Model. 2010 ,		1
1969	Bacterial diversity in <i>Amblyomma americanum</i> (Acari: Ixodidae) with a focus on members of the genus <i>Rickettsia</i> . 2010 , 47, 258-68		52
1968	Application of molecular techniques to elucidate the influence of cellulosic waste on the bacterial community structure at a simulated low-level-radioactive-waste site. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 3106-15	4.8	32
1967	Vertical distribution of ammonia-oxidizing crenarchaeota and methanogens in the epipelagic waters of Lake Kivu (Rwanda-Democratic Republic of the Congo). <i>Applied and Environmental Microbiology</i> , 2010 , 76, 6853-63	4.8	75
1966	Subseafloor Ocean Crust Microbial Observatories: Development of FLOCS (Flow-through Osmo Colonization System) and Evaluation of Borehole Construction Materials. 2010 , 27, 143-157		46
1965	Expansion of the protein repertoire in newly explored environments: human gut microbiome specific protein families. 2010 , 6, e1000798		48
1964	The microbiota mediates pathogen clearance from the gut lumen after non-typhoidal <i>Salmonella</i> diarrhea. 2010 , 6, e1001097		252
1963	Like will to like: abundances of closely related species can predict susceptibility to intestinal colonization by pathogenic and commensal bacteria. 2010 , 6, e1000711		304
1962	Comparative metagenomics and population dynamics of the gut microbiota in mother and infant. 2010 , 2, 53-66		176
1961	A primer on metagenomics. 2010 , 6, e1000667		412
1960	Cyanobacterial communities on Qiyi glacier, Qilian Shan, China. 2010 , 51, 135-144		23

1959	Phylogenetic evidence of noteworthy microflora from the subsurface of the former Homestake gold mine, Lead, South Dakota. 2010 , 31, 979-91	6
1958	Comparative analyses of the bacterial microbiota of the human nostril and oropharynx. 2010 , 1,	213
1957	The human oral microbiome. 2010 , 192, 5002-17	1929
1956	The effects of alignment quality, distance calculation method, sequence filtering, and region on the analysis of 16S rRNA gene-based studies. 2010 , 6, e1000844	257
1955	Diversity of benzyl- and alkylsuccinate synthase genes in hydrocarbon-impacted environments and enrichment cultures. 2010 , 44, 7287-94	137
1954	Unlocking Environmental DNA Derived Gene Clusters Using a Metagenomics Approach. 2010 , 455-474	1
1953	Bacterial communities in two Antarctic ice cores analyzed by 16S rRNA gene sequencing analysis. 2010 , 4, 215-227	41
1952	Diversity of rock varnish bacterial communities from Black Canyon, New Mexico. 2010 , 115, n/a-n/a	53
1951	A persistent and diverse airway microbiota present during chronic obstructive pulmonary disease exacerbations. 2010 , 14, 9-59	178
1950	Identification of species by multiplex analysis of variable-length sequences. 2010 , 38, e203	42
1949	A global network of coexisting microbes from environmental and whole-genome sequence data. 2010 , 20, 947-59	305
1948	Microbial community transcriptomes reveal microbes and metabolic pathways associated with dissolved organic matter turnover in the sea. 2010 , 107, 16420-7	297
1947	V-Xtractor: an open-source, high-throughput software tool to identify and extract hypervariable regions of small subunit (16S/18S) ribosomal RNA gene sequences. 2010 , 83, 250-3	93
1946	Endotracheal tube biofilm inoculation of oral flora and subsequent colonization of opportunistic pathogens. 2010 , 300, 503-11	55
1945	Bacterial communities from soil sediments of a mountain oasis in northern Oman. 2010 , 82, 102-111	2
1944	Identification of bacterial populations in drinking water using 16S rRNA-based sequence analyses. 2010 , 44, 1353-60	83
1943	Pyrosequencing of the 16S rRNA gene to reveal bacterial pathogen diversity in biosolids. 2010 , 44, 4252-60	127
1942	Delivery mode shapes the acquisition and structure of the initial microbiota across multiple body habitats in newborns. 2010 , 107, 11971-5	2914

1941	Microbial Diversity of Cave Ecosystems. 2010 , 219-238		38
1940	Indigenous ectosymbiotic bacteria associated with diverse hydrothermal vent invertebrates. 2010 , 2, 479-88		56
1939	Sediment-associated microdiversity within the Marine Group I Crenarchaeota. 2010 , 2, 693-703		65
1938	Novel microbial diversity retrieved by autonomous robotic exploration of the world's deepest vertical phreatic sinkhole. 2010 , 10, 201-13		27
1937	From structure to function: the ecology of host-associated microbial communities. 2010 , 74, 453-76		251
1936	PyNASt: a flexible tool for aligning sequences to a template alignment. 2010 , 26, 266-7		2728
1935	Ecophysiology of Fe-cycling bacteria in acidic sediments. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 8174-83	4.8	106
1934	Detection of prokaryotic cells with fluorescence in situ hybridization. 2010 , 659, 349-62		3
1933	Clone Libraries of Ribosomal RNA Gene Sequences for Characterization of Bacterial and Fungal Communities. 2010 , 3969-3993		8
1932	High Performance Computing in Science and Engineering, Garching/Munich 2009. 2010 ,		3
1931	Identification and Quantification of Abundant Species from Pyrosequences of 16S rRNA by Consensus Alignment. 2011 , 2010, 153-157		72
1930	Ecological role of a seaweed secondary metabolite for a colonizing bacterial community. 2011 , 27, 579-88		30
1929	Microbial Mobilization of Major and Trace Elements from Catchment Rock Samples of a High Mountain Lake in the European Alps. 2011 , 43, 465-473		5
1928	An Open-source Collaboration Environment for Metagenomics Research. 2011 ,		1
1927	PTPan--overcoming memory limitations in oligonucleotide string matching for primer/probe design. 2011 , 27, 2797-805		2
1926	Parallel Metagenomic Sequence Clustering Via Sketching and Maximal Quasi-clique Enumeration on Map-Reduce Clouds. 2011 ,		10
1925	rCAD: A Novel Database Schema for the Comparative Analysis of RNA. 2011 , 2011, 15-22		5
1924	Partial genome assembly for a candidate division OP11 single cell from an anoxic spring (Zodletone Spring, Oklahoma). <i>Applied and Environmental Microbiology</i> , 2011 , 77, 7804-14	4.8	55

1923	Analysis of streptococcal CRISPRs from human saliva reveals substantial sequence diversity within and between subjects over time. 2011 , 21, 126-36		90
1922	Metabolite-based mutualism between <i>Pseudomonas aeruginosa</i> PA14 and <i>Enterobacter aerogenes</i> enhances current generation in bioelectrochemical systems. 2011 , 4, 4550		94
1921	PCR amplification-independent methods for detection of microbial communities by the high-density microarray PhyloChip. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 6313-22	4.8	62
1920	Effects of the antimicrobial sulfamethoxazole on groundwater bacterial enrichment. 2011 , 45, 3096-101		147
1919	Hydrocarbon-degrading bacteria and the bacterial community response in gulf of Mexico beach sands impacted by the deepwater horizon oil spill. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 7962-74	4.8	609
1918	Airway microbiota and bronchial hyperresponsiveness in patients with suboptimally controlled asthma. 2011 , 127, 372-381.e1-3		486
1917	Diversity of 23S rRNA Genes within Individual Prokaryotic Genomes. 2011 , 17-27		
1916	The Enduring Legacy of Small Subunit rRNA in Microbiology. 2011 , 123-128		1
1915	The Metagenomics RAST Server: A Public Resource for the Automatic Phylogenetic and Functional Analysis of Metagenomes. 2011 , 325-331		24
1914	SILVA: Comprehensive Databases for Quality Checked and Aligned Ribosomal RNA Sequence Data Compatible with ARB. 2011 , 393-398		3
1913	The PhyloWARE Project: A Software Framework for Phylogenomic Virtue. 2011 , 407-416		3
1912	Identification of a novel subgroup of uncultured gammaproteobacterial glycogen-accumulating organisms in enhanced biological phosphorus removal sludge. 2011 , 157, 2287-2296		10
1911	Application of Phylogenetic Oligonucleotide Microarrays in Microbial Analysis. 2011 , 551-566		1
1910	Novelty and Uniqueness Patterns of Rare Members of the Soil Biosphere. 2011 , 143-150		
1909	Extensive Phylogenetic Analysis of a Soil Bacterial Community Illustrates Extreme Taxon Evenness and the Effects of Amplicon Length, Degree of Coverage, and DNA Fractionation on Classification and Ecological Parameters. 2011 , 151-163		
1908	Bacterial Community Structure and Dynamics in a Seasonally Anoxic Fjord: Saanich Inlet, British Columbia. 2011 , 253-267		10
1907	Ecology drives a global network of gene exchange connecting the human microbiome. 2011 , 480, 241-4		573
1906	3 Environmental DNA Analysis and the Expansion of the Fungal Tree of Life. 2011 , 37-54		7

1905	Pathogenic bacteria in sewage treatment plants as revealed by 454 pyrosequencing. 2011 , 45, 7173-9		164
1904	Parallel-META: A high-performance computational pipeline for metagenomic data analysis. 2011 ,		1
1903	Community Analysis-Based Methods. 2011 , 251-282		6
1902	Microbial Source Tracking: Methods, Applications, and Case Studies. 2011 ,		47
1901	Assessing and improving methods used in operational taxonomic unit-based approaches for 16S rRNA gene sequence analysis. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 3219-26	4.8	497
1900	Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons. 2011 , 21, 494-504		2174
1899	A bioinformatics pipeline for sequence-based analyses of fungal biodiversity. 2011 , 722, 141-55		22
1898	Metagenomic analyses: past and future trends. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 1153-618		490
1897	The Use of rRNA Gene Sequence Data in the Classification and Identification of Prokaryotes. 2011 , 349-384		4
1896	Moving pictures of the human microbiome. 2011 , 12, R50		723
1895	EMIRGE: reconstruction of full-length ribosomal genes from microbial community short read sequencing data. 2011 , 12, R44		256
1894	Capture of Planktonic Microbial Diversity in Fractures by Long-Term Monitoring of Flowing Boreholes, Evander Basin, South Africa. 2011 , 28, 275-300		25
1893	Isolation of Succinivibrionaceae implicated in low methane emissions from Tammar wallabies. 2011 , 333, 646-8		119
1892	Metagenomic analysis of a permafrost microbial community reveals a rapid response to thaw. 2011 , 480, 368-71		499
1891	Application of leftover sample material from waterborne protozoa monitoring for the molecular detection of Bacteroidales and fecal source tracking markers. 2011 , 86, 337-43		6
1890	Analysis of the bacterial community in a laboratory-scale nitrification reactor and a wastewater treatment plant by 454-pyrosequencing. 2011 , 45, 4390-8		203
1889	Fine-scale bacterial community dynamics and the taxa-time relationship within a full-scale activated sludge bioreactor. 2011 , 45, 5476-88		117
1888	A novel method for determining microflora composition using dynamic phylogenetic analysis of 16S ribosomal RNA deep sequencing data. 2011 , 98, 253-9		9

1887	Complete genome sequence of the filamentous gliding predatory bacterium <i>Herpetosiphon aurantiacus</i> type strain (114-95(T)). 2011 , 5, 356-70	35
1886	<i>Chthonomonas calidirosea</i> gen. nov., sp. nov., an aerobic, pigmented, thermophilic micro-organism of a novel bacterial class, <i>Chthonomonadetes classis</i> nov., of the newly described phylum <i>Armatimonadetes</i> originally designated candidate division OP10. 2011 , 61, 2482-2490	50
1885	The activated sludge bulking filament Eikelboom morphotype 0914 is a member of the Chloroflexi. 2011 , 3, 159-65	18
1884	Compositional differences in particle-associated and free-living microbial assemblages from an extreme deep-ocean environment. 2011 , 3, 449-58	122
1883	The larval sponge holobiont exhibits high thermal tolerance. 2011 , 3, 756-62	48
1882	Transitions in bacterial communities along the 2000 km salinity gradient of the Baltic Sea. 2011 , 5, 1571-9	1381
1881	Probing individual environmental bacteria for viruses by using microfluidic digital PCR. 2011 , 333, 58-62	171
1880	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing β standard operating procedure, version 1.0. 2011 ,	3
1879	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing β standard operating procedure, version 1.0. 2011 ,	
1878	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing β standard operating procedure, version 1.0. 2011 ,	3
1877	High prevalence of DNA from non- <i>H. pylori</i> helicobacters in the gastric mucosa of Venezuelan pet dogs and its histological alterations. 2011 , 53, 207-12	9
1876	Studying the Enteric Microbiome in Inflammatory Bowel Diseases: Getting through the Growing Pains and Moving Forward. 2011 , 2, 144	19
1875	Tidying up international nucleotide sequence databases: ecological, geographical and sequence quality annotation of its sequences of mycorrhizal fungi. 2011 , 6, e24940	46
1874	Stalking the fourth domain in metagenomic data: searching for, discovering, and interpreting novel, deep branches in marker gene phylogenetic trees. 2011 , 6, e18011	72
1873	Characterization of trapped lignin-degrading microbes in tropical forest soil. 2011 , 6, e19306	143
1872	Application of two-part statistics for comparison of sequence variant counts. 2011 , 6, e20296	38
1871	Exploring the diversity of <i>Gardnerella vaginalis</i> in the genitourinary tract microbiota of monogamous couples through subtle nucleotide variation. 2011 , 6, e26732	147
1870	Branched chain fatty acids reduce the incidence of necrotizing enterocolitis and alter gastrointestinal microbial ecology in a neonatal rat model. 2011 , 6, e29032	113

1869	Ecological and Clinical Consequences of Antibiotic Subsistence by Environmental Microbes. 2011 , 29-41	3
1868	Microbial communities of the upper respiratory tract and otitis media in children. 2011 , 2, e00245-10	146
1867	Development of a Novel Strategy to Cultivate Enhanced Biological Phosphorus Removal (EBPR) Microorganisms. 2011 , 2011, 4833-4851	1
1866	Complete genome sequence of <i>Leadbetterella byssophila</i> type strain (4M15). 2011 , 4, 2-12	15
1865	Complete genome sequence of <i>Hydrogenobacter thermophilus</i> type strain (TK-6). 2011 , 4, 131-43	8
1864	Complete genome sequence of <i>Paludibacter propionigenes</i> type strain (WB4). 2011 , 4, 36-44	24
1863	Complete genome sequence of <i>Bacteroides helcogenes</i> type strain (P 36-108). 2011 , 4, 45-53	7
1862	Complete genome sequence of <i>Weeksella virosa</i> type strain (9751). 2011 , 4, 81-90	8
1861	Complete genome sequence of <i>Desulfobulbus propionicus</i> type strain (1pr3). 2011 , 4, 100-10	39
1860	Complete genome sequence of <i>Marivirga tractuosa</i> type strain (H-43). 2011 , 4, 154-62	15
1859	Complete genome sequence of <i>Desulfurococcus mucosus</i> type strain (O7/1). 2011 , 4, 173-82	9
1858	Complete genome sequence of <i>Cellulophaga lytica</i> type strain (LIM-21). 2011 , 4, 221-32	23
1857	Non-contiguous finished genome sequence of <i>Bacteroides coprosuis</i> type strain (PC139). 2011 , 4, 233-43	4
1856	Complete genome sequence of <i>Rhodospirillum rubrum</i> type strain (S1). 2011 , 4, 293-302	31
1855	Complete genome sequence of the extremely halophilic <i>Halanaerobium praevalens</i> type strain (GSL). 2011 , 4, 312-21	24
1854	Complete genome sequence of <i>Nitratifactor salsuginis</i> type strain (E9I37-1). 2011 , 4, 322-30	10
1853	Complete genome sequence of <i>Mahella australiensis</i> type strain (50-1 BON). 2011 , 4, 331-41	6
1852	Complete genome sequence of <i>Treponema succinifaciens</i> type strain (6091). 2011 , 4, 361-70	20

1851	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FLGlyRT). 2011 , 4, 371-380	9
1850	Complete genome sequence of the hyperthermophilic chemolithoautotroph <i>Pyrolobus fumarii</i> type strain (1A). 2011 , 4, 381-92	10
1849	Complete genome sequence of the acetate-degrading sulfate reducer <i>Desulfobacca acetoxidans</i> type strain (ASRB2). 2011 , 4, 393-401	19
1848	Complete genome sequence of the thermophilic, hydrogen-oxidizing <i>Bacillus tusciae</i> type strain (T2) and reclassification in the new genus, <i>Kyrpidia</i> gen. nov. as <i>Kyrpidia tusciae</i> comb. nov. and emendation of the family <i>Alicyclobacillaceae</i> da Costa and Rainey, 2010. 2011 , 5, 121-34	35
1847	Complete genome sequence of the gliding, heparinolytic <i>Pedobacter saltans</i> type strain (113). 2011 , 5, 30-40	11
1846	Non-contiguous finished genome sequence of the opportunistic oral pathogen <i>Prevotella multisaccharivorax</i> type strain (PPPA20). 2011 , 5, 41-9	2
1845	Complete genome sequence of <i>Tolomonas auensis</i> type strain (TA 4). 2011 , 5, 112-20	4
1844	Complete genome sequence of <i>Hirschia baltica</i> type strain (IFAM 1418(T)). 2011 , 5, 287-97	8
1843	Complete genome sequence of the halophilic and highly halotolerant <i>Chromohalobacter salexigens</i> type strain (1H11(T)). 2011 , 5, 379-88	28
1842	Genome sequence of the filamentous, gliding <i>Thiothrix nivea</i> neotype strain (JP2(T)). 2011 , 5, 398-406	9
1841	Complete genome sequence of the thermophilic sulfur-reducer <i>Desulfurobacterium thermolithotrophum</i> type strain (BSA(T)) from a deep-sea hydrothermal vent. 2011 , 5, 407-15	10
1840	Complete genome sequence of <i>Calditerrivibrio nitroreducens</i> type strain (Yu37-1). 2011 , 4, 54-62	9
1839	Complete genome sequence of <i>Truepera radiovictrix</i> type strain (RQ-24). 2011 , 4, 91-9	37
1838	The Viral MetaGenome Annotation Pipeline (VMGAP): an automated tool for the functional annotation of viral Metagenomic shotgun sequencing data. 2011 , 4, 418-29	35
1837	Complete genome sequence of <i>Bacteroides salanitronis</i> type strain (BL78). 2011 , 4, 191-9	8
1836	Complete genome sequence of <i>Odoribacter splanchnicus</i> type strain (1651/6). 2011 , 4, 200-9	62
1835	Complete genome sequence of <i>Oceanithermus profundus</i> type strain (506). 2011 , 4, 210-20	3
1834	Complete genome sequence of <i>Tsukamurella paurometabola</i> type strain (no. 33). 2011 , 4, 342-51	8

1833	Non-contiguous finished genome sequence and contextual data of the filamentous soil bacterium <i>Ktedonobacter racemifer</i> type strain (SOSP1-21). 2011 , 5, 97-111	72
1832	Complete genome sequence of <i>Isosphaera pallida</i> type strain (IS1B). 2011 , 4, 63-71	40
1831	Complete genome sequence of <i>Cellulophaga algicola</i> type strain (IC166). 2011 , 4, 72-80	22
1830	Complete genome sequence of <i>Riemerella anatipestifer</i> type strain (ATCC 11845T). 2011 , 4, 144-153	26
1829	Complete genome sequence of the thermophilic sulfur-reducer <i>Hippea maritima</i> type strain (MH(2)). 2011 , 4, 303-11	6
1828	Complete genome sequence of <i>Haliscomenobacter hydrossis</i> type strain (O). 2011 , 4, 352-60	17
1827	Complete genome sequence of the gliding freshwater bacterium <i>Fluviicola taffensis</i> type strain (RW262). 2011 , 5, 21-9	19
1826	Genome sequence of the moderately thermophilic halophile <i>Flexistipes sinusarabici</i> strain (MAS10). 2011 , 5, 86-96	8
1825	Phylogenetic Binning of Metagenome Sequence Samples. 2011 , 353-358	
1824	16S rRNA gene microarray analysis of microbial communities in ethanol-stimulated subsurface sediment. 2011 , 26, 261-5	2
1823	Differential growth responses of soil bacterial taxa to carbon substrates of varying chemical recalcitrance. 2011 , 2, 94	333
1822	Complete genome sequence of <i>Deinococcus maricopensis</i> type strain (LB-34). 2011 , 4, 163-72	11
1821	Evolutionary trade-offs among decomposers determine responses to nitrogen enrichment. 2011 , 14, 933-8	60
1820	Non-target sites with single nucleotide insertions or deletions are frequently found in 16S rRNA sequences and can lead to false positives in fluorescence in situ hybridization (FISH). 2011 , 13, 33-47	19
1819	Global patterns in the biogeography of bacterial taxa. 2011 , 13, 135-144	279
1818	A comparative molecular analysis of water-filled limestone sinkholes in north-eastern Mexico. 2011 , 13, 226-240	19
1817	Acidobacteria, Rubrobacteridae and Chloroflexi are abundant among very slow-growing and mini-colony-forming soil bacteria. 2011 , 13, 798-805	118
1816	Seasonal differences in bacterial community composition following nutrient additions in a eutrophic lake. 2011 , 13, 887-99	66

1815	Ribosomal tag pyrosequencing of DNA and RNA from benthic coral reef microbiota: community spatial structure, rare members and nitrogen-cycling guilds. 2011 , 13, 1138-52	78
1814	Microbial communities in bulk fluids and biofilms of an oil facility have similar composition but different structure. 2011 , 13, 1078-90	47
1813	Archaeal diversity along a subterranean salt core from the Salar Grande (Chile). 2011 , 13, 2105-21	66
1812	The bacterial biogeography of British soils. 2011 , 13, 1642-54	564
1811	Ammonia oxidation, denitrification and dissimilatory nitrate reduction to ammonium in two US Great Basin hot springs with abundant ammonia-oxidizing archaea. 2011 , 13, 2371-86	83
1810	Microbial diversity and stratification of South Pacific abyssal marine sediments. 2011 , 13, 3219-34	101
1809	On the suitability of short reads of 16S rRNA for phylogeny-based analyses in environmental surveys. 2011 , 13, 3000-9	44
1808	Molecular diversity of the foregut bacteria community in the dromedary camel (<i>Camelus dromedarius</i>). 2011 , 13, 3024-35	42
1807	Microbial community composition and dynamics in a semi-industrial-scale facility operating under the MixAlcoBioconversion platform. 2011 , 110, 587-96	17
1806	Molecular analysis of the prevalent microbiota of human male and female forehead skin compared to forearm skin and the influence of make-up. 2011 , 110, 1381-9	64
1805	Selection of antagonistic bacteria isolated from the <i>Physalis peruviana</i> rhizosphere against <i>Fusarium oxysporum</i> . 2011 , 111, 707-16	20
1804	The methane cycle in ferruginous Lake Matano. 2011 , 9, 61-78	141
1803	Low temperature S(0) biomineralization at a supraglacial spring system in the Canadian High Arctic. 2011 , 9, 360-75	28
1802	Carotenoid biomarkers as an imperfect reflection of the anoxygenic phototrophic community in meromictic Fayetteville Green Lake. 2011 , 9, 321-9	44
1801	Viral metagenome analysis to guide human pathogen monitoring in environmental samples. 2011 , 52, 386-92	74
1800	Evidence of compositional differences between the extracellular and intracellular DNA of a granular sludge biofilm. 2011 , 53, 1-7	8
1799	Development of a colorimetric colony-screening assay for detection of defluorination by micro-organisms. 2011 , 53, 417-23	6
1798	V-REVCOMP: automated high-throughput detection of reverse complementary 16S rRNA gene sequences in large environmental and taxonomic datasets. 2011 , 319, 140-5	10

1797	Linking bacterial identities and ecosystem processes: can 'omic' analyses be more than the sum of their parts?. 2011 , 75, 2-16	92
1796	Halomonas and Marinobacter ecotypes from hydrothermal vent, seafloor and deep-sea environments. 2011 , 75, 123-33	59
1795	Microbial consortia of gorgonian corals from the Aleutian islands. 2011 , 76, 109-20	50
1794	Evidence for syntrophic butyrate metabolism under sulfate-reducing conditions in a hydrocarbon-contaminated aquifer. 2011 , 76, 289-300	21
1793	ThermoPhyl: a software tool for selecting phylogenetically optimized conventional and quantitative-PCR taxon-targeted assays for use with complex samples. 2011 , 77, 17-27	6
1792	Electron acceptor-dependent identification of key anaerobic toluene degraders at a tar-oil-contaminated aquifer by Pyro-SIP. 2011 , 78, 165-75	84
1791	Characterization of culturable bacteria isolated from the cold-water coral <i>Lophelia pertusa</i> . 2011 , 77, 333-46	28
1790	Denaturing gradient gel electrophoresis analyses of the vertical distribution and diversity of <i>Vibrio</i> spp. populations in the Cariaco Basin. 2011 , 77, 347-56	13
1789	Rethinking taxon sampling in the light of environmental sequencing. 2011 , 27, 197-203	18
1788	Comparative metagenomics of bathypelagic plankton and bottom sediment from the Sea of Marmara. 2011 , 5, 285-304	113
1787	Analysis of human and animal fecal microbiota for microbial source tracking. 2011 , 5, 362-5	73
1786	Microbial biodegradation of aromatic alkanolic naphthenic acids is affected by the degree of alkyl side chain branching. 2011 , 5, 486-96	71
1785	Structure of the human gastric bacterial community in relation to <i>Helicobacter pylori</i> status. 2011 , 5, 574-9	199
1784	Spatial variability in airborne bacterial communities across land-use types and their relationship to the bacterial communities of potential source environments. 2011 , 5, 601-12	288
1783	Partitioning core and satellite taxa from within cystic fibrosis lung bacterial communities. 2011 , 5, 780-91	177
1782	Integrated metatranscriptomic and metagenomic analyses of stratified microbial assemblages in the open ocean. 2011 , 5, 999-1013	178
1781	Depleted dissolved organic carbon and distinct bacterial communities in the water column of a rapid-flushing coral reef ecosystem. 2011 , 5, 1374-87	78
1780	Chemolithotrophic acetogenic H ₂ /CO ₂ utilization in Italian rice field soil. 2011 , 5, 1526-39	32

1779	Ovine pedomics: the first study of the ovine foot 16S rRNA-based microbiome. 2011 , 5, 1426-37	32
1778	Effect of warming and drought on grassland microbial communities. 2011 , 5, 1692-700	223
1777	Archaea in Yellowstone Lake. 2011 , 5, 1784-95	49
1776	Land-use history has a stronger impact on soil microbial community composition than aboveground vegetation and soil properties. 2011 , 43, 2184-2193	276
1775	High-throughput clone library analysis of the mucosa-associated microbiota reveals dysbiosis and differences between inflamed and non-inflamed regions of the intestine in inflammatory bowel disease. 2011 , 11, 7	455
1774	Bacteria and Archaea community structure in the rumen microbiome of goats (<i>Capra hircus</i>) from the semiarid region of Brazil. 2011 , 17, 118-24	58
1773	Involvement of <i>Clostridium gasigenes</i> and <i>C. algidicarnis</i> in 'blown pack' spoilage of Brazilian vacuum-packed beef. 2011 , 148, 156-63	26
1772	Microbial ecology of the dark ocean above, at, and below the seafloor. 2011 , 75, 361-422	425
1771	A guide to the natural history of freshwater lake bacteria. 2011 , 75, 14-49	914
1770	Comparative analysis of microbial diversity in <i>Longitarsus</i> flea beetles (Coleoptera: Chrysomelidae). 2011 , 139, 541-50	30
1769	Impacts of microbial community composition on isotope fractionation during reductive dechlorination of tetrachloroethylene. 2011 , 22, 431-44	22
1768	Analysis of bacterial communities in rhizosphere soil of healthy and diseased cotton (<i>Gossypium</i> sp.) at different plant growth stages. 2011 , 339, 447-455	45
1767	Metaxa: a software tool for automated detection and discrimination among ribosomal small subunit (12S/16S/18S) sequences of archaea, bacteria, eukaryotes, mitochondria, and chloroplasts in metagenomes and environmental sequencing datasets. 2011 , 100, 471-5	61
1766	Assessing gut microbial diversity from feces and rectal mucosa. 2011 , 61, 123-33	116
1765	Molecular studies of microbial community structure on stained pages of Leonardo da Vinci's Atlantic Codex. 2011 , 61, 214-22	29
1764	Annual and seasonal variation in the phyllosphere bacterial community associated with leaves of the southern Magnolia (<i>Magnolia grandiflora</i>). 2011 , 61, 113-22	62
1763	Identification of sulfur-cycle prokaryotes in a low-sulfate lake (Lake Pavin) using <i>aprA</i> and 16S rRNA gene markers. 2011 , 61, 313-27	35
1762	STITCH: algorithm to splice, trim, identify, track, and capture the uniqueness of 16S rRNAs sequence pairs using public or in-house database. 2011 , 61, 669-75	3

1761	Aquatic microbial habitats within a neotropical rainforest: bromeliads and pH-associated trends in bacterial diversity and composition. 2011 , 61, 529-42	36
1760	Ammonia-oxidizing archaea and ammonia-oxidizing bacteria in six full-scale wastewater treatment bioreactors. 2011 , 91, 1215-25	117
1759	Analyses of bacterial communities in meju, a Korean traditional fermented soybean bricks, by cultivation-based and pyrosequencing methods. 2011 , 49, 340-8	84
1758	Diversity and novelty of the gut microbial community of an herbivorous rodent (<i>Neotoma bryanti</i>). 2011 , 54, 47-54	29
1757	Simrank: Rapid and sensitive general-purpose k-mer search tool. 2011 , 11, 11	21
1756	Preliminary characterization of the oral microbiota of Chinese adults with and without gingivitis. 2011 , 11, 33	82
1755	Polytomy identification in microbial phylogenetic reconstruction. 2011 , 5 Suppl 3, S2	8
1754	Variance adjusted weighted UniFrac: a powerful beta diversity measure for comparing communities based on phylogeny. 2011 , 12, 118	78
1753	i-rDNA: alignment-free algorithm for rapid in silico detection of ribosomal gene fragments from metagenomic sequence data sets. 2011 , 12 Suppl 3, S12	0
1752	Comparative fecal metagenomics unveils unique functional capacity of the swine gut. 2011 , 11, 103	254
1751	Analysis of the hydrogenotrophic microbiota of wild and captive black howler monkeys (<i>Alouatta pigra</i>) in palenque national park, Mexico. 2011 , 73, 909-19	38
1750	Disease phenotype and genotype are associated with shifts in intestinal-associated microbiota in inflammatory bowel diseases. 2011 , 17, 179-84	445
1749	Distinct microbiome in pouchitis compared to healthy pouches in ulcerative colitis and familial adenomatous polyposis. 2011 , 17, 1092-100	58
1748	Investigation of intermittent air exposure on four-stage and one-stage anaerobic semi-continuous mixed-acid fermentations. 2011 , 102, 5066-75	15
1747	Stimulating denitrification in a stream mesocosm with elemental sulfur as an electron donor. 2011 , 37, 580-588	18
1746	Characterization of an alkane-degrading methanogenic enrichment culture from production water of an oil reservoir after 274 days of incubation. 2011 , 65, 444-450	85
1745	Computational Genomic Signatures. 2011 , 6, 1-129	3
1744	Microbial life in a liquid asphalt desert. 2011 , 11, 241-58	46

1743	Effect of sodium bisulfite injection on the microbial community composition in a brackish-water-transporting pipeline. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 6908-17	4.8	62
1742	Human oral, gut, and plaque microbiota in patients with atherosclerosis. 2011 , 108 Suppl 1, 4592-8		679
1741	Bacterial biogeography of the human digestive tract. 2011 , 1, 170		268
1740	Enteral tube feeding alters the oral indigenous microbiota in elderly adults. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 6739-45	4.8	23
1739	A limited microbial consortium is responsible for extended bioreduction of uranium in a contaminated aquifer. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 5955-65	4.8	81
1738	Influence of the drilling mud formulation process on the bacterial communities in thermogenic natural gas wells of the Barnett Shale. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 4744-53	4.8	79
1737	Hoeflea anabaenae sp. nov., an epiphytic symbiont that attaches to the heterocysts of a strain of Anabaena. 2011 , 61, 2439-2444		18
1736	The incidence of necrotizing enterocolitis is increased following probiotic administration to preterm pigs. 2011 , 141, 223-30		35
1735	Sources of bacteria in outdoor air across cities in the midwestern United States. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 6350-6	4.8	195
1734	Isolation and characterization of Methanothermobacter crinale sp. nov., a novel hydrogenotrophic methanogen from the Shengli oil field. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 5212-9	4.8	67
1733	FastSP: linear time calculation of alignment accuracy. 2011 , 27, 3250-8		36
1732	Seasonal changes of freshwater ammonia-oxidizing archaeal assemblages and nitrogen species in oligotrophic alpine lakes. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 1937-45	4.8	82
1731	Target region selection is a critical determinant of community fingerprints generated by 16S pyrosequencing. 2011 , 6, e20956		174
1730	Comprehensive and relaxed search for oligonucleotide signatures in hierarchically clustered sequence datasets. 2011 , 27, 1546-54		13
1729	Fecal bacteroidales diversity and decay in response to variations in temperature and salinity. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 2563-72	4.8	44
1728	Pan-genome of the dominant human gut-associated archaeon, Methanobrevibacter smithii, studied in twins. 2011 , 108 Suppl 1, 4599-606		165
1727	Dynamics of microbial community structure of and enhanced biological phosphorus removal by aerobic granules cultivated on propionate or acetate. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 8041-51	4.8	69
1726	Tobacco smoking affects bacterial acquisition and colonization in oral biofilms. 2011 , 79, 4730-8		156

1725	Evidence for an evolutionary antagonism between Mrr and Type III modification systems. 2011 , 39, 5991-6001	16
1724	Bacterial community comparisons by taxonomy-supervised analysis independent of sequence alignment and clustering. 2011 , 108, 14637-42	66
1723	Novel biphenyl-oxidizing bacteria and dioxygenase genes from a korean tidal mudflat. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 3888-91	4.8 25
1722	Chemical basis of the synergism and antagonism in microbial communities in the nests of leaf-cutting ants. 2011 , 108, 1955-60	136
1721	Bacterial community structures are unique and resilient in full-scale bioenergy systems. 2011 , 108, 4158-63	325
1720	Phylogenetic Microarrays (PhyloChips) for Analysis of Complex Microbial Communities. 2011 , 521-532	
1719	STROMATOLITES: Interaction of Microbes with Sediments. 2011 ,	7
1718	Experimental Evidence for Microbially Mediated Carbonate Dissolution from the Saline Water Zone of the Edwards Aquifer, Central Texas. 2011 , 28, 313-327	14
1717	PhylOTU: a high-throughput procedure quantifies microbial community diversity and resolves novel taxa from metagenomic data. 2011 , 7, e1001061	62
1716	Validation of heavy-water stable isotope probing for the characterization of rapidly responding soil bacteria. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 4589-96	4.8 55
1715	PrimerProspector: de novo design and taxonomic analysis of barcoded polymerase chain reaction primers. 2011 , 27, 1159-61	273
1714	Phylogenomic analysis of the uracil-DNA glycosylase superfamily. 2011 , 28, 1307-17	24
1713	Mobilization of Metals from Pristine Mineral Soil by Nitrifying and Sulfur-Oxidizing Bacteria [The Leaching Potential of Indigenous Culture Enrichments. 2011 , 28, 212-220	2
1712	TreeLign. 2011 ,	
1711	Comparative 16S rRNA gene surveys of granular sludge from three upflow anaerobic bioreactors treating purified terephthalic acid (PTA) wastewater. 2011 , 64, 1406-12	12
1710	Chemolithotrophic Metal Mobilization from Dolomite. 2011 , 28, 651-659	2
1709	Complete genome sequence of <i>Thermomonospora curvata</i> type strain (B9). 2011 , 4, 13-22	24
1708	Consumption of lysozyme-rich milk can alter microbial fecal populations. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 6153-60	4.8 70

1707	Incorporating 16S gene copy number information improves estimates of microbial diversity and abundance. 2012 , 8, e1002743		303
1706	Identification and removal of ribosomal RNA sequences from metatranscriptomes. 2012 , 28, 433-5		148
1705	Unexpected stability of Bacteroidetes and Firmicutes communities in laboratory biogas reactors fed with different defined substrates. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 2106-19	4.8	144
1704	Targeted recovery of novel phylogenetic diversity from next-generation sequence data. 2012 , 6, 2067-77		42
1703	Chapter 12: Human microbiome analysis. 2012 , 8, e1002808		310
1702	The Protist Ribosomal Reference database (PR2): a catalog of unicellular eukaryote small sub-unit rRNA sequences with curated taxonomy. 2013 , 41, D597-604		744
1701	Bioinformatics for the Human Microbiome Project. 2012 , 8, e1002779		54
1700	Microbial dysbiosis in pediatric patients with Crohn's disease. 2012 , 50, 3258-66		89
1699	Grinder: a versatile amplicon and shotgun sequence simulator. 2012 , 40, e94		137
1698	Comparison of gull feces-specific assays targeting the 16S rRNA genes of <i>Catelliboccus marimammalium</i> and <i>Streptococcus</i> spp. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 1909-16	4.8	46
1697	DECIPHER, a search-based approach to chimera identification for 16S rRNA sequences. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 717-25	4.8	474
1696	Factors that affect large subunit ribosomal DNA amplicon sequencing studies of fungal communities: classification method, primer choice, and error. 2012 , 7, e35749		45
1695	Increased levels of multiresistant bacteria and resistance genes after wastewater treatment and their dissemination into lake Geneva, Switzerland. 2012 , 3, 106		249
1694	Identifying genomic and metabolic features that can underlie early successional and opportunistic lifestyles of human gut symbionts. 2012 , 22, 1974-84		97
1693	Nurture trumps nature in a longitudinal survey of salivary bacterial communities in twins from early adolescence to early adulthood. 2012 , 22, 2146-52		131
1692	Denitrifying bacteria from the genus <i>Rhodanobacter</i> dominate bacterial communities in the highly contaminated subsurface of a nuclear legacy waste site. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 1039-47	4.8	134
1691	Significant and persistent impact of timber harvesting on soil microbial communities in Northern coniferous forests. 2012 , 6, 2199-218		203
1690	Culture-dependent and -independent investigations of microbial diversity on urinary catheters. 2012 , 50, 3901-8		31

1689	Bioinformatic approaches for functional annotation and pathway inference in metagenomics data. 2012 , 13, 696-710		60
1688	Responses in digestion, rumen fermentation and microbial populations to inhibition of methane formation by a halogenated methane analogue. 2012 , 108, 482-91		77
1687	Efficient relaxed search in hierarchically clustered sequence datasets. 2012 , 17,		
1686	Interleukin-1 β (IL-1 β) promotes susceptibility of Toll-like receptor 5 (TLR5) deficient mice to colitis. 2012 , 61, 373-84		59
1685	Identification of novel positive-strand RNA viruses by metagenomic analysis of archaea-dominated Yellowstone hot springs. 2012 , 86, 5562-73		92
1684	Convergent development of anodic bacterial communities in microbial fuel cells. 2012 , 6, 2002-13		142
1683	Wide distribution of closely related, antibiotic-producing <i>Arthrobacter</i> strains throughout the Arctic Ocean. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 2039-42	4.8	27
1682	Cellulolytic bacteria in the foregut of the dromedary camel (<i>Camelus dromedarius</i>). <i>Applied and Environmental Microbiology</i> , 2012 , 78, 8836-9	4.8	18
1681	Impact of training sets on classification of high-throughput bacterial 16s rRNA gene surveys. 2012 , 6, 94-103		385
1680	Extraction of bacterial RNA from soil: challenges and solutions. 2012 , 27, 111-21		44
1679	Pyrosequencing as a tool for better understanding of human microbiomes. 2012 , 4,		94
1678	Bacterial communities in women with bacterial vaginosis: high resolution phylogenetic analyses reveal relationships of microbiota to clinical criteria. 2012 , 7, e37818		410
1677	Diversity and partitioning of bacterial populations within the accessory nidamental gland of the squid <i>Euprymna scolopes</i> . <i>Applied and Environmental Microbiology</i> , 2012 , 78, 4200-8	4.8	53
1676	Novel high-rank phylogenetic lineages within a sulfur spring (Zodletone Spring, Oklahoma), revealed using a combined pyrosequencing-sanger approach. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 2677-88	4.8	29
1675	Development and evaluation of a quantitative PCR assay targeting sandhill crane (<i>Grus canadensis</i>) fecal pollution. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 4338-45	4.8	26
1674	Genome sequence of the moderately thermophilic, amino-acid-degrading and sulfur-reducing bacterium <i>Thermovirga lienii</i> type strain (Cas60314(T)). 2012 , 6, 230-9		21
1673	Recruitment of members from the rare biosphere of marine bacterioplankton communities after an environmental disturbance. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 1361-9	4.8	87
1672	Vertical segregation and phylogenetic characterization of ammonia-oxidizing Archaea in a deep oligotrophic lake. 2012 , 6, 1786-97		87

1671	Evaluation of the GenBank, EzTaxon, and BIBI services for molecular identification of clinical blood culture isolates that were unidentifiable or misidentified by conventional methods. 2012 , 50, 1792-5	25
1670	Identification of triclosan-degrading bacteria using stable isotope probing, fluorescence in situ hybridization and microautoradiography. 2012 , 158, 2796-2804	34
1669	TaxMan: a server to trim rRNA reference databases and inspect taxonomic coverage. 2012 , 40, W82-7	29
1668	Metagenomics to Unveil Microbiome of Human Body. 2012 , 04,	
1667	Genome sequence of the orange-pigmented seawater bacterium <i>Owenweeksia hongkongensis</i> type strain (UST20020801(T)). 2012 , 7, 120-30	11
1666	Anaerobic decomposition of switchgrass by tropical soil-derived feedstock-adapted consortia. 2012 , 3,	16
1665	Complete genome sequence of the moderately thermophilic mineral-sulfide-oxidizing firmicute <i>Sulfobacillus acidophilus</i> type strain (NAL(T)). 2012 , 6, 1-13	20
1664	Complete genome sequence of the termite hindgut bacterium <i>Spirochaeta coccoides</i> type strain (SPN1(T)), reclassification in the genus <i>Sphaerochaeta</i> as <i>Sphaerochaeta coccoides</i> comb. nov. and emendations of the family Spirochaetaceae and the genus <i>Sphaerochaeta</i> . 2012 , 6, 194-209	46
1663	Permanent draft genome sequence of the gliding predator <i>Saprospira grandis</i> strain Sa g1 (= HR1). 2012 , 6, 210-9	1
1662	Soil Diffusion System Enriches the Growth of Diverse and Previously Uncultivated Bacterial Taxa. 2012 , 76, 463-474	4
1661	Genome sequence of the soil bacterium <i>Saccharomonospora azurea</i> type strain (NA-128(T)). 2012 , 6, 220-9	10
1660	Complete genome sequence of the facultatively anaerobic, appendaged bacterium <i>Muricauda ruestringensis</i> type strain (B1(T)). 2012 , 6, 185-93	8
1659	Complete genome sequence of <i>Polynucleobacter necessarius</i> subsp. <i>asymbioticus</i> type strain (QLW-P1DMWA-1(T)). 2012 , 6, 74-83	27
1658	Complete genome sequence of the aerobic, heterotroph <i>Marinithermus hydrothermalis</i> type strain (T1(T)) from a deep-sea hydrothermal vent chimney. 2012 , 6, 21-30	6
1657	Complete genome sequence of the aquatic bacterium <i>Runella slithyformis</i> type strain (LSU 4(T)). 2012 , 6, 145-54	16
1656	Genome sequence of the ocean sediment bacterium <i>Saccharomonospora marina</i> type strain (XMU15(T)). 2012 , 6, 265-75	3
1655	Complete genome sequence of the thermophilic sulfate-reducing ocean bacterium <i>Thermodesulfator indicus</i> type strain (CIR29812(T)). 2012 , 6, 155-64	9
1654	Genome sequence of the homoacetogenic bacterium <i>Holophaga foetida</i> type strain (TMBS4(T)). 2012 , 6, 174-84	23

1653	Complete genome sequence of the orange-red pigmented, radioresistant <i>Deinococcus proteolyticus</i> type strain (MRP(T)). 2012 , 6, 240-50	7
1652	Genome sequence of the flexirubin-pigmented soil bacterium <i>Niabella soli</i> type strain (JS13-8(T)). 2012 , 7, 210-20	0
1651	Genome sequence of the Antarctic rhodopsins-containing flavobacterium <i>Gillisia limnaea</i> type strain (R-8282(T)). 2012 , 7, 107-19	9
1650	Complete genome sequence of the sulfate-reducing firmicute <i>Desulfotomaculum ruminis</i> type strain (DL(T)). 2012 , 7, 304-19	18
1649	Complete genome sequencing and analysis of <i>Saprospira grandis</i> str. Lewin, a predatory marine bacterium. 2012 , 6, 84-93	19
1648	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium <i>Starkeya novella</i> type strain (ATCC 8093(T)). 2012 , 7, 44-58	12
1647	Global biogeography of SAR11 marine bacteria. 2012 , 8, 595	146
1646	Metagenomic analysis of a southern maritime antarctic soil. 2012 , 3, 403	84
1645	Stimulated bacterioplankton growth and selection for certain bacterial taxa in the vicinity of the ctenophore <i>Mnemiopsis leidyi</i> . 2012 , 3, 302	29
1644	PCR Advances Towards the Identification of Individual and Mixed Populations of Biotechnology Microbes. 2012 ,	
1643	Discrimination of the oral microbiota associated with high hydrogen sulfide and methyl mercaptan production. 2012 , 2, 215	54
1642	Complete genome sequence of the sulfur compounds oxidizing chemolithoautotroph <i>Sulfuricurvum kujiense</i> type strain (YK-1(T)). 2012 , 6, 94-103	31
1641	Microbiomes. 2012 ,	
1640	A memory efficient method for structure-based RNA multiple alignment. 2012 , 9, 1-11	1
1639	Cultured fungal associates from the deep-sea coral <i>Lophelia pertusa</i> . 2012 , 67, 12-20	15
1638	Life and death of deep-sea vents: bacterial diversity and ecosystem succession on inactive hydrothermal sulfides. 2012 , 3, e00279-11	95
1637	Novel bacterial community associated with 500-year-old unpreserved archaeological wood from King Henry VIII's Tudor Warship the Mary Rose. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 8822-8828	4.8 8
1636	Comparative survey of rumen microbial communities and metabolites across one caprine and three bovine groups, using bar-coded pyrosequencing and ^1H nuclear magnetic resonance spectroscopy. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 5983-93	4.8 109

1635	Molecular methods to measure intestinal bacteria: a review. 2012 , 95, 5-23		39
1634	Central role of dynamic tidal biofilms dominated by aerobic hydrocarbonoclastic bacteria and diatoms in the biodegradation of hydrocarbons in coastal mudflats. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 3638-48	4.8	73
1633	Electrosynthesis of commodity chemicals by an autotrophic microbial community. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 8412-20	4.8	307
1632	Deep sequencing reveals extensive variation in the gut microbiota of wild mosquitoes from Kenya. 2012 , 21, 5138-50		189
1631	Oral and airway microbiota in HIV-infected pneumonia patients. 2012 , 50, 2995-3002		56
1630	OTU analysis using metagenomic shotgun sequencing data. 2012 , 7, e49785		19
1629	Treatment of alcohol distillery wastewater using a Bacteroidetes-dominant thermophilic microbial fuel cell. 2012 , 46, 3022-30		87
1628	Detecting unknown sequences with DNA microarrays: explorative probe design strategies. 2012 , 14, 356-71		31
1627	A metagenomic study of diet-dependent interaction between gut microbiota and host in infants reveals differences in immune response. 2012 , 13, r32		173
1626	Resistance to thermal stress in corals without changes in symbiont composition. 2012 , 279, 1100-7		99
1625	Distinct approaches for the detection and removal of chimeric 16S rRNA sequences can significantly affect the outcome of between-site comparisons. 2012 , 66, 13-21		3
1624	Impact of commercial natural gas production on geochemistry and microbiology in a shale-gas reservoir. 2012 , 332-333, 15-25		35
1623	Advances in the methods for studying gut microbiota and their relevance to the research of dietary fiber functions. 2012 , 48, 916-929		38
1622	The transcription factor T-bet regulates intestinal inflammation mediated by interleukin-7 receptor+ innate lymphoid cells. 2012 , 37, 674-84		244
1621	Profiling of the metabolically active community from a production-scale biogas plant by means of high-throughput metatranscriptome sequencing. 2012 , 158, 248-58		170
1620	The Western English Channel contains a persistent microbial seed bank. 2012 , 6, 1089-93		140
1619	An Accurate Scalable Template-based Alignment Algorithm. 2012 , 2012, 1-7		7
1618	Bacterial diversity of bryophyte-dominant biological soil crusts and associated mites. 2012 , 87, 110-117		35

1617	Bacterial Associations with Weathering Minerals at the Regolith-Bedrock Interface, Luquillo Experimental Forest, Puerto Rico. 2012 , 29, 792-803	19
1616	The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. 2013 , 41, D590-6	11640
1615	Measuring the microbiome: perspectives on advances in DNA-based techniques for exploring microbial life. 2012 , 13, 420-9	31
1614	SINA: accurate high-throughput multiple sequence alignment of ribosomal RNA genes. 2012 , 28, 1823-9	2017
1613	Methanogen colonisation does not significantly alter acetogen diversity in lambs isolated 17 h after birth and raised aseptically. 2012 , 64, 628-40	31
1612	Bacterial succession during 500 years of soil development under agricultural use. 2012 , 27, 793-807	29
1611	Ultrafast clustering algorithms for metagenomic sequence analysis. 2012 , 13, 656-68	294
1610	Phylogenetic microarray analysis of a microbial community performing reductive dechlorination at a TCE-contaminated site. 2012 , 46, 1044-54	28
1609	Microbial community structure of Arctic multiyear sea ice and surface seawater by 454 sequencing of the 16S RNA gene. 2012 , 6, 11-20	135
1608	Comparative ocular microbial communities in humans with and without blepharitis. 2012 , 53, 5585-93	103
1607	Differences in crop bacterial community structure between hoatzins from different geographical locations. 2012 , 163, 211-20	16
1606	The structure and spatio-temporal distribution of the Archaea in a horizontal subsurface flow constructed wetland. 2012 , 435-436, 465-71	17
1605	Efficient electricity generation from sewage sludge using biocathode microbial fuel cell. 2012 , 46, 43-52	143
1604	C16S - a Hidden Markov Model based algorithm for taxonomic classification of 16S rRNA gene sequences. 2012 , 99, 195-201	5
1603	Saliva microbiomes distinguish caries-active from healthy human populations. 2012 , 6, 1-10	245
1602	Denaturing gradient gel electrophoresis and barcoded pyrosequencing reveal unprecedented archaeal diversity in mangrove sediment and rhizosphere samples. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 5520-8	4.8 171
1601	Phenazine content in the cystic fibrosis respiratory tract negatively correlates with lung function and microbial complexity. 2012 , 47, 738-45	140
1600	Fermentation, hydrogen, and sulfur metabolism in multiple uncultivated bacterial phyla. 2012 , 337, 1661-5	464

1599	Time-series analysis of two hydrothermal plumes at 9°50'N East Pacific Rise reveals distinct, heterogeneous bacterial populations. 2012 , 10, 178-92	40
1598	Microbial diversity under extreme euxinia: Mahoney Lake, Canada. 2012 , 10, 223-35	38
1597	Cyanobacterial diversity and activity in modern conical microbialites. 2012 , 10, 384-401	42
1596	Reference databases for taxonomic assignment in metagenomics. 2012 , 13, 682-95	68
1595	Taxonomic binning of metagenome samples generated by next-generation sequencing technologies. 2012 , 13, 646-55	78
1594	<i>Deferrisoma camini</i> gen. nov., sp. nov., a moderately thermophilic, dissimilatory iron(III)-reducing bacterium from a deep-sea hydrothermal vent that forms a distinct phylogenetic branch in the Deltaproteobacteria. 2012 , 62, 2463-2468	36
1593	Use of a culture-independent approach to characterize aerosolized bacteria near an open-freestall dairy operation. 2012 , 41, 8-14	19
1592	Characterization and control of microbial black spot spoilage in dry-cured Iberian ham. 2012 , 23, 128-136	6
1591	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. 2012 , 6, 1715-27	420
1590	Sequencing our way towards understanding global eukaryotic biodiversity. 2012 , 27, 233-43	322
1589	A comparative evaluation of sequence classification programs. 2012 , 13, 92	80
1588	Metagenomic analysis reveals a functional signature for biomass degradation by cecal microbiota in the leaf-eating flying squirrel (<i>Petaurista alborufus lena</i>). 2012 , 13, 466	19
1587	Molecular analysis of meso- and thermophilic microbiota associated with anaerobic biowaste degradation. 2012 , 12, 121	28
1586	The effect of training set on the classification of honey bee gut microbiota using the Naïve Bayesian Classifier. 2012 , 12, 221	40
1585	BactQuant: an enhanced broad-coverage bacterial quantitative real-time PCR assay. 2012 , 12, 56	110
1584	Coverage evaluation of universal bacterial primers using the metagenomic datasets. 2012 , 12, 66	130
1583	Characterization of a biogas-producing microbial community by short-read next generation DNA sequencing. 2012 , 5, 41	262
1582	High-throughput isotopic analysis of RNA microarrays to quantify microbial resource use. 2012 , 6, 1210-21	51

1581	Phylum XXVI. Actinobacteria phyl. nov.. 2012 , 33-2028	43
1580	The Inter-Valley Soil Comparative Survey: the ecology of Dry Valley edaphic microbial communities. 2012 , 6, 1046-57	196
1579	Isolation and survey of novel fluoroacetate-degrading bacteria belonging to the phylum Synergistetes. 2012 , 80, 671-84	36
1578	Thermophilic enrichment of microbial communities in the presence of the ionic liquid 1-ethyl-3-methylimidazolium acetate. 2012 , 113, 1362-70	25
1577	Nitrogen metabolism and rumen microbial enumeration in lactating cows with divergent residual feed intake fed high-digestibility pasture. 2012 , 95, 5024-5034	89
1576	Archaea in organic-lean and organic-rich marine subsurface sediments: an environmental gradient reflected in distinct phylogenetic lineages. 2012 , 3, 168	75
1575	Evidence of a robust resident bacteriophage population revealed through analysis of the human salivary virome. 2012 , 6, 915-26	211
1574	The gut microbiota in IBD. 2012 , 9, 599-608	759
1573	Species-level analysis of DNA sequence data from the NIH Human Microbiome Project. 2012 , 7, e47075	116
1572	Virus genes in Arctic marine bacteria identified by metagenomic analysis. 2012 , 66, 107-116	17
1571	Bacterial communities and the nitrogen cycle in the gypsum soils of Cuatro Ciñegas Basin, coahuila: a Mars analogue. 2012 , 12, 699-709	45
1570	Comparative metagenomics of two microbial mats at Cuatro Ciñegas Basin II: community structure and composition in oligotrophic environments. 2012 , 12, 659-73	55
1569	Defining the core Arabidopsis thaliana root microbiome. 2012 , 488, 86-90	1613
1568	Millimeter-scale patterns of phylogenetic and trait diversity in a salt marsh microbial mat. 2012 , 3, 293	34
1567	Microbial Community Changes Along a Land-Use Gradient of Desert Soil Origin. 2012 , 22, 593-603	25
1566	The active bacterial community in a pristine confined aquifer. 2012 , 48,	16
1565	The interpersonal and intrapersonal diversity of human-associated microbiota in key body sites. 2012 , 129, 1204-8	207
1564	Bacterial diversity of siliciclastic sediments in a Thalassia testudinum meadow and the implications for Lucinisca nassula chemosymbiosis. 2012 , 112, 153-161	9

1563	Shifts in phylogenetic diversity of archaeal communities in mangrove sediments at different sites and depths in southeastern Brazil. 2012 , 163, 366-77	29
1562	Environmental microbiology through the lens of high-throughput DNA sequencing: synopsis of current platforms and bioinformatics approaches. 2012 , 91, 106-13	90
1561	Methanogenic Microbial Community Composition of Oily Sludge and Its Enrichment Amended with Alkanes Incubated for Over 500 Days. 2012 , 29, 716-726	25
1560	Isolation of biosurfactant-producing bacteria from the Rancho La Brea Tar Pits. 2012 , 28, 3261-7	15
1559	Hydrogen production in photosynthetic microbial mats in the Elkhorn Slough estuary, Monterey Bay. 2012 , 6, 863-74	41
1558	Analysis of gut microbial regulation of host gene expression along the length of the gut and regulation of gut microbial ecology through MyD88. 2012 , 61, 1124-31	261
1557	An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea. 2012 , 6, 610-8	3287
1556	High-Throughput Characterization and Comparison of Microbial Communities. 2012 , 37-57	
1555	<i>Geodermatophilus arenarius</i> sp. nov., a xerophilic actinomycete isolated from Saharan desert sand in Chad. 2012 , 16, 903-9	44
1554	Microbes. 2012 , 490-499	3
1553	Defining seasonal marine microbial community dynamics. 2012 , 6, 298-308	656
1552	Selection of primers for optimal taxonomic classification of environmental 16S rRNA gene sequences. 2012 , 6, 1440-4	243
1551	Metagenomic approaches to the discovery of cellulases. 2012 , 510, 375-94	7
1550	<i>Acetatifactor muris</i> gen. nov., sp. nov., a novel bacterium isolated from the intestine of an obese mouse. 2012 , 194, 901-7	42
1549	Bacterial communities associated with production facilities of two newly drilled thermogenic natural gas wells in the Barnett Shale (Texas, USA). 2012 , 64, 942-54	66
1548	Long-term characterization of free-living and particle-associated bacterial communities in Lake Tiefwaren reveals distinct seasonal patterns. 2012 , 64, 571-83	57
1547	Microbial and geochemical assessment of bauxitic un-mined and post-mined chronosequence soils from Mocho Mountains, Jamaica. 2012 , 64, 738-49	14
1546	Species-level classification of the vaginal microbiome. 2012 , 13 Suppl 8, S17	114

1545	Shifts in human skin and nares microbiota of healthy children and adults. 2012 , 4, 77	218
1544	Inflammatory bowel diseases phenotype, <i>C. difficile</i> and NOD2 genotype are associated with shifts in human ileum associated microbial composition. 2012 , 7, e26284	178
1543	Host genes related to paneth cells and xenobiotic metabolism are associated with shifts in human ileum-associated microbial composition. 2012 , 7, e30044	18
1542	Predatory Bacteriovorax communities ordered by various prey species. 2012 , 7, e34174	33
1541	Comparison of DNA extraction methods for microbial community profiling with an application to pediatric bronchoalveolar lavage samples. 2012 , 7, e34605	104
1540	Bacterial communities of the coronal sulcus and distal urethra of adolescent males. 2012 , 7, e36298	133
1539	Bacterial communities in the sediments of Dianchi Lake, a partitioned eutrophic waterbody in China. 2012 , 7, e37796	98
1538	Testing the limits of 454 pyrotag sequencing: reproducibility, quantitative assessment and comparison to T-RFLP fingerprinting of aquifer microbes. 2012 , 7, e40467	126
1537	Phylogenetic and functional metagenomic profiling for assessing microbial biodiversity in environmental monitoring. 2012 , 7, e43630	38
1536	Exploring bacterial diversity in hospital environments by GS-FLX Titanium pyrosequencing. 2012 , 7, e44105	40
1535	The role of coral-associated bacterial communities in Australian Subtropical White Syndrome of <i>Turbinaria mesenterina</i> . 2012 , 7, e44243	24
1534	A direct PCR approach to accelerate analyses of human-associated microbial communities. 2012 , 7, e44563	52
1533	Analysis of the gut microbiota in the old order Amish and its relation to the metabolic syndrome. 2012 , 7, e43052	161
1532	Routine habitat change: a source of unrecognized transient alteration of intestinal microbiota in laboratory mice. 2012 , 7, e47416	42
1531	Phylogenetic analysis of microbial communities in different regions of the gastrointestinal tract in <i>Panaque nigrolineatus</i> , a wood-eating fish. 2012 , 7, e48018	33
1530	Next generation sequencing to define prokaryotic and fungal diversity in the bovine rumen. 2012 , 7, e48289	182
1529	Statistical object data analysis of taxonomic trees from human microbiome data. 2012 , 7, e48996	12
1528	CREST--classification resources for environmental sequence tags. 2012 , 7, e49334	167

1527	Commensal bacteria and MAMPs are necessary for stress-induced increases in IL-1 β and IL-18 but not IL-6, IL-10 or MCP-1. 2012 , 7, e50636	56
1526	The bacterial composition within the <i>Sarracenia purpurea</i> model system: local scale differences and the relationship with the other members of the food web. 2012 , 7, e50969	16
1525	Insights from characterizing extinct human gut microbiomes. 2012 , 7, e51146	141
1524	RNA-based assessment of diversity and composition of active archaeal communities in the German Bight. 2012 , 2012, 695826	32
1523	Widespread Oceanospirillaceae Bacteria in Porites spp.. 2012 , 2012, 1-7	29
1522	Carbon, metals, and grain size correlate with bacterial community structure in sediments of a high arsenic aquifer. 2012 , 3, 82	19
1521	A Streamlined Strategy for Biohydrogen Production with <i>Halanaerobium hydrogeniformans</i> , an Alkaliphilic Bacterium. 2012 , 3, 93	17
1520	Microbial communities at the borehole observatory on the Costa Rica Rift flank (Ocean Drilling Program Hole 896A). 2012 , 3, 232	15
1519	Detection of autotrophic verrucomicrobial methanotrophs in a geothermal environment using stable isotope probing. 2012 , 3, 303	49
1518	Co-occurrence patterns of plants and soil bacteria in the high-alpine subnival zone track environmental harshness. 2012 , 3, 347	44
1517	Microbial communities associated with wet flue gas desulfurization systems. 2012 , 3, 412	7
1516	Advancements in Molecular Techniques and Applications in Environmental Engineering. 2012 , 84, 814-844	2
1515	Computational methods for the analysis of tag sequences in metagenomics studies. 2012 , 4, 1333-43	2
1514	Molecular analysis of the microbial community structures in water-flooding petroleum reservoirs with different temperatures. 2012 , 9, 4645-4659	46
1513	<i>Thermosulfurimonas dismutans</i> gen. nov., sp. nov., an extremely thermophilic sulfur-disproportionating bacterium from a deep-sea hydrothermal vent. 2012 , 62, 2565-2571	60
1512	Computational Challenges in Characterization of Bacteria and Bacteria-Host Interactions Based on Genomic Data. 2012 , 27, 225-239	7
1511	Early life antibiotic-driven changes in microbiota enhance susceptibility to allergic asthma. 2012 , 13, 440-7	566
1510	Spatial and temporal dynamics of the microbial community in the Hanford unconfined aquifer. 2012 , 6, 1665-76	81

1509	Phylogenetic diversities and community structure of members of the extremely halophilic Archaea (order Halobacteriales) in multiple saline sediment habitats. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 1332-44	4.8	67
1508	Archaeal diversity: temporal variation in the arsenic-rich creek sediments of Carnoulès Mine, France. 2012 , 16, 645-57		36
1507	Microbial interactions: from networks to models. 2012 , 10, 538-50		1607
1506	Diversity of Bacteria and Archaea in hypersaline sediment from Death Valley National Park, California. 2012 , 1, 135-48		17
1505	Short-term effects of temperature on the abundance and diversity of magnetotactic cocci. 2012 , 1, 53-63		17
1504	Diversity and structure of soil bacterial communities associated with vultures in an African savanna. 2012 , 3, art47		17
1503	Microbial ecology of expanding oxygen minimum zones. 2012 , 10, 381-94		325
1502	Analysis of Metagenomics Data. 2012 , 219-229		1
1501	Comparison of Illumina paired-end and single-direction sequencing for microbial 16S rRNA gene amplicon surveys. 2012 , 6, 1273-6		79
1500	Qualitative variation in colour morphotypes of <i>Ianthella basta</i> (Porifera: Verongida). 2012 , 687, 191-203		7
1499	Microbiological and environmental issues in show caves. 2012 , 28, 2453-64		38
1498	Human microbiome and HIV/AIDS. 2012 , 9, 44-51		56
1497	Genotypic distribution of a specialist model microorganism, <i>Methanosaeta</i> , along an estuarine gradient: does metabolic restriction limit niche differentiation potential?. 2012 , 63, 856-64		5
1496	Performance and microbial community dynamics of a sulfate-reducing bioreactor treating coal generated acid mine drainage. 2012 , 23, 415-29		42
1495	Uranium reduction and microbial community development in response to stimulation with different electron donors. 2012 , 23, 535-46		22
1494	Transcriptional responses of surface water marine microbial assemblages to deep-sea water amendment. 2012 , 14, 191-206		57
1493	Consistent effects of nitrogen amendments on soil microbial communities and processes across biomes. 2012 , 18, 1918-1927		715
1492	Experimental and analytical tools for studying the human microbiome. 2011 , 13, 47-58		491

1491	The roles of host evolutionary relationships (genus: <i>Nasonia</i>) and development in structuring microbial communities. 2012 , 66, 349-62	98
1490	Temporal and spatial changes in the microbial bioaerosol communities in green-waste composting. 2012 , 79, 229-39	37
1489	A specific mix of generalists: bacterial symbionts in Mediterranean <i>Ircinia</i> spp. 2012 , 79, 619-37	63
1488	Soil bacterial communities of a calcium-supplemented and a reference watershed at the Hubbard Brook Experimental Forest (HBEF), New Hampshire, USA. 2012 , 79, 728-40	22
1487	Phylogenetic diversity, composition and distribution of bacterioplankton community in the Dongjiang River, China. 2012 , 80, 30-44	76
1486	Bacterial communities associated with healthy and <i>Acropora</i> white syndrome-affected corals from American Samoa. 2012 , 80, 509-20	26
1485	Pyrosequencing reveals unique microbial signatures associated with healthy and failing dental implants. 2012 , 39, 425-33	215
1484	Size-resolved emission rates of airborne bacteria and fungi in an occupied classroom. 2012 , 22, 339-51	245
1483	Antibiotic effects on bacterial profile in osteonecrosis of the jaw. 2012 , 18, 85-95	47
1482	Differentiation of mixed lactic acid bacteria communities in beverage fermentations using targeted terminal restriction fragment length polymorphism. 2012 , 31, 126-32	37
1481	Phylogenetic diversity of microbial communities associated with the crude-oil, large-insoluble-particle and formation-water components of the reservoir fluid from a non-flooded high-temperature petroleum reservoir. 2012 , 113, 204-10	58
1480	Seasonal variability in airborne bacterial communities at a high-elevation site. 2012 , 50, 41-49	184
1479	Increased temperature and altered summer precipitation have differential effects on biological soil crusts in a dryland ecosystem. 2012 , 18, 2583-2593	86
1478	Molecular profiling of oral microbiota in jawbone samples of bisphosphonate-related osteonecrosis of the jaw. 2012 , 18, 602-12	37
1477	In situ TCE degradation mediated by complex dehalorespiring communities during biostimulation processes. 2012 , 5, 642-53	38
1476	Phylogenetic clustering increases with elevation for microbes. 2012 , 4, 217-26	118
1475	Molecular methods for pathogen and microbial community detection and characterization: current and potential application in diagnostic microbiology. 2012 , 12, 505-21	104
1474	Bacterial community structure and function change in association with colonizer plants during early primary succession in a glacier forefield. 2012 , 46, 172-180	146

1473	Digging deeper to find unique microbial communities: The strong effect of depth on the structure of bacterial and archaeal communities in soil. 2012 , 50, 58-65	429
1472	A suite of citrate-derived siderophores from a marine <i>Vibrio</i> species isolated following the Deepwater Horizon oil spill. 2012 , 107, 90-5	22
1471	Inter-individual variation in the dominant intestinal microbiota of reared Atlantic cod (<i>Gadus morhua</i> L.) larvae. 2012 , 43, 1499-1508	40
1470	Exploration of community traits as ecological markers in microbial metagenomes. 2012 , 21, 1909-17	55
1469	Highly similar microbial communities are shared among related and trophically similar ant species. 2012 , 21, 2282-96	118
1468	Experience matters: prior exposure to plant toxins enhances diversity of gut microbes in herbivores. 2012 , 15, 1008-15	74
1467	Towards a taxonomy of Bacteria and Archaea based on interactive and cumulative data repositories. 2012 , 14, 318-34	49
1466	Vertical stratification of subsurface microbial community composition across geological formations at the Hanford Site. 2012 , 14, 414-25	86
1465	Cyanobacterial construction of hot spring siliceous stromatolites in Yellowstone National Park. 2012 , 14, 1182-97	52
1464	Geographic distance and pH drive bacterial distribution in alkaline lake sediments across Tibetan Plateau. 2012 , 14, 2457-66	353
1463	Biodiversity soup: metabarcoding of arthropods for rapid biodiversity assessment and biomonitoring. 2012 , 3, 613-623	414
1462	Parallel-META: efficient metagenomic data analysis based on high-performance computation. 2012 , 6 Suppl 1, S16	29
1461	Metagenomics - a guide from sampling to data analysis. 2012 , 2, 3	507
1460	In-depth characterization via complementing culture-independent approaches of the microbial community in an acidic hot spring of the Colombian Andes. 2012 , 63, 103-15	84
1459	Effect of antimicrobial growth promoter administration on the intestinal microbiota of beef cattle. 2013 , 5, 8	32
1458	Large-scale survey of gut microbiota associated with MHE Via 16S rRNA-based pyrosequencing. 2013 , 108, 1601-11	104
1457	<i>Geodermatophilus saharensis</i> sp. nov., isolated from sand of the Saharan desert in Chad. 2013 , 195, 153-9	27
1456	<i>Streptococcus danieliae</i> sp. nov., a novel bacterium isolated from the caecum of a mouse. 2013 , 195, 43-9	15

1455	Species diversity of magnetotactic bacteria from the Olkhovka River, Russia. 2013 , 82, 335-340	9
1454	Dysbiosis signature of fecal microbiota in colorectal cancer patients. 2013 , 66, 462-70	286
1453	Profiling bacterial diversity and taxonomic composition on speleothem surfaces in Kartchner Caverns, AZ. 2013 , 65, 371-83	57
1452	The influence of in situ chemical oxidation on microbial community composition in groundwater contaminated with chlorinated solvents. 2013 , 65, 39-49	18
1451	Intergenerational transfer of specific bacteria in corals and possible implications for offspring fitness. 2013 , 65, 227-31	41
1450	Functional and compositional succession of bacterioplankton in response to a gradient in bioavailable dissolved organic carbon. 2013 , 15, 2616-28	37
1449	Changes in microbial dynamics during long-term decomposition in tropical forests. 2013 , 66, 60-68	42
1448	Taxonomic and functional metagenomic profiling of gastrointestinal tract microbiome of the farmed adult turbot (<i>Scophthalmus maximus</i>). 2013 , 86, 432-43	112
1447	Survival in hostile territory: the microbiota of the stomach. 2013 , 37, 736-61	99
1446	Methanotrophic bacteria in oilsands tailings ponds of northern Alberta. 2013 , 7, 908-21	79
1445	<i>Thermoanaerobaculum aquaticum</i> gen. nov., sp. nov., the first cultivated member of Acidobacteria subdivision 23, isolated from a hot spring. 2013 , 63, 4149-4157	55
1444	The Inflammasome. 2013 ,	4
1443	Romance of the three domains: how cladistics transformed the classification of cellular organisms. 2013 , 4, 664-76	4
1442	Diversity, distribution and sources of bacteria in residential kitchens. 2013 , 15, 588-96	137
1441	MetaPathways: a modular pipeline for constructing pathway/genome databases from environmental sequence information. 2013 , 14, 202	75
1440	M-pick, a modularity-based method for OTU picking of 16S rRNA sequences. 2013 , 14, 43	26
1439	Functional microbial diversity explains groundwater chemistry in a pristine aquifer. 2013 , 13, 146	120
1438	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. 2013 , 31, 814-21	5270

1437	PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes. 2013 , 4, 2304	511
1436	Mineralogy Drives Bacterial Biogeography of Hydrothermally Inactive Seafloor Sulfide Deposits. 2013 , 30, 313-326	36
1435	Succession of bacterial communities during composting process as detected by 16S rRNA clone libraries analysis. 2013 , 78, 58-66	78
1434	Ecological Inferences from a deep screening of the Complex Bacterial Consortia associated with the coral, <i>Porites astreoides</i> . 2013 , 22, 4349-4362	43
1433	Secondary structure improves OTU assignments of 16S rRNA gene sequences. 2013 , 7, 457-60	46
1432	Previously unclassified bacteria dominate during thermophilic and mesophilic anaerobic pre-treatment of primary sludge. 2013 , 36, 281-90	20
1431	UPARSE: highly accurate OTU sequences from microbial amplicon reads. 2013 , 10, 996-8	8067
1430	Composition diversity and nutrition conditions for accumulation of polyhydroxyalkanoate (PHA) in a bacterial community from activated sludge. 2013 , 97, 9377-87	25
1429	Bacterial communities in different sections of a municipal wastewater treatment plant revealed by 16S rDNA 454 pyrosequencing. 2013 , 97, 2681-90	227
1428	<i>Thermodesulfobacterium geofontis</i> sp. nov., a hyperthermophilic, sulfate-reducing bacterium isolated from Obsidian Pool, Yellowstone National Park. 2013 , 17, 251-63	22
1427	Analysis of microbiota alterations in inflammasome-deficient mice. 2013 , 1040, 185-94	23
1426	Sewage reflects the distribution of human faecal Lachnospiraceae. 2013 , 15, 2213-27	75
1425	Filtering and ranking techniques for automated selection of high-quality 16S rRNA gene sequences. 2013 , 36, 549-59	4
1424	Magma-To-Microbe Networks in the Context of Sulfide Hosted Microbial Ecosystems. 2013 , 233-258	2
1423	Characterizing the microbiota across the gastrointestinal tract of a Brazilian Nelore steer. 2013 , 164, 307-14	103
1422	Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. 2013 , 41, e1	3890
1421	Microbial community dynamics during acetate biostimulation of RDX-contaminated groundwater. 2013 , 47, 7672-8	30
1420	Selective occurrence of Rhizobiales in frost flowers on the surface of young sea ice near Barrow, Alaska and distribution in the polar marine rare biosphere. 2013 , 5, 575-82	12

1419	GPU-Meta-Storms: Computing the similarities among massive microbial communities using GPU. 2013 ,		1
1418	SIV-induced instability of the chimpanzee gut microbiome. 2013 , 14, 340-5		62
1417	Metabolic modeling of species interaction in the human microbiome elucidates community-level assembly rules. 2013 , 110, 12804-9		251
1416	Pyrosequencing-based profiling of archaeal and bacterial 16S rRNA genes identifies a novel archaeon associated with black band disease in corals. 2013 , 15, 2994-3007		18
1415	The core faecal bacterial microbiome of Irish Thoroughbred racehorses. 2013 , 57, 492-501		62
1414	Slowing PCR ramp speed reduces chimera formation from environmental samples. 2013 , 93, 203-5		32
1413	Differential recovery of bacterial and archaeal 16S rRNA genes from ruminal digesta in response to glycerol as cryoprotectant. 2013 , 95, 381-3		17
1412	High-throughput sequencing and metagenomics: moving forward in the culture-independent analysis of food microbial ecology. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 3148-55	4.8	334
1411	Identification of trigger factors selecting for polyphosphate- and glycogen-accumulating organisms in aerobic granular sludge sequencing batch reactors. 2013 , 47, 7006-18		53
1410	Isosteric and nonisosteric base pairs in RNA motifs: molecular dynamics and bioinformatics study of the sarcin-ricin internal loop. 2013 , 117, 14302-19		18
1409	Sensitive and substrate-specific detection of metabolically active microorganisms in natural microbial consortia using community isotope arrays. 2013 , 342, 70-5		3
1408	Screening metatranscriptomes for toxin genes as functional drivers of human colorectal cancer. 2013 , 27, 85-99		28
1407	Deoxygenation alters bacterial diversity and community composition in the ocean's largest oxygen minimum zone. 2013 , 4, 2705		52
1406	Gut microbiota from twins discordant for obesity modulate metabolism in mice. 2013 , 341, 1241214		2251
1405	Quikr: a method for rapid reconstruction of bacterial communities via compressive sensing. 2013 , 29, 2096-102		32
1404	Environmental bio-monitoring with high-throughput sequencing. 2013 , 14, 575-88		23
1403	Use of bifidobacterial specific terminal restriction fragment length polymorphisms to complement next generation sequence profiling of infant gut communities. 2013 , 19, 62-9		18
1402	Removing environmental sources of variation to gain insight on symbionts vs. transient microbes in high and low microbial abundance sponges. 2013 , 15, 3008-19		38

1401	Two accurate sequence, structure, and phylogenetic template-based RNA alignment systems. 2013 , 7 Suppl 4, S13	9
1400	Alignment-free supervised classification of metagenomes by recursive SVM. 2013 , 14, 641	21
1399	Genome resolved analysis of a premature infant gut microbial community reveals a <i>Varibaculum cambriense</i> genome and a shift towards fermentation-based metabolism during the third week of life. 2013 , 1, 30	39
1398	Culture dependent and independent analysis of bacterial communities associated with commercial salad leaf vegetables. 2013 , 13, 274	132
1397	High throughput sequencing methods and analysis for microbiome research. 2013 , 95, 401-14	167
1396	Nitrite oxidation in the upper water column and oxygen minimum zone of the eastern tropical North Pacific Ocean. 2013 , 7, 2192-205	71
1395	Alterations in the gut microbiota associated with HIV-1 infection. 2013 , 14, 329-39	284
1394	Assessing the human gut microbiota in metabolic diseases. 2013 , 62, 3341-9	289
1393	Simultaneous pyrosequencing of the 16S rRNA, IncP-1 trfA, and merA genes. 2013 , 95, 280-4	5
1392	Assembling full-length rRNA genes from short-read metagenomic sequence datasets using EMIRGE. 2013 , 531, 333-52	7
1391	Computational methods for high-throughput comparative analyses of natural microbial communities. 2013 , 531, 353-70	23
1390	Advancing our understanding of the human microbiome using QIIME. 2013 , 531, 371-444	373
1389	Diversity and population structure of Marine Group A bacteria in the Northeast subarctic Pacific Ocean. 2013 , 7, 256-68	52
1388	Temporal change in the gut community of rats fed high amylose cornstarch is driven by endogenous urea rather than strictly on carbohydrate availability. 2013 , 114, 1516-28	31
1387	Higher seasonal variation of actinobacterial communities than spatial heterogeneity in the surface sediments of Taihu Lake, China. 2013 , 59, 353-8	2
1386	Short communication: Evidence that microbial translocation occurs in HIV-infected children in the United Kingdom. 2013 , 29, 1589-93	14
1385	The DNA60IFX contest. 2013 , 14, 124	
1384	Dynamics of cathode-associated microbial communities and metabolite profiles in a glycerol-fed bioelectrochemical system. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 4008-14	4.8 53

1383	The Paint Pots, Kootenay National Park, Canada: A natural acid spring analogue for Mars. 2013 , 50, 94-108	19
1382	Ectobiotic and endobiotic bacteria associated with <i>Eutreptiella</i> sp. isolated from Long Island Sound. 2013 , 164, 60-74	32
1381	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. 2013 , 10, 57-9	2167
1380	16S rRNA survey revealed complex bacterial communities and evidence of bacterial interference on human adenoids. 2013 , 15, 535-47	27
1379	Ocean acidification reduces induction of coral settlement by crustose coralline algae. 2013 , 19, 303-15	97
1378	Advances in computational analysis of metagenome sequences. 2013 , 15, 1-5	30
1377	Taxon-specific C/N relative use efficiency for amino acids in an estuarine community. 2013 , 83, 402-12	18
1376	Ammonia-oxidizing archaea and nitrite-oxidizing nitrospiras in the biofilter of a shrimp recirculating aquaculture system. 2013 , 83, 17-25	72
1375	Microbial community structure across fluid gradients in the Juan de Fuca Ridge hydrothermal system. 2013 , 83, 324-39	40
1374	RNA secondary structure, an important bioinformatics tool to enhance multiple sequence alignment: a case study (<i>Sordariomycetes</i> , Fungi). 2013 , 12, 305-319	11
1373	Comparing metabolic functionalities, community structures, and dynamics of herbicide-degrading communities cultivated with different substrate concentrations. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 367-75	4.8 28
1372	Tackling the minority: sulfate-reducing bacteria in an archaea-dominated subsurface biofilm. 2013 , 7, 635-51	51
1371	Characterization of sulfate-reducing granular sludge in the SANI() process. 2013 , 47, 7042-52	77
1370	Novel bacterial phylotypes associated with the healthy feline oral cavity and feline chronic gingivostomatitis. 2013 , 94, 428-32	15
1369	Molecular characterization of microbial populations in full-scale biofilters treating iron, manganese and ammonia containing groundwater in Harbin, China. 2013 , 147, 234-239	48
1368	Sensitivity of soil respiration and microbial communities to altered snowfall. 2013 , 57, 217-227	87
1367	Establishing a relationship between bacteria in the human gut and complex regional pain syndrome. 2013 , 29, 62-69	14
1366	Intrinsic rates of petroleum hydrocarbon biodegradation in Gulf of Mexico intertidal sandy sediments and its enhancement by organic substrates. 2013 , 244-245, 537-44	29

1365	Using Water Chemistry, Isotopes and Microbiology to Evaluate Groundwater Sources, Flow Paths and Geochemical Reactions in the Death Valley Flow System, USA. 2013 , 7, 842-845	11
1364	A comparison of microbial communities in deep-sea polymetallic nodules and the surrounding sediments in the Pacific Ocean. 2013 , 79, 40-49	41
1363	Investigation of the koala (<i>Phascolarctos cinereus</i>) hindgut microbiome via 16S pyrosequencing. 2013 , 167, 554-64	37
1362	Chronic N-amended soils exhibit an altered bacterial community structure in Harvard Forest, MA, USA. 2013 , 83, 478-93	64
1361	Meconium microbiota types dominated by lactic acid or enteric bacteria are differentially associated with maternal eczema and respiratory problems in infants. 2013 , 43, 198-211	238
1360	Stool substitute transplant therapy for the eradication of <i>Clostridium difficile</i> infection: 'RePOOPulating' the gut. 2013 , 1, 3	503
1359	<i>Altererythrobacter gangjinensis</i> sp. nov., a marine bacterium isolated from a tidal flat. 2013 , 63, 971-976	41
1358	Effect of media composition, including gelling agents, on isolation of previously uncultured rumen bacteria. 2013 , 56, 63-70	19
1357	Antagonism influences assembly of a <i>Bacillus</i> guild in a local community and is depicted as a food-chain network. 2013 , 7, 487-97	68
1356	Enrichment and dynamics of novel syntrophs in a methanogenic hexadecane-degrading culture from a Chinese oilfield. 2013 , 83, 757-66	42
1355	Colorless Sulfur Bacteria. 2013 , 555-588	12
1354	Characterization of rhizosphere prokaryotic diversity in a horizontal subsurface flow constructed wetland using a PCR cloning-sequencing based approach. 2013 , 97, 4221-31	18
1353	The <i>Montastraea faveolata</i> microbiome: ecological and temporal influences on a Caribbean reef-building coral in decline. 2013 , 15, 2082-94	52
1352	Temporal variability in soil microbial communities across land-use types. 2013 , 7, 1641-50	299
1351	Experimentally induced habitat filtering in marine bacterial communities. 2013 , 477, 77-86	11
1350	Bacterial succession in Antarctic soils of two glacier forefields on Larsemann Hills, East Antarctica. 2013 , 85, 128-42	66
1349	Sediment microbial communities in Great Boiling Spring are controlled by temperature and distinct from water communities. 2013 , 7, 718-29	106
1348	Genomes of the class <i>Erysipelotrichia</i> clarify the firmicute origin of the class <i>Mollicutes</i> . 2013 , 63, 2727-2741	31

- 1347 Low acetate concentrations favor polyphosphate-accumulating organisms over glycogen-accumulating organisms in enhanced biological phosphorus removal from wastewater. **2013**, 47, 3816-24 61
- 1346 Effects of oxygen on biodegradation of fuels in a corroding environment. **2013**, 81, 114-126 28
- 1345 Phylogenetic analysis of nitrate- and sulfate-reducing bacteria in a hydrogen-fed biofilm. **2013**, 85, 158-67 35
- 1344 *Geodermatophilus telluris* sp. nov., an actinomycete isolated from Saharan desert sand. **2013**, 63, 2254-2259 26
- 1343 Effects of multiple electron acceptors on microbial interactions in a hydrogen-based biofilm. **2013**, 47, 7396-403 43
- 1342 A phylogenetic analysis of the phylum Fibrobacteres. **2013**, 36, 376-82 18
- 1341 Community transcriptomic assembly reveals microbes that contribute to deep-sea carbon and nitrogen cycling. **2013**, 7, 1962-73 82
- 1340 Microbial communities in the subglacial waters of the Vatnajökull ice cap, Iceland. **2013**, 7, 427-37 49
- 1339 Phylogeographic analysis of filterable bacteria with special reference to Rhizobiales strains that occur in cryospheric habitats. **2013**, 25, 219-228 18
- 1338 Long-term operation of microbial electrosynthesis systems improves acetate production by autotrophic microbiomes. **2013**, 47, 6023-9 238
- 1337 The Influence of Vegetation on Microbial Enzyme Activity and Bacterial Community Structure in Freshwater Constructed Wetland Sediments. **2013**, 33, 365-378 38
- 1336 Screening and expression of genes from metagenomes. **2013**, 83, 1-68 39
- 1335 In situ chemistry and microbial community compositions in five deep-sea hydrothermal fluid samples from Irina II in the Logatchev field. **2013**, 15, 1551-60 36
- 1334 Phylogenetic stratigraphy in the Guerrero Negro hypersaline microbial mat. **2013**, 7, 50-60 147
- 1333 Metagenomic exploration reveals high levels of microbial arsenic metabolism genes in activated sludge and coastal sediments. **2013**, 97, 9579-88 52
- 1332 *Arabidopsis thaliana* as Model for Studies on the Bacterial Root Microbiota. **2013**, 243-256 5
- 1331 Integrating niche-based process and spatial process in biogeography of magnetotactic bacteria. **2013**, 3, 1643 50
- 1330 Detecting human bacterial pathogens in wastewater treatment plants by a high-throughput shotgun sequencing technique. **2013**, 47, 5433-41 147

1329	Microbial community adaptation to quaternary ammonium biocides as revealed by metagenomics. 2013 , 15, 2850-64	60
1328	<i>Sagittula marina</i> sp. nov., isolated from seawater and emended description of the genus <i>Sagittula</i> . 2013 , 63, 2101-2107	4
1327	<i>Geodermatophilus siccatus</i> sp. nov., isolated from arid sand of the Saharan desert in Chad. 2013 , 103, 449-56	35
1326	From molecules to dynamic biological communities. 2013 , 28, 241-259	12
1325	Exploring the interaction patterns in seasonal marine microbial communities with network analysis. 2013 ,	2
1324	Improving the coverage of the cyanobacterial phylum using diversity-driven genome sequencing. 2013 , 110, 1053-8	566
1323	<i>Geodermatophilus tzadiensis</i> sp. nov., a UV radiation-resistant bacterium isolated from sand of the Saharan desert. 2013 , 36, 177-82	29
1322	Transcriptional response of bathypelagic marine bacterioplankton to the Deepwater Horizon oil spill. 2013 , 7, 2315-29	118
1321	Suppression of methanogenesis in cellulose-fed microbial fuel cells in relation to performance, metabolite formation, and microbial population. 2013 , 129, 281-8	61
1320	Patient-specific analysis of periodontal and peri-implant microbiomes. 2013 , 92, 168S-75S	117
1319	Bacterial diversity of surface sand samples from the Gobi and Taklamaken deserts. 2013 , 66, 850-60	74
1318	Probiotic dosing of <i>Ruminococcus flavefaciens</i> affects rumen microbiome structure and function in reindeer. 2013 , 66, 840-9	13
1317	Using a two-stage hydrogen-based membrane biofilm reactor (MBfR) to achieve complete perchlorate reduction in the presence of nitrate and sulfate. 2013 , 47, 1565-72	66
1316	Encyclopedia of Metagenomics. 2013 , 1-6	
1315	Bacterial diversity, community structure and potential growth rates along an estuarine salinity gradient. 2013 , 7, 210-20	270
1314	Genomic Sequence Fragment Identification using Quasi-Alignment. 2013 ,	1
1313	Bacterial community response to petroleum hydrocarbon amendments in freshwater, marine, and hypersaline water-containing microcosms. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 5927-35	4.8 75
1312	<i>Parvibacter caecicola</i> gen. nov., sp. nov., a bacterium of the family Coriobacteriaceae isolated from the caecum of a mouse. 2013 , 63, 2642-2648	15

1311	Comparative genomic analysis of the microbiome [corrected] of herbivorous insects reveals eco-environmental adaptations: biotechnology applications. 2013 , 9, e1003131		46
1310	Probabilistic inference of biochemical reactions in microbial communities from metagenomic sequences. 2013 , 9, e1002981		12
1309	The role of microbial communities in parturition: is there evidence of association with preterm birth and perinatal morbidity and mortality?. 2013 , 30, 613-24		28
1308	Preliminary Analysis of Life within a Former Subglacial Lake Sediment in Antarctica. 2013 , 5, 680-702		13
1307	Molecular diversity of Bacteroidales in fecal and environmental samples and swine-associated subpopulations. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 816-24	4.8	7
1306	Crohn's disease may be differentiated into 2 distinct biotypes based on the detection of bacterial genomic sequences and virulence genes within submucosal tissues. 2013 , 47, 612-20		15
1305	Overview of organohalide-respiring bacteria and a proposal for a classification system for reductive dehalogenases. 2013 , 368, 20120322		201
1304	Optimization of routine identification of clinically relevant Gram-negative bacteria by use of matrix-assisted laser desorption ionization-time of flight mass spectrometry and the Bruker Biotyper. 2013 , 51, 1412-20		72
1303	Novel cultivation-based approach to understanding the miscellaneous crenarchaeotic group (MCG) archaea from sedimentary ecosystems. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 6400-6	4.8	32
1302	Bacterial DNA sifted from the <i>Trichoplax adhaerens</i> (Animalia: Placozoa) genome project reveals a putative rickettsial endosymbiont. 2013 , 5, 621-45		60
1301	Alignment-free genome tree inference by learning group-specific distance metrics. 2013 , 5, 1470-84		13
1300	Transcriptional response of nitrifying communities to wetting of dry soil. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 3294-302	4.8	84
1299	Impact of long-term diesel contamination on soil microbial community structure. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 619-30	4.8	238
1298	Assessment of bacterial and structural dynamics in aerobic granular biofilms. 2013 , 4, 175		73
1297	Large cryoconite aggregates on a Svalbard glacier support a diverse microbial community including ammonia-oxidizing archaea. 2013 , 8, 035044		40
1296	Analytical tools and databases for metagenomics in the next-generation sequencing era. 2013 , 11, 102-13		98
1295	Species identification and profiling of complex microbial communities using shotgun Illumina sequencing of 16S rRNA amplicon sequences. 2013 , 8, e60811		72
1294	Distinct distal gut microbiome diversity and composition in healthy children from Bangladesh and the United States. 2013 , 8, e53838		224

1293	Bacterial communities in Fe/Mn films, sulphate crusts, and aluminium glazes from Swedish Lapland: implications for astrobiology on Mars. 2013 , 12, 345-356	7
1292	Evolving concepts: how diet and the intestinal microbiome act as modulators of breast malignancy. 2013 , 2013, 693920	39
1291	Bacterial Infections across the Ants: Frequency and Prevalence of Wolbachia, Spiroplasma, and Asaia. 2013 , 2013, 1-11	32
1290	Unique vaginal microbiota that includes an unknown Mycoplasma-like organism is associated with Trichomonas vaginalis infection. 2013 , 207, 1922-31	53
1289	Fe-phylosilicate redox cycling organisms from a redox transition zone in Hanford 300 Area sediments. 2013 , 4, 388	35
1288	Free-living bacterial communities associated with tubeworm (<i>Ridgeia piscesae</i>) aggregations in contrasting diffuse flow hydrothermal vent habitats at the Main Endeavour Field, Juan de Fuca Ridge. 2013 , 2, 259-75	33
1287	Active bacterial flora surrounding foraminifera (xenophyophorea) living on the deep-sea floor. 2013 , 77, 381-4	11
1286	Benzene and sulfide removal from groundwater treated in a microbial fuel cell. 2013 , 110, 3104-13	41
1285	Altered enteric microbiota ecology in interleukin 10-deficient mice during development and progression of intestinal inflammation. 2013 , 4, 316-24	91
1284	. 2013 ,	
1283	Analysis of the bacterial communities associated with two ant-plant symbioses. 2013 , 2, 276-83	28
1282	Evidence and characteristics of a diverse and metabolically active microbial community in deep subsurface clay borehole water. 2013 , 86, 458-73	34
1281	Temperature-driven shifts in the epibiotic bacterial community composition of the brown macroalga <i>Fucus vesiculosus</i> . 2013 , 2, 338-49	66
1280	Microbial diversity in The Cedars, an ultrabasic, ultrareducing, and low salinity serpentinizing ecosystem. 2013 , 110, 15336-41	72
1279	Maximum likelihood estimation of frequencies of known haplotypes from pooled sequence data. 2013 , 30, 1145-58	38
1278	Microbiome of the upper troposphere: species composition and prevalence, effects of tropical storms, and atmospheric implications. 2013 , 110, 2575-80	297
1277	The role of the gastrointestinal microbiome in <i>Helicobacter pylori</i> pathogenesis. 2013 , 4, 505-31	129
1276	Collaborative cloud-enabled tools allow rapid, reproducible biological insights. 2013 , 7, 461-4	14

1275	Evidence for a persistent microbial seed bank throughout the global ocean. 2013 , 110, 4651-5	158
1274	Microbiome assembly across multiple body sites in low-birthweight infants. 2013 , 4, e00782-13	103
1273	Bacterial communities in pigmented biofilms formed on the sandstone bas-relief walls of the Bayon Temple, Angkor Thom, Cambodia. 2013 , 28, 422-31	47
1272	Genome Diversity of Spore-Forming Firmicutes. 2013 , 1,	114
1271	Different bacterial communities in ectomycorrhizae and surrounding soil. 2013 , 3, 3471	62
1270	Transcriptomic and phylogenetic analysis of a bacterial cell cycle reveals strong associations between gene co-expression and evolution. 2013 , 14, 450	41
1269	Sputum smear concentration may misidentify acid-fast bacilli as <i>Mycobacterium tuberculosis</i> in HIV-infected patients. 2013 , 63, 168-77	8
1268	Phylogeny-driven target selection for large-scale genome-sequencing (and other) projects. 2013 , 8, 360-74	42
1267	Genome of the marine alphaproteobacterium <i>Hoeflea phototrophica</i> type strain (DFL-43(T)). 2013 , 7, 440-8	7
1266	Complete genome sequence of <i>Coriobacterium glomerans</i> type strain (PW2(T)) from the midgut of <i>Pyrrhocoris apterus</i> L. (red soldier bug). 2013 , 8, 15-25	5
1265	Complete genome sequence of the bile-resistant pigment-producing anaerobe <i>Alistipes finegoldii</i> type strain (AHN2437(T)). 2013 , 8, 26-36	6
1264	High-quality-draft genome sequence of the yellow-pigmented flavobacterium <i>Joostella marina</i> type strain (En5(T)). 2013 , 8, 37-46	4
1263	Complete genome sequence of the moderate thermophile <i>Anaerobaculum mobile</i> type strain (NGA(T)). 2013 , 8, 47-57	10
1262	Genome sequence of the free-living aerobic spirochete <i>Turneriella parva</i> type strain (H(T)), and emendation of the species <i>Turneriella parva</i> . 2013 , 8, 228-38	8
1261	Genome sequence of the phage-gene rich marine <i>Phaeobacter arcticus</i> type strain DSM 23566(T). 2013 , 8, 450-64	9
1260	Genome sequence of the <i>Leisingera aquimarina</i> type strain (DSM 24565(T)), a member of the marine <i>Roseobacter</i> clade rich in extrachromosomal elements. 2013 , 8, 389-402	16
1259	Genome sequence of <i>Phaeobacter caeruleus</i> type strain (DSM 24564T), a surface-associated member of the marine <i>Roseobacter</i> clade. 2013 , 8, 403-419	12
1258	Genome sequence of the chemoheterotrophic soil bacterium <i>Saccharomonospora cyanea</i> type strain (NA-134(T)). 2013 , 9, 28-41	1

1257	Genome sequence of the moderately thermophilic sulfur-reducing bacterium <i>Thermanaerovibrio velox</i> type strain (Z-9701(T)) and emended description of the genus <i>Thermanaerovibrio</i> . 2013 , 9, 57-70	4
1256	Genome sequence of the <i>Litoreibacter arenae</i> type strain (DSM 19593(T)), a member of the <i>Roseobacter</i> clade isolated from sea sand. 2013 , 9, 117-27	6
1255	Genome sequence of <i>Frateuria aurantia</i> type strain (Kond67(T)), a xanthomonade isolated from <i>Lilium auratum</i> Lindl. 2013 , 9, 83-92	1
1254	Genome of the R-body producing marine alphaproteobacterium <i>Labrenzia alexandrii</i> type strain (DFL-11(T)). 2013 , 7, 413-26	8
1253	The Gut Microbiotassay: a high-throughput qPCR approach combinable with next generation sequencing to study gut microbial diversity. 2013 , 14, 788	62
1252	Genome sequence of the thermophilic fresh-water bacterium <i>Spirochaeta caldaria</i> type strain (H1(T)), reclassification of <i>Spirochaeta caldaria</i> , <i>Spirochaeta stenostrepta</i> , and <i>Spirochaeta zuelzeriae</i> in the genus <i>Treponema</i> as <i>Treponema caldaria</i> comb. nov., <i>Treponema stenostrepta</i> comb. nov., and <i>Treponema zuelzeriae</i> comb. nov. and emendation of the genus <i>Treponema</i> . 2013 , 8, 165-76	24
1251	Complete genome sequence of the halophilic bacterium <i>Spirochaeta africana</i> type strain (Z-7692(T)) from the alkaline Lake Magadi in the East African Rift. 2013 , 8, 165-76	2
1250	Genome sequence of the phylogenetically isolated spirochete <i>Leptonema illini</i> type strain (3055(T)). 2013 , 8, 177-87	4
1249	Genome sequence of the reddish-pigmented <i>Rubellimicrobium thermophilum</i> type strain (DSM 16684(T)), a member of the <i>Roseobacter</i> clade. 2013 , 8, 480-90	3
1248	Genome sequence of <i>Phaeobacter inhibens</i> type strain (T5(T)), a secondary metabolite producing representative of the marine <i>Roseobacter</i> clade, and emendation of the species description of <i>Phaeobacter inhibens</i> . 2013 , 9, 334-50	19
1247	Microbial flora of cochlear implants by gene pyrosequencing. 2013 , 34, e65-71	14
1246	Histamine-2 receptor blockers alter the fecal microbiota in premature infants. 2013 , 56, 397-400	80
1245	Diffuse flow environments within basalt- and sediment-based hydrothermal vent ecosystems harbor specialized microbial communities. 2013 , 4, 182	31
1244	A microbial clock provides an accurate estimate of the postmortem interval in a mouse model system. 2013 , 2, e01104	183
1243	A multifactor analysis of fungal and bacterial community structure in the root microbiome of mature <i>Populus deltoides</i> trees. 2013 , 8, e76382	186
1242	QC-Chain: fast and holistic quality control method for next-generation sequencing data. 2013 , 8, e60234	49
1241	Colonization patterns of soil microbial communities in the Atacama Desert. 2013 , 1, 28	132
1240	16S rRNA gene-based identification of microbiota associated with the parthenogenetic troglobiont sand fly <i>Deanemyia maruaga</i> (Diptera, Psychodidae) from central Amazon, Brazil. 2013 , 44, 325-8	2

1239	The characterization of microorganisms in dairy wastewater storage ponds. 2013 , 42, 1583-8	5
1238	Highly variable microbiota development in the chicken gastrointestinal tract. 2013 , 8, e84290	155
1237	Stimulatory effect of xenobiotics on oxidative electron transport of chemolithotrophic nitrifying bacteria used as biosensing element. 2013 , 8, e53484	3
1236	Evolution of a pathogen: a comparative genomics analysis identifies a genetic pathway to pathogenesis in <i>Acinetobacter</i> . 2013 , 8, e54287	88
1235	Sputum microbiota in tuberculosis as revealed by 16S rRNA pyrosequencing. 2013 , 8, e54574	67
1234	Base-calling algorithm with vocabulary (BCV) method for analyzing population sequencing chromatograms. 2013 , 8, e54835	6
1233	Pyrosequencing reveals high-temperature cellulolytic microbial consortia in Great Boiling Spring after in situ lignocellulose enrichment. 2013 , 8, e59927	33
1232	phyloseq: an R package for reproducible interactive analysis and graphics of microbiome census data. 2013 , 8, e61217	6869
1231	Shedding light on the microbial community of the macropod foregut using 454-amplicon pyrosequencing. 2013 , 8, e61463	25
1230	Assembly-driven community genomics of a hypersaline microbial ecosystem. 2013 , 8, e61692	71
1229	Metagenomic identification of bacterioplankton taxa and pathways involved in microcystin degradation in lake erie. 2013 , 8, e61890	77
1228	The culturable soil antibiotic resistome: a community of multi-drug resistant bacteria. 2013 , 8, e65567	104
1227	Factors Controlling Soil Microbial Biomass and Bacterial Diversity and Community Composition in a Cold Desert Ecosystem: Role of Geographic Scale. 2013 , 8, e66103	75
1226	Phylogenetic analysis of a microbialite-forming microbial mat from a hypersaline lake of the Kiritimati atoll, Central Pacific. 2013 , 8, e66662	111
1225	DNA-SIP reveals that Syntrophaceae play an important role in methanogenic hexadecane degradation. 2013 , 8, e66784	50
1224	Culture-independent investigation of the microbiome associated with the nematode <i>Acrobeloides maximus</i> . 2013 , 8, e67425	33
1223	Light structures phototroph, bacterial and fungal communities at the soil surface. 2013 , 8, e69048	16
1222	Antibiotic resistance of bacteria isolated from the internal organs of edible snow crabs. 2013 , 8, e70887	16

1221	Microbial life in a fjord: metagenomic analysis of a microbial mat in Chilean patagonia. 2013 , 8, e71952	15
1220	Soil-borne bacterial structure and diversity does not reflect community activity in Pampa biome. 2013 , 8, e76465	39
1219	Systematic identification of gene families for use as "markers" for phylogenetic and phylogeny-driven ecological studies of bacteria and archaea and their major subgroups. 2013 , 8, e77033	123
1218	Deep sequencing identifies ethnicity-specific bacterial signatures in the oral microbiome. 2013 , 8, e77287	124
1217	An in vitro model of the horse gut microbiome enables identification of lactate-utilizing bacteria that differentially respond to starch induction. 2013 , 8, e77599	54
1216	Distinct phyllosphere bacterial communities on Arabidopsis wax mutant leaves. 2013 , 8, e78613	59
1215	Evidence of unique and generalist microbes in distantly related sympatric intertidal marine sponges (Porifera: Demospongiae). 2013 , 8, e80653	20
1214	Microbial ecology of the hive and pollination landscape: bacterial associates from floral nectar, the alimentary tract and stored food of honey bees (<i>Apis mellifera</i>). 2013 , 8, e83125	167
1213	Same, same but different: symbiotic bacterial associations in GBR sponges. 2012 , 3, 444	43
1212	Low temperature geomicrobiology follows host rock composition along a geochemical gradient in lau basin. 2013 , 4, 61	32
1211	Metagenomic evidence for sulfur lithotrophy by Epsilonproteobacteria as the major energy source for primary productivity in a sub-aerial arctic glacial deposit, Borup Fiord Pass. 2013 , 4, 63	26
1210	Metagenome sequence analysis of filamentous microbial communities obtained from geochemically distinct geothermal channels reveals specialization of three aquificales lineages. 2013 , 4, 84	58
1209	Multilocus sequence analysis of <i>Thermoanaerobacter</i> isolates reveals recombining, but differentiated, populations from geothermal springs of the Uzon Caldera, Kamchatka, Russia. 2013 , 4, 169	5
1208	Microbial diversity and methanogenic activity of Antrim Shale formation waters from recently fractured wells. 2013 , 4, 367	63
1207	Archaeal assemblages inhabiting temperate mixed forest soil fluctuate in taxon composition and spatial distribution over time. 2013 , 2013, 870825	8
1206	Dynamic succession of soil bacterial community during continuous cropping of peanut (<i>Arachis hypogaea</i> L.). 2014 , 9, e101355	41
1205	Changes in abundance of oral microbiota associated with oral cancer. 2014 , 9, e98741	197
1204	Strengths and limitations of 16S rRNA gene amplicon sequencing in revealing temporal microbial community dynamics. 2014 , 9, e93827	323

1203	Structure, composition and metagenomic profile of soil microbiomes associated to agricultural land use and tillage systems in Argentine Pampas. 2014 , 9, e99949	129
1202	The effects of Mary Rose conservation treatment on iron oxidation processes and microbial communities contributing to acid production in marine archaeological timbers. 2014 , 9, e84169	19
1201	Application of microarray and functional-based screening methods for the detection of antimicrobial resistance genes in the microbiomes of healthy humans. 2014 , 9, e86428	45
1200	Bacterial communities of surface mixed layer in the Pacific sector of the western Arctic Ocean during sea-ice melting. 2014 , 9, e86887	27
1199	Airborne bacterial communities in residences: similarities and differences with fungi. 2014 , 9, e91283	99
1198	First evidence for the presence of iron oxidizing zetaproteobacteria at the Levantine continental margins. 2014 , 9, e91456	21
1197	High concentrations of methyl fluoride affect the bacterial community in a thermophilic methanogenic sludge. 2014 , 9, e92604	2
1196	Novel PCR primers for the archaeal phylum Thaumarchaeota designed based on the comparative analysis of 16S rRNA gene sequences. 2014 , 9, e96197	5
1195	Microbial communities in sunken wood are structured by wood-boring bivalves and location in a submarine canyon. 2014 , 9, e96248	20
1194	Escherichia coli O157:H7 super-shedder and non-shedder feedlot steers harbour distinct fecal bacterial communities. 2014 , 9, e98115	35
1193	Coupling genetic and chemical microbiome profiling reveals heterogeneity of archaeome and bacteriome in subsurface biofilms that are dominated by the same archaeal species. 2014 , 9, e99801	22
1192	Identification of the microbiota in carious dentin lesions using 16S rRNA gene sequencing. 2014 , 9, e103712	49
1191	Diversity and community composition of methanogenic archaea in the rumen of Scottish upland sheep assessed by different methods. 2014 , 9, e106491	22
1190	Alterations in ileal mucosa bacteria related to diet complexity and growth performance in young pigs. 2014 , 9, e108472	22
1189	Relationships between bacterial community composition, functional trait composition and functioning are context dependent--but what is the context?. 2014 , 9, e112409	2
1188	Maternal obesity is associated with alterations in the gut microbiome in toddlers. 2014 , 9, e113026	112
1187	Bacteria and methanogens differ along the gastrointestinal tract of Chinese roe deer (Capreolus pygargus). 2014 , 9, e114513	37
1186	Diversity, distribution and hydrocarbon biodegradation capabilities of microbial communities in oil-contaminated cyanobacterial mats from a constructed wetland. 2014 , 9, e114570	41

1185	IM-TORNADO: a tool for comparison of 16S reads from paired-end libraries. 2014 , 9, e114804	76
1184	Investigation of bacterial diversity in the feces of cattle fed different diets. 2014 , 92, 683-94	99
1183	Pyruvic oxime nitrification and copper and nickel resistance by a <i>Cupriavidus pauculus</i> , an active heterotrophic nitrifier-denitrifier. 2014 , 2014, 901702	6
1182	Gastrointestinal Bacterial and Methanogenic Archaea Diversity Dynamics Associated with Condensed Tannin-Containing Pine Bark Diet in Goats Using 16S rDNA Amplicon Pyrosequencing. 2014 , 2014, 141909	34
1181	Seasonal effects in a lake sediment archaeal community of the Brazilian Savanna. 2014 , 2014, 957145	9
1180	An antimethanogenic nutritional intervention in early life of ruminants modifies ruminal colonization by Archaea. 2014 , 2014, 841463	49
1179	Assessment of the Deepwater Horizon oil spill impact on Gulf coast microbial communities. 2014 , 5, 130	128
1178	<i>Pinus flexilis</i> and <i>Picea engelmannii</i> share a simple and consistent needle endophyte microbiota with a potential role in nitrogen fixation. 2014 , 5, 333	60
1177	Evaluation of automated ribosomal intergenic spacer analysis for bacterial fingerprinting of rumen microbiome compared to pyrosequencing technology. 2014 , 3, 109-20	19
1176	High-Throughput Sequencing, a Versatile Weapon to Support Genome-Based Diagnosis in Infectious Diseases: Applications to Clinical Bacteriology. 2014 , 3, 258-79	19
1175	Diversity of bacterial communities of fitness center surfaces in a U.S. metropolitan area. 2014 , 11, 12544-61	30
1174	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. 2014 , 2, e545	395
1173	Membership and behavior of ultra-low-diversity pathogen communities present in the gut of humans during prolonged critical illness. 2014 , 5, e01361-14	203
1172	<i>Saccharomyces boulardii</i> administration changes gut microbiota and reduces hepatic steatosis, low-grade inflammation, and fat mass in obese and type 2 diabetic db/db mice. 2014 , 5, e01011-14	158
1171	Bacterial community structure influenced by <i>Coscinodiscus</i> sp. in the Vistula river plume**This research was carried out with the support of a grant from the Polish Ministry of Science and Higher Education (No. NN304 025334) and statutory activities of the Department of Fisheries Oceanography and Marine Ecology of the National Marine Fisheries Research Institute (project	5
1170	The loss of topography in the microbial communities of the upper respiratory tract in the elderly. 2014 , 11, 513-21	124
1169	Effects of high hydrostatic pressure on coastal bacterial community abundance and diversity. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 5992-6003	4.8 18
1168	History and impact of RDP: a legacy from Carl Woese to microbiology. 2014 , 11, 239-43	15

1167	Meta-analyses of human gut microbes associated with obesity and IBD. 2014 , 588, 4223-33	514
1166	A phylogenomic view of ecological specialization in the Lachnospiraceae, a family of digestive tract-associated bacteria. 2014 , 6, 703-13	402
1165	Diet and exercise orthogonally alter the gut microbiome and reveal independent associations with anxiety and cognition. 2014 , 9, 36	184
1164	Effects of farmhouse hotel and paper mill effluents on bacterial community structures in sediment and surface water of Nanxi River, China. 2014 , 68, 773-84	4
1163	Respiratory tract clinical sample selection for microbiota analysis in patients with pulmonary tuberculosis. 2014 , 2, 29	40
1162	A comparative study of microbial communities in soils amended by manures from pigs fed with organic versus synthetic feeds. 2014 , 96, 426-441	1
1161	Modulation of fecal Clostridiales bacteria and butyrate by probiotic intervention with <i>Lactobacillus paracasei</i> DG varies among healthy adults. 2014 , 144, 1787-96	127
1160	An expanded genomic representation of the phylum cyanobacteria. 2014 , 6, 1031-45	186
1159	The gut microbiota of Colombians differs from that of Americans, Europeans and Asians. 2014 , 14, 311	125
1158	The effect of omeprazole on the development of experimental autoimmune encephalomyelitis in C57BL/6J and SJL/J mice. 2014 , 7, 605	15
1157	Dietary supplementation with lactose or artificial sweetener enhances swine gut <i>Lactobacillus</i> population abundance. 2014 , 111 Suppl 1, S30-5	64
1156	MyTaxa: an advanced taxonomic classifier for genomic and metagenomic sequences. 2014 , 42, e73	240
1155	Genomic properties of Marine Group A bacteria indicate a role in the marine sulfur cycle. 2014 , 8, 455-68	61
1154	Reprogramming of gut microbiome energy metabolism by the FUT2 Crohn's disease risk polymorphism. 2014 , 8, 2193-206	140
1153	Microbial cargo: do bacteria on symbiotic propagules reinforce the microbiome of lichens?. 2014 , 16, 3743-52	54
1152	pH of drinking water influences the composition of gut microbiome and type 1 diabetes incidence. 2014 , 63, 632-44	74
1151	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
1150	Oral microbiota and host innate immune response in bisphosphonate-related osteonecrosis of the jaw. 2014 , 6, 219-26	33

1149	Primers: Functional Genes for Anaerobic Hydrocarbon Degrading Microbes. 2014 , 39-55	3
1148	Identification of bacterial community composition in freshwater aquaculture system farming of <i>Litopenaeus vannamei</i> reveals distinct temperature-driven patterns. 2014 , 15, 13663-80	37
1147	Biogeography of anaerobic ammonia-oxidizing (anammox) bacteria. 2014 , 5, 399	126
1146	Molecular methods for studying biocorrosion. 2014 , 57-75	1
1145	Characterizing the avian gut microbiota: membership, driving influences, and potential function. 2014 , 5, 223	220
1144	Soil bacterial community structure remains stable over a 5-year chronosequence of insect-induced tree mortality. 2014 , 5, 681	24
1143	Taxonomically and functionally diverse microbial communities in deep crystalline rocks of the Fennoscandian shield. 2014 , 8, 126-38	81
1142	Applications of Next-Generation Sequencing Technologies to the Study of the Human Microbiome. 2014 , 75-106	
1141	Immersing undergraduate students into research on the metagenomics of the plant rhizosphere: a pedagogical strategy to engage civic-mindedness and retain undergraduates in STEM. 2014 , 5, 157	10
1140	Antibiotic Resistance in <i>Aeromonas</i> Upstream and Downstream of a Water Resource Recovery Facility. 2014 , 86, 835-843	2
1139	Illuminating microbial dark matter in meromictic Sakinaw Lake. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 6807-18	4.8 79
1138	Mining seasonal marine microbial pattern with greedy heuristic clustering and symmetrical nonnegative matrix factorization. 2014 , 2014, 189590	2
1137	Ecological consistency of SSU rRNA-based operational taxonomic units at a global scale. 2014 , 10, e1003594	58
1136	A novel nutritional predictor links microbial fastidiousness with lowered ubiquity, growth rate, and cooperativeness. 2014 , 10, e1003726	19
1135	Bacterial population succession and adaptation affected by insecticide application and soil spraying history. 2014 , 5, 457	70
1134	Site- and horizon-specific patterns of microbial community structure and enzyme activities in permafrost-affected soils of Greenland. 2014 , 5, 541	62
1133	<i>Bacteroides dorei</i> dominates gut microbiome prior to autoimmunity in Finnish children at high risk for type 1 diabetes. 2014 , 5, 678	159
1132	Bacterial communities in the rumen of Holstein heifers differ when fed orchardgrass as pasture vs. hay. 2014 , 5, 689	26

1131	Captivity results in disparate loss of gut microbial diversity in closely related hosts. 2014 , 2, cou009	88
1130	GPU-Meta-Storms: computing the structure similarities among massive amount of microbial community samples using GPU. 2014 , 30, 1031-3	15
1129	PhyloPDb: a 16S rRNA oligonucleotide probe database for prokaryotic identification. 2014 , 2014, bau036	13
1128	Depth-dependent geochemical and microbiological gradients in Fe(III) deposits resulting from coal mine-derived acid mine drainage. 2014 , 5, 215	28
1127	Fe-oxide grain coatings support bacterial Fe-reducing metabolisms in 1.7-2.0 km-deep subsurface quartz arenite sandstone reservoirs of the Illinois Basin (USA). 2014 , 5, 511	10
1126	Comparisons of the composition and biogeographic distribution of the bacterial communities occupying South African thermal springs with those inhabiting deep subsurface fracture water. 2014 , 5, 679	46
1125	Differences between the rhizosphere microbiome of <i>Beta vulgaris</i> ssp. <i>maritima</i> -ancestor of all beet crops-and modern sugar beets. 2014 , 5, 415	73
1124	Microbial dysbiosis is associated with human breast cancer. 2014 , 9, e83744	233
1123	A comprehensive aligned nifH gene database: a multipurpose tool for studies of nitrogen-fixing bacteria. 2014 , 2014, bau001	112
1122	Prevalence of unclassified bacteria in tropical coastal waters of malaysia revealed by metagenomic approach. 2014 , 2,	3
1121	Exposure to a social stressor disrupts the community structure of the colonic mucosa-associated microbiota. 2014 , 14, 189	203
1120	Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition. 2014 , 15, R76	150
1119	DNA extraction protocols cause differences in 16S rRNA amplicon sequencing efficiency but not in community profile composition or structure. 2014 , 3, 910-21	64
1118	Protocols for Investigating the Microbiology of Drilling Fluids, Hydraulic Fracturing Fluids, and Formations in Unconventional Natural Gas Reservoirs. 2014 , 133-156	1
1117	Infectious Microecology. 2014 ,	4
1116	Prolonged use of a proton pump inhibitor reduces microbial diversity: implications for <i>Clostridium difficile</i> susceptibility. 2014 , 2, 42	100
1115	Fast dendrogram-based OTU clustering using sequence embedding. 2014 ,	3
1114	Characterization of bacteriophage communities and CRISPR profiles from dental plaque. 2014 , 14, 175	41

1113	Draft Genome Sequence of the Lignin-Degrading Burkholderia sp. Strain LIG30, Isolated from Wet Tropical Forest Soil. 2014 , 2,	22
1112	Altered oral viral ecology in association with periodontal disease. 2014 , 5, e01133-14	108
1111	Microbial community composition and in silico predicted metabolic potential reflect biogeochemical gradients between distinct peatland types. 2014 , 90, 633-46	21
1110	Temporal changes and the effect of subtherapeutic concentrations of antibiotics in the gut microbiota of swine. 2014 , 90, 599-608	42
1109	Bacterial Typing and Identification By Genomic Analysis of 16S Ω 3S rRNA Intergenic Transcribed Spacer (ITS) Sequences. 2014 , 41, 253-274	10
1108	Hibernation alters the diversity and composition of mucosa-associated bacteria while enhancing antimicrobial defence in the gut of 13-lined ground squirrels. 2014 , 23, 4658-69	43
1107	Shotgun microbial profiling of fossil remains. 2014 , 23, 1780-98	43
1106	Intertidal epilithic bacteria diversity changes along a naturally occurring carbon dioxide and pH gradient. 2014 , 89, 670-8	28
1105	Shifts in microbial community structure and function in light- and dark-grown biofilms driven by warming. 2014 , 16, 2550-67	29
1104	The Sphagnum microbiome supports bog ecosystem functioning under extreme conditions. 2014 , 23, 4498-510	69
1103	Host-specific microbial communities in three sympatric North Sea sponges. 2014 , 90, 390-403	21
1102	Characterization of growing bacterial populations in McMurdo Dry Valley soils through stable isotope probing with (18) O-water. 2014 , 89, 415-25	31
1101	Mouse Genetics. 2014 ,	2
1100	Spatial distribution of microbial communities associated with dune landform in the Gurbantunggut Desert, China. 2014 , 52, 898-907	16
1099	Indoor airborne bacterial communities are influenced by ventilation, occupancy, and outdoor air source. 2014 , 24, 41-8	197
1098	The effect of long-term macrolide treatment on respiratory microbiota composition in non-cystic fibrosis bronchiectasis: an analysis from the randomised, double-blind, placebo-controlled BLESS trial. 2014 , 2, 988-96	108
1097	The microbiome of New World vultures. 2014 , 5, 5498	177
1096	Individuals' diet diversity influences gut microbial diversity in two freshwater fish (threespine stickleback and Eurasian perch). 2014 , 17, 979-87	178

1095	Challenges of studying viral aerosol metagenomics and communities in comparison with bacterial and fungal aerosols. 2014 , 357, 1-9		39
1094	Mathematical tools to optimize the design of oligonucleotide probes and primers. 2014 , 98, 9595-608		11
1093	Variations in potential CH ₄ flux and CO ₂ respiration from freshwater wetland sediments that differ by microsite location, depth and temperature. 2014 , 72, 84-94		15
1092	Similarity and differentiation between bacteria associated with skin of salamanders (<i>Plethodon jordani</i>) and free-living assemblages. 2014 , 88, 482-94		44
1091	Unique and shared responses of the gut microbiota to prolonged fasting: a comparative study across five classes of vertebrate hosts. 2014 , 90, 883-94		134
1090	The All-Species Living Tree Project. 2014 , 41, 45-59		3
1089	Herbivorous rodents (<i>Neotoma</i> spp.) harbour abundant and active foregut microbiota. 2014 , 16, 2869-78		54
1088	Marek's disease virus influences the core gut microbiome of the chicken during the early and late phases of viral replication. 2014 , 90, 300-12		22
1087	Exercise prevents weight gain and alters the gut microbiota in a mouse model of high fat diet-induced obesity. 2014 , 9, e92193		344
1086	Bacterial diversity assessment in Antarctic terrestrial and aquatic microbial mats: a comparison between bidirectional pyrosequencing and cultivation. 2014 , 9, e97564		49
1085	Phylogenetic signal in the community structure of host-specific microbiomes of tropical marine sponges. 2014 , 5, 532		107
1084	Microbiota of human breast tissue. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 3007-14	4.8	248
1083	Comparison of environmental and isolate <i>Sulfobacillus</i> genomes reveals diverse carbon, sulfur, nitrogen, and hydrogen metabolisms. 2014 , 15, 1107		54
1082	Bacterial community composition of chronic periodontitis and novel oral sampling sites for detecting disease indicators. 2014 , 2, 32		54
1081	Intestinal anastomotic injury alters spatially defined microbiome composition and function. 2014 , 2, 35		99
1080	Investigation of a new acetogen isolated from an enrichment of the tammar wallaby forestomach. 2014 , 14, 314		22
1079	Altered microbiota associated with abnormal humoral immune responses to commensal organisms in enthesitis-related arthritis. 2014 , 16, 486		134
1078	The lung microbiome after lung transplantation. 2014 , 8, 221-31		14

1077	Deep sequencing analysis reveals temporal microbiota changes associated with development of bovine digital dermatitis. 2014 , 82, 3359-73	69
1076	Broad scope method for creating humanized animal models for animal health and disease research through antibiotic treatment and human fecal transfer. 2014 , 5, 183-91	58
1075	Effects of polysaccharopeptide from <i>Trametes versicolor</i> and amoxicillin on the gut microbiome of healthy volunteers: a randomized clinical trial. 2014 , 5, 458-67	46
1074	Diversity of bacteria cultured from the blood of lesser electric rays caught in the northern gulf of Mexico. 2014 , 26, 225-32	11
1073	Analysis, optimization and verification of Illumina-generated 16S rRNA gene amplicon surveys. 2014 , 9, e94249	237
1072	Severity-related changes of bronchial microbiome in chronic obstructive pulmonary disease. 2014 , 52, 4217-23	127
1071	Restricted streptomycin use in apple orchards did not adversely alter the soil bacteria communities. 2013 , 4, 383	22
1070	The Variation of Microbial Communities in a Depth Profile of an Acidic, Nutrient-Poor Boreal Bog in Southwestern Finland. 2014 , 04, 832-859	30
1069	A rod-like bacterium is responsible for high molybdenum concentrations in the tropical sponge <i>Halichondria phakellioides</i> . 2014 , 65, 838	2
1068	The structures of the colonic mucosa-associated and luminal microbial communities are distinct and differentially affected by a prolonged murine stressor. 2014 , 5, 748-60	66
1067	Deterministic processes guide long-term synchronised population dynamics in replicate anaerobic digesters. 2014 , 8, 2015-28	224
1066	Host-associated bacterial taxa from Chlorobi, Chloroflexi, GN02, Synergistetes, SR1, TM7, and WPS-2 Phyla/candidate divisions. 2014 , 6,	55
1065	Selective proliferation of intestinal <i>Barnesiella</i> under fucosyllactose supplementation in mice. 2014 , 111, 1602-10	55
1064	Iron supplementation promotes gut microbiota metabolic activity but not colitis markers in human gut microbiota-associated rats. 2014 , 111, 2135-45	42
1063	. 2014 ,	6
1062	Application of Bioinformatics in Microbial Ecology. 2014 , 955-959, 276-280	
1061	Validation of IMP dehydrogenase inhibitors in a mouse model of cryptosporidiosis. 2014 , 58, 1603-14	44
1060	Metabolic alterations to the mucosal microbiota in inflammatory bowel disease. 2014 , 20, 723-31	55

1059	Soil Acidobacterial 16S rRNA Gene Sequences Reveal Subgroup Level Differences between Savanna-Like Cerrado and Atlantic Forest Brazilian Biomes. 2014 , 2014, 156341	23
1058	Variations of Bacterial Community Structure and Composition in Mangrove Sediment at Different Depths in Southeastern Brazil. 2014 , 6, 827-843	36
1057	MPI-blastn and NCBI-TaxCollector: improving metagenomic analysis with high performance classification and wide taxonomic attachment. 2014 , 12, 1450013	7
1056	Characterization of bacterial community shift in human Ulcerative Colitis patients revealed by Illumina based 16S rRNA gene amplicon sequencing. 2014 , 6, 22	60
1055	Microbes in the neonatal intensive care unit resemble those found in the gut of premature infants. 2014 , 2, 1	251
1054	Host lifestyle affects human microbiota on daily timescales. 2014 , 15, R89	548
1053	Resistance and resilience of the forest soil microbiome to logging-associated compaction. 2014 , 8, 226-44	194
1052	The amphibian skin-associated microbiome across species, space and life history stages. 2014 , 23, 1238-50	220
1051	Characterization of bacterial communities in solarized soil amended with lignocellulosic organic matter. 2014 , 73, 97-104	33
1050	Interactions in the microbiome: communities of organisms and communities of genes. 2014 , 38, 90-118	135
1049	Skin microbiome imbalance in patients with STAT1/STAT3 defects impairs innate host defense responses. 2014 , 6, 253-62	67
1048	Host-specific adaptation governs the interaction of the marine diatom, <i>Pseudo-nitzschia</i> and their microbiota. 2014 , 8, 63-76	85
1047	Using high-throughput sequencing to assess the impacts of treated and untreated wastewater discharge on prokaryotic communities in an urban river. 2014 , 98, 1841-51	45
1046	Bacterial diversity in Greenlandic soils as affected by potato cropping and inorganic versus organic fertilization. 2014 , 37, 61-71	41
1045	Illumina sequencing of the V4 hypervariable region 16S rRNA gene reveals extensive changes in bacterial communities in the cecum following carbohydrate oral infusion and development of early-stage acute laminitis in the horse. 2014 , 168, 436-41	37
1044	Metabolic profiles of prokaryotic and eukaryotic communities in deep-sea sponge <i>Neamphius huxleyi</i> [corrected], indicated by metagenomics. 2014 , 4, 3895	33
1043	Metagenomics using next-generation sequencing. 2014 , 1096, 183-201	55
1042	Metagenomic analysis of sludge from full-scale anaerobic digesters operated in municipal wastewater treatment plants. 2014 , 98, 5709-18	147

1041	Convergence of gut microbiomes in myrmecophagous mammals. 2014 , 23, 1301-17	179
1040	Environmental Microbiology. 2014 ,	5
1039	Phylogenetic and functional analysis of gut microbiota of a fungus-growing higher termite: Bacteroidetes from higher termites are a rich source of β -glucosidase genes. 2014 , 68, 416-25	35
1038	Divergent responses of soil fungi functional groups to short-term warming. 2014 , 68, 708-15	45
1037	Detecting the nonviable and heat-tolerant bacteria in activated sludge by minimizing DNA from dead cells. 2014 , 67, 829-36	18
1036	The temporal scaling of bacterioplankton composition: high turnover and predictability during shrimp cultivation. 2014 , 67, 256-64	45
1035	A systematic search for discriminating sites in the 16S ribosomal RNA gene. 2014 , 4, 2	15
1034	Characterization of bacterial communities in sediments receiving various wastewater effluents with high-throughput sequencing analysis. 2014 , 67, 612-23	51
1033	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
1032	Diversity of the vaginal microbiome correlates with preterm birth. 2014 , 21, 32-40	183
1031	Rumen bacterial community evaluated by 454 pyrosequencing and terminal restriction fragment length polymorphism analyses in dairy sheep fed marine algae. 2014 , 97, 1661-9	55
1030	Enhanced microbial diversity in the saliva microbiome induced by short-term probiotic intake revealed by 16S rRNA sequencing on the IonTorrent PGM platform. 2014 , 190, 30-9	26
1029	Salt tolerance and polyphyly in the cyanobacterium <i>Chroococidiopsis</i> (Pleurocapsales). 2014 , 50, 472-82	14
1028	Hydrocarbon-related microbial processes in the deep sediments of the Eastern Mediterranean Levantine Basin. 2014 , 87, 780-96	22
1027	Salinity affects compositional traits of epibacterial communities on the brown macroalga <i>Fucus vesiculosus</i> . 2014 , 88, 272-9	29
1026	Mosquitoes rely on their gut microbiota for development. 2014 , 23, 2727-39	263
1025	An analysis of the ruminal bacterial microbiota in West African Dwarf sheep fed grass- and tree-based diets. 2014 , 116, 1094-105	21
1024	Comparative analysis of gingival tissue antigen presentation pathways in ageing and periodontitis. 2014 , 41, 327-39	31

1023	Microbial community dynamics and stability during an ammonia-induced shift to syntrophic acetate oxidation. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 3375-83	4.8	100
1022	Methane emission and dynamics of methanotrophic and methanogenic communities in a flooded rice field ecosystem. 2014 , 88, 195-212		74
1021	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
1020	Improved group-specific primers based on the full SILVA 16S rRNA gene reference database. 2014 , 16, 2389-407		28
1019	Characterization of the gut microbiota of three commercially valuable warmwater fish species. 2014 , 116, 1396-404		212
1018	A glimpse of <i>Escherichia coli</i> O157:H7 survival in soils from eastern China. 2014 , 476-477, 49-56		21
1017	Microbial community structures of novel Icelandic hot spring systems revealed by PhyloChip G3 analysis. 2014 , 14, 229-40		11
1016	Characterizing changes in soil bacterial community structure in response to short-term warming. 2014 , 89, 281-92		75
1015	Spatial and temporal variations of microbial community in a mixed plug-flow loop reactor fed with dairy manure. 2014 , 7, 332-46		41
1014	Diversity and structure of bacterial communities associated with <i>Phanerochaete chrysosporium</i> during wood decay. 2014 , 16, 2238-52		38
1013	Molecular and lipid biomarker analysis of a gypsum-hosted endoevaporitic microbial community. 2014 , 12, 62-82		16
1012	<i>Muc5b</i> is required for airway defence. 2014 , 505, 412-6		450
1011	Diet rapidly and reproducibly alters the human gut microbiome. 2014 , 505, 559-63		5264
1010	Bacterial communities in manures of piglets and adult pigs bred with different feeds revealed by 16S rDNA 454 pyrosequencing. 2014 , 98, 2657-65		45
1009	Soil microbial community responses to a decade of warming as revealed by comparative metagenomics. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 1777-86	4.8	94
1008	Enzyme activities of aerobic lignocellulolytic bacteria isolated from wet tropical forest soils. 2014 , 37, 60-7		87
1007	Continuous syngas fermentation for the production of ethanol, n-propanol and n-butanol. 2014 , 151, 69-77		104
1006	Bacterial structure and spatiotemporal distribution in a horizontal subsurface flow constructed wetland. 2014 , 98, 3191-203		28

1005	Mineral Microniches Control the Diversity of Subsurface Microbial Populations. 2014 , 31, 246-261		44
1004	Metagenomic Evidence for Sulfide Oxidation in Extremely Acidic Cave Biofilms. 2014 , 31, 194-204		21
1003	EBI metagenomics--a new resource for the analysis and archiving of metagenomic data. 2014 , 42, D600-6		104
1002	Comparison of two approaches for the classification of 16S rRNA gene sequences. 2014 , 63, 1311-1315		9
1001	Microbial heterotrophic production in an oligotrophic acidic geothermal lake: responses to organic amendments and terrestrial plant litter. 2014 , 89, 606-24		3
1000	Partner associations across sympatric broad-headed bug species and their environmentally acquired bacterial symbionts. 2014 , 23, 1333-47		31
999	A new species of Burkholderia isolated from sugarcane roots promotes plant growth. 2014 , 7, 142-54		63
998	Free-Living and Particle-Associated Bacterioplankton in Large Rivers of the Mississippi River Basin Demonstrate Biogeographic Patterns. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 7186-95	4.8	40
997	Directly sampling the lung of a young child with cystic fibrosis reveals diverse microbiota. 2014 , 11, 1049-55		50
996	Comparative analysis of deep-sea bacterioplankton OMICS revealed the occurrence of habitat-specific genomic attributes. 2014 , 17, 1-8		7
995	Biofouling and microbial communities in membrane distillation and reverse osmosis. 2014 , 48, 13155-64		59
994	Internal porosity of mineral coating supports microbial activity in rapid sand filters for groundwater treatment. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 7010-20	4.8	27
993	Native microbiome impedes vertical transmission of Wolbachia in Anopheles mosquitoes. 2014 , 111, 12498-503		153
992	Soil microbial responses to increased moisture and organic resources along a salinity gradient in a polar desert. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 3034-43	4.8	103
991	Microbial community composition and dynamics in high-temperature biogas reactors using industrial bioethanol waste as substrate. 2014 , 98, 9095-106		28
990	Regulatory B cells are induced by gut microbiota-driven interleukin-1 β and interleukin-6 production. 2014 , 20, 1334-9		282
989	Microbial biogeography of wine grapes is conditioned by cultivar, vintage, and climate. 2014 , 111, E139-48		557
988	Amphiphilic siderophore production by oil-associating microbes. 2014 , 6, 1150-5		24

987	Effects of river sediment addition to the beach microbial communities. 2014 , 96, 68-83		1
986	Hand bacterial communities vary across two different human populations. 2014 , 160, 1144-1152		44
985	Construction of aligned database of <i>dsrA</i> , a gene encoding dissimilatory sulfite reductase alpha subunit, for metagenomic studies of sulfate-reducing bacteria. 2014 , 57, 419-427		0
984	Temperature response of denitrification and anaerobic ammonium oxidation rates and microbial community structure in Arctic fjord sediments. 2014 , 16, 3331-44		68
983	Responsiveness of cardiometabolic-related microbiota to diet is influenced by host genetics. 2014 , 25, 583-99		48
982	Rapid fucosylation of intestinal epithelium sustains host-commensal symbiosis in sickness. 2014 , 514, 638-41		343
981	Inhalable microorganisms in Beijing's PM2.5 and PM10 pollutants during a severe smog event. 2014 , 48, 1499-507		446
980	Nitrate shaped the selenate-reducing microbial community in a hydrogen-based biofilm reactor. 2014 , 48, 3395-402		86
979	<i>Lactobacillus rhamnosus</i> HN001 decreases the severity of necrotizing enterocolitis in neonatal mice and preterm piglets: evidence in mice for a role of TLR9. 2014 , 306, G1021-32		79
978	High-fat-diet-mediated dysbiosis promotes intestinal carcinogenesis independently of obesity. 2014 , 514, 508-12		284
977	16S rRNA-targeted oligonucleotide probes for direct detection of <i>Propionibacterium freudenreichii</i> in presence of <i>Lactococcus lactis</i> with multicolour fluorescence in situ hybridization. 2014 , 59, 320-7		7
976	Temporal dynamics of the cecal gut microbiota of juvenile arctic ground squirrels: a strong litter effect across the first active season. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 4260-8	4.8	13
975	Sequentially aerated membrane biofilm reactors for autotrophic nitrogen removal: microbial community composition and dynamics. 2014 , 7, 32-43		36
974	The role of the human microbiome in otolaryngology-head and neck surgery: a contemporary review. 2014 , 124, 1352-7		1
973	Characterization of novel polycyclic aromatic hydrocarbon dioxygenases from the bacterial metagenomic DNA of a contaminated soil. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 6591-600	4.8	47
972	Smoking decreases structural and functional resilience in the subgingival ecosystem. 2014 , 41, 1037-47		54
971	Molecular analysis for screening human bacterial pathogens in municipal wastewater treatment and reuse. 2014 , 48, 11610-9		56
970	Microbial distribution in an eroded landscape: Buried A horizons support abundant and unique communities. 2014 , 196, 94-102		32

969	Plant defence inducers rapidly influence the diversity of bacterial communities in a potting mix. 2014 , 84, 1-5		23
968	Agricultural Bioinformatics. 2014 ,		1
967	Microbial iron uptake as a mechanism for dispersing iron from deep-sea hydrothermal vents. 2014 , 5, 3192		54
966	Comparison of identification systems for psychrotrophic bacteria isolated from raw bovine milk. 2014 , 189, 26-38		43
965	A comprehensive insight into bacterial virulence in drinking water using 454 pyrosequencing and Illumina high-throughput sequencing. 2014 , 109, 15-21		50
964	Evidence of environmental and vertical transmission of Burkholderia symbionts in the oriental chinch bug, Cavalerius saccharivorus (Heteroptera: Blissidae). <i>Applied and Environmental Microbiology</i> , 2014 , 80, 5974-83	4.8	70
963	Correlation between viral production and carbon mineralization under nitrate-reducing conditions in aquifer sediment. 2014 , 8, 1691-703		25
962	Improved resolution of bacteria by high throughput sequence analysis of the rRNA internal transcribed spacer. 2014 , 105, 82-7		21
961	Individual diet has sex-dependent effects on vertebrate gut microbiota. 2014 , 5, 4500		330
960	Getting started with microbiome analysis: sample acquisition to bioinformatics. 2014 , 82, 18.8.1-29		79
959	Molecular methods for biofilms. 2014 , 87-137		
958	Evaluation of bifidobacterial community composition in the human gut by means of a targeted amplicon sequencing (ITS) protocol. 2014 , 90, 493-503		62
957	Gastrointestinal microbiota of wild and inbred individuals of two house mouse subspecies assessed using high-throughput parallel pyrosequencing. 2014 , 23, 5048-60		47
956	Exercise induction of gut microbiota modifications in obese, non-obese and hypertensive rats. 2014 , 15, 511		171
955	Conservation of streptococcal CRISPRs on human skin and saliva. 2014 , 14, 146		15
954	Comparative assessment of the bacterial communities associated with Aedes aegypti larvae and water from domestic water storage containers. 2014 , 7, 391		43
953	The interplay between Campylobacter and Helicobacter species and other gastrointestinal microbiota of commercial broiler chickens. 2014 , 6, 18		67
952	Characterization of the nasopharyngeal microbiota in health and during rhinovirus challenge. 2014 , 2, 22		87

951	Effect of chemotherapy on the microbiota and metabolome of human milk, a case report. 2014 , 2, 24		67
950	Artificial sweeteners induce glucose intolerance by altering the gut microbiota. 2014 , 514, 181-6		1088
949	Human oral viruses are personal, persistent and gender-consistent. 2014 , 8, 1753-67		107
948	Pyrosequencing reveals transient cystic fibrosis lung microbiome changes with intravenous antibiotics. 2014 , 44, 922-30		61
947	A hidden pitfall in the preparation of agar media undermines microorganism cultivability. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 7659-66	4.8	133
946	Power generation and oil sands process-affected water treatment in microbial fuel cells. 2014 , 169, 581-587		19
945	Primate vaginal microbiomes exhibit species specificity without universal <i>Lactobacillus</i> dominance. 2014 , 8, 2431-44		110
944	Patterns of bacterial diversity along a long-term mercury-contaminated gradient in the paddy soils. 2014 , 68, 575-83		50
943	Pioneer microbial communities of the Fimmvörðuháls lava flow, Eyjafjallajökull, Iceland. 2014 , 68, 504-18		36
942	International Space Station environmental microbiome - microbial inventories of ISS filter debris. 2014 , 98, 6453-66		73
941	Diversity, abundance, and spatial distribution of riverine microbial communities response to effluents from swine farm versus farmhouse restaurant. 2014 , 98, 7597-608		5
940	Enhancing the culturability of bacteria from the gastrointestinal tract of farmed adult turbot <i>Scophthalmus maximus</i> . 2014 , 32, 316-325		4
939	Bacterial diversity in snow on North Pole ice floes. 2014 , 18, 945-51		19
938	Gastro-intestinal microbiota of two migratory shorebird species during spring migration staging in Delaware Bay, USA. 2014 , 155, 969-977		22
937	Niche partitioning of bacterial communities in biological crusts and soils under grasses, shrubs and trees in the Kalahari. 2014 , 23, 1709-1733		38
936	Bacterial communities on classroom surfaces vary with human contact. 2014 , 2, 7		99
935	Spatial biodiversity of bacteria along the largest Arctic river determined by next-generation sequencing. 2014 , 89, 442-50		32
934	Probiotic administration attenuates myocardial hypertrophy and heart failure after myocardial infarction in the rat. 2014 , 7, 491-9		158

933	Benchmarking of methods for genomic taxonomy. 2014 , 52, 1529-39		141
932	Marine rust tubercles harbour iron corroding archaea and sulphate reducing bacteria. 2014 , 83, 189-197		55
931	Effects of season and host physiological state on the diversity, density, and activity of the arctic ground squirrel cecal microbiota. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 5611-22	4.8	52
930	DegePrime, a program for degenerate primer design for broad-taxonomic-range PCR in microbial ecology studies. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 5116-23	4.8	210
929	mtDNA haplogroup and single nucleotide polymorphisms structure human microbiome communities. 2014 , 15, 257		57
928	Processing faecal samples: a step forward for standards in microbial community analysis. 2014 , 14, 112		99
927	Discovery of novel enzymes with industrial potential from a cold and alkaline environment by a combination of functional metagenomics and culturing. 2014 , 13, 72		72
926	Investigation of the microbial metabolism of carbon dioxide and hydrogen in the kangaroo foregut by stable isotope probing. 2014 , 8, 1855-65		29
925	Amphibian skin may select for rare environmental microbes. 2014 , 8, 2207-17		150
924	Intestinal microbiota and species diversity of <i>Campylobacter</i> and <i>Helicobacter</i> spp. in migrating shorebirds in Delaware Bay. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 1838-47	4.8	36
923	<i>Bifidobacterium longum</i> subsp. <i>infantis</i> in experimental necrotizing enterocolitis: alterations in inflammation, innate immune response, and the microbiota. 2014 , 76, 326-33		69
922	Metatranscriptomics of the human oral microbiome during health and disease. 2014 , 5, e01012-14		250
921	An insight into the microbiome of the <i>Amblyomma maculatum</i> (Acari: Ixodidae). 2014 , 51, 119-29		90
920	Bacterial community variations in an alfalfa-rice rotation system revealed by 16S rRNA gene 454-pyrosequencing. 2014 , 87, 650-63		58
919	Wastewater irrigation increases the abundance of potentially harmful gammaproteobacteria in soils in Mezquital Valley, Mexico. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 5282-91	4.8	51
918	Pyrosequencing analysis yields comprehensive assessment of microbial communities in pilot-scale two-stage membrane biofilm reactors. 2014 , 48, 7511-8		33
917	Benthic foraminifera from the deep-water Niger delta (Gulf of Guinea): Assessing present-day and past activity of hydrate pockmarks. 2014 , 94, 87-106		23
916	Response of soil-associated microbial communities to intrusion of coal mine-derived acid mine drainage. 2014 , 48, 8556-63		40

915	Variation in the hindgut microbial communities of the Florida manatee, <i>Trichechus manatus latirostris</i> over winter in Crystal River, Florida. 2014 , 87, 601-15	24
914	Members of the human gut microbiota involved in recovery from <i>Vibrio cholerae</i> infection. 2014 , 515, 423-6	249
913	Reactor performance and microbial community dynamics during anaerobic co-digestion of municipal wastewater sludge with restaurant grease waste at steady state and overloading stages. 2014 , 172, 232-240	48
912	Cold seep biogenic carbonate crust in the Levantine basin is inhabited by burrowing <i>Phascolosoma</i> aff. <i>turnerae</i> , a sipunculan worm hosting a distinctive microbiota. 2014 , 90, 17-26	2
911	Impact of sampler selection on the characterization of the indoor microbiome via high-throughput sequencing. 2014 , 80, 274-282	41
910	Managing the interactions between sulfate- and perchlorate-reducing bacteria when using hydrogen-fed biofilms to treat a groundwater with a high perchlorate concentration. 2014 , 55, 215-24	52
909	The source of inoculum plays a defining role in the development of MEC microbial consortia fed with acetic and propionic acid mixtures. 2014 , 182-183, 11-8	42
908	Bacterioplankton assemblages as biological indicators of shrimp health status. 2014 , 38, 218-224	61
907	Two necrotic enteritis predisposing factors, dietary fishmeal and <i>Eimeria</i> infection, induce large changes in the caecal microbiota of broiler chickens. 2014 , 169, 188-97	117
906	Substrate type drives variation in reactor microbiomes of anaerobic digesters. 2014 , 151, 397-401	61
905	Variations in 16S rRNA-based microbiome profiling between pyrosequencing runs and between pyrosequencing facilities. 2014 , 52, 355-65	25
904	Seasonal fluctuations in ionic concentrations drive microbial succession in a hypersaline lake community. 2014 , 8, 979-90	58
903	Dynamics of bacterial community succession in a salt marsh chronosequence: evidences for temporal niche partitioning. 2014 , 8, 1989-2001	140
902	Rapidly expanding knowledge on the role of the gut microbiome in health and disease. 2014 , 1842, 1981-1992	110
901	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. 2014 , 24, 1517-25	197
900	Unraveling the outcome of 16S rDNA-based taxonomy analysis through mock data and simulations. 2014 , 30, 1530-8	27
899	Disruption of <i>Pten</i> speeds onset and increases severity of spontaneous colitis in <i>Il10(-/-)</i> mice. 2014 , 147, 667-679.e10	23
898	Biodegradation of oil sands process affected water in sequencing batch reactors and microbial community analysis by high-throughput pyrosequencing. 2014 , 92, 79-85	20

897	Impact of influent COD/N ratio on disintegration of aerobic granular sludge. 2014 , 62, 127-35	123
896	Short communication: effect of milk and milk containing <i>Lactobacillus casei</i> on the intestinal microbiota of mice. 2014 , 97, 2049-55	17
895	Effects of enhanced denitrification on hydrodynamics and microbial community structure in a soil column system. 2014 , 111, 112-9	26
894	Incorporation of therapeutically modified bacteria into gut microbiota inhibits obesity. 2014 , 124, 3391-406	171
893	Integrative workflows for metagenomic analysis. 2014 , 2, 70	28
892	Novel gut-based pharmacology of metformin in patients with type 2 diabetes mellitus. 2014 , 9, e100778	171
891	Assessing impacts of unconventional natural gas extraction on microbial communities in headwater stream ecosystems in Northwestern Pennsylvania. 2014 , 5, 522	28
890	Molecular Methods To Study Complex Microbial Communities. 2014 , 323-345	
889	Localized electron transfer rates and microelectrode-based enrichment of microbial communities within a phototrophic microbial mat. 2014 , 5, 11	25
888	Nitrogen cycling processes and microbial community composition in bed sediments in the Yukon River at Pilot Station. 2014 , 119, 2328-2344	19
887	Temperature-dependent variations in sulfate-reducing communities associated with a terrestrial hydrocarbon seep. 2014 , 29, 377-87	11
886	Time-resolved DNA stable isotope probing links <i>Desulfobacterales</i> - and <i>Coriobacteriaceae</i> -related bacteria to anaerobic degradation of benzene under methanogenic conditions. 2014 , 29, 191-9	34
885	The effects of intestinal tract bacterial diversity on mortality following allogeneic hematopoietic stem cell transplantation. 2014 , 124, 1174-82	531
884	PATTERNS OF UNCULTURED BACTERIA PHYLA IN DIFFERENT WASTEWATER TREATMENT SLUDGES. 2014 , 70, 42-52	1
883	HIGH ORGANIC LOADING TREATMENT OF MOLASSES WASTEWATER BY COMBINED SYSTEM CONSISTED OF THERMOPHILIC MULTI-STAGED UASB REACTOR AND MESOPHILIC UASB REACTOR. 2014 , 70, III_151-III_158	
882	Molecular analysis of the benthos microbial community in Zavarzin thermal spring (Uzon Caldera, Kamchatka, Russia). 2014 , 15 Suppl 12, S12	32
881	Genome sequence of the <i>Thermotoga thermarum</i> type strain (LA3(T)) from an African solfataric spring. 2014 , 9, 1105-17	4
880	Genome sequence of the anaerobic bacterium <i>Bacillus</i> sp. strain ZYK, a selenite and nitrate reducer from paddy soil. 2014 , 9, 646-54	5

879	High quality draft genome sequence of <i>Olivibacter sitiensis</i> type strain (AW-6(T)), a diphenol degrader with genes involved in the catechol pathway. 2014 , 9, 783-93	8
878	High quality draft genome sequence of the slightly halophilic bacterium <i>Halomonas zhanjiangensis</i> type strain JSM 078169(T) (DSM 21076(T)) from a sea urchin in southern China. 2014 , 9, 1020-30	8
877	Complete genome sequence of the bacteriochlorophyll a-containing <i>Roseibacterium elongatum</i> type strain (DSM 19469(T)), a representative of the <i>Roseobacter</i> group isolated from Australian coast sand. 2014 , 9, 840-54	3
876	CUDSwap: Tolerating Memory Exhaustion Failures in Cloud Computing. 2014 ,	
875	Bacterial symbiont sharing in <i>Megalomyrmex</i> social parasites and their fungus-growing ant hosts. 2015 , 24, 3151-69	23
874	The development and application of a molecular community profiling strategy to identify polymicrobial bacterial DNA in the whole blood of septic patients. 2015 , 15, 215	19
873	Effect of Electron Donor to Sulfate Ratio on Mercury Methylation in Floodplain Sediments under Saturated Flow Conditions. 2015 , 32, 924-933	13
872	Coral-the world's most diverse symbiotic ecosystem. 2015 , 24, 5330-47	106
871	Biodiversity hot spot on a hot spot: novel extremophile diversity in Hawaiian fumaroles. 2015 , 4, 267-281	10
870	Pyrosequencing analysis of a bacterial community associated with lava-formed soil from the Gotjawal forest in Jeju, Korea. 2015 , 4, 301-312	10
869	Dynamics of marine bacterial community diversity of the coastal waters of the reefs, inlets, and wastewater outfalls of southeast Florida. 2015 , 4, 390-408	48
868	Brassica seed meal soil amendments transform the rhizosphere microbiome and improve apple production through resistance to pathogen reinfestation. 2015 , 105, 460-9	97
867	River bacterioplankton community responses to a high inflow event. 2015 , 75, 187-205	16
866	Probiotics modify human intestinal mucosa-associated microbiota in patients with colorectal cancer. 2015 , 12, 6119-27	63
865	Microbial ecology and geoelectric responses across a groundwater plume. 2015 , 3, SAB9-SAB21	2
864	Impact of oil spills on coral reefs can be reduced by bioremediation using probiotic microbiota. 2015 , 5, 18268	59
863	Agent-Based Modelling as a Service on Amazon EC2: Opportunities and Challenges. 2015 ,	1
862	Intrinsic challenges in ancient microbiome reconstruction using 16S rRNA gene amplification. 2015 , 5, 16498	95

861	Habitat fragmentation is associated to gut microbiota diversity of an endangered primate: implications for conservation. 2015 , 5, 14862	107
860	The commensal infant gut meta-mobilome as a potential reservoir for persistent multidrug resistance integrons. 2015 , 5, 15317	24
859	Insights into the distribution and abundance of the ubiquitous candidatus Saccharibacteria phylum following tag pyrosequencing. 2014 , 4, 3957	48
858	Dietary silver nanoparticles can disturb the gut microbiota in mice. 2016 , 13, 38	101
857	The hidden 'mycobacteriome' of the human healthy oral cavity and upper respiratory tract. 2015 , 7, 26094	24
856	Niche differentiation of bacterial communities at a millimeter scale in Shark Bay microbial mats. 2015 , 5, 15607	71
855	The Impact of Injections of Different Nutrients on the Bacterial Community and Its Dechlorination Activity in Chloroethene-Contaminated Groundwater. 2015 , 30, 164-71	30
854	Shifts in the Midgut/Pyloric Microbiota Composition within a Honey Bee Apiary throughout a Season. 2015 , 30, 235-44	47
853	Do you kiss your mother with that mouth? An authentic large-scale undergraduate research experience in mapping the human oral microbiome. 2015 , 16, 50-60	14
852	MICCA: a complete and accurate software for taxonomic profiling of metagenomic data. 2015 , 5, 9743	158
851	Potential applications of next generation DNA sequencing of 16S rRNA gene amplicons in microbial water quality monitoring. 2015 , 72, 1962-72	40
850	Microbial Community Analysis Using High-Throughput Amplicon Sequencing. 2015 , 2.4.2-1-2.4.2-26	3
849	Generation and Analysis of Microbial Metatranscriptomes. 2015 , 2.4.5-1-2.4.5-19	1
848	Characterising the bacterial microbiota across the gastrointestinal tracts of dairy cattle: membership and potential function. 2015 , 5, 16116	276
847	Distinct composition of the oral indigenous microbiota in South Korean and Japanese adults. 2014 , 4, 6990	46
846	In vitro characterisation of the fermentation profile and prebiotic capacity of gold-fleshed kiwifruit. 2015 , 6, 829-39	9
845	Cecum microbial communities from steers differing in feed efficiency. 2015 , 93, 5327-40	31
844	Analysis of composition of microbiomes: a novel method for studying microbial composition. 2015 , 26, 27663	717

843	Robust species taxonomy assignment algorithm for 16S rRNA NGS reads: application to oral carcinoma samples. 2015 , 7, 28934	64
842	Cohort profile: LifeLines DEEP, a prospective, general population cohort study in the northern Netherlands: study design and baseline characteristics. 2015 , 5, e006772	136
841	The upper respiratory tract microbiome of hospitalised patients with community-acquired pneumonia of unknown aetiology: a pilot study. 2015 , 6, 83-89	0
840	Microbiomes of the dust particles collected from the International Space Station and Spacecraft Assembly Facilities. 2015 , 3, 50	113
839	Genome sequence of the <i>Roseovarius mucosus</i> type strain (DSM 17069(T)), a bacteriochlorophyll a-containing representative of the marine <i>Roseobacter</i> group isolated from the dinoflagellate <i>Alexandrium ostenfeldii</i> . 2015 , 10, 17	8
838	Inhibition of the endosymbiont " <i>Candidatus Midichloria mitochondrii</i> " during 16S rRNA gene profiling reveals potential pathogens in <i>Ixodes</i> ticks from Australia. 2015 , 8, 345	74
837	Lactobacilli with probiotic potential in the prairie vole (<i>Microtus ochrogaster</i>). 2015 , 7, 35	9
836	Potassium permanganate elicits a shift of the external fish microbiome and increases host susceptibility to columnaris disease. 2015 , 46, 82	41
835	Potential association of vacuum cleaning frequency with an altered gut microbiota in pregnant women and their 2-year-old children. 2015 , 3, 65	7
834	Modulation of gut microbiota in rats fed high-fat diets by processing whole-grain barley to barley malt. 2015 , 59, 2066-76	127
833	METAXA2: improved identification and taxonomic classification of small and large subunit rRNA in metagenomic data. 2015 , 15, 1403-14	252
832	The core microbiome bonds the Alpine bog vegetation to a transkingdom metacommunity. 2015 , 24, 4795-807	44
831	Draft genome sequence of <i>Halomonas lutea</i> strain YIM 91125(T) (DSM 23508(T)) isolated from the alkaline Lake Ebinur in Northwest China. 2015 , 10, 1	31
830	High quality draft genome sequence and analysis of <i>Pontibacter roseus</i> type strain SRC-1(T) (DSM 17521(T)) isolated from muddy waters of a drainage system in Chandigarh, India. 2015 , 10, 8	4
829	SPINGO: a rapid species-classifier for microbial amplicon sequences. 2015 , 16, 324	91
828	DectICO: an alignment-free supervised metagenomic classification method based on feature extraction and dynamic selection. 2015 , 16, 323	5
827	The rumen microbial metagenome associated with high methane production in cattle. 2015 , 16, 839	186
826	Improved taxonomic assignment of human intestinal 16S rRNA sequences by a dedicated reference database. 2015 , 16, 1056	87

825	Development of gut inflammation in mice colonized with mucosa-associated bacteria from patients with ulcerative colitis. 2015 , 7, 32	36
824	Maternal fucosyltransferase 2 status affects the gut bifidobacterial communities of breastfed infants. 2015 , 3, 13	244
823	An accurate and efficient experimental approach for characterization of the complex oral microbiota. 2015 , 3, 48	63
822	Chemostat culture systems support diverse bacteriophage communities from human feces. 2015 , 3, 58	16
821	Relative and contextual contribution of different sources to the composition and abundance of indoor air bacteria in residences. 2015 , 3, 61	68
820	High-quality permanent draft genome sequence of the extremely osmotolerant diphenol degrading bacterium <i>Halotalea alkalilenta</i> AW-7(T), and emended description of the genus <i>Halotalea</i> . 2015 , 10, 52	4
819	Combining metagenomics with metaproteomics and stable isotope probing reveals metabolic pathways used by a naturally occurring marine methyloph. 2015 , 17, 4007-18	45
818	Continental-scale variation in seaweed host-associated bacterial communities is a function of host condition, not geography. 2015 , 17, 4078-88	88
817	Impact of dietary deviation on disease progression and gut microbiome composition in lupus-prone SNF1 mice. 2015 , 181, 323-37	87
816	Barite encrustation of benthic sulfur-oxidizing bacteria at a marine cold seep. 2015 , 13, 588-603	28
815	An insight into the functional role of thioredoxin reductase, a selenoprotein, in maintaining normal native microbiota in the Gulf Coast tick (<i>Amblyomma maculatum</i>). 2015 , 24, 570-81	24
814	Draft Genome Sequence of Bacteroidales Strain 6E, Isolated from a Rice Paddy Field in Japan. 2015 , 3,	1
813	The relationship between microbial community evenness and function in slow sand filters. 2015 , 6, e00729-15	26
812	Seasonal assemblages and short-lived blooms in coastal north-west Atlantic Ocean bacterioplankton. 2015 , 17, 3642-61	30
811	A comparative study on microbiota from the intestine of Prussian carp (<i>Carassius gibelio</i>) and their aquatic environmental compartments, using different molecular methods. 2015 , 119, 948-61	30
810	High diversity of viable bacteria isolated from lymph nodes of slaughter pigs and its possible impacts for food safety. 2015 , 119, 1420-32	8
809	Resistivity and induced polarization monitoring of biogas combined with microbial ecology at a brownfield site. 2015 , 3, SAB43-SAB56	2
808	Differences in major bacterial populations in the intestines of mature broilers after feeding virginiamycin or bacitracin methylene disalicylate. 2015 , 119, 1515-26	31

807	Atmospheric N deposition alters connectance, but not functional potential among saprotrophic bacterial communities. 2015 , 24, 3170-80	31
806	Lactobacillus rhamnosus GG Dosage Affects the Adjuvanticity and Protection Against Rotavirus Diarrhea in Gnotobiotic Pigs. 2015 , 60, 834-43	26
805	The effect of antibiotics on the microbiome in acute exacerbations of chronic rhinosinusitis. 2015 , 5, 884-93	32
804	Fecal microbiota composition of breast-fed infants is correlated with human milk oligosaccharides consumed. 2015 , 60, 825-33	152
803	Melting glacier impacts community structure of Bacteria, Archaea and Fungi in a Chilean Patagonia fjord. 2015 , 17, 3882-97	34
802	PhytoREF: a reference database of the plastidial 16S rRNA gene of photosynthetic eukaryotes with curated taxonomy. 2015 , 15, 1435-45	90
801	Arsenic rich Himalayan hot spring metagenomics reveal genetically novel predator-prey genotypes. 2015 , 7, 812-23	36
800	Chemotherapy-driven dysbiosis in the intestinal microbiome. 2015 , 42, 515-28	223
799	Ecosystem productivity is associated with bacterial phylogenetic distance in surface marine waters. 2015 , 24, 5785-95	19
798	Draft Genome Sequence of Bacteroidales Strain TBC1, a Novel Isolate from a Methanogenic Wastewater Treatment System. 2015 , 3,	4
797	The Potential of High-throughput Metagenomic Sequencing of Aquatic Bacterial Communities to Estimate the Postmortem Submersion Interval. 2015 , 60, 1500-10	49
796	Microbial diversity in shallow-water hydrothermal sediments of Kueishan Island, Taiwan as revealed by pyrosequencing. 2015 , 55, 1308-18	22
795	Bacterial biogeography in the coastal waters of northern Zhejiang, East China Sea is highly controlled by spatially structured environmental gradients. 2015 , 17, 3898-913	56
794	Enhanced salinities, as a proxy of seawater desalination discharges, impact coastal microbial communities of the eastern Mediterranean Sea. 2015 , 17, 4105-20	22
793	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
792	MinION—New, Long Read, Portable Nucleic Acid Sequencing Device. 2015 , 45, 285	5
791	THE HUMAN MICROBIOTA: THE ROLE OF MICROBIAL COMMUNITIES IN HEALTH AND DISEASE. 2015 , 21,	1
790	Comparative Evaluation of DNA Extraction Methods from Feces of Multiple Host Species for Downstream Next-Generation Sequencing. 2015 , 10, e0143334	75

789	Deuteromethylactin B from a Freshwater-derived Streptomyces sp.. 2015 , 21, 261	4
788	Hidden biosphere in an oxygen-deficient Atlantic open-ocean eddy: future implications of ocean deoxygenation on primary production in the eastern tropical North Atlantic. 2015 , 12, 7467-7482	24
787	Emerging Perspectives on the Natural Microbiome of Fresh Produce Vegetables. 2015 , 5, 170-187	36
786	Computational Studies of the Intestinal Host-Microbiota Interactome. 2015 , 3, 2-28	5
785	Prebiotics Modulate the Effects of Antibiotics on Gut Microbial Diversity and Functioning in Vitro. 2015 , 7, 4480-97	35
784	riboFrame: An Improved Method for Microbial Taxonomy Profiling from Non-Targeted Metagenomics. 2015 , 6, 329	12
783	The Road to Metagenomics: From Microbiology to DNA Sequencing Technologies and Bioinformatics. 2015 , 6, 348	168
782	Table_1.xlsx. 2020 ,	
781	Table_2.xlsx. 2020 ,	
780	Image_3.TIF. 2020 ,	
779	Table_3.xlsx. 2020 ,	
778	Table_4.xlsx. 2020 ,	
777	Table_5.xlsx. 2020 ,	
776	Table_6.xlsx. 2020 ,	
775	Image_1.PDF. 2019 ,	
774	Image_2.PDF. 2019 ,	
773	Table_1.docx. 2019 ,	
772	Table_2.docx. 2019 ,	

771 Data_Sheet_1.FASTA. 2020,

770 Image_1.EPS. 2020,

769 Image_10.EPS. 2020,

768 Image_11.EPS. 2020,

767 Image_2.EPS. 2020,

766 Image_3.EPS. 2020,

765 Image_4.EPS. 2020,

764 Image_5.EPS. 2020,

763 Image_6.EPS. 2020,

762 Image_7.EPS. 2020,

761 Image_8.EPS. 2020,

760 Image_9.EPS. 2020,

759 Table_1.XLSX. 2020,

758 Table_2.XLSX. 2020,

757 Table_3.XLSX. 2020,

756 Table_4.XLSX. 2020,

755 Table_5.XLSX. 2020,

754 Table_6.DOCX. 2020,

753 Image_1.pdf. **2021,**

752 Image_2.pdf. **2021,**

751 Image_3.pdf. **2021,**

750 Table_1.xlsx. **2021,**

749 Table_10.xlsx. **2021,**

748 Table_11.xlsx. **2021,**

747 Table_12.xlsx. **2021,**

746 Table_2.xlsx. **2021,**

745 Table_3.xlsx. **2021,**

744 Table_4.xlsx. **2021,**

743 Table_5.xlsx. **2021,**

742 Table_6.xlsx. **2021,**

741 Table_7.xlsx. **2021,**

740 Table_8.xlsx. **2021,**

739 Table_9.xlsx. **2021,**

738 Data_Sheet_1.zip. **2019,**

737 Data_Sheet_1.ZIP. **2019,**

736 Data_Sheet_2.zip. **2019,**

735 Data_Sheet_1.DOCX. 2018,

734 Image_1.JPEG. 2018,

733 Image_2.JPEG. 2018,

732 Data_Sheet_1.PDF. 2020,

731 Table_1.XLSX. 2020,

730 Table_10.XLSX. 2020,

729 Table_11.XLSX. 2020,

728 Table_12.XLSX. 2020,

727 Table_13.XLSX. 2020,

726 Table_2.XLSX. 2020,

725 Table_3.XLSX. 2020,

724 Table_4.XLSX. 2020,

723 Table_5.XLSX. 2020,

722 Table_6.XLSX. 2020,

721 Table_7.XLSX. 2020,

720 Table_8.XLSX. 2020,

719 Table_9.XLSX. 2020,

718 Data_Sheet_1.PDF. 2020,

717 Data_Sheet_2.PDF. **2020**,

716 Data_Sheet_3.docx. **2020**,

715 Data_Sheet_1.docx. **2020**,

714 Data_Sheet_1.pdf. **2020**,

713 Table_6.xlsx. **2020**,

712 Table_1.docx. **2019**,

711 Data_Sheet_1.docx. **2019**,

710 Data_Sheet_1.pdf. **2020**,

709 Image_1.TIFF. **2020**,

708 Image_2.TIFF. **2020**,

707 Table_1.XLSX. **2020**,

706 Table_2.XLSX. **2020**,

705 Table_3.XLSX. **2020**,

704 Table_4.XLSX. **2020**,

703 Table_5.XLSX. **2020**,

702 Table_6.XLSX. **2020**,

701 Data_Sheet_1.PDF. **2020**,

700 Table_1.XLSX. **2019**,

699 Table_10.DOCX. 2019,

698 Table_11.DOCX. 2019,

697 Table_2.DOCX. 2019,

696 Table_3.DOCX. 2019,

695 Table_4.DOCX. 2019,

694 Table_5.XLSX. 2019,

693 Image_1.jpg. 2020,

692 Data_Sheet_1.pdf. 2020,

691 Data_Sheet_2.xlsx. 2020,

690 Data_Sheet_1.docx. 2020,

689 Data_Sheet_2.xlsx. 2020,

688 Data_Sheet_1.pdf. 2020,

687 Image_1.TIF. 2020,

686 Image_2.TIF. 2020,

685 Image_3.TIF. 2020,

684 Table_1.XLSX. 2020,

683 Table_2.XLSX. 2020,

682 Table_3.XLSX. 2020,

681 Table_4.XLSX. 2020,

680 Table_5.XLSX. 2020,

679 Table_6.XLSX. 2020,

678 Table_7.XLSX. 2020,

677 Table_8.XLSX. 2020,

676 DataSheet_1.docx. 2020,

675 DataSheet_2.pdf. 2020,

674 Data_Sheet_1.xlsx. 2020,

673 Image_1.TIF. 2020,

672 Image_2.TIF. 2020,

671 Image_3.TIF. 2020,

670 Image_4.TIFF. 2020,

669 Image_5.TIF. 2020,

668 Data_Sheet_1.docx. 2020,

667 Table_1.DOC. 2019,

666 Data_Sheet_1.PDF. 2019,

665 Table_1.DOCX. 2020,

664 Table_1.docx. 2019,

663 Presentation_1.pdf. **2019,**

662 Presentation_1.pdf. **2019,**

661 Table_1.DOCX. **2019,**

660 Presentation_1.pdf. **2020,**

659 Table_1.DOCX. **2019,**

658 Image_1.TIF. **2020,**

657 DataSheet_1.docx. **2019,**

656 Table_1.docx. **2019,**

655 Image1.TIF. **2018,**

654 Image10.TIF. **2018,**

653 Image2.TIF. **2018,**

652 Image3.TIF. **2018,**

651 Image4.TIF. **2018,**

650 Image5.TIF. **2018,**

649 Image6.TIF. **2018,**

648 Image7.TIF. **2018,**

647 Image8.TIF. **2018,**

646 Image9.TIF. **2018,**

645 Table1.XLS. 2018,

644 Table2.XLSX. 2018,

643 Table3.XLSX. 2018,

642 Table4.XLS. 2018,

641 Table5.XLSX. 2018,

640 Image_1.tif. 2019,

639 Image_2.tif. 2019,

638 Image_1.pdf. 2020,

637 Table_1.xlsx. 2020,

636 Image1.pdf. 2018,

635 Image2.pdf. 2018,

634 Image3.pdf. 2018,

633 Image4.pdf. 2018,

632 Image5.pdf. 2018,

631 Image6.pdf. 2018,

630 Image7.pdf. 2018,

629 Table1.pdf. 2018,

628 Table2.pdf. 2018,

627 Table3.pdf. **2018,**

626 Table4.pdf. **2018,**

625 Table5.pdf. **2018,**

624 Table6.pdf. **2018,**

623 Table7.pdf. **2018,**

622 Table8.pdf. **2018,**

621 Image_1.JPEG. **2020,**

620 Table_1.XLSX. **2020,**

619 Data_Sheet_1.pdf. **2018,**

618 Table_1.DOCX. **2020,**

617 Table_2.DOCX. **2020,**

616 Table_3.DOCX. **2020,**

615 Table_4.DOCX. **2020,**

614 Table_5.xlsx. **2020,**

613 Table_6.docx. **2020,**

612 Table_1.PDF. **2018,**

611 Image_1.TIF. **2019,**

610 Image_2.TIF. **2019,**

609 Table_1.pdf. **2019**,

608 Table_1.docx. **2019**,

607 Cytokine-inducible SH2 domain containing protein contributes to regulation of adiposity, food intake, and glucose metabolism.. **2022**, 36, e22320 1

606 Metagenomic Tracking of Antibiotic Resistance Genes through a Pre-harvest Vegetable Production System: An Integrated Lab-, Microcosm-, and Greenhouse-Scale Study.. **2022**, 1

605 Precision Probiotics in Agroecosystems: Multiple Strategies of Native Soil Microbiotas for Conquering the Competitor *Ralstonia solanacearum*.. **2022**, e0115921 0

604 The influence of primer choice on archaeal phylogenetic analyses based on 16S rRNA gene PCR. **2021**, 83, e247529 0

603 Clinical response and changes in the fecal microbiota and metabolite levels after fecal microbiota transplantation in patients with inflammatory bowel disease and recurrent infection.. **2021**, 7, 87-98 0

602 Effect of dry matter content on the microbial community and on the effectiveness of a microbial inoculant to improve the aerobic stability of corn silage.. **2022**, 1

601 Can the Salivary Microbiome Predict Cardiovascular Diseases? Lessons Learned From the Qatari Population.. **2021**, 12, 772736 0

600 Dietary Diversity during Early Infancy Increases Microbial Diversity and Prevents Egg Allergy in High-Risk Infants.. **2022**, 22, e17

599 OUP accepted manuscript. 1

598 Hyaluronic Acid 35 kDa Protects against a Hyperosmotic, Formula Feeding Model of Necrotizing Enterocolitis.. **2022**, 14, 0

597 Uremic Toxin-Producing Species Prevail in the Gut Microbiota of Taiwanese CKD Patients: An Analysis Using the New Taiwan Microbiome Baseline.. **2022**, 12, 726256 1

596 Taxonomy Informed Clustering, an Optimized Method for Purer and More Informative Clusters in Diversity Analysis and Microbiome Profiling. **2022**, 2, 0

595 Not All Liver Abscesses Are Created Equal: The Impact of Tylosin and Antibiotic Alternatives on Bovine Liver Abscess Microbial Communities and a First Look at Bacteroidetes-Dominated Communities.. **2022**, 13, 882419 0

594 Effects of the non-chlorine oxidizer potassium monopersulfate on the water quality, growth performance and microbial community of Pacific white shrimp (*Penaeus vannamei*) culture systems with limited water exchange. 1

593 Altered Salivary Microbiota Following *Bifidobacterium animalis* Subsp. *Lactis* BL-11 Supplementation Are Associated with Anthropometric Growth and Social Behavior Severity in Individuals with Prader-Willi Syndrome.. **2022**, 1

592 Sewage treatment effect of AOA-SBR under different C/P value and its mechanism of nitrogen and phosphorus removal. **2022**, 102774 0

591	Administration of Hookworm Excretory/Secretory Proteins Improves Glucose Tolerance in a Mouse Model of Type 2 Diabetes. 2022 , 12, 637	1
590	Increased Diversity of Rhizosphere Bacterial Community Confers Adaptability to Coastal Environment for <i>Sapium sebiferum</i> Trees. 2022 , 13, 667	1
589	Functional Redundancy in Soil Microbial Community Based on Metagenomics Across the Globe.. 2022 , 13, 878978	0
588	Maternal consumption of a fermented diet protects offspring against intestinal inflammation by regulating the gut microbiota.. 2022 , 14, 2057779	3
587	Fate of face masks after being discarded into seawater: aging and microbial colonization. 2022 , 129084	1
586	Analysis of Environmental and Pathogenic Bacteria Attached to Aerosol Particles Size-Separated with a Metal Mesh Device.. 2022 , 19,	
585	Social Interaction is Unnecessary for Hindgut Microbiome Transmission in Honey Bees: The Effect of Diet and Social Exposure on Tissue-Specific Microbiome Assembly.. 2022 ,	3
584	Beneficial Effects of a Low-Glycemic Diet on Serum Metabolites and Gut Microbiota in Obese Women With and Enterotypes: A Randomized Clinical Trial.. 2022 , 9, 861880	0
583	Wastewater reuse for tree irrigation: Influence on rhizosphere microbial communities. 2022 , 100063	0
582	Prevalence of bacterial genes in the phage fraction of food viromes. 2022 , 111342	0
581	Marine Sponge Endosymbionts: Structural and Functional Specificity of the Microbiome within Cells.. 2022 , e0229621	0
580	Subgingival Microbiome in Pregnancy and a Potential Relationship to Early Term Birth. 2022 , 12,	0
579	<i>Glycyrrhiza uralensis</i> Fisch. Root-associated microbiota: the multifaceted hubs associated with environmental factors, growth status and accumulation of secondary metabolites.. 2022 , 17, 23	2
578	Acetaminophen Levels Found in Recycled Wastewater Alter Soil Microbial Community Structure and Functional Diversity.. 2022 , 1	0
577	Microbiota Comparison of Amur ide (<i>Leuciscus waleckii</i>) Intestine and Waters at Alkaline Water and Freshwater as the Living Environment. 2022 , 13,	0
576	A putatively new family of alphaproteobacterial chloromethane degraders from a deciduous forest soil revealed by stable isotope probing and metagenomics.. 2022 , 17, 24	
575	The impact of dromedary camel milk on mice gut microbiota. 2022 , 65,	0
574	Effects of Low-Carbohydrate Diet and Exercise Training on Gut Microbiota.. 2022 , 9, 884550	1

573	Comparative Analysis of Metagenomics and Metataxonomics for the Characterization of Vermicompost Microbiomes. 2022 , 13,	
572	Two isolates of <i>Rhizophagus irregularis</i> select different strategies for improving plants phosphorus uptake at moderate soil P availability. 2022 , 421, 115910	0
571	Nitrogen fixation contribution to nitrogen cycling during cyanobacterial blooms in Utah Lake.. 2022 , 302, 134784	0
570	Increased Relative Abundance of <i>Is</i> Associated With Reduced Cardiovascular Risk in an Obese Population.. 2022 , 9, 849005	1
569	Arbuscular mycorrhizal fungi have a greater role than root hairs of maize for priming the rhizosphere microbial community and enhancing rhizosphere organic P mineralization. 2022 , 108713	1
568	Insights into Prokaryotic Community and Its Potential Functions in Nitrogen Metabolism in the Bay of Bengal, a Pronounced Oxygen Minimum Zone.. 2022 , e0089221	0
567	COInr and mkCOInr: Building and customizing a non-redundant barcoding reference database from BOLD and NCBI using a lightweight pipeline.	1
566	Bacteroidetes and Firmicutes Drive Differing Microbial Diversity and Community Composition Among Micro-Environments in the Bovine Rumen. 2022 , 9,	0
565	Differences in composition of interdigital skin microbiota predict sheep and feet that develop footrot. 2022 , 12,	
564	Chlorate addition enhances perchlorate reduction in denitrifying membrane-biofilm reactors.	0
563	Monocot diet sources drive diversity of gut bacterial communities in <i>Spodoptera frugiperda</i> (Lepidoptera: Noctuidae) larvae.	0
562	Quercetin Reduces Inflammation and Protects Gut Microbiota in Broilers. 2022 , 27, 3269	3
561	Biodiversity risk assessment of genetically modified <i>Chaetoceros gracilis</i> for outdoor cultivation. 2022 ,	
560	Pollutant Removal Performance and Microbial Diversity of Simulated Vertical Flow Constructed Wetlands with Different Modified Biochar Additions.	
559	Controlled-Release Fertilizer Microplastics Can Dynamically Affect the Available State of Cd by Controlling Fe Morphology and Doc Content in Soil.	
558	Interaction effect between NAFLD severity and high carbohydrate diet on gut microbiome alteration and hepatic de novo lipogenesis. 2022 , 14,	2
557	Comparison of the Gut Microbiota in Healthy Infants With Different Delivery Modes and Feeding Types: A Cohort Study. 2022 , 13,	1
556	The Gut Microbiome of Preterm Infants Treated With Aminophylline Is Closely Related to the Occurrence of Feeding Intolerance and the Weight Gain. 2022 , 9,	1

- 555 Supranutritional Selenium-Yeast Supplementation of Beef Cows during the Last Trimester of Pregnancy Results in Higher Whole-Blood Selenium Concentrations in Their Calves at Weaning, but Not Enough to Improve Nasal Microbial Diversity. **2022**, 12, 1360
- 554 M-CAMPTM: A cloud-based web platform with a novel approach for species-level classification of 16S rRNA microbiome sequences. **2022**, 17,
- 553 Exploring Trade-offs in Scalable Phylogenetic Placement Methods.
- 552 Characteristics of the gut microbiota in women with premenstrual symptoms: A cross-sectional study. **2022**, 17, e0268466 ○
- 551 Different Exercise Intensity Associates with Varied Disease Biomarkers of Guts-Microbiome Genera Change in Rats: Preliminary Study.
- 550 The abundances and occurrences of foliar microbes are poorly predicted by variation in plant traits and abiotic conditions.
- 549 Metagenomics Analysis on Bacterial Communities Seasonal Diversity in the Urban Lake Jinghu, Central of China.
- 548 Autophagy controls mucus secretion from intestinal goblet cells by alleviating ER stress.
- 547 Rhizosphere microbiome of forest trees is connected to their resistance to soil-borne pathogens. ○
- 546 Impact of *Paenarthrobacter ureafaciens* ZF1 on the soil enzyme activity and microbial community during the bioremediation of atrazine-contaminated soils. **2022**, 22, 1
- 545 Comparative and analytical characterization of the oral bacteriome of smokeless tobacco users with oral squamous cell carcinoma. ○
- 544 Changes in Ambient Bacterial Community in Northern Taiwan during Long-Range Transport: Asian Dust Storm and Frontal Pollution. **2022**, 13, 841 ○
- 543 High-throughput sequencing to evaluate the effects of methamphetamine on the succession of the bacterial community to estimate the postmortem interval. 1-12 ○
- 542 Metagenomic Analysis Using Phylogenetic Placement—A Review of the First Decade. **2022**, 2, 2
- 541 Culturing the uncultured microbial majority in activated sludge: A critical review. 1-24 ○
- 540 The Microbiome and Volatile Organic Compounds Reflect the State of Decomposition in an Indoor Environment.
- 539 Impact of a 7-day homogeneous diet on interpersonal variation in human gut microbiomes and metabolomes. **2022**, 1
- 538 Whey protein and xylitol complex alleviate type 2 diabetes in C57BL/6 mice by regulating the intestinal microbiota. **2022**, 111454 ○

- 537 Seasonal and spatial variability of zooplankton diversity in the Poyang Lake Basin using DNA metabarcoding. **2022**, 12, 0
- 536 Altered Gut Microbiota and Short-Chain Fatty Acids After Vonoprazan-Amoxicillin Dual Therapy for *Helicobacter pylori* Eradication. **2022**, 12, 1
- 535 *Wolbachia* interacts with the microbiome to shape fitness-associated traits during seasonal adaptation in *Drosophila melanogaster*.
- 534 Multiomic Analyses of Nascent Preterm Infant Microbiomes Differentiation Suggest Opportunities for Targeted Intervention. 2101313 0
- 533 Microbial Community Structure Is Mostly Strongly Associated With Geographical Distance and pH in Salt Lake Sediments. **2022**, 13,
- 532 A health survey of the reef forming scleractinian cold-water corals *Lophelia pertusa* and *Madrepora oculata* in a remote submarine canyon on the European continental margin, NE Atlantic. **2022**, 107782
- 531 Root traits and soil nutrient and carbon availability drive soil microbial diversity and composition in a northern temperate forest. 1
- 530 Composition and Diversity of Gut Bacterial Community in Different Life Stages of a Leaf Beetle *Gastrolina depressa*. 1
- 529 Gut bacterial isoamylamine promotes age-related cognitive dysfunction by promoting microglial cell death. **2022**, 0
- 528 A metagenomic approach to the molecular analysis of bacterial communities in tailings of a gold mine.
- 527 Full Issue PDF. **2022**, 6, 108-182
- 526 Chewing differences in consumers affect the digestion and colonic fermentation outcomes: In vitro studies.
- 525 A potential oral microbiome signature associated with coronary artery disease in Tunisia.
- 524 Dose-Response Effect of Nitrogen on Microbial Community during Hydrocarbon Biodegradation in Simplified Model System. **2022**, 12, 6012 0
- 523 The Seasonal Patterns, Ecological Function and Assembly Processes of Bacterioplankton Communities in the Danjiangkou Reservoir, China. 13,
- 522 Dual-Hit Model of Parkinson's Disease: Impact of Dysbiosis on 6-Hydroxydopamine-Insulted Mice. Neuroprotective and Anti-Inflammatory Effects of Butyrate. **2022**, 23, 6367 0
- 521 Metagenome Analysis Reveals a Response of the Antibiotic Resistome to Mars-like Extraterrestrial Conditions. 0
- 520 Precision environmental health monitoring by longitudinal exposome and multi-omics profiling. **2022**, 32, 1199-1214 0

- 519 Using Surface Washing to Remove the Environmental Component from Flea Microbiome Analysis. **2022**, 108,
- 518 Biogeographical Patterns of Bacterial Communities and Their Antibiotic Resistomes in the Inland Waters of Southeast China. ○
- 517 Gut microbiota modulation in response to combination of *Escherichia coli* Nissle 1917 and sugars: Lessons from comparative analysis of fecal microbiota of two healthy donors from 2019-2021.
- 516 Metformin Influence on the Intestinal Microbiota and Organism of Rats with Metabolic Syndrome. **2022**, 23, 6837 ○
- 515 *Sparus aurata* and *Lates calcarifer* skin microbiota under healthy and diseased conditions in UV and non-UV treated water. **2022**, 4,
- 514 Heat stress impacts the multi-domain ruminal microbiota and some of the functional features independent of its effect on feed intake in lactating dairy cows. **2022**, 13, ○
- 513 Comparative study between the effects of aged and fresh Chinese baijiu on gut microbiota and host metabolism. **2022**, 101859
- 512 Bacterial endophytes as indicators of susceptibility to *Cercospora* Leaf Spot (CLS) disease in *Beta vulgaris* L.. **2022**, 12, ○
- 511 Profile of the Lower Respiratory Tract Microbiome in Human Immunodeficiency Virus/Acquired Immunodeficiency Syndrome and Lung Disease. 13, ○
- 510 Gut microbiota in mucosa and feces of newly diagnosed, treatment-naïve adult inflammatory bowel disease and irritable bowel syndrome patients. **2022**, 14, 3
- 509 Copper-Nanocoated Ultra-Small Cells in Grain Boundaries Inside an Extinct Vent Chimney. 13, ○
- 508 An evaluation of the microbiota of the upper reproductive tract of women with and without epithelial ovarian cancer. **2022**, 42, 101017 ○
- 507 Structural and functional spatial dynamics of microbial communities in aerated and non-aerated horizontal flow treatment wetlands. **2022**, 838, 156600
- 506 Comprehensive understanding the impacts of dietary exposure to polyethylene microplastics on genetically improved farmed tilapia (*Oreochromis niloticus*): tracking from growth, microbiota, metabolism to gene expressions. **2022**, 841, 156571 2
- 505 The removal mechanisms of microcystin-LR through electrolysis biofilters. **2022**, 447, 137413 ○
- 504 Response of Bacterial Diversity and Community Structure to Heavy Metals in Mangrove Sediments from South China.
- 503 Recent trends of polyphasic approach in taxonomy and cyanobacterial diversity. **2022**, 1-49
- 502 Contrasting Patterns of Nitrogen Release from Fine Roots and Leaves Driven by Microbial Communities During Decomposition.

501	Comparison and Correlation Analysis of Immune Function and Gut Microbiota of Broiler Chickens Raised in Double-Layer Cages and Litter Floor Pens.	0
500	Divergent gut microbiota in two closely related house mouse subspecies under common garden conditions.	1
499	Postbiotic heat-killed lactobacilli modulates on body weight associated with gut microbiota in a pig model. 2022 , 12,	1
498	Climate dictates microbial community composition and diversity in Australian biological soil crusts (biocrusts).	0
497	Increase in Bifidobacterium is a characteristic of the difference in the salivary microbiota of pregnant and non-pregnant women. 2022 , 22,	0
496	Feeding Fiber-Bound Polyphenol Ingredients at Different Levels Modulates Colonic Postbiotics to Improve Gut Health in Cats. 2022 , 12, 1654	0
495	Emu: species-level microbial community profiling of full-length 16S rRNA Oxford Nanopore sequencing data. 2022 , 19, 845-853	3
494	Effects on community composition and function Pinus massoniana infected by Bursaphelenchus xylophilus. 2022 , 22,	0
493	Insights into the Antimicrobial Activities and Metabolomes of Aquimarina (Flavobacteriaceae, Bacteroidetes) Species from the Rare Marine Biosphere. 2022 , 20, 423	1
492	Identification of Nordic Berries with Beneficial Effects on Cognitive Outcomes and Gut Microbiota in High-Fat-Fed Middle-Aged C57BL/6J Mice. 2022 , 14, 2734	1
491	Octanoate Alleviates Dietary Soybean Oil-Induced Intestinal Physical Barrier Damage, Oxidative Stress, Inflammatory Response and Microbial Dysbiosis in Large Yellow Croaker (Larimichthys Crocea). 13,	0
490	Analysis of bacterial diversity and genetic evolution of Lacticaseibacillus paracasei isolates in fermentation pit mud.	
489	Dietary Utilization Drives the Differentiation of Gut Bacterial Communities between Specialist and Generalist Drosophilid Flies.	0
488	Microbial community shifts correspond with suppression of decomposition 25 years after liming of acidic forest soils.	0
487	Microbiome Heritability and Its Role in Adaptation of Hosts to Novel Resources. 13,	0
486	Riverine bacterioplankton and phytoplankton assembly along an environmental gradient induced by urbanization.	0
485	Effects of Salinity on the Growth, Physiological Characteristics, and Intestinal Microbiota of the Echiura Worm (Urechis uncinatus). 9,	
484	Estimating the time since deposition (T _{sD}) in saliva stains using temporal changes in microbial markers. 2022 , 102747	

- 483 Watershed-scale liming reveals the short- and long-term effects of pH on the forest soil microbiome and carbon cycling. 0
- 482 Nisin and Nisin Probiotic Disrupt Oral Pathogenic Biofilms and Restore Their Microbiome Composition towards Healthy Control Levels in a Peri-Implantitis Setting. **2022**, 10, 1336 0
- 481 A single respiratory tract infection early in life reroutes healthy microbiome development and affects adult metabolism in a preclinical animal model. **2022**, 8, 0
- 480 Engineering probiotics to inhibit *Clostridioides difficile* infection by dynamic regulation of intestinal metabolism. **2022**, 13, 5
- 479 Snaq: A Dynamic Snakemake Pipeline for Microbiome Data Analysis With QIIME2. 2,
- 478 Fecal microbiota transplantation in the treatment of irritable bowel syndrome: a single-center prospective study in Japan. **2022**, 22, 0
- 477 Dysbiosis and Predicted Functions of the Dental Biofilm of Dairy Goats with Periodontitis. 1
- 476 Beneficial Shifts in the Gut Bacterial Community of Gilthead Seabream (*Sparus aurata*) Juveniles Supplemented with Allium-Derived Compound Propyl Propane Thiosulfonate (PTSO). **2022**, 12, 1821 0
- 475 Associations Between Gut Microbes and Social Behavior in Healthy 2-Year-Old Children. Publish Ahead of Print,
- 474 Comparison Between Full-Length 16S rRNA Metabarcoding and Whole Metagenome Sequencing Suggests the Use of Either Is Suitable for Large-Scale Microbiome Studies. **2022**, 19, 495-504 0
- 473 Changes in soil microecology of gangue reclamation areas after 10 years of in situ restoration with herbaceous plants (*Artemisia sacrorum* and *Imperata cylindrica*) and trees (*Populus* spp.). **2022**, 182, 106719 0
- 472 Optimizing the bacterial community structure and function in rhizosphere soil of sesame continuous cropping by the appropriate nitrate ammonium ratio. **2022**, 23, 100550 0
- 471 Bacterial Succession in Microbial Biofilm as a Potential Indicator for Postmortem Submersion Interval Estimation. 13, 0
- 470 Rhizosphere bacterial communities and soil nutrient conditions reveal sexual dimorphism of *Populus deltoides*. 0
- 469 The impact of symbiotic population crash (or reduction) on microbiome structure and composition. 1-12
- 468 *Rickettsia helvetica* infection is associated with microbiome modulation in *Ixodes ricinus* collected from humans in Serbia. **2022**, 12, 0
- 467 Effects of Phytoremediation on Microbial Biomass, Composition, and Function in a Sulphide-Rich Tailing From a Metal-Contaminated Region. 10, 0
- 466 Organelle 16S rRNA amplicon sequencing enables profiling of active gut microbiota in murine model.

- 465 Supercarriers of antibiotic resistome in a world's large river. **2022**, 10, 1
- 464 Whole plant microbiome profiling reveals a novel geminivirus associated with soybean stay-green disease. 0
- 463 Histamine production by the gut microbiota induces visceral hyperalgesia through histamine 4 receptor signaling in mice. **2022**, 14, 6
- 462 MOCHI: a comprehensive cross-platform tool for amplicon-based microbiota analysis.
- 461 Natural Environmental Variation Determines Microbial Diversity Patterns in Serum Fluid Dish, a Traditional Chinese Fermented Vegetable Food. **2022**, 79, 1
- 460 Methanol utilizers of the rhizosphere and phyllosphere of a common grass and forb host species. **2022**, 17,
- 459 Prophylactic Treatment of Undernourished Mice with Cotrimoxazole Induces a Different Profile of Dysbiosis with Functional Metabolic Alterations. **2022**, 11, 2278
- 458 Comparative analysis of the gut microbiota of sand fly vectors of zoonotic visceral leishmaniasis (ZVL) in Iran; host-environment interplay shapes diversity. **2022**, 16, e0010609 0
- 457 Water Accommodated Fraction of Macondo Oil Has Limited Effects on Nitrate Reduction in Northern Gulf of Mexico Salt Marsh Sediments Regardless of Prior Oiling History. **2022**, 233,
- 456 Metagenomic profiling pipelines improve taxonomic classification for 16S amplicon sequencing data. 0
- 455 PCR based fingerprinting techniques to transpire the microbial populations diversity of biofilm based nitrifying packed bed bioreactor in the bioremediation of aquaculture wastewater. **2022**, 2,
- 454 Bisphenol F induces liver-gut alteration in zebrafish. **2022**, 157974 0
- 453 A pilot study characterizing longitudinal changes in fecal microbiota of patients with Hirschsprung-associated enterocolitis. 1
- 452 Peanuts as a nighttime snack enrich butyrate-producing bacteria compared to an isocaloric lower-fat higher-carbohydrate snack in adults with elevated fasting glucose: A randomized crossover trial. **2022**, 1
- 451 Isolated Grauer's gorilla populations differ in diet and gut microbiome. 1
- 450 Changes in the Vaginal Microbiota of Women With Secondary Localized Provoked Vulvodynia. Publish Ahead of Print,
- 449 Proof of concept for developing novel feeds for cattle from wasted food and crop biomass to enhance agri-food system efficiency. **2022**, 12, 0
- 448 Bacterial Keystone Taxa Regulate Carbon Metabolism in the Earthworm Gut.

447	Flavonoids affect the endophytic bacterial community in Ginkgo biloba leaves with increasing altitude. 13,	1
446	Cecal microbiota of feedlot cattle fed a four-species Bacillus supplement.	
445	High-Temperature-and-Humidity Reduces Plasma Insulin and Gut Hormones through FXR Activation Accompanied by a Metabolic Compensatory Gut Microbiota.	
444	Modeling spatial interaction networks of the gut microbiota. 2022, 14,	0
443	Alterations in the vaginal microbiota of patients with preterm premature rupture of membranes. 12,	1
442	Estimating biodiversity across the tree of life on Mount Everest's southern flank with environmental DNA. 2022, 104848	0
441	Bacterial communities of hookah tobacco products are diverse and differ across brands and flavors. 2022, 106, 5785-5795	0
440	Alginate oligosaccharides increase boar semen quality by affecting gut microbiota and metabolites in blood and sperm. 13,	0
439	Interrelated Effects of Zinc Deficiency and the Microbiome on Group B Streptococcal Vaginal Colonization.	1
438	16S-ITGDB: An Integrated Database for Improving Species Classification of Prokaryotic 16S Ribosomal RNA Sequences. 2,	
437	Carbon monoxide (CO) correlates with symptom severity, autoimmunity, and responses to probiotics treatment in a cohort of children with autism spectrum disorder (ASD): a post-hoc analysis of a randomized controlled trial. 2022, 22,	0
436	Assembly and dynamics of the apple carposphere microbiome during fruit development and storage. 13,	1
435	Dietary ellagic acid supplementation attenuates intestinal damage and oxidative stress by regulating gut microbiota in weanling piglets. 2022,	0
434	Intermittent fasting positively modulates human gut microbial diversity and ameliorates blood lipid profile. 13,	0
433	Alterations in Microbiota and Metabolites Related to Spontaneous Diabetes and Pre-Diabetes in Rhesus Macaques. 2022, 13, 1513	
432	Performance of an anaerobic-oxic (AOA) system in the simultaneous removal of nutrients and triclosan and bacterial community. 1-15	1
431	Differential Susceptibility of the Gut Microbiota to DSS Treatment Interferes in the Conserved Microbiome Association in Mouse Models of Colitis and Is Related to the Initial Gut Microbiota Difference. 2022, 2022, 1-20	3
430	Postnatal exposure to ambient air pollutants is associated with the composition of the infant gut microbiota at 6-months of age. 2022, 14,	0

- 429 Attention Deficit Hyperactivity Disorder and the gut microbiome: An ecological perspective.
- 428 Cascading effects of habitat loss on ectoparasite-associated bacterial microbiomes. **2022**, 2, 1
- 427 Consortium of Indigenous Fecal Bacteria in the Treatment of Metabolic Syndrome. **2022**, 10, 1574 0
- 426 Termite diet rather than geographical origin determines the microbiome composition and functional genetic structure of nests from South American and African representatives, as revealed by a multiomics approach.
- 425 MinION Nanopore Sequencing Accelerates Progress towards Ubiquitous Genetics in Water Research. **2022**, 14, 2491 0
- 424 A new pathway for anaerobic biotransformation of marine toxin domoic acid. 0
- 423 Local adaptation of host-species specific gut microbiota. 0
- 422 Antibiotic resistance genes correlate with metal resistances and accumulate in the deep water layers of the Black Sea. **2022**, 120033 0
- 421 Liver abscess microbiota of feedlot steers finished in natural and traditional management programs.
- 420 Different Intestinal Microbiota with Growth Stages of Three-Breed Hybrid Pig. **2022**, 2022, 1-9 0
- 419 Individual Nutrition Is Associated with Altered Gut Microbiome Composition for Adults with Food Insecurity. **2022**, 14, 3407
- 418 Does swab type matter? Comparing methods for *Mannheimia haemolytica* recovery and upper respiratory microbiome characterization in feedlot cattle. **2022**, 4,
- 417 Plasma Microbiome in COVID-19 Subjects: An Indicator of Gut Barrier Defects and Dysbiosis. **2022**, 23, 9141 4
- 416 Biological aspects of phage therapy versus antibiotics against *Salmonella enterica* serovar Typhimurium infection of chickens. 12, 1
- 415 Epidemiological Studies of Children's Gut Microbiota: Validation of Sample Collection and Storage Methods and Microbiota Analysis of Toddlers' Feces Collected from Diapers. **2022**, 14, 3315
- 414 Relationship between flavor compounds and changes of microbial community in the solid fermented vinegar. 0
- 413 An integrative bioinformatics pipeline shows that honeybee-associated microbiomes are driven primarily by pollen composition.
- 412 Biochar addition regulates soil and earthworm gut microbiome and multifunctionality. **2022**, 173, 108810 1

411	Impacts of microplastics addition on sediment environmental properties, enzymatic activities and bacterial diversity. 2022 , 307, 135836	1
410	Comparative anaerobic digestion of sewage sludge at different temperatures with and without heat pre-treatment. 2022 , 307, 135808	0
409	nTiO ₂ alleviates the toxic effects of TCPP on mussels by adjusting respiratory metabolism and gut microbiota. 2022 , 851, 158176	0
408	Response of bacterial diversity and community structure to metals in mangrove sediments from South China. 2022 , 850, 157969	0
407	Exploring bacterioplankton communities and their temporal dynamics in the rearing water of a biofloc-based shrimp (<i>Litopenaeus vannamei</i>) aquaculture system. 13,	1
406	Lactiplantibacillus plantarum Regulated Intestinal Microbial Community and Cytokines to Inhibit Salmonella typhimurium Infection.	0
405	Metagenomics and Metatranscriptomics. 2022 , 147-184	0
404	The Intestinal Microbiome, Dietary Habits, and Physical and Psychological Resilience in Postpartum Women.	0
403	Microbiome Changes during Regenerative Endodontic Treatment Using Different Methods of Disinfection. 2022 , 48, 1273-1284	0
402	Understanding of the interrelationship between methane production and microorganisms in high-solid anaerobic co-digestion using microbial analysis and machine learning. 2022 , 373, 133848	0
401	Testing for differential abundance in compositional counts data, with application to microbiome studies. 2022 , 16,	1
400	Generalists and specialists decomposing labile and aromatic biochar compounds and sequestering carbon in soil. 2022 , 428, 116176	0
399	Pathologic, transcriptomic and microbiomic insight into the pathogenesis of intestinal parasitic tapeworm in cultured Chinese soft-shelled turtle (<i>Pelodiscus sinensis</i>). 2023 , 562, 738788	0
398	Contrasting patterns of nitrogen release from fine roots and leaves driven by microbial communities during decomposition. 2023 , 855, 158809	0
397	Growth, health status and gut microbiota of the scalloped spiny lobster (<i>Panulirus homarus</i>) at different salinities. 2023 , 562, 738779	0
396	Positive effects of steamed <i>Polygonatum sibiricum</i> polysaccharides including a glucofructan on fatty acids and intestinal microflora. 2023 , 402, 134068	1
395	Ankle brachial indices and anaerobes: is peripheral arterial disease associated with anaerobic bacteria in diabetic foot ulcers?. 2022 , 13, 204201882211187	0
394	Gut Microbiome and Neurodegeneration: A Bioinformatics Approach. 2022 , 297-311	0

- 393 Metagenomic Approaches for Studying Plant-Microbe Interactions. **2022**, 243-254 ○
- 392 Tools to Study Gut Microbiome. **2022**, 253-270 ○
- 391 Comprehensive Evaluation of Shotgun Metagenomics, Amplicon Sequencing and Harmonization of Said Platforms for Epidemiological Studies Using the Large Multi-Center HCHS/SOL Cohort. ○
- 390 Metagenomic approaches for understanding microbial communities in contaminated environments: Bioinformatic tools, case studies and future outlook. **2023**, 103-156 ○
- 389 RiboTaxa: combined approaches for rRNA genes taxonomic resolution down to the species level from metagenomics data revealing novelties. **2022**, 4, ○
- 388 Spatial assortment of soil organisms supports the size-plasticity hypothesis. ○
- 387 Application of Microbiome in Forensics. **2022**, ○
- 386 Analysis of oral microbiota alterations induced by Helicobacter pylori infection and vonoprazan-amoxicillin dual therapy for Helicobacter pylori eradication. **2022**, 27, ○
- 385 Skin Microbiota Profiles from Tape Stripping and Skin Biopsy Samples of Patients with Psoriasis Treated with Narrowband Ultraviolet B. Volume 15, 1767-1778 1
- 384 Constitution of mucosa-associated microbiota in the lower digestive tract does not change in early stage of non-alcoholic fatty liver disease with fecal dysbiosis. ○
- 383 Host Species and Captivity Distinguish the Microbiome Compositions of a Diverse Zoo-Resident Non-Human Primate Population. **2022**, 14, 715 ○
- 382 Characteristics of lower respiratory tract microbiota in the patients with post-hematopoietic stem cell transplantation pneumonia. 12, ○
- 381 Strongyloides stercoralis infection induces gut dysbiosis in chronic kidney disease patients. **2022**, 16, e0010302 ○
- 380 Two modes of evolution shape bacterial strain diversity in the mammalian gut for thousands of generations. **2022**, 13, 1
- 379 Increased diversity of a cervical microbiome associates with cervical cancer. 12, ○
- 378 Gut microbiome of multiple sclerosis patients and paired household healthy controls reveal associations with disease risk and course. **2022**, 185, 3467-3486.e16 4
- 377 Pyrolyzed or Composted Sewage Sludge Application Induces Short-Term Changes in the Terra Rossa Soil Bacterial and Fungal Communities. **2022**, 14, 11382 ○
- 376 Modulation of gut microbiota: The effects of a fruits and vegetables supplement. 9, ○

375	Seasonal precipitation and soil microbial community influence plant growth response to warming and N addition in a desert steppe.	1
374	Effect of sex on the gut microbiota characteristics of passerine migratory birds. 13,	0
373	Functional signatures of ex-vivo dental caries onset. 2022 , 14,	1
372	Nicotinamide adenine dinucleotide supplementation drives gut microbiota variation in Alzheimer's mouse model. 14,	1
371	Sex-specific effects of maternal weight loss on offspring cardiometabolic outcomes in the obese preeclamptic-like mouse model, BPH /5. 2022 , 10,	0
370	Machine Learning and Canine Chronic Enteropathies: A New Approach to Investigate FMT Effects. 2022 , 9, 502	2
369	The combined impact of low temperatures and shifting phosphorus availability on the competitive ability of cyanobacteria. 2022 , 12,	0
368	Climate warming restructures seasonal dynamics of grassland soil microbial communities. 2022 , 1, 245-256	0
367	Experimental removal of extracellular egg-associated microbes has long-lasting effects for larval performance.	0
366	Culture dependent and independent characterization of endophytic bacteria in the seeds of highland barley. 13,	0
365	Unbiased screen for pathogens in human paraffin-embedded tissue samples by whole genome sequencing and metagenomics. 12,	0
364	The Relationship of Tumor Microbiome and Oral Bacteria and Intestinal Dysbiosis in Canine Mammary Tumor. 2022 , 23, 10928	1
363	Cross-biome microbial networks reveal functional redundancy and suggest genome reduction through functional complementarity.	0
362	Correlation and Influence of Seasonal Variation of Diet with Gut Microbiota Diversity and Metabolism Profile of Chipmunk. 2022 , 12, 2586	0
361	Xenobiotic estradiol-17 β alters gut microbiota of hatchling American Alligators (Alligator mississippiensis).	0
360	Predator Presence Alters Intestinal Microbiota in Mussel.	0
359	Exploring the Healthy Eye Microbiota Niche in a Multicenter Study. 2022 , 23, 10229	2
358	The genetic and evolution characterization of the gut microbiota in pigs.	0

- 357 Interaction networks reveal highly antagonistic endophytic bacteria in native maize seeds from traditional milpa agroecosystems. 1
- 356 Fecal Microbiota Transplantation Combined with a Low FODMAP Diet for the Treatment of Irritable Bowel Syndrome with Predominant Diarrhea. **2022**, 2022, 1-24 0
- 355 The Microbiota of Human Lung of Pulmonary Tuberculosis and the Alteration Caused by Anti-tuberculosis Drugs. **2022**, 79, 0
- 354 An Insight into the Endophytic Bacterial Community of Tomato after Spray Application of Propiconazole and *Bacillus subtilis* Strain NBRI-W9. 1
- 353 *Mikania* sesquiterpene lactones enhance soil bacterial diversity and fungal and bacterial activities. 0
- 352 Chronological analysis of the gut microbiome for efficacy of atezolizumab-based immunotherapy in non-small cell lung cancer: Protocol for a multicenter prospective observational study. **2022**, 13, 2829-2833 0
- 351 Comparative metagenomic analysis of human intervertebral disc nucleus pulposus and cartilaginous end plates. 9, 0
- 350 High fat diet-induced hyperlipidemia and tissue steatosis in rabbits through modulating ileal microbiota. 0
- 349 *Drosophila melanogaster* microbiome is shaped by strict filtering and neutrality along a latitudinal cline. 0
- 348 Post-harvest quality changes and shelf-life determination of washed and blanched sugar kelp (*Saccharina latissima*). 2, 0
- 347 Temporal Changes in the Faecal Microbiota of Beef Cattle on Feedlot Placement. **2022**, 12, 2500 0
- 346 Genotype and organ effect on the occupancy of phyllosphere prokaryotes in different rice landraces. **2022**, 204, 0
- 345 Specific gut bacterial and fungal microbiota pattern in the first half of pregnancy is linked to the development of gestational diabetes mellitus in the cohort including obese women. 13, 0
- 344 Zinc Supplementation Partially Decreases the Harmful Effects of a Cafeteria Diet in Rats but Does Not Prevent Intestinal Dysbiosis. **2022**, 14, 3921 0
- 343 Altered gut microbiota in patients with small intestinal bacterial overgrowth. 2
- 342 Changes in Microbial Diversity, Soil Function, and Plant Biomass of Cotton Rhizosphere Soil Under the Influence of Chlorpyrifos. **2022**, 79, 1
- 341 Chronic stress exposure alters the gut barrier: sex-specific effects on microbiota and jejunum tight junctions. 0
- 340 Diversity of bacterial community in Jerusalem artichoke (*Helianthus tuberosus* L.) during storage is associated with the genotype and carbohydrates. 13, 0

- 339 Diversity of the gut, vaginal and oral microbiome among pregnant women in South Africa with and without pre-eclampsia. 3, 0
- 338 Synbiotic Supplementation Modulates Gut Microbiota, Regulates β Catenin Expression and Prevents Weight Gain in ob/ob Mice: Preliminary Findings. **2022**, 23, 10483 0
- 337 Microorganisms associated with *Sporobolus anglicus*, an invasive dimethylsulfoniopropionate producing salt marsh plant, are an unrecognized sink for dimethylsulfide. 13, 0
- 336 Oral Absorbent AST-120 Is Associated with Compositional and Functional Adaptations of Gut Microbiota and Modification of Serum Short and Medium-Chain Fatty Acids in Advanced CKD Patients. **2022**, 10, 2234 0
- 335 Leaf endophytic microbiomes of different almond cultivars grafted to the same rootstock. 0
- 334 Copy number variation on ABCC2-DNMBP loci impacts the diversity and composition of the gut microbiota in pigs. 0
- 333 Soil chemistry and fungal communities are associated with dieback in an Endangered Australian shrub. 1
- 332 Acute exposure to microplastics induces metabolic disturbances and gut dysbiosis in adult zebrafish (*Danio rerio*). **2022**, 245, 114125 1
- 331 Evaluation of sedimentary bacterial community dynamics and contamination assessment of lower Des Plaines River. **2022**, 100177 1
- 330 Reevaluation of old data with new techniques reveals novel insights into the celiac microbiome. 0
- 329 Analysis of the gut microbiota of healthy CARI-Nirbheek (Aseel cross) Chickens: A Metagenomic Approaches. **2022**, 100304 0
- 328 Uncovering the core principles of the gut-lung axis to enhance innate immunity in the chicken. 13, 0
- 327 Physicochemical and biological factors determining the patchy distribution of soil water repellency among species of dominant vegetation in loess hilly region of China. 13, 0
- 326 An exploratory study of the gut microbiota in major depression with anxious distress. **2022**, 1
- 325 FANGORN: A quality-checked and publicly available database of full-length 16S-ITS-23S rRNA operon sequences. 0
- 324 Quantification and characterization of mouse and human tissue-resident microbiota by qPCR and 16S sequencing. **2022**, 3, 101765 0
- 323 Structure and Functional Potential of Arctic Sea Sediment Microbiota. **2022**, 0
- 322 Tuft cells mediate commensal remodeling of the small intestinal antimicrobial landscape. 0

321	Effects of Proteases from Pineapple and Papaya on Protein Digestive Capacity and Gut Microbiota in Healthy C57BL/6 Mice and Dose-Manner Response on Mucosal Permeability in Human Reconstructed Intestinal 3D Tissue Model. 2022 , 12, 1027	1
320	The lung microbiome, peripheral gene expression, and recurrence-free survival after resection of stage II non-small cell lung cancer. 2022 , 14,	0
319	Functional Interpretation of Cross-Talking Pathways with Emphasis on Amino Acid Metabolism in Rhizosphere Microbiome of the Wild Plant <i>Moringa oleifera</i> . 2022 , 12, 1814	1
318	Tick transmission of <i>Borrelia burgdorferi</i> to the murine host is not influenced by environmentally acquired midgut microbiota. 2022 , 10,	0
317	C-section delivery induces gut barrier-microbiota imbalances in early life and leads to higher sensitivity to inflammation.	0
316	3L, three-Lactobacilli on recovering of microbiome and immune-damage by cyclophosphamide chemotherapy.	0
315	Daqu microbiota adaptability to altered temperature determines the formation of characteristic compounds. 2022 , 109995	2
314	The rectal mucosal immune environment and HIV susceptibility among young men who have sex with men. 13,	0
313	Elucidating the gut microbiome alterations of tribal community of Arunachal Pradesh: perspectives on their lifestyle or food habits. 2022 , 12,	0
312	Indoor microbiome and allergic diseases: from theoretical advances to prevention strategies. 2022 ,	1
311	Association between Gut Microbiota and Emotional-Behavioral Symptoms in Children with Attention-Deficit/Hyperactivity Disorder. 2022 , 12, 1634	0
310	Investigating the oral microbiome in retrospective and prospective cases of prostate, colon, and breast cancer.	0
309	Emerald ash borer invasion of riparian forests alters organic matter and bacterial subsidies to south Michigan headwater streams.	0
308	Therapeutic role of ursodeoxycholic acid in colitis-associated cancer via gut microbiota modulation. 2022 ,	0
307	Low-abundance populations distinguish microbiome performance in plant cell wall deconstruction. 2022 , 10,	0
306	16S rRNA gene-based assessment of common broiler chicken sampling methods: Evaluating intra-flock sample size, cecal pair similarity, and cloacal swab similarity to other alimentary tract locations. 13,	0
305	Gut microbial ecology of Philippine gekkonids: ecoevolutionary effects on microbiome compositions.	0
304	Plastic mulch stimulates denitrification by interaction between soil environment and denitrifying bacteria.	1

- 303 More than an anthropogenic phenomenon: Antimicrobial resistance in ungulates from natural and agricultural environments. **2022**, 159789 ○
- 302 Relationship between healing status and microbial dissimilarity in wound and peri-wound skin in pressure injuries. **2022**, ○
- 301 Assessing the relationship between physical activity and the gut microbiome in a large, population-based sample of Wisconsin adults. **2022**, 17, e0276684 1
- 300 Rumen Microbial Predictors for Short-Chain Fatty Acid Levels and the Grass-Fed Regimen in Angus Cattle. **2022**, 12, 2995 1
- 299 Pretreatment with probiotics *Enterococcus faecium* NCIMB 11181 attenuated *Salmonella* Typhimurium-induced gut injury through modulating intestinal microbiome and immune responses with barrier function in broiler chickens. **2022**, 13, ○
- 298 The First Evidence of Bacterial Foci in the Hair Part and Dermal Papilla of Scalp Hair Follicles: A Pilot Comparative Study in Alopecia Areata. **2022**, 23, 11956 ○
- 297 Cytomegalovirus infection disrupts the influence of short-chain fatty acid producers on Treg/Th17 balance. **2022**, 10, ○
- 296 Rice growth stages modulate rhizosphere bacteria and archaea co-occurrence and sensitivity to long-term inorganic fertilization. ○
- 295 Spatial assortment of soil organisms supports the size-plasticity hypothesis. **2022**, 2, ○
- 294 Microbiome of *Citrullus colocynthis* (L.) Schrad. Reveals a Potential Association with Non-Photosynthetic Cyanobacteria. **2022**, 10, 2083 ○
- 293 Metagenomics analysis on the microbiota of chicken manure anaerobic digestion materials in biogas production. ○
- 292 Gut microbiota diversity and specific composition during immunotherapy in responders with non-small cell lung cancer. 9, ○
- 291 High-throughput sequencing-based metagenomic and transcriptomic analysis of intestine in piglets infected with salmonella. ○
- 290 Tapping into Plant Microbiome Interactions through the Lens of Multi-Omics Techniques. **2022**, 11, 3254 ○
- 289 Influence of Flax Seeds on the Gut Microbiota of Elderly Patients with Constipation. Volume 15, 2407-2418 ○
- 288 Warming alters elevation distributions of soil bacterial and fungal communities in alpine grasslands. **2022**, 39, e02306 ○
- 287 The Role of the Microbiome in the Metabolic Health of People with Schizophrenia and Related Psychoses: Cross-Sectional and Pre-Post Lifestyle Intervention Analyses. **2022**, 11, 1279 ○
- 286 Effects of rice-brayfish co-culture on ammonia-oxidizing microbial abundance and community structure. ○

285	Impacts of Dietary Protein and Niacin Deficiency on Reproduction Performance, Body Growth, and Gut Microbiota of Female Hamsters (<i>Tscherskia triton</i>) and Their Offspring.	1
284	Application of ecosystem-specific reference databases for increased taxonomic resolution in soil microbial profiling. 13,	0
283	Regulatory effects of <i>Auricularia cornea</i> var. <i>Li.</i> polysaccharides on immune system and gut microbiota in cyclophosphamide-induced mice. 13,	0
282	Impact of Probiotic <i>Geotrichum candidum</i> QAUGC01 on Health, Productivity, and Gut Microbial Diversity of Dairy Cattle. 2022 , 79,	0
281	Change of the structure and assembly of bacterial and photosynthetic communities by the ecological engineering practices in Dianchi Lake. 2022 , 315, 120386	1
280	Changes in the gut microbial community of larvae of the harlequin lady beetle in response to cannibalism and intraguild predation. 2022 , 176, 105090	0
279	Contrasting diversity patterns and community assembly mechanisms of bacterioplankton among different aquatic habitats in Lake Taihu, a large eutrophic shallow lake in China. 2022 , 315, 120342	0
278	Soil sample storage conditions impact extracellular enzyme activity and bacterial amplicon diversity metrics in a semi-arid ecosystem. 2022 , 175, 108858	0
277	Microbiota DNA isolation, 16S rRNA amplicon sequencing, and bioinformatic analysis for bacterial microbiome profiling of rodent fecal samples. 2022 , 3, 101772	0
276	Native soil organic-carbon contents shape distinct bacterial communities associated with priming effect. 2022 , 95, 150842	0
275	The controlled-release nitrogen fertilizer driving the symbiosis of microbial communities to improve wheat productivity and soil fertility. 2022 , 289, 108712	0
274	Whole-genome sequencing for food safety. 2023 , 854-870	0
273	Airway microbiome and asthma. 2023 , 47-62	0
272	Characteristics and interactions of soil bacteria, phytocommunity and soil properties in rocky desertification ecosystems of Southwest China. 2023 , 220, 106731	1
271	Soil microbial community structure dynamics shape the rhizosphere priming effect patterns in the paddy soil. 2023 , 857, 159459	0
270	A survey of soil bacterial diversity across a northeast Louisiana federal wildlife refuge. 2021 , 95, 104-120	0
269	Unravelling Diabetes-related Pathways Using 16S rRNA Microbiome Data from Human Gut and Nasal Cavity. 2022 ,	0
268	Characteristics of oral microbiome of healthcare workers in different clinical scenarios: a cross-sectional analysis. 2022 , 22,	0

267	Bifidobacterial carbohydrate/nucleoside metabolism enhances oxidative phosphorylation in white adipose tissue to protect against diet-induced obesity. 2022 , 10,	0
266	Sociability in a non-captive macaque population is associated with beneficial gut bacteria. 13,	0
265	Diet-induced modifications to human microbiome reshape colonic homeostasis in irritable bowel syndrome. 2022 , 41, 111657	1
264	Impact of lactobacillus-originated metabolites on enterohemorrhagic E. coli in rumen fluid.	0
263	Composition and factors influencing community structure of lactic acid bacterial in dairy products from Nyingchi Prefecture of Tibet. 2022 ,	0
262	Alterations of the Mucosal Immune Response and Microbial Community of the Skin upon Viral Infection in Rainbow Trout (<i>Oncorhynchus mykiss</i>). 2022 , 23, 14037	2
261	Dietary L-Arginine or N-Carbamylglutamate Alleviates Colonic Barrier Injury, Oxidative Stress, and Inflammation by Modulation of Intestinal Microbiota in Intrauterine Growth-Retarded Suckling Lambs. 2022 , 11, 2251	1
260	Causality Verification for the Correlation between the Presence of Nonstarter Bacteria and Flavor Characteristics in Soft-Type Ripened Cheeses.	0
259	High polyphenolic cranberry beverage alters specific fecal microbiota but not gut permeability following aspirin challenge in healthy obese adults: A randomized, double-blind, crossover trial. 2022 , 99, 105332	0
258	Data set on the diversity and core members of bacterial community associated with two specialist fruit flies <i>Bactrocera melastomatos</i> and <i>B. umbrosa</i> (Insecta, Tephritidae). 2022 , 45, 108727	0
257	Effects of Intestinal Bacterial Hydrogen Gas Production on Muscle Recovery following Intense Exercise in Adult Men: A Pilot Study. 2022 , 14, 4875	0
256	Unraveling the effect of the combination of modified atmosphere packaging and Epolylysine on the physicochemical properties and bacterial community of greater amberjack (<i>Seriola dumerili</i>). 9,	0
255	Effect of <i>Entamoeba histolytica</i> infection on gut microbial diversity and composition in diarrheal patients from New Delhi.	0
254	Evaluation of Environmental Hygiene in Railway Vehicles Using Microbiome Analysis. 2022 , 63, 283-288	1
253	Effects of <i>Salmonella enteritidis</i> Infection on TLR Genes Expression and Microbial Diversity in Laying Hens.	0
252	Analysis and Interpretation of metagenomics data: an approach. 2022 , 24,	1
251	Early life microbiota transplantation from highly feed-efficient broiler improved weight gain by reshaping the gut microbiota in laying chicken. 13,	0
250	Inclusion of a fish oil processing fraction as additive in diets for weaning piglets. 2023 , 295, 115517	0

- 249 Community-integrated multi-omics facilitates the isolation of an organohalide dehalogenation microorganism. **2023**, 4, 100355 ○
- 248 Use of wood and cork in biofilters for the simultaneous removal of nitrates and pesticides from groundwater. **2023**, 313, 137502 ○
- 247 Community adaptation to temperature explains abrupt soil bacterial community shift along a geothermal gradient on Iceland. **2023**, 177, 108914 ○
- 246 *Bifidobacterium lactis* Probio-M8 ameliorated the symptoms of type 2 diabetes mellitus mice by changing ileum FXR-CYP7A1. **2022**, 17, 2072-2084 ○
- 245 *Scrophulariae Radix-Atractylodes sinensis* pair and metformin inhibit inflammation by modulating gut microbiota of high-fat diet/streptozotocin-induced diabetes in rats. 13, ○
- 244 Starter culture-related changes in free amino acids, biogenic amines profile, and antioxidant properties of fermented red beetroot grown in Poland. **2022**, 12, ○
- 243 Exercise and Gut Microbiome: Trends and Advances in Research Methods. **2022**, 31, 428-437 ○
- 242 Gastrointestinal, vaginal, nasopharyngeal, and breast milk microbiota profiles and breast milk metabolomic changes in Gambian infants over the first two months of lactation: A prospective cohort study. **2022**, 101, e31419 ○
- 241 Challenges of Comparing Marine Microbiome Community Composition Data Provided by Different Commercial Laboratories and Classification Databases. **2022**, 14, 3855 ○
- 240 Different tissues in the maternal-fetal interface harbor distinct microbiomes showing associations related to their anatomical position or function. ○
- 239 Gut microbiome alterations in preclinical Alzheimer's disease. **2022**, 17, e0278276 ○
- 238 Effect of diet on gut microbiota diversity in mandarin ducks (*Aix galericulata*) revealed by Illumina high-throughput sequencing. **2022**, 204, ○
- 237 A comparative study to determine the association of gut microbiome with schizophrenia in Zhejiang, China. **2022**, 22, ○
- 236 Microbiome Classification for Heart Disease Detection. **2022**, ○
- 235 Deep Learning for Predicting 16S rRNA Copy Number. ○
- 234 Metagenomic decoding and oxidation pond-based treatment of domestic wastewater using 16's V3-V4 rRNA sequencing tool. ○
- 233 The divergent effects of moderate climate warming on the gut microbiota and energetic state of cold-climate lizards from open and semi-closed microhabitats. 13, ○
- 232 Molecular characterization of gut microbiome in weaning pigs supplemented with multi-strain probiotics using metagenomic, culturomic, and metabolomic approaches. **2022**, 4, ○

- 231 Gut Microbiome Studies in Livestock: Achievements, Challenges, and Perspectives. **2022**, 12, 3375 ○
- 230 Evaluation of the Microbial Community and Geochemistry in Produced Waters Collected from CO₂ EOR in the Niagaran Pinnacle Reef. **2022**, 6, 2972-2982 ○
- 229 Genetic and Environmental Investigation of a Novel Phenylamino Acetamide Inhibitor of the *Pseudomonas aeruginosa* Type III Secretion System. ○
- 228 Exploring variation in the fecal microbial communities of Kasaragod Dwarf and Holstein crossbred cattle. ○
- 227 Comparative analysis of intestinal flora between rare wild red-crowned crane and white-naped crane. 13, ○
- 226 Gut microbiota alterations in patients with juvenile idiopathic arthritis. **2022**, ○
- 225 Metagenomic Analysis of Garden Soil-Derived Microbial Consortia and Unveiling Their Metabolic Potential in Mitigating Toxic Hexavalent Chromium. **2022**, 12, 2094 1
- 224 Gut bacteria reflect the adaptation of *Diastrammena japonica* (Orthoptera: Rhaphidophoridae) to the cave. 13, ○
- 223 Elevated inflammatory fecal immune factors in men who have sex with men with HIV associate with microbiome composition and gut barrier function. 13, 1
- 222 Bacterial colonizers of *Nematostella vectensis* are initially selected by the host before interactions between bacteria determine further succession. ○
- 221 Alterations of the vaginal microbiome in healthy pregnant women positive for group B *Streptococcus* colonization during the third trimester. **2022**, 22, ○
- 220 Longitudinal analysis of the faecal microbiome in pigs fed *Cyberlindnera jadinii* yeast as a protein source during the weanling period followed by a rapeseed- and faba bean-based grower-finisher diet. **2022**, 4, ○
- 219 The effect of a multi-carbohydrase enzyme and yeast-derived product on intestinal microbiome structure, activity, and gut function of turkeys. ○
- 218 Effects of rearing system and antibiotic treatment on immune function, gut microbiota and metabolites of broiler chickens. **2022**, 13, ○
- 217 Assessment of Microbial Diversity during Thermophilic Anaerobic Co-Digestion for an Effective Valorization of Food Waste and Wheat Straw. **2023**, 16, 55 ○
- 216 Investigating the effects of glyphosate on the bumblebee proteome and microbiota. **2022**, 161074 1
- 215 Kombuchas from Green and Black Tea Modulate the Gut Microbiota and Improve the Intestinal Health of Wistar Rats Fed a High-Fat High-Fructose Diet. **2022**, 14, 5234 1
- 214 Characterization of the bacterial microbiome of *Amblyomma scalpturatum* and *Amblyomma ovale* collected from *Tapirus terrestris* and *Amblyomma sabanerae* collected from *Chelonoidis denticulata*, Madre de Dios- Peru. **2022**, 22, ○

213	Exploration of the relationship between gut microbiota and fecal microRNAs in patients with major depressive disorder. 2022 , 12,	1
212	Leveraging phylogenetic signal to unravel microbial community function and assembly rules.	0
211	Diversity of bacterial communities in the plasmodia of myxomycetes. 2022 , 22,	0
210	Impact of cafeteria diet and n3 supplementation on the intestinal microbiota, fatty acids levels, neuroinflammatory markers and social memory in male rats. 2022 , 114068	0
209	Quantitative analysis of disease-related metabolic dysregulation of human microbiota. 2022 , 105868	0
208	Analysis of Bacterial Microbiota of Aerated Compost Teas and Effect on Tomato Growth.	0
207	8-HQA Adjusts the Number and Diversity of Bacteria in the Gut Microbiome of <i>Spodoptera littoralis</i> .	0
206	Effect of Chemotherapy on the Gut Microbiome of Breast Cancer Patients During the First Year of Treatment. Volume 14, 433-451	0
205	Microbiota analysis in the hemodialysis population - Focusing on Enterobacteriaceae. 2022 ,	0
204	PGRP-SC shapes gut microbiota richness, diversity, and composition by modulating immunity in the house fly <i>Musca domestica</i> .	0
203	Untargeted Fecal Metabolomic Analyses across an Industrialization Gradient Reveal Shared Metabolites and Impact of Industrialization on Fecal Microbiome-Metabolome Interactions. 2022 , 7,	0
202	Effect of chicken manure on soil microbial community diversity in poultry keeping areas.	0
201	Prokaryotic and eukaryotic microbial communities associated with coral species have high host specificity in the South China Sea. 2022 , 161185	0
200	Internal and external microbiota of home-caught <i>Anopheles coluzzii</i> (Diptera: Culicidae) from Côte d'Ivoire, Africa: Mosquitoes are filthy. 2022 , 17, e0278912	0
199	Tea Consumption and the Gut Microbiome in Older Chinese Adults. 2022 ,	0
198	Unveiling the Wheat Microbiome under Varied Agricultural Field Conditions. 2022 , 10,	0
197	Combined Culture and DNA Metabarcoding Analysis of Cyanobacterial Community Structure in Response to Coral Reef Health Status in the South China Sea. 2022 , 10, 1984	1
196	Gut Microbiota, Intestinal Morphometric Characteristics, and Gene Expression in Relation to the Growth Performance of Chickens. 2022 , 12, 3474	0

- 195 Karst tiankeng shapes the differential composition and structure of bacterial and fungal communities in karst land. ○
- 194 Detection of horizontal sequence transfer in microorganisms in the genomic era. ○
- 193 Hydropower dam alters the microbial structure of fish gut in different habitats in upstream and downstream rivers. ○
- 192 Interaction between rhizobacterial community assembly and host responses determines poplar salt tolerance. ○
- 191 Allium-Derived Compound Propyl Propane Thiosulfonate (PTSO) Reduces *Vibrio* Populations and Increases Body Weight of European Seabass (*Dicentrarchus labrax*) Juveniles. **2023**, 12, 134 ○
- 190 Biogeochemical properties of blue carbon sediments influence the distribution and monomer composition of bacterial polyhydroxyalkanoates (PHA). ○
- 189 6His-tatritin promotes antimicrobial defense via regulating immune ability and intestinal microbial community in grass carp (*Ctenopharyngodon idella*). **2023**, 108532 ○
- 188 Phylogenetic comparative approach reveals evolutionary conservatism, ancestral composition, and integration of vertebrate gut microbiota. ○
- 187 Influence of structural features and feruloylation on fermentability and ability to modulate gut microbiota of arabinoxylan in in vitro fermentation. 13, ○
- 186 8-HQA adjusts the number and diversity of bacteria in the gut microbiome of *Spodoptera littoralis*. 14, ○
- 185 Imbalanced gut microbiota predicts and drives the progression of nonalcoholic fatty liver disease and nonalcoholic steatohepatitis in a fast-food diet mouse model. ○
- 184 Effect of Long-Term Inorganic Fertilization on Diversity and Abundance of Bacterial and Archaeal Communities at Tillage in Irrigated Rice Field. **2023**, 14, 18-33 ○
- 183 Dome1/JAK/STAT signaling between parasite and host integrates vector immunity and development. **2023**, 379, ○
- 182 3L, three-Lactobacilli on recovering of microbiome and immune-damage by cyclophosphamide chemotherapy A pilot experiment in rats ○
- 181 Compositional Changes in the Vaginal Bacterial Microbiome of Healthy Pregnant Women across the Three Gestational Trimesters in Ismailia, Egypt. **2023**, 11, 139 1
- 180 Mutualistic Interactions between Dinoflagellates and Pigmented Bacteria Mitigate Environmental Stress. ○
- 179 Involucrin modulates vitamin D receptor activity in the epidermis. **2023**, ○
- 178 Abundance, diversity, and composition of root-associated microbial communities varied with tall fescue cultivars under water deficit. 13, ○

- 177 Inflammatory Responses Induced by the Monophasic Variant of Salmonella Typhimurium in Pigs Play a Role in the High Shedder Phenotype and Fecal Microbiota Composition. 2
- 176 3L, three-Lactobacilli on recovering of microbiome and immune-damage by cyclophosphamide chemotherapy A pilot experiment 0
- 175 Grain, Gluten, and Dietary Fiber Intake Influence Gut Microbial Diversity: Data from the Food and Microbiome Longitudinal Investigation. **2023**, 3, 43-53 0
- 174 Field demonstration of biostimulation with wine pomace extract at a chloroethene contaminated site. **2023**, 21, 101322 0
- 173 Exploring plant and soil microbial communities as indicators of soil organic carbon in a California rangeland. **2023**, 178, 108952 0
- 172 High-throughput sequencing and marker pigment analysis of freshwater phytoplankton: A direct comparison with microscopic count data in the tropical crater lakes of Western Uganda. **2023**, 99, 126052 0
- 171 Effects of a *Saccharomyces cerevisiae* fermentation product on fecal characteristics, metabolite concentrations, and microbiota populations of dogs subjected to exercise challenge. 0
- 170 Photodynamic therapy treats acne by altering the composition of the skin microbiota. **2023**, 29, 0
- 169 Soil moisture affects soil microbial community diversity, structure and phenotypic characteristics on the south shore of Hulun Lake in Inner Mongolia of China. 0
- 168 Habitability and Biosignature Formation in Simulated Martian Aqueous Environments. 0
- 167 Bacterial and Fungal Symbionts in Pollen Provisions of a Native Solitary Bee in Urban and Rural Environments. 0
- 166 New Insights into the Effect of Fipronil on the Soil Bacterial Community. **2023**, 11, 52 0
- 165 Cross Cultivation on Homologous/Heterologous Plant-Based Culture Media Empowers Host-Specific and Real Time In Vitro Signature of Plant Microbiota. **2023**, 15, 46 0
- 164 Using the Gut Microbiome to Assess Stocking Efforts of the Endangered Pallid Sturgeon, *Scaphirhynchus albus*. **2023**, 13, 309 0
- 163 SCAMPP+FastTree: Improving Scalability for Likelihood-based Phylogenetic Placement. 0
- 162 Improvements in gut microbiota dysbiosis in aged mice transplanted with adipose-derived stem cells. 0
- 161 The community profiles of symbiotic bacteria at the different life stages of coral *Dipsastraea favus*. 10, 0
- 160 Antimicrobial Resistance Profiles of Bacterial Community in Premise Plumbing before and after Water Stagnation. **2023**, 21, 19-29 0

- 159 High-throughput amplicon sequencing of gut microbiome sea cucumber in Pahang, Malaysia. **2023**, ○
- 158 Plant selection and ecological microhabitat drive domestications of shrub-associated microbiomes in a revegetated shrub ecosystem. ○
- 157 The Effects of 6 Weeks of Resistance Training on the Gut Microbiome and Cardiometabolic Health in Young Adults with Overweight and Obesity. ○
- 156 Strengthening and microbial regulation mechanism of *Bacillus* on purification device for grass carp culture wastewater. 11, ○
- 155 Residual Effects of Transgenic Cotton on the Intestinal Microbiota of *Dysdercus concinnus*. **2023**, 11, 261 ○
- 154 The Dietary Fermentable Fiber Inulin Alters the Intestinal Microbiome and Improves Chronic Kidney Disease Mineral-Bone Disorder in a Rat Model of CKD. ○
- 153 Biogeography and potential ecological functions of prokaryotes in the hydrothermal and non-hydrothermal field sediments of the Indian Ocean Ridges. 9, ○
- 152 Comprehensive evaluation of shotgun metagenomics, amplicon sequencing, and harmonization of these platforms for epidemiological studies. **2023**, 3, 100391 ○
- 151 PhoD Harboring Microbial Community and Alkaline Phosphatase as Affected by Long Term Fertilization Regimes on a Calcareous Soil. **2023**, 13, 363 ○
- 150 Omics Technologies in Environmental Microbiology and Microbial Ecology. **2023**, 433-454 ○
- 149 A High Dose of Dietary Berberine Improves Gut Wall Morphology, Despite an Expansion of Enterobacteriaceae and a Reduction in Beneficial Microbiota in Broiler Chickens. ○
- 148 Gut Dysbiosis in Experimental Kidney Disease: A Meta-Analysis of Rodent Repository Data. **2023**, Publish Ahead of Print, ○
- 147 Uncovering the effect of *Moringa oleifera* Lam. leaves addition on Fuzhuan Brick Tea on sensory, volatile profiles and anti-obesity activity. ○
- 146 Gallbladder microbiota in healthy dogs and dogs with mucocele formation. **2023**, 18, e0281432 ○
- 145 Best practice for wildlife gut microbiome research: A comprehensive review of methodology for 16S rRNA gene investigations. 14, ○
- 144 *Moringa oleifera* Leaf Powder as New Source of Protein-Based Feedstuff Improves Growth Performance and Cecal Microbial Diversity of Broiler Chicken. **2023**, 13, 1104 ○
- 143 In silico evaluation and selection of the best 16S rRNA gene primers for use in next-generation sequencing to detect oral bacteria and archaea. **2023**, 11, ○
- 142 Cecal Microbial Succession and Its Apparent Association with Nutrient Metabolism in Broiler Chickens. ○

- 141 Meta-analysis reveals *Helicobacter pylori* mutual exclusivity and reproducible gastric microbiome alterations during gastric carcinoma progression. **2023**, 15, ○
- 140 Microbiome Metabolome Integration Platform (MMIP): a web-based platform for microbiome and metabolome data integration and feature identification. ○
- 139 Environmental Factors Affect the Bacterial Community in *Diaphorina citri*, an Important Vector of *Candidatus Liberibacter asiaticus* **2023**, 11, ○
- 138 Microbial ecology of Australian commercial rice koji and soybean miso. ○
- 137 Nickel exposure induces gut microbiome disorder and serum uric acid elevation. **2023**, 324, 121349 ○
- 136 *Limosilactobacillus reuteri* ameliorates preeclampsia in mice via improving gut dysbiosis and endothelial dysfunction. **2023**, 161, 114429 ○
- 135 Fecal microbiota transplantation affects the recovery of AD-skin lesions and enhances gut microbiota homeostasis. **2023**, 118, 110005 ○
- 134 Long-term implementation of a silvopastoral system enhances soil P availability and bacterial diversity. **2023**, 433, 116458 ○
- 133 Effects of Granular Activated Carbon Amendment, Temperature, and Organic Loading Rate on Microbial Communities in Up-Flow Anaerobic Sludge Blanket Reactors. **2023**, 149, ○
- 132 Stress-buster *Enterobacter* sp. alleviates salinity stress in *Cajanus cajan* together with impacting its rhizospheric microbiome. **2023**, 156, 202-212 ○
- 131 Ammonia tolerance and microbial community in thermophilic co-digestion of sewage sludge initiated with lignocellulosic biomass. **2023**, 376, 128834 ○
- 130 Straw is more effective than biochar in mobilizing soil organic phosphorus mineralization in saline-alkali paddy soil. **2023**, 186, 104848 ○
- 129 Microbial assessment of water, sanitation, and hygiene (WaSH) in temporary and permanent settlements two years after Nepal 2015 earthquake. **2023**, 877, 162867 ○
- 128 Insight into the spatiotemporal distribution of antibiotic resistance genes in estuarine sediments during long-term ecological restoration. **2023**, 335, 117472 ○
- 127 Integrated omics analysis on the bacterial community in the anaerobic digestion of chicken manure materials in biogas production farm. **2023**, 22, 101424 ○
- 126 An in vitro model of the chicken gastrointestinal tract with special emphasis to the cecal microbiota. **2023**, 102, 102654 ○
- 125 Changes in soil bacterial communities and functional groups beneath coarse woody debris across a subalpine forest successional series. **2023**, 43, e02436 ○
- 124 Revealing the relative importance among plant species, slope positions, and soil types on rhizosphere microbial communities in northern tropical karst and non-karst seasonal rainforests of China. 14, ○

- 123 The power of DNA based methods in probiotic authentication. 14, 0
- 122 Integrated omics analysis on the bacterial community in the anaerobic digestion of chicken manure materials in biogas production farm. 0
- 121 A review on Impact of dietary interventions, drugs, and traditional herbal supplements on the gut microbiome. **2023**, 271, 127346 0
- 120 Biofilm colonization of stone materials from an Australian outdoor sculpture: Importance of geometry and exposure. **2023**, 339, 117948 0
- 119 Dynamic changes of microbial community composition and diversity in metal contaminated and reclaimed lands assessed by Illumina MiSeq sequencing. **2023**, 26, 100163 0
- 118 Revisiting Mt Fuji groundwater origins with helium, vanadium and environmental DNA tracers. **2023**, 1, 60-73 0
- 117 Bioaugmentation removal and microbiome analysis of the synthetic estrogen 17 β -ethynylestradiol from hostile conditions and environmental samples by *Pseudomonas citronellolis* SJTE-3. **2023**, 317, 137893 0
- 116 Different types of land use influence soil physiochemical properties, the abundance of nitrifying bacteria, and microbial interactions in tropical urban soil. **2023**, 869, 161722 0
- 115 Dietary montmorillonite clay improved *Penaeus vannamei* survival from acute hepatopancreatic necrosis disease and modulated stomach microbiota. **2023**, 297, 115581 0
- 114 Dietary Application of the Microalga *Lobosphaera incisa* P127 Reduces Severity of Intestinal Inflammation, Modulates Gut-Associated Gene Expression, and Microbiome in the Zebrafish Model of IBD. **2023**, 67, 2200253 0
- 113 Characterization and Hydrocarbon Degradation Potential of *Variovorax* sp. Strain N23 Isolated from the Antarctic Soil. **2023**, 14, 91-103 0
- 112 Non-Surgical Periodontal Treatment Impact on Subgingival Microbiome and Intra-Oral Halitosis. **2023**, 24, 2518 0
- 111 Association of serum homocysteine levels with intestinal flora and cognitive function in schizophrenia. **2023**, 159, 258-265 0
- 110 Comparative metagenomics at Solfatara and Pisciarelli hydrothermal systems in Italy reveal that ecological differences across substrates are not ubiquitous. 14, 0
- 109 The influence of maternal factors on the neonatal microbiome and health. 0
- 108 Autophagy controls mucus secretion from intestinal goblet cells by alleviating ER stress. **2023**, 31, 433-446.e4 2
- 107 Gut microbiome variations in *Rhinopithecus roxellanae* caused by changes in the environment. **2023**, 24, 1
- 106 Rhizobiome Signature and Its Alteration Due to Watering in the Wild Plant *Moringa oleifera*. **2023**, 15, 2745 0

- 105 Postbiotic gel relieves clinical symptoms of bacterial vaginitis by regulating the vaginal microbiota. 13, ○
- 104 Functional Prediction of Microbial Communities in Sediment Microbial Fuel Cells. **2023**, 10, 199 ○
- 103 Microbial community stratification in scale-up Anaerobic Fluidized Bed Reactor applied for 4-Nonylphenol degradation. **2023**, 21, 101359 ○
- 102 StrainSelect: A novel microbiome reference database that disambiguates all bacterial strains, genome assemblies and extant cultures worldwide. **2023**, 9, e13314 ○
- 101 Changes of gut microbiome and metabolome in the AOM/DSS mouse model of colorectal cancer with FLASH radiation. **2023**, 4, 1-10 ○
- 100 Antarctic Ardley Island terrace [An ideal place to study the marine to terrestrial succession of microbial communities. 14, ○
- 99 Replacement of water yam (*Dioscorea alata* L.) indigenous root endophytes and rhizosphere bacterial communities via inoculation with a synthetic bacterial community of dominant nitrogen-fixing bacteria. 14, ○
- 98 The effects of a *Bacillus licheniformis* and phytase mixture added to broiler diets on growth performance, nutrient digestibility, and cecal microecosystem. **2023**, ○
- 97 500. The gut microbiome profile varies among two maternal rabbit lines with different longevity. **2022**, ○
- 96 A comparative study on the impact of five *Desmodium* species on soil microbiome reveals enrichment of selected bacterial and fungal taxa. ○
- 95 Nitrate determines the bacterial habitat specialization and impacts microbial functions in a subsurface karst cave. 14, ○
- 94 Vaginal microbial dynamics and pathogen colonization in a humanized microbiota mouse model. 1 ○
- 93 Exposure at low tide leads to a different microbial abundance of intertidal coral *Acropora pulchra*. **2022**, 18, 520-530 ○
- 92 Butyrate in Human Milk: Associations with Milk Microbiota, Milk Intake Volume, and Infant Growth. **2023**, 15, 916 ○
- 91 A newly developed solution for the preservation of short-chain fatty acids, bile acids, and microbiota in fecal specimens. **2023**, ○
- 90 A network meta-analysis on comparison of invasive and non-invasive sampling methods to characterize intestinal microbiota of birds. **2023**, 14, 100086 ○
- 89 Reliability of species detection in 16S microbiome analysis: Comparison of five widely used pipelines and recommendations for a more standardized approach. **2023**, 18, e0280870 ○
- 88 Microbiomes of Antarctic pearlwort (*Colobanthus quitensis*) of the maritime Antarctic: distinct diversity and core microbes in rhizosphere and endosphere compartments of the plant. **2022**, 20, ○

- 87 Gut Microbiome Composition Reveals the Distinctiveness between the Bengali people and the Indigenous Ethnicities in Bangladesh. ○
- 86 Structural characteristics and diversity of the rhizosphere bacterial communities of wild *Fritillaria przewalskii* Maxim. in the northeastern Tibetan Plateau. 14, ○
- 85 Effects of feeding *Saccharomyces cerevisiae* fermentation postbiotic on the fecal microbial community of Holstein dairy calves. **2023**, 5, ○
- 84 Long-term immersion of compostable plastics in marine aquarium: Microbial biofilm evolution and polymer degradation. **2023**, 189, 114711 ○
- 83 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
- 82 The gut microbiota correlate with the disease characteristics and immune status of patients with untreated diffuse large B-cell lymphoma. 14, ○
- 81 Dynamic variation of *Paris polyphylla* root-associated microbiome assembly with planting years. **2023**, 257, ○
- 80 HIV, asymptomatic STI, and the rectal mucosal immune environment among young men who have sex with men. ○
- 79 The vaginal microbiota among the different status of human papillomavirus infection and bacterial vaginosis. **2023**, 95, ○
- 78 Predicting Foodborne Pathogens and Probiotics Taxa within Poultry-Related Microbiomes Using a Machine Learning Approach. ○
- 77 Dynamics of bacterial community in the foregut and hindgut of earthworms with the nutrition supplied by kitchen waste during vermicomposting. **2023**, 374, 128777 ○
- 76 A trade-off between space exploration and mobilization of organic phosphorus through associated microbiomes enables niche differentiation of arbuscular mycorrhizal fungi on the same root. ○
- 75 Host Hybridization Dominates over Cohabitation in Affecting Gut Microbiota of Intrageneric Hybrid *Takifugu Pufferfish*. ○
- 74 Comparison of the diversity and structure of the rhizosphere microbial community between the straight and twisted trunk types of *Pinus yunnanensis*. 14, ○
- 73 Validation of 16S rRNA Gene Sequencing of the Periocular Microbiome and Lack of Alteration by Topical Eyedrops. **2023**, 12, 32 ○
- 72 Matrine alleviates depressive-like behaviors via modulating microbiota-gut-brain axis in CUMS-induced mice. **2023**, 21, ○
- 71 Avian Malaria Parasites Modulate Gut Microbiome Assembly in Canaries. **2023**, 11, 563 ○
- 70 Rise and metabolic roles of *Vibrio* during the fermentation of crab paste. 10, ○

- 69 Characterization of Gut Microbiome Composition in Patients with Triple-Negative Breast Cancer Treated with Neoadjuvant Chemotherapy. ○
- 68 Age-Dependent and Body Composition-Dependent Association of Child Gut Microbial Enterotype With Puberty Timing: A Chinese Cohort. ○
- 67 Evaluation of the lignocellulose degradation potential of Mediterranean forests soil microbial communities through diversity and targeted functional metagenomics. 14, ○
- 66 Nano Fe_2O_3 Self-Assembled Hybrid Biofilm Boosts Hydrogen Autotrophic Denitrification in a Three-Dimensional Biofilm Electrode Reactor. **2023**, 3, 557-567 ○
- 65 Gut-Microbiota Dysbiosis in Stroke-Prone Spontaneously Hypertensive Rats with Diet-Induced Steatohepatitis. **2023**, 24, 4603 ○
- 64 Changes in Bacterial Communities and Their Effects on Soil Carbon Storage in *Spartina alterniflora* Invasion Areas, Coastal Wetland Bare Flats, and *Suaeda salsa* Areas. **2023**, 20, 4308 ○
- 63 The Gut Microbiome of an Indigenous Agropastoralist Population in a Remote Area of Colombia with High Rates of Gastrointestinal Infections and Dysbiosis. **2023**, 11, 625 ○
- 62 Microbial community profiling and culturing reveal functional groups of bacteria associated with Thai commercial stingless worker bees (*Tetragonula pagdeni*). **2023**, 18, e0280075 ○
- 61 A New Technique for Use in Culturing Prokaryotes Comprising the Mouse Intestinal Microbiome. **2023**, 13, 119-147 ○
- 60 Habitat severity characteristics structure soil communities at regional and local spatial scales along the Antarctica Peninsula. 1-17 ○
- 59 Stronger linkage of diversity-carbon decomposition for rare rather than abundant bacteria in woodland soils. 14, ○
- 58 Microbiome analysis revealed distinct microbial communities occupying different sized nodules in field-grown peanut. 14, ○
- 57 Participants in the Trans-Antarctic Winter Traverse Expedition Showed Increased Bacterial Load and Diversity in Saliva but Maintained Individual Differences within Stool Microbiota and Across Metabolite Fingerprints. **2023**, 24, 4850 ○
- 56 Antibiotic-induced gut microbiota dysbiosis altered host metabolism. ○
- 55 Evaluation of the effects of Lake H₂S sulfur thermal water on skin microbiome in plaque psoriasis: An open label, pilot study. **2023**, 67, 661-673 ○
- 54 Influence of Pesticides and Mineral Fertilizers on the Bacterial Community of Arable Soils under Pea and Chickpea Crops. **2023**, 13, 750 ○
- 53 Diel modifications in the oral and anal microflora of the *Pygoscelis papua* Penguins. **2023**, 54, 351-368 ○
- 52 *Lactobacillus gasseri* LG-G12 Restores Gut Microbiota and Intestinal Health in Obesity Mice on Ceftriaxone Therapy. **2023**, 12, 1092 ○

- 51 *Giardia duodenalis* Colonization Slightly Affects Gut Microbiota and Hematological Parameters in Clinically Healthy Dogs. **2023**, 13, 958 ○
- 50 Citrus Flavonoids Supplementation as an Alternative to Replace Zinc Oxide in Weanling Pigs Diets Minimizing the Use of Antibiotics. **2023**, 13, 967 ○
- 49 Inoculation strategies affect the physicochemical properties and flavor of Zhenjiang aromatic vinegar. 14, ○
- 48 Impact of high altitude on composition and functional profiling of oral microbiome in Indian male population. **2023**, 13, ○
- 47 The Effects of Lakitelek Thermal Water and Tap Water on Skin Microbiome, a Randomized Control Pilot Study. **2023**, 13, 746 ○
- 46 Effects of nuclease-treated fermentation product of *Lactobacillus rhamnosus* GCC-3 on growth, hepatic health and gut microbiota of zebrafish (*Danio rerio*) fed a high-fat diet. **2023**, 29, 101529 ○
- 45 *Chrysophyllum albidum* Deterioration Entails Decline in *Pseudomonas* and Increase in *Acetobacter* Abundance. ○
- 44 The tropical cookbook: Termite diet and phylogenetics Over geographical origin Drive the microbiome and functional genetic structure of nests. 14, ○
- 43 Rhizosphere microbial community assembly and association networks strongly differ based on vegetation type at a local environment scale. 14, ○
- 42 The gut microbiota diversity of five Orthoptera (Insecta, Polyneoptera) insects determined by DNA metabarcoding. 11, ○
- 41 Dopamine receptor D2 confers colonization resistance via gut microbial metabolites. ○
- 40 *Camellia* oil (*Camellia oleifera* Abel.) alleviates gastric injury induced by ethanol associated with modulation of gut microbiota in mice. **2023**, 8, 61-71 ○
- 39 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 ○
- 38 Response of intestinal microbiota to saline-alkaline water in mud crab (*Scylla paramamosain*) based on multiple low salinity culture modes. 10, ○
- 37 SARS-CoV-2 infection alters the gut microbiome in diabetes patients: A cross-sectional study from Bangladesh. **2023**, 95, ○
- 36 Dysbiosis of gut microbiota due to diet, alcohol intake, body mass index, and gastrointestinal diseases in India. **2023**, 107, 2547-2560 ○
- 35 Evaluation of the effectiveness of personalised therapy for the patients with irritable bowel syndrome. **2023**, 14, 119-129 ○
- 34 Scaling deep phylogenetic embedding to ultra-large reference trees: a tree-aware ensemble approach. ○

- 33 Effect of *Limosilactobacillus reuteri* ZJF036 on Growth Performance and Gut Microbiota in Juvenile Beagle Dogs. **2023**, 80,
- 32 The effect of colonic pH on microbial activity and metabolite production using common prebiotics as substrates: an in vitro study.
- 31 Oral microbiome correlates with selected clinical biomarkers in individuals with no significant systemic disease. 13,
- 30 Analysis of microbiota-host communication mediated by butyrate in Atlantic Salmon. **2023**,
- 29 Oral metagenomes from Native American Ancestors reveal distinct microbial lineages in the pre-contact era.
- 28 Enhancement of micropollutant biotransformation by adding manganese sand in constructed wetlands. **2023**, 9, e15092
- 27 Unveiling the role of emerging metagenomics for the examination of hypersaline environments. 1-39
- 26 Alterations of Epidermal Lipid Profiles and Skin Microbiome in Children With Atopic Dermatitis. **2023**, 15, 186
- 25 Big Data for a Small World: A Review on Databases and Resources for Studying Microbiomes.
- 24 Agroecosystem edge effects on vegetation, soil properties, and the soil microbial community in the Canadian prairie. **2023**, 18, e0283832
- 23 Gut Microbiota Contribution to Weight-Independent Glycemic Improvements after Gastric Bypass Surgery.
- 22 Inflammatory cytokines and a diverse cervicovaginal microbiome are associated with cervical disease in Hispanics living in Puerto Rico.
- 21 Integrated Microbiota and Metabolite Changes following Rice Bran Intake during Murine Inflammatory Colitis-Associated Colon Cancer and in Colorectal Cancer Survivors. **2023**, 15, 2231
- 20 Exploration of Soil Microbial Diversity and Community Structure along Mid-Subtropical Elevation Gradients in Southeast China. **2023**, 14, 769
- 19 Body Size Poorly Predicts Host-Associated Microbial Diversity in Wild Birds.
- 18 The microbial removal of bisphenols in aquatic microcosms and associated alteration in bacterial community.
- 17 MiSurv: an Integrative Web Cloud Platform for User-Friendly Microbiome Data Analysis with Survival Responses.
- 16 Chimera alert! The threat of chimeric sequences causing inaccurate taxonomic classification of phytoplasmal strains.

- 15 The Effect of the Microalgae *Chlorella vulgaris* on the Gut Microbiota of Juvenile Nile Tilapia (*Oreochromis niloticus*) Is Feeding-Time Dependent. **2023**, 11, 1002 ○
- 14 A comparison between Greengenes, SILVA, RDP, and NCBI reference databases in four published microbiota datasets. ○
- 13 *Bifidobacterium* and *Lactobacillus* improve inflammatory bowel disease in zebrafish of different ages by regulating the intestinal mucosal barrier and microbiota. **2023**, 121699 ○
- 12 Correlation between microbial diversity and flavor metabolism in Huangshui: A by-product of solid-state fermentation Baijiu. **2023**, 181, 114767 ○
- 11 Relationship between pepper (*Capsicum annum* L.) root morphology, inter-root soil bacterial community structure and diversity under waterBir intercropping conditions. **2023**, 257, ○
- 10 Conjugated bile acids are nutritionally re-programmable antihypertensive metabolites. Publish Ahead of Print, ○
- 9 Soil bacterial community structure at different plant maturity stages in an annual grassLegume production system. 7, ○
- 8 Sociobiome - Individual and neighborhood socioeconomic status influence the gut microbiome in a multi-ethnic population in the US. ○
- 7 Integrating Multi-Omics Data to Construct Reliable Interconnected Models of Signaling, Gene Regulatory, and Metabolic Pathways. **2023**, 139-151 ○
- 6 *Vibrio cholerae* Invasion Dynamics of the Chironomid Host Are Strongly Influenced by Aquatic Cell Density and Can Vary by Strain. ○
- 5 Microbiome Diversity and Cellulose Decomposition Processes by Microorganisms on the Ancient Wooden Seawall of Qiantang River of Hangzhou, China. ○
- 4 DeepMicroGen: a generative adversarial network-based method for longitudinal microbiome data imputation. **2023**, 39, ○
- 3 Exploring Microbial Diversity and Functional Potential along the Bay of Bengal Coastline in Bangladesh: Insights from Amplicon Sequencing and Shotgun Metagenomics. ○
- 2 Effect of salinity on the denitrification of the sulfur-based autotrophic denitrification system. **2023**, 4, 95-103 ○
- 1 Biodegradation of polyvinyl chloride by *Citrobacter koseri* isolated from superworms (*Zophobas atratus* larvae). 14, ○