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UCHIME improves sensitivity and speed of chimera detection

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2200	Characteristics of a Self-Forming Dynamic Membrane Coupled with a Bioreactor in Application of Anammox Processes.		
2199	Mutual Interaction of Phenolic Compounds and Microbiota: Metabolism of Complex Phenolic ApigeninC- and KaempferolODerivatives by Human Fecal Samples.		
2198	Wetland management strategies lead to tradeoffs in ecological structure and function. <b>2017</b> , 5,		
2197	Effects of triclosan on bacterial community composition and <i>Vibrio</i> populations in natural seawater microcosms. <b>2017</b> , 5,		
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2010	Fecal microbiota diversity in survivors of adolescent/young adult Hodgkin lymphoma: a study of twins. <b>2013</b> , 108, 1163-7	34
2009	Variations in diversity and richness of gut bacterial communities of termites ( <i>Reticulitermes flavipes</i> ) fed with grassy and woody plant substrates. <b>2013</b> , 65, 531-6	43
2008	The microbiome extends to subepidermal compartments of normal skin. <b>2013</b> , 4, 1431	280
2007	Strong coupling of plant and fungal community structure across western Amazonian rainforests. <b>2013</b> , 7, 1852-61	235
2006	Testing three pipelines for 18S rDNA-based metabarcoding of soil faunal diversity. <b>2013</b> , 56, 73-81	20
2005	Identifying active foraminifera in the Sea of Japan using metatranscriptomic approach. <b>2013</b> , 86-87, 214-220	29
2004	Analysis of soil fungal communities by amplicon pyrosequencing: current approaches to data analysis and the introduction of the pipeline SEED. <b>2013</b> , 49, 1027-1037	146
2003	Subgingival microbiome in smokers and non-smokers in periodontitis: an exploratory study using traditional targeted techniques and a next-generation sequencing. <b>2013</b> , 40, 483-92	83
2002	Microbial communities in the subglacial waters of the Vatnajökull ice cap, Iceland. <b>2013</b> , 7, 427-37	49
2001	Coral reef invertebrate microbiomes correlate with the presence of photosymbionts. <b>2013</b> , 7, 1452-8	105
2000	Long-term operation of microbial electrosynthesis systems improves acetate production by autotrophic microbiomes. <b>2013</b> , 47, 6023-9	238
1999	Topographic diversity of fungal and bacterial communities in human skin. <b>2013</b> , 498, 367-70	693
1998	Application of <sup>13</sup> C-stable isotope probing to identify RDX-degrading microorganisms in groundwater. <b>2013</b> , 178, 350-60	28
1997	pH dominates variation in tropical soil archaeal diversity and community structure. <b>2013</b> , 86, 303-11	65
1996	Modulation of systemic immune responses through commensal gastrointestinal microbiota. <b>2013</b> , 8, e53969	36
1995	Bacterial communities in tetrachloroethene-polluted groundwaters: a case study. <b>2013</b> , 454-455, 517-27	50
1994	Pharmaceuticals suppress algal growth and microbial respiration and alter bacterial communities in stream biofilms. <b>2013</b> , 23, 583-93	129

1993	Arabidopsis thaliana as Model for Studies on the Bacterial Root Microbiota. <b>2013</b> , 243-256	5
1992	Regional variability in eukaryotic protist communities in the Amundsen Sea. <b>2013</b> , 25, 741-751	24
1991	Short-term dynamics of diversity patterns: evidence of continual reassembly within lacustrine small eukaryotes. <b>2013</b> , 15, 1745-58	105
1990	Microbial biodiversity in saline shallow lakes of the Monegros Desert, Spain. <b>2013</b> , 85, 503-18	53
1989	Effects of surface charge and hydrophobicity on anodic biofilm formation, community composition, and current generation in bioelectrochemical systems. <b>2013</b> , 47, 7563-70	234
1988	Illumina sequencing of 16S rRNA tag revealed spatial variations of bacterial communities in a mangrove wetland. <b>2013</b> , 66, 96-104	230
1987	Illumina metabarcoding of a soil fungal community. <b>2013</b> , 65, 128-132	280
1986	High genetic diversity and novelty in planktonic protists inhabiting inland and coastal high salinity water bodies. <b>2013</b> , 85, 27-36	31
1985	Contemporary environmental variation determines microbial diversity patterns in acid mine drainage. <b>2013</b> , 7, 1038-50	235
1984	Bacteriohopanepolyols in a stratified cyanobacterial mat from Kiritimati (Christmas Island, Kiribati). <b>2013</b> , 55, 55-62	12
1983	Contrasting Euryarchaeota communities between upland and paddy soils exhibited similar pH-impacted biogeographic patterns. <b>2013</b> , 64, 18-27	61
1982	A single betaproteobacterium dominates the microbial community of the crambescidine-containing sponge <i>Crambe crambe</i> . <b>2013</b> , 3, 2583	45
1981	SOAPBarcode: revealing arthropod biodiversity through assembly of Illumina shotgun sequences of PCR amplicons. <b>2013</b> , 4, 1142-1150	42
1980	Probiotic dosing of <i>Ruminococcus flavefaciens</i> affects rumen microbiome structure and function in reindeer. <b>2013</b> , 66, 840-9	13
1979	Elucidating the microbial resuscitation cascade in biological soil crusts following a simulated rain event. <b>2013</b> , 15, 2799-815	73
1978	Microbial community changes in hydraulic fracturing fluids and produced water from shale gas extraction. <b>2013</b> , 47, 13141-50	120
1977	Effects of plant host species and plant community richness on streptomycete community structure. <b>2013</b> , 83, 596-606	28
1976	Monotonous diets protect against acute colitis in mice: epidemiologic and therapeutic implications. <b>2013</b> , 56, 544-50	15

1975	More effective cell-based therapy through biofilm suppression. <b>2013</b> , 22, 26-31		11
1974	Standard methods for research on <i>Apis mellifera</i> gut symbionts. <b>2013</b> , 52, 1-24		62
1973	Microbiome in human health and disease. <b>2013</b> , 96, 153-70		17
1972	Male circumcision significantly reduces prevalence and load of genital anaerobic bacteria. <b>2013</b> , 4, e00076		81
1971	Reestablishment of recipient-associated microbiota in the lung allograft is linked to reduced risk of bronchiolitis obliterans syndrome. <b>2013</b> , 187, 640-7		89
1970	VSL#3 probiotic modifies mucosal microbial composition but does not reduce colitis-associated colorectal cancer. <b>2013</b> , 3, 2868		74
1969	Reduced colonic microbial diversity is associated with colitis in NHE3-deficient mice. <b>2013</b> , 305, G667-77		57
1968	FunFrame: functional gene ecological analysis pipeline. <i>Bioinformatics</i> , <b>2013</b> , 29, 1212-4	7.2	10
1967	454 pyrosequencing to describe microbial eukaryotic community composition, diversity and relative abundance: a test for marine haptophytes. <b>2013</b> , 8, e74371		98
1966	Upper Arctic Ocean water masses harbor distinct communities of heterotrophic flagellates. <b>2013</b> , 10, 4273-4286		21
1965	Population genetics of the filarial worm <i>wuchereria bancrofti</i> in a post-treatment region of Papua New Guinea: insights into diversity and life history. <b>2013</b> , 7, e2308		12
1964	Comparison of Gut Microbiota between Sasang Constitutions. <b>2013</b> , 2013, 171643		10
1963	HIV-1 superinfection occurs less frequently than initial infection in a cohort of high-risk Kenyan women. <b>2013</b> , 9, e1003593		34
1962	Scrapheap challenge: a novel bulk-bone metabarcoding method to investigate ancient DNA in faunal assemblages. <b>2013</b> , 3, 3371		53
1961	EBARDenovo: highly accurate de novo assembly of RNA-Seq with efficient chimera-detection. <i>Bioinformatics</i> , <b>2013</b> , 29, 1004-10	7.2	28
1960	Density-based hierarchical clustering of pyro-sequences on a large scale--the case of fungal ITS1. <i>Bioinformatics</i> , <b>2013</b> , 29, 1268-74	7.2	14
1959	Gene capture coupled to high-throughput sequencing as a strategy for targeted metagenome exploration. <b>2013</b> , 20, 185-96		37
1958	How are plant and fungal communities linked to each other in belowground ecosystems? A massively parallel pyrosequencing analysis of the association specificity of root-associated fungi and their host plants. <b>2013</b> , 3, 3112-24		57

1957	Application of natural blends of phytochemicals derived from the root exudates of Arabidopsis to the soil reveal that phenolic-related compounds predominantly modulate the soil microbiome. <b>2013</b> , 288, 4502-12	324
1956	Analytical tools and databases for metagenomics in the next-generation sequencing era. <b>2013</b> , 11, 102-13	98
1955	FunGene: the functional gene pipeline and repository. <b>2013</b> , 4, 291	368
1954	Structural and functional variation in soil fungal communities associated with litter bags containing maize leaf. <b>2013</b> , 84, 519-31	48
1953	Temporal molecular and isotopic analysis of active bacterial communities in two New Zealand sponges. <b>2013</b> , 85, 195-205	27
1952	Distribution-based clustering: using ecology to refine the operational taxonomic unit. <b>2013</b> , 79, 6593-603	102
1951	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. <b>2013</b> , 2, 259-75	33
1950	Microbial communities in flowback water impoundments from hydraulic fracturing for recovery of shale gas. <b>2013</b> , 86, 567-80	92
1949	Community composition of root-associated fungi in a <i>Quercus</i> -dominated temperate forest: "codominance" of mycorrhizal and root-endophytic fungi. <b>2013</b> , 3, 1281-93	92
1948	Evaluating bacterial community structures in oil collected from the sea surface and sediment in the northern Gulf of Mexico after the Deepwater Horizon oil spill. <b>2013</b> , 2, 492-504	114
1947	Habitat- and host-related variation in sponge bacterial symbiont communities in Indonesian waters. <b>2013</b> , 85, 465-82	73
1946	The transition from freshwater to marine iron-oxidizing bacterial lineages along a salinity gradient on the Sheepscot River, Maine, USA. <b>2013</b> , 5, 453-63	51
1945	Pyrosequencing Analysis of Bench-Scale Nitrifying Biofilters Removing Trihalomethanes. <b>2013</b> , 30, 582-588	12
1944	Changes in the rumen epimural bacterial diversity of beef cattle as affected by diet and induced ruminal acidosis. <b>2013</b> , 79, 3744-55	128
1943	High-throughput DNA sequence analysis reveals stable engraftment of gut microbiota following transplantation of previously frozen fecal bacteria. <b>2013</b> , 4, 125-35	218
1942	Structure of the rare archaeal biosphere and seasonal dynamics of active ecotypes in surface coastal waters. <b>2013</b> , 110, 6004-9	175
1941	Large-Scale Clustering of Short Reads for Metagenomics On GPUs. <b>2013</b> , 1003-1022	
1940	Metatranscriptomics reveal differences in in situ energy and nitrogen metabolism among hydrothermal vent snail symbionts. <b>2013</b> , 7, 1556-67	53



1939	Molecular evidence for an active endogenous microbiome beneath glacial ice. <b>2013</b> , 7, 1402-12	91
1938	Broad distribution of diverse anaerobic ammonium-oxidizing bacteria in Chinese agricultural soils. <b>2013</b> , 79, 6167-72	74
1937	Medical therapy reduces microbiota diversity and evenness in surgically recalcitrant chronic rhinosinusitis. <b>2013</b> , 3, 775-81	58
1936	Microbiome assembly across multiple body sites in low-birthweight infants. <b>2013</b> , 4, e00782-13	103
1935	De novo semi-alignment of 16S rRNA gene sequences for deep phylogenetic characterization of next generation sequencing data. <b>2013</b> , 28, 211-6	37
1934	Sputum smear concentration may misidentify acid-fast bacilli as <i>Mycobacterium tuberculosis</i> in HIV-infected patients. <b>2013</b> , 63, 168-77	8
1933	Impact of ethnicity, geography, and disease on the microbiota in health and inflammatory bowel disease. <b>2013</b> , 19, 2906-18	59
1932	A multifactor analysis of fungal and bacterial community structure in the root microbiome of mature <i>Populus deltoides</i> trees. <b>2013</b> , 8, e76382	186
1931	Assessing Long Term Effects of Bioremediation: Soil Bacterial Communities 14 Years after Polycyclic Aromatic Hydrocarbon Contamination and Introduction of a Genetically Engineered Microorganism. <b>2013</b> , 04,	2
1930	Colonization patterns of soil microbial communities in the Atacama Desert. <b>2013</b> , 1, 28	132
1929	Up to Species-level Community Analysis of Human Gut Microbiota by 16S rRNA Amplicon Pyrosequencing. <b>2013</b> , 32, 69-76	12
1928	Highly variable microbiota development in the chicken gastrointestinal tract. <b>2013</b> , 8, e84290	155
1927	Alterations in the colonic microbiota in response to osmotic diarrhea. <b>2013</b> , 8, e55817	80
1926	A multi-omic systems-based approach reveals metabolic markers of bacterial vaginosis and insight into the disease. <b>2013</b> , 8, e56111	84
1925	Molecular mapping to species level of the tonsillar crypt microbiota associated with health and recurrent tonsillitis. <b>2013</b> , 8, e56418	92
1924	Assessing the consequences of denoising marker-based metagenomic data. <b>2013</b> , 8, e60458	49
1923	Bacterial community profiling of milk samples as a means to understand culture-negative bovine clinical mastitis. <b>2013</b> , 8, e61959	91
1922	Impact of colonoscopy bowel preparation on intestinal microbiota. <b>2013</b> , 8, e62815	60

1921	Phylogenetic analysis of a microbialite-forming microbial mat from a hypersaline lake of the Kiritimati atoll, Central Pacific. <b>2013</b> , 8, e66662	111
1920	Comparison of DNA extraction methods in analysis of salivary bacterial communities. <b>2013</b> , 8, e67699	62
1919	Light structures phototroph, bacterial and fungal communities at the soil surface. <b>2013</b> , 8, e69048	16
1918	Bacterial community development in experimental gingivitis. <b>2013</b> , 8, e71227	132
1917	Surprising prokaryotic and eukaryotic diversity, community structure and biogeography of Ethiopian soda lakes. <b>2013</b> , 8, e72577	68
1916	Metagenomic profiling reveals lignocellulose degrading system in a microbial community associated with a wood-feeding beetle. <b>2013</b> , 8, e73827	87
1915	Shifts in the microbial community composition of Gulf Coast beaches following beach oiling. <b>2013</b> , 8, e74265	60
1914	Methane-carbon flow into the benthic food web at cold seeps--a case study from the Costa Rica subduction zone. <b>2013</b> , 8, e74894	47
1913	Campylobacter jejuni colonization is associated with a dysbiosis in the cecal microbiota of mice in the absence of prominent inflammation. <b>2013</b> , 8, e75325	16
1912	Diverse vaginal microbiomes in reproductive-age women with vulvovaginal candidiasis. <b>2013</b> , 8, e79812	73
1911	Characterization of the core rumen microbiome in cattle during transition from forage to concentrate as well as during and after an acidotic challenge. <b>2013</b> , 8, e83424	208
1910	Comparison of the bacterial composition and structure in symptomatic and asymptomatic endodontic infections associated with root-filled teeth using pyrosequencing. <b>2013</b> , 8, e84960	43
1909	The role of tetraether lipid composition in the adaptation of thermophilic archaea to acidity. <b>2013</b> , 4, 62	41
1908	An analysis of thaumarchaeota populations from the northern gulf of Mexico. <b>2013</b> , 4, 72	56
1907	Characterization of eukaryotic microbial diversity in hypersaline Lake Tyrrell, Australia. <b>2013</b> , 4, 115	40
1906	A comparative study of microbial diversity and community structure in marine sediments using poly(A) tailing and reverse transcription-PCR. <b>2013</b> , 4, 160	11
1905	Microbial communities associated with ferromanganese nodules and the surrounding sediments. <b>2013</b> , 4, 161	38
1904	The epsomitic phototrophic microbial mat of Hot Lake, Washington: community structural responses to seasonal cycling. <b>2013</b> , 4, 323	60

1903	Functional gene pyrosequencing and network analysis: an approach to examine the response of denitrifying bacteria to increased nitrogen supply in salt marsh sediments. <b>2013</b> , 4, 342	37
1902	Characterizing microbial diversity and the potential for metabolic function at -15 °c in the Basal ice of Taylor Glacier, Antarctica. <b>2013</b> , 2, 1034-53	32
1901	The human urinary microbiome; bacterial DNA in voided urine of asymptomatic adults. <b>2013</b> , 3, 41	199
1900	Intra-aggregate Pore Structure Influences Phylogenetic Composition of Bacterial Community in Macroaggregates. <b>2014</b> , 78, 1924-1939	52
1899	Free glycogen in vaginal fluids is associated with Lactobacillus colonization and low vaginal pH. <b>2014</b> , 9, e102467	113
1898	The impact of selective-logging and forest clearance for oil palm on fungal communities in Borneo. <b>2014</b> , 9, e111525	32
1897	Network analysis reveals ecological links between N-fixing bacteria and wood-decaying fungi. <b>2014</b> , 9, e88141	82
1896	Microbial communities of three sympatric Australian stingless bee species. <b>2014</b> , 9, e105718	31
1895	Bacterial communities in Malagasy soils with differing levels of disturbance affecting botanical diversity. <b>2014</b> , 9, e85097	6
1894	Diversity and spatial structure of belowground plant-fungal symbiosis in a mixed subtropical forest of ectomycorrhizal and arbuscular mycorrhizal plants. <b>2014</b> , 9, e86566	53
1893	Characterization of the gut microbiota in the red panda ( <i>Ailurus fulgens</i> ). <b>2014</b> , 9, e87885	41
1892	Microbial community structure in lake and wetland sediments from a high Arctic polar desert revealed by targeted transcriptomics. <b>2014</b> , 9, e89531	27
1891	Diversity of rumen bacteria in Canadian cervids. <b>2014</b> , 9, e89682	49
1890	Airborne bacterial communities in residences: similarities and differences with fungi. <b>2014</b> , 9, e91283	99
1889	Analysis of plant-bacteria interactions in their native habitat: bacterial communities associated with wild tobacco are independent of endogenous jasmonic acid levels and developmental stages. <b>2014</b> , 9, e94710	33
1888	The bacterial communities associated with honey bee ( <i>Apis mellifera</i> ) foragers. <b>2014</b> , 9, e95056	162
1887	Spatial segregation and aggregation of ectomycorrhizal and root-endophytic fungi in the seedlings of two <i>Quercus</i> species. <b>2014</b> , 9, e96363	23
1886	Should we build "obese" or "lean" anaerobic digesters?. <b>2014</b> , 9, e97252	18

1885	Escherichia coli O157:H7 super-shedder and non-shedder feedlot steers harbour distinct fecal bacterial communities. <b>2014, 9, e98115</b>	35
1884	Changes in the bacterial community of soybean rhizospheres during growth in the field. <b>2014, 9, e100709</b>	140
1883	Improved yield of high molecular weight DNA coincides with increased microbial diversity access from iron oxide cemented sub-surface clay environments. <b>2014, 9, e102826</b>	18
1882	Intracellular diversity of the V4 and V9 regions of the 18S rRNA in marine protists (radiolarians) assessed by high-throughput sequencing. <b>2014, 9, e104297</b>	49
1881	Snow surface microbiome on the High Antarctic Plateau (DOME C). <b>2014, 9, e104505</b>	26
1880	Differential responses of cecal microbiota to fishmeal, Eimeria and Clostridium perfringens in a necrotic enteritis challenge model in chickens. <b>2014, 9, e104739</b>	110
1879	Microbial community structure of relict niter-beds previously used for saltpeter production. <b>2014, 9, e104752</b>	4
1878	Acute effects of TiO <sub>2</sub> nanomaterials on the viability and taxonomic composition of aquatic bacterial communities assessed via high-throughput screening and next generation sequencing. <b>2014, 9, e106280</b>	32
1877	Application of ion torrent sequencing to the assessment of the effect of alkali ballast water treatment on microbial community diversity. <b>2014, 9, e107534</b>	20
1876	The largest subunit of RNA polymerase II as a new marker gene to study assemblages of arbuscular mycorrhizal fungi in the field. <b>2014, 9, e107783</b>	44
1875	Effect of oral administration of metronidazole or prednisolone on fecal microbiota in dogs. <b>2014, 9, e107909</b>	67
1874	Specific microbiome changes in a mouse model of parenteral nutrition associated liver injury and intestinal inflammation. <b>2014, 9, e110396</b>	51
1873	Stable composition of the nano- and picoplankton community during the ocean iron fertilization experiment LOHAFEX. <b>2014, 9, e113244</b>	13
1872	Succession of bacterial community structure and diversity in soil along a chronosequence of reclamation and re-vegetation on coal mine spoils in China. <b>2014, 9, e115024</b>	45
1871	Bacterial community composition in three freshwater reservoirs of different alkalinity and trophic status. <b>2014, 9, e116145</b>	65
1870	An antimethanogenic nutritional intervention in early life of ruminants modifies ruminal colonization by Archaea. <b>2014, 2014, 841463</b>	49
1869	Characterization of the Vaginal Microbiota of Ewes and Cows Reveals a Unique Microbiota with Low Levels of Lactobacilli and Near-Neutral pH. <b>2014, 1, 19</b>	71
1868	Effect of an oxygenating agent on oral bacteria in vitro and on dental plaque composition in healthy young adults. <b>2014, 4, 95</b>	10

1867	Zooplankton diversity across three Red Sea reefs using pyrosequencing. <b>2014</b> , 1,	31
1866	Potential benefits of the application of yeast starters in table olive processing. <b>2012</b> , 5, 34	93
1865	Effects of different compost amendments on the abundance and composition of <i>alkB</i> harboring bacterial communities in a soil under industrial use contaminated with hydrocarbons. <b>2014</b> , 5, 96	28
1864	Phototrophic biofilm assembly in microbial-mat-derived unicyanobacterial consortia: model systems for the study of autotroph-heterotroph interactions. <b>2014</b> , 5, 109	84
1863	<i>Pinus flexilis</i> and <i>Picea engelmannii</i> share a simple and consistent needle endophyte microbiota with a potential role in nitrogen fixation. <b>2014</b> , 5, 333	60
1862	Water content differences have stronger effects than plant functional groups on soil bacteria in a steppe ecosystem. <b>2014</b> , 9, e115798	9
1861	Pyrosequencing-based analysis of the bacterial community during fermentation of Alaska pollock sikhae: traditional Korean seafood. <b>2014</b> , 60, 227-33	3
1860	Meat Science and Muscle Biology Symposium: <i>Escherichia coli</i> O157:H7, diet, and fecal microbiome in beef cattle. <b>2014</b> , 92, 1345-55	12
1859	Origin and effect of Alpha 2.2 <i>Acetobacteraceae</i> in honey bee larvae and description of <i>Parasaccharibacter apium</i> gen. nov., sp. nov. <b>2014</b> , 80, 7460-72	85
1858	A metagenomics-based approach to the top-down effect on the detritivore food web: a salamanders influence on fungal communities within a deciduous forest. <b>2014</b> , 4, 4106-16	7
1857	Microbial community composition and diversity via 16S rRNA gene amplicons: evaluating the Illumina platform. <b>2014</b> ,	2
1856	Microbial Communities Promoting Mn(II) Oxidation in Ashumet Pond, a Historically Polluted Freshwater Pond Undergoing Remediation. <b>2014</b> , 31, 605-616	23
1855	Induction of diabetes in the RIP-B7.1 mouse model is critically dependent on TLR3 and MyD88 pathways and is associated with alterations in the intestinal microbiome. <b>2014</b> , 63, 619-31	40
1854	Profiling bacterial community in upper respiratory tracts. <b>2014</b> , 14, 583	48
1853	Association between cigarette smoking and the vaginal microbiota: a pilot study. <b>2014</b> , 14, 471	74
1852	16S rRNA gene pyrosequencing of reference and clinical samples and investigation of the temperature stability of microbiome profiles. <b>2014</b> , 2, 31	46
1851	Two grass species fail to display differing species-specific effects on soil bacterial community structures after one season of greenhouse growth. <b>2014</b> , 385, 241-254	8
1850	Sequence exploration reveals information bias among molecular markers used in phylogenetic reconstruction for <i>Colletotrichum</i> species. <b>2014</b> , 3, 614	2

1849	Functional genomics and microbiome profiling of the Asian longhorned beetle ( <i>Anoplophora glabripennis</i> ) reveal insights into the digestive physiology and nutritional ecology of wood feeding beetles. <b>2014</b> , 15, 1096	68
1848	Integrated 'omics analysis for studying the microbial community response to a pH perturbation of a cellulose-degrading bioreactor culture. <b>2014</b> , 90, 802-15	9
1847	A review of software for analyzing molecular sequences. <b>2014</b> , 7, 830	37
1846	Solution hybrid selection capture for the recovery of functional full-length eukaryotic cDNAs from complex environmental samples. <b>2014</b> , 21, 685-94	16
1845	Reproducibility of pyrosequencing data for biodiversity assessment in complex communities. <b>2014</b> , 5, 881-890	30
1844	Differences in gastric mucosal microbiota profiling in patients with chronic gastritis, intestinal metaplasia, and gastric cancer using pyrosequencing methods. <b>2014</b> , 19, 407-16	160
1843	Detection of bacterial DNA in lymph nodes of Crohn's disease patients using high throughput sequencing. <b>2014</b> , 63, 1596-606	53
1842	In-depth analyses of deep subsurface sediments using 454-pyrosequencing reveals a reservoir of buried fungal communities at record-breaking depths. <b>2014</b> , 90, 908-21	36
1841	Acetoclastic methane formation from Eucalyptus detritus in pristine hydrocarbon-rich river sediments by Methanosarcinales. <b>2014</b> , 90, 587-98	4
1840	Core functional traits of bacterial communities in the Upper Mississippi River show limited variation in response to land cover. <b>2014</b> , 5, 414	64
1839	Identification of bacterial community composition in freshwater aquaculture system farming of <i>Litopenaeus vannamei</i> reveals distinct temperature-driven patterns. <b>2014</b> , 15, 13663-80	37
1838	Activity and abundance of methane-oxidizing bacteria in secondary forest and manioc plantations of Amazonian Dark Earth and their adjacent soils. <b>2014</b> , 5, 550	14
1837	Metagenomic ventures into outer sequence space. <b>2014</b> , 4, e979664	22
1836	A rickettsial endosymbiont inhabiting the cytoplasm of <i>Volvox carteri</i> (Volvocales, Chlorophyceae). <b>2014</b> , 53, 95-99	12
1835	Characterizing the avian gut microbiota: membership, driving influences, and potential function. <b>2014</b> , 5, 223	220
1834	Validation of a novel murine wound model of <i>Acinetobacter baumannii</i> infection. <b>2014</b> , 58, 1332-42	51
1833	Applications of Next-Generation Sequencing Technologies to the Study of the Human Microbiome. <b>2014</b> , 75-106	
1832	Convergent bacterial microbiotas in the fungal agricultural systems of insects. <b>2014</b> , 5, e02077	68

1831	Bacterial community structure is indicative of chemical inputs in the Upper Mississippi River. <b>2014</b> , 5, 524	61
1830	Eutrophication has no short-term effect on the <i>Cymbastela stipitata</i> holobiont. <b>2014</b> , 5, 216	38
1829	Aerobic methanotrophic communities at the Red Sea brine-seawater interface. <b>2014</b> , 5, 487	24
1828	Ecological consistency of SSU rRNA-based operational taxonomic units at a global scale. <b>2014</b> , 10, e1003594	58
1827	Effects of bifidobacterial supplementation to pregnant women and infants in the prevention of allergy development in infants and on fecal microbiota. <b>2014</b> , 63, 575-85	102
1826	Oligotyping reveals differences between gut microbiomes of free-ranging sympatric Namibian carnivores ( <i>Acinonyx jubatus</i> , <i>Canis mesomelas</i> ) on a bacterial species-like level. <b>2014</b> , 5, 526	29
1825	Carbadox has both temporary and lasting effects on the swine gut microbiota. <b>2014</b> , 5, 276	48
1824	Molecular analysis of the microbiota in hard feces from healthy rabbits ( <i>Oryctolagus cuniculus</i> ) medicated with long term oral meloxicam. <b>2014</b> , 10, 62	22
1823	Comparisons of the composition and biogeographic distribution of the bacterial communities occupying South African thermal springs with those inhabiting deep subsurface fracture water. <b>2014</b> , 5, 679	46
1822	A compositional look at the human gastrointestinal microbiome and immune activation parameters in HIV infected subjects. <b>2014</b> , 10, e1003829	259
1821	Late winter under ice pelagic microbial communities in the high Arctic Ocean and the impact of short-term exposure to elevated CO <sub>2</sub> levels. <b>2014</b> , 5, 490	18
1820	The crypt-dwelling primary bacterial symbiont of the polyphagous pentatomid pest <i>Halyomorpha halys</i> (Hemiptera: Pentatomidae). <b>2014</b> , 43, 617-25	35
1819	Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition. <b>2014</b> , 15, R76	150
1818	Anal microbiota profiles in HIV-positive and HIV-negative MSM. <b>2014</b> , 28, 753-60	54
1817	Linking geology and microbiology: inactive pockmarks affect sediment microbial community structure. <b>2014</b> , 9, e85990	9
1816	Fast dendrogram-based OTU clustering using sequence embedding. <b>2014</b> ,	3
1815	The female urinary microbiome: a comparison of women with and without urgency urinary incontinence. <b>2014</b> , 5, e01283-14	346
1814	Evaluation of the nasal microbiota in slaughter-age pigs and the impact on nasal methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) carriage. <b>2014</b> , 10, 69	37

1813	Single clinical isolates from acute uncomplicated urinary tract infections are representative of dominant in situ populations. <b>2014</b> , 5, e01064-13	27
1812	Multiple omics uncovers host-gut microbial mutualism during prebiotic fructooligosaccharide supplementation. <b>2014</b> , 21, 469-80	62
1811	Hive-stored pollen of honey bees: many lines of evidence are consistent with pollen preservation, not nutrient conversion. <b>2014</b> , 23, 5904-17	127
1810	Nitrogen deposition alters plant-fungal relationships: linking belowground dynamics to aboveground vegetation change. <b>2014</b> , 23, 1364-78	51
1809	Diversity and geochemical structuring of bacterial communities along a salinity gradient in a carbonate aquifer subject to seawater intrusion. <b>2014</b> , 90, 922-34	28
1808	Temporal changes and the effect of subtherapeutic concentrations of antibiotics in the gut microbiota of swine. <b>2014</b> , 90, 599-608	42
1807	Molecular analyses of gut contents: elucidating the feeding of co-occurring salps in the Lazarev Sea from a different perspective. <b>2014</b> , 26, 545-553	11
1806	<i>Hartmannibacter diazotrophicus</i> gen. nov., sp. nov., a phosphate-solubilizing and nitrogen-fixing alphaproteobacterium isolated from the rhizosphere of a natural salt-meadow plant. <b>2014</b> , 64, 3160-3167	18
1805	Correlates of gut community composition across an ant species ( <i>Cephalotes varians</i> ) elucidate causes and consequences of symbiotic variability. <b>2014</b> , 23, 1284-300	60
1804	Hyperimmune bovine colostrum as a novel therapy to combat <i>Clostridium difficile</i> infection. <b>2015</b> , 211, 1334-41	24
1803	Amplicon pyrosequencing reveals the soil microbial diversity associated with invasive Japanese barberry ( <i>Berberis thunbergii</i> DC.). <b>2014</b> , 23, 1318-32	26
1802	Spatial distribution patterns of benthic microbial communities along the Pearl Estuary, China. <b>2014</b> , 37, 578-89	58
1801	Major faecal microbiota shifts in composition and diversity with age in a geographically restricted cohort of mothers and their children. <b>2014</b> , 87, 280-90	121
1800	Deodorization of pig slurry and characterization of bacterial diversity using 16S rDNA sequence analysis. <b>2014</b> , 52, 918-29	7
1799	Association of Growth Substrates and Bacterial Genera with Benzo[ <i>a</i> ]pyrene Mineralization in Contaminated Soil. <b>2014</b> , 31, 689-697	27
1798	The giraffe ( <i>Giraffa camelopardalis</i> ) rumen microbiome. <b>2014</b> , 90, 237-46	23
1797	Distribution and diversity of <i>Prochlorococcus</i> ecotypes in the Red Sea. <b>2014</b> , 356, 118-26	22
1796	NxrB encoding the beta subunit of nitrite oxidoreductase as functional and phylogenetic marker for nitrite-oxidizing <i>Nitrospira</i> . <b>2014</b> , 16, 3055-71	193



1795	Analysis of the factors affecting the formation of the microbiome associated with chronic osteomyelitis of the jaw. <b>2014</b> , 20, O309-17	17
1794	Seasonal dynamics of fungal communities in a temperate oak forest soil. <b>2014</b> , 201, 269-278	230
1793	Anaerobic oxidation of methane by sulfate in hypersaline groundwater of the Dead Sea aquifer. <b>2014</b> , 12, 511-28	34
1792	The microbiome of New World vultures. <b>2014</b> , 5, 5498	177
1791	Microbiome diversity of <i>Aphis glycines</i> with extensive superinfection in native and invasive populations. <b>2014</b> , 6, 57-69	34
1790	Onset and establishment of diazotrophs and other bacterial associates in the early life history stages of the coral <i>Acropora millepora</i> . <b>2014</b> , 23, 4682-95	68
1789	Impact of drinking water conditions and copper materials on downstream biofilm microbial communities and <i>Legionella pneumophila</i> colonization. <b>2014</b> , 117, 905-18	45
1788	A morphogenetic survey on ciliate plankton from a mountain lake pinpoints the necessity of lineage-specific barcode markers in microbial ecology. <b>2014</b> , 16, 430-44	81
1787	Human microbiota characterization in the course of renal transplantation. <b>2014</b> , 14, 416-27	99
1786	The potential role of lung microbiota in lung cancer attributed to household coal burning exposures. <b>2014</b> , 55, 643-51	116
1785	Effect of CO <sub>2</sub> (aq) Exposure on a Freshwater Aquifer Microbial Community from Simulated Geologic Carbon Storage Leakage. <b>2014</b> , 1, 479-483	7
1784	First evidence of amoebae-mycobacteria association in drinking water network. <b>2014</b> , 48, 11872-82	85
1783	An increasing opine carbon bias in artificial exudation systems and genetically modified plant rhizospheres leads to an increasing reshaping of bacterial populations. <b>2014</b> , 23, 4846-61	29
1782	Ribosomal Database Project: data and tools for high throughput rRNA analysis. <b>2014</b> , 42, D633-42	2527
1781	Anthropogenic land use shapes the composition and phylogenetic structure of soil arbuscular mycorrhizal fungal communities. <b>2014</b> , 90, 609-21	104
1780	Distribution of PAHs and the PAH-degrading bacteria in the deep-sea sediments of the high-latitude Arctic Ocean. <b>2014</b> ,	5
1779	Epidemic <i>Clostridium difficile</i> strains demonstrate increased competitive fitness compared to nonepidemic isolates. <b>2014</b> , 82, 2815-25	49
1778	Bacterial diversity assessment in Antarctic terrestrial and aquatic microbial mats: a comparison between bidirectional pyrosequencing and cultivation. <b>2014</b> , 9, e97564	49

1777	Analysis of plant microbe interactions in the era of next generation sequencing technologies. <b>2014</b> , 5, 216	150
1776	Rheinheimera hassiensis sp. nov. and Rheinheimera muenzenbergensis sp. nov., two species from the rhizosphere of Hordeum secalinum. <b>2014</b> , 64, 1202-1209	21
1775	Simultaneous assessment of the macrobiome and microbiome in a bulk sample of tropical arthropods through DNA metasytematics. <b>2014</b> , 111, 8007-12	196
1774	Characterization and use of microbial communities in Doenjang to control the unpleasant odor of Ginkgo epicarp. <b>2014</b> , 23, 1959-1964	1
1773	Effect of long-term different fertilization on bacterial community structures and diversity in citrus orchard soil of volcanic ash. <b>2014</b> , 52, 995-1001	22
1772	Mitochondrial and nuclear phylogenetic analysis with Sanger and next-generation sequencing shows that, in Ñea de Conservaci3n Guanacaste, northwestern Costa Rica, the skipper butterfly named Urbanus belli (family Hesperiiidae) comprises three morphologically cryptic species. <b>2014</b> , 11, 153	23
1771	Comparison of environmental and isolate Sulfolobus genomes reveals diverse carbon, sulfur, nitrogen, and hydrogen metabolisms. <b>2014</b> , 15, 1107	54
1770	Characterization and comparison of bacterial communities in benign vocal fold lesions. <b>2014</b> , 2, 43	19
1769	ITS1, 5.8S and ITS2 secondary structure modelling for intra-specific differentiation among species of the Colletotrichum gloeosporioides sensu lato species complex. <b>2014</b> , 3, 684	26
1768	Sñnce: reference-based phylogenetic analysis for 18S rRNA studies. <b>2014</b> , 14, 235	8
1767	Bacterial associates of seed-parasitic wasps (Hymenoptera: Megastigmus). <b>2014</b> , 14, 224	15
1766	Alcohol and tobacco consumption affects bacterial richness in oral cavity mucosa biofilms. <b>2014</b> , 14, 250	42
1765	Diet disparity among sympatric herbivorous cichlids in the same ecomorphs in Lake Tanganyika: amplicon pyrosequences on algal farms and stomach contents. <b>2014</b> , 12, 90	22
1764	Evaluation of the impact of refrigeration on next generation sequencing-based assessment of the canine and feline fecal microbiota. <b>2014</b> , 10, 230	12
1763	Elucidation of bacteria found in car interiors and strategies to reduce the presence of potential pathogens. <b>2014</b> , 30, 337-46	17
1762	Broad scope method for creating humanized animal models for animal health and disease research through antibiotic treatment and human fecal transfer. <b>2014</b> , 5, 183-91	58
1761	Microbial community stratification linked to utilization of carbohydrates and phosphorus limitation in a boreal peatland at Marcell Experimental Forest, Minnesota, USA. <b>2014</b> , 80, 3518-30	79
1760	Analysis, optimization and verification of Illumina-generated 16S rRNA gene amplicon surveys. <b>2014</b> , 9, e94249	237

1759	Pyrosequencing 16S rRNA genes of bacteria associated with wild tiger mosquito <i>Aedes albopictus</i> : a pilot study. <b>2014</b> , 4, 59	46
1758	Dietary history contributes to enterotype-like clustering and functional metagenomic content in the intestinal microbiome of wild mice. <b>2014</b> , 111, E2703-10	107
1757	Acquisition and structuring of midgut bacterial communities in gypsy moth ( <i>Lepidoptera</i> : <i>Erebidae</i> ) larvae. <b>2014</b> , 43, 595-604	73
1756	A possible link between food and mood: dietary impact on gut microbiota and behavior in BALB/c mice. <b>2014</b> , 9, e103398	103
1755	Deterministic processes guide long-term synchronised population dynamics in replicate anaerobic digesters. <b>2014</b> , 8, 2015-28	224
1754	Importance of saprotrophic freshwater fungi for pollen degradation. <b>2014</b> , 9, e94643	74
1753	Iron supplementation promotes gut microbiota metabolic activity but not colitis markers in human gut microbiota-associated rats. <b>2014</b> , 111, 2135-45	42
1752	Consumption of acidic water alters the gut microbiome and decreases the risk of diabetes in NOD mice. <b>2014</b> , 62, 237-50	55
1751	Microbial diversity in hummock and hollow soils of three wetlands on the Qinghai-Tibetan Plateau revealed by 16S rRNA pyrosequencing. <b>2014</b> , 9, e103115	48
1750	Characterization of intestinal bacteria in wild and domesticated adult black tiger shrimp ( <i>Penaeus monodon</i> ). <b>2014</b> , 9, e91853	156
1749	Microbes in the neonatal intensive care unit resemble those found in the gut of premature infants. <b>2014</b> , 2, 1	251
1748	Association between the vaginal microbiota, menopause status, and signs of vulvovaginal atrophy. <b>2014</b> , 21, 450-8	198
1747	Resistance and resilience of the forest soil microbiome to logging-associated compaction. <b>2014</b> , 8, 226-44	194
1746	Bacterial diversity associated with the tunic of the model chordate <i>Ciona intestinalis</i> . <b>2014</b> , 8, 309-20	30
1745	Unearthing carrion beetles' microbiome: characterization of bacterial and fungal hindgut communities across the Silphidae. <b>2014</b> , 23, 1251-67	65
1744	Early empiric antibiotic use in preterm infants is associated with lower bacterial diversity and higher relative abundance of <i>Enterobacter</i> . <b>2014</b> , 165, 23-9	225
1743	The anti-obesity effect of <i>Ephedra sinica</i> through modulation of gut microbiota in obese Korean women. <b>2014</b> , 152, 532-9	59
1742	Characterization of the oral microbiota of healthy cats using next-generation sequencing. <b>2014</b> , 201, 223-9	51

1741	Influence of <i>Panax ginseng</i> on obesity and gut microbiota in obese middle-aged Korean women. <b>2014</b> , 38, 106-15	57
1740	Habitat preferences, distribution, and temporal persistence of a novel fungal taxon in Alaskan boreal forest soils. <b>2014</b> , 12, 70-77	2
1739	Molecular characterization of bacterial communities associated with sediments in the Laurentian Great Lakes. <b>2014</b> , 40, 640-645	12
1738	Successional development of biofilms in moving bed biofilm reactor (MBBR) systems treating municipal wastewater. <b>2014</b> , 98, 1429-40	76
1737	Genus-wide acid tolerance accounts for the biogeographical distribution of soil Burkholderia populations. <b>2014</b> , 16, 1503-12	72
1736	16S rDNA pyrosequencing analysis of bacterial community in heavy metals polluted soils. <b>2014</b> , 67, 635-47	167
1735	Bacterial diversity in Greenlandic soils as affected by potato cropping and inorganic versus organic fertilization. <b>2014</b> , 37, 61-71	41
1734	Detection of the horizontal spatial structure of soil fungal communities in a natural forest. <b>2014</b> , 56, 301-310	23
1733	Pyrosequencing-based characterization of gastrointestinal bacteria of Atlantic salmon ( <i>Salmo salar</i> L.) within a commercial mariculture system. <b>2014</b> , 117, 18-27	98
1732	Prokaryotic communities in pit mud from different-aged cellars used for the production of Chinese strong-flavored liquor. <b>2014</b> , 80, 2254-60	105
1731	Effects of water-saving irrigation on emissions of greenhouse gases and prokaryotic communities in rice paddy soil. <b>2014</b> , 68, 271-83	30
1730	Mouse Paneth cell antimicrobial function is independent of Nod2. <b>2014</b> , 63, 903-10	81
1729	Pathogens and host immunity in the ancient human oral cavity. <b>2014</b> , 46, 336-44	353
1728	Amplicon pyrosequencing reveals spatial and temporal consistency in diazotroph assemblages of the <i>Acropora millepora</i> microbiome. <b>2014</b> , 16, 3345-59	71
1727	Analysis of the gut microbiota by high-throughput sequencing of the V5-V6 regions of the 16S rRNA gene in donkey. <b>2014</b> , 68, 657-62	28
1726	Comparison of brush and biopsy sampling methods of the ileal pouch for assessment of mucosa-associated microbiota of human subjects. <b>2014</b> , 2, 5	72
1725	Protist community composition in the Pacific sector of the Southern Ocean during austral summer 2010. <b>2014</b> , 37, 375-389	26
1724	The composition and stability of the vaginal microbiota of normal pregnant women is different from that of non-pregnant women. <b>2014</b> , 2, 4	447

1723	Diversity and abundance of Bacteria and nirS-encoding denitrifiers associated with the Juan de Fuca Ridge hydrothermal system. <b>2014</b> , 64, 1691-1705	11
1722	Genetic data generated from virus-host complexes obtained by membrane co-immobilization are equivalent to data obtained from tangential filtrate virus concentrates and virus cultures. <b>2014</b> , 48, 160-7	2
1721	High-throughput DNA sequencing of the ruminal bacteria from moose ( <i>Alces alces</i> ) in Vermont, Alaska, and Norway. <b>2014</b> , 68, 185-95	37
1720	When the forest dies: the response of forest soil fungi to a bark beetle-induced tree dieback. <b>2014</b> , 8, 1920-31	95
1719	Ontogenetic variation in epibiont community structure in the deep-sea yeti crab, <i>Kiwa puravida</i> : convergence among crustaceans. <b>2014</b> , 23, 1457-72	24
1718	nifH pyrosequencing reveals the potential for location-specific soil chemistry to influence N <sub>2</sub> -fixing community dynamics. <b>2014</b> , 16, 3211-23	80
1717	Rich and cold: diversity, distribution and drivers of fungal communities in patterned-ground ecosystems of the North American Arctic. <b>2014</b> , 23, 3258-72	102
1716	Molecular analysis of point-of-use municipal drinking water microbiology. <b>2014</b> , 49, 225-35	79
1715	Gene-targeted metagenomic analysis of glucan-branching enzyme gene profiles among human and animal fecal microbiota. <b>2014</b> , 8, 493-503	23
1714	Dynamics of the bacterial community structure in the rhizosphere of a maize cultivar. <b>2014</b> , 68, 392-401	230
1713	Resilience of the natural phyllosphere microbiota of the grapevine to chemical and biological pesticides. <b>2014</b> , 80, 3585-96	99
1712	Elevated atmospheric CO <sub>2</sub> stimulates soil fungal diversity through increased fine root production in a semiarid shrubland ecosystem. <b>2014</b> , 20, 2555-65	23
1711	Dynamics and associations of microbial community types across the human body. <b>2014</b> , 509, 357-60	529
1710	Evaluating the potential of 18S rDNA clone libraries to complement pyrosequencing data of marine protists with near full-length sequence information. <b>2014</b> , 10, 771-780	5
1709	Large-scale fungal diversity assessment in the Andean Yungas forests reveals strong community turnover among forest types along an altitudinal gradient. <b>2014</b> , 23, 2452-72	107
1708	Bacterial community structure and dissolved organic matter in repeatedly flooded subsurface karst water pools. <b>2014</b> , 89, 111-26	39
1707	Accuracy of allele frequency estimation using pooled RNA-Seq. <b>2014</b> , 14, 381-92	45
1706	Root-colonizing and soil-borne communities of arbuscular mycorrhizal fungi in a temperate forest understorey. <b>2014</b> , 92, 277-285	76

1705	Diversity of diversity: conceptual and methodological differences in biodiversity estimates of eukaryotic microbes as compared to bacteria. <b>2014</b> , 22, 432-7	32
1704	Performance comparison of genetic markers for high-throughput sequencing-based biodiversity assessment in complex communities. <b>2014</b> , 14, 1049-59	69
1703	Stability and phylogenetic correlation in gut microbiota: lessons from ants and apes. <b>2014</b> , 23, 1268-83	168
1702	Ancient DNA sheds new light on the Svalbard foraminiferal fossil record of the last millennium. <b>2014</b> , 12, 277-88	28
1701	Improved group-specific primers based on the full SILVA 16S rRNA gene reference database. <b>2014</b> , 16, 2389-407	28
1700	Atmospheric N deposition increases bacterial laccase-like multicopper oxidases: implications for organic matter decay. <b>2014</b> , 80, 4460-8	37
1699	Bacteria, phages and pigs: the effects of in-feed antibiotics on the microbiome at different gut locations. <b>2014</b> , 8, 1566-76	224
1698	Mathematical modeling of primary succession of murine intestinal microbiota. <b>2014</b> , 111, 439-44	130
1697	Community fingerprinting in a sequencing world. <b>2014</b> , 89, 316-30	124
1696	Comparative analysis of the microbial communities in agricultural soil amended with enhanced biochars or traditional fertilisers. <b>2014</b> , 191, 73-82	133
1695	HIV-1 interacts with human endogenous retrovirus K (HML-2) envelopes derived from human primary lymphocytes. <b>2014</b> , 88, 6213-23	35
1694	Species richness of arbuscular mycorrhizal fungi: associations with grassland plant richness and biomass. <b>2014</b> , 203, 233-44	176
1693	Contrasting elevational diversity patterns between eukaryotic soil microbes and plants. <b>2014</b> , 95, 3190-3202	110
1692	Enrichment of specific bacterial and eukaryotic microbes in the rhizosphere of switchgrass ( <i>Panicum virgatum</i> L.) through root exudates. <b>2014</b> , 6, 293-306	38
1691	AIEC pathobiont instigates chronic colitis in susceptible hosts by altering microbiota composition. <b>2014</b> , 63, 1069-80	149
1690	Meta-analysis of deep-sequenced fungal communities indicates limited taxon sharing between studies and the presence of biogeographic patterns. <b>2014</b> , 201, 623-635	86
1689	Phylogenetic differences in attached and free-living bacterial communities in a temperate coastal lagoon during summer, revealed via high-throughput 16S rRNA gene sequencing. <b>2014</b> , 80, 2071-83	73
1688	Multistate assessment of wetland restoration on CO <sub>2</sub> and N <sub>2</sub> O emissions and soil bacterial communities. <b>2014</b> , 76, 87-94	13

1687	Phylogenetic diversity of eukaryotic marine microbial plankton on the Scotian Shelf Northwestern Atlantic Ocean. <b>2014</b> , 36, 344-363	18
1686	Urine is not sterile: use of enhanced urine culture techniques to detect resident bacterial flora in the adult female bladder. <b>2014</b> , 52, 871-6	458
1685	Variation in forest soil fungal diversity along a latitudinal gradient. <b>2014</b> , 64, 305-315	82
1684	Removal of nonylphenol by earthworms and bacterial community change. <b>2014</b> , 96, 9-17	13
1683	Microplastic is an abundant and distinct microbial habitat in an urban river. <b>2014</b> , 48, 11863-71	711
1682	Effect of feeding dried distillers grains with solubles on ruminal biohydrogenation, intestinal fatty acid profile, and gut microbial diversity evaluated through DNA pyro-sequencing. <b>2014</b> , 92, 733-43	16
1681	Molecular community profiling reveals impacts of time, space, and disease status on the bacterial community associated with the Caribbean sponge <i>Aplysina cauliformis</i> . <b>2014</b> , 87, 268-79	38
1680	Spatial-temporal survey and occupancy-abundance modeling to predict bacterial community dynamics in the drinking water microbiome. <b>2014</b> , 5, e01135-14	124
1679	Impact of a hormone-releasing intrauterine system on the vaginal microbiome: a prospective baboon model. <b>2014</b> , 43, 89-99	18
1678	Shifts in archaeoplankton community structure along ecological gradients of Pearl Estuary. <b>2014</b> , 90, 424-35	31
1677	Abundance, diversity and seasonal dynamics of predatory bacteria in aquaculture zero discharge systems. <b>2014</b> , 89, 149-61	51
1676	Establishment of ruminal bacterial community in dairy calves from birth to weaning is sequential. <b>2014</b> , 116, 245-57	155
1675	Tissue storage and primer selection influence pyrosequencing-based inferences of diversity and community composition of endolichenic and endophytic fungi. <b>2014</b> , 14, 1032-48	66
1674	Diazotrophic potential among bacterial communities associated with wild and cultivated <i>Agave</i> species. <b>2014</b> , 90, 844-57	43
1673	Free-Living and Particle-Associated Bacterioplankton in Large Rivers of the Mississippi River Basin Demonstrate Biogeographic Patterns. <b>2014</b> , 80, 7186-95	40
1672	Microbial diversity and biogenic methane potential of a thermogenic-gas coal mine. <b>2014</b> , 134-135, 96-107	35
1671	Internal porosity of mineral coating supports microbial activity in rapid sand filters for groundwater treatment. <b>2014</b> , 80, 7010-20	27
1670	Prebiotic effects of cassava bagasse in TNO's in vitro model of the colon in lean versus obese microbiota. <b>2014</b> , 11, 210-220	31

1669	Microbiota transplantation restores normal fecal bile acid composition in recurrent <i>Clostridium difficile</i> infection. <b>2014</b> , 306, G310-9	254
1668	Microbial community composition and dynamics in high-temperature biogas reactors using industrial bioethanol waste as substrate. <b>2014</b> , 98, 9095-106	28
1667	Utilizing "omics" tools to study the complex gut ecosystem. <b>2014</b> , 817, 25-38	7
1666	Gill bacteria enable a novel digestive strategy in a wood-feeding mollusk. <b>2014</b> , 111, E5096-104	67
1665	Effect of wastewater disposal on the bacterial and archaeal community of sea sediment in an industrial area in China. <b>2014</b> , 88, 320-32	27
1664	Microbial community structure and dynamics during co-digestion of whey permeate and cow manure in continuous stirred tank reactor systems. <b>2014</b> , 171, 350-9	50
1663	Bacterial epibionts of <i>Daphnia</i> : a potential route for the transfer of dissolved organic carbon in freshwater food webs. <b>2014</b> , 8, 1808-19	49
1662	Systematic evaluation of bias in microbial community profiles induced by whole genome amplification. <b>2014</b> , 16, 643-57	27
1661	Shifts in abundance and diversity of mobile genetic elements after the introduction of diverse pesticides into an on-farm biopurification system over the course of a year. <b>2014</b> , 80, 4012-20	48
1660	Development of methane emission from lambs fed milk replacer and cream for a prolonged period. <b>2014</b> , 198, 38-48	6
1659	Exploring the diversity of extremely halophilic archaea in food-grade salts. <b>2014</b> , 191, 36-44	33
1658	Microbial community composition is unaffected by anode potential. <b>2014</b> , 48, 1352-8	141
1657	Assessing Symbiodinium diversity in scleractinian corals via next-generation sequencing-based genotyping of the ITS2 rDNA region. <b>2014</b> , 23, 4418-33	161
1656	Cultivation-based multiplex phenotyping of human gut microbiota allows targeted recovery of previously uncultured bacteria. <b>2014</b> , 5, 4714	91
1655	Application of ARISA to assess the influence of salt content and cation type on microbiological diversity of Cheddar cheese. <b>2014</b> , 59, 207-16	10
1654	Pyrosequencing for assessing diversity of eukaryotic microbes: analysis of data on marine planktonic ciliates and comparison with traditional methods. <b>2014</b> , 16, 2752-63	52
1653	Tongue images and tongue coating microbiome in patients with colorectal cancer. <b>2014</b> , 77, 1-6	28
1652	In vitro fermentability of sugar beet pulp derived oligosaccharides using human and pig fecal inocula. <b>2014</b> , 62, 1079-87	54



1651	Protons accumulation during anodic phase turned to advantage for oxygen reduction during cathodic phase in reversible bioelectrodes. <b>2014</b> , 173, 224-230	38
1650	Research on neonatal microbiomes: what neonatologists need to know. <b>2014</b> , 105, 14-24	11
1649	Bacterial community characterization in the soils of native and restored rainforest fragments. <b>2014</b> , 106, 947-57	1
1648	Characterization of ancient DNA supports long-term survival of Haloarchaea. <b>2014</b> , 14, 553-60	16
1647	Investigation of ruminal bacterial diversity in dairy cattle fed supplementary monensin alone and in combination with fat, using pyrosequencing analysis. <b>2014</b> , 60, 65-71	15
1646	Off-site impacts of agricultural composting: role of terrestrially derived organic matter in structuring aquatic microbial communities and their metabolic potential. <b>2014</b> , 90, 622-32	14
1645	Spore dispersal of basidiomycete fungi at the landscape scale is driven by stochastic and deterministic processes and generates variability in plant-fungal interactions. <b>2014</b> , 204, 180-191	123
1644	Biofilm community dynamics in bench-scale annular reactors simulating arrestment of chloraminated drinking water nitrification. <b>2014</b> , 48, 5448-57	26
1643	Design and validation of four new primers for next-generation sequencing to target the 18S rRNA genes of gastrointestinal ciliate protozoa. <b>2014</b> , 80, 5515-21	24
1642	Down under the tunic: bacterial biodiversity hotspots and widespread ammonia-oxidizing archaea in coral reef ascidians. <b>2014</b> , 8, 575-588	56
1641	Predominant bacterial and fungal assemblages in agricultural soils during a record drought/heat wave and linkages to enzyme activities of biogeochemical cycling. <b>2014</b> , 84, 69-82	81
1640	Plant defence inducers rapidly influence the diversity of bacterial communities in a potting mix. <b>2014</b> , 84, 1-5	23
1639	Differential resistance of drinking water bacterial populations to monochloramine disinfection. <b>2014</b> , 48, 4038-47	112
1638	Picoeukaryote plankton composition off West Spitsbergen at the entrance to the Arctic Ocean. <b>2014</b> , 61, 569-79	36
1637	Conducting a microbiome study. <b>2014</b> , 158, 250-262	428
1636	Microbial ecology dynamics reveal a succession in the core microbiota involved in the ripening of pasta filata caciocavallo pugliese cheese. <b>2014</b> , 80, 6243-55	56
1635	Human mitochondrial DNA and endogenous bacterial surrogates for risk assessment of graywater reuse. <b>2014</b> , 48, 7993-8002	16
1634	Influence of hand rearing and bird age on the fecal microbiota of the critically endangered kakapo. <b>2014</b> , 80, 4650-8	34

1633	The human gut microbiome as a screening tool for colorectal cancer. <b>2014</b> , 7, 1112-21	316
1632	Host species and developmental stage, but not host social structure, affects bacterial community structure in socially polymorphic bees. <b>2014</b> , 88, 398-406	41
1631	Microbial genomic analysis reveals the essential role of inflammation in bacteria-induced colorectal cancer. <b>2014</b> , 5, 4724	222
1630	Identification and characterization of microbial biofilm communities associated with corroded oil pipeline surfaces. <b>2014</b> , 30, 823-35	67
1629	A microbial ecosystem beneath the West Antarctic ice sheet. <b>2014</b> , 512, 310-3	191
1628	TRIF signaling drives homeostatic intestinal epithelial antimicrobial peptide expression. <b>2014</b> , 193, 4223-34	25
1627	Molecular methods for biofilms. <b>2014</b> , 87-137	
1626	Distinct bacterial assemblages reside at different depths in Arctic multiyear sea ice. <b>2014</b> , 90, 115-25	20
1625	Characterization of the intestinal microbiota in Pacific white shrimp, <i>Litopenaeus vannamei</i> , fed diets with different lipid sources. <b>2014</b> , 434, 449-455	119
1624	Functional diversification within bacterial lineages promotes wide functional overlapping between taxonomic groups in a Mediterranean forest soil. <b>2014</b> , 90, 54-67	16
1623	Exploring the immediate and long-term impact on bacterial communities in soil amended with animal and urban organic waste fertilizers using pyrosequencing and screening for horizontal transfer of antibiotic resistance. <b>2014</b> , 90, 206-24	55
1622	Bacterial community composition and diversity of five different permafrost-affected soils of Northeast Greenland. <b>2014</b> , 89, 426-41	51
1621	The vaginal microbiota of pregnant women who subsequently have spontaneous preterm labor and delivery and those with a normal delivery at term. <b>2014</b> , 2, 18	236
1620	Structure of the gut microbiome following colonization with human feces determines colonic tumor burden. <b>2014</b> , 2, 20	176
1619	Characterization of the nasopharyngeal microbiota in health and during rhinovirus challenge. <b>2014</b> , 2, 22	87
1618	The nasal cavity microbiota of healthy adults. <b>2014</b> , 2, 27	103
1617	Impact of primer choice on characterization of orchid mycorrhizal communities using 454 pyrosequencing. <b>2014</b> , 14, 679-99	75
1616	Rate-specific responses of prokaryotic diversity and structure to nitrogen deposition in the <i>Leymus chinensis</i> steppe. <b>2014</b> , 79, 81-90	125

1615	Diversity of dechlorination pathways and organohalide respiring bacteria in chlorobenzene dechlorinating enrichment cultures originating from river sludge. <b>2014</b> , 25, 757-76	14
1614	Microbiota characterization of a Belgian protected designation of origin cheese, Herve cheese, using metagenomic analysis. <b>2014</b> , 97, 6046-56	106
1613	Shallow water marine sediment bacterial community shifts along a natural CO <sub>2</sub> gradient in the Mediterranean Sea off Vulcano, Italy. <b>2014</b> , 67, 819-28	48
1612	Spatial scaling effects on soil bacterial communities in Malaysian tropical forests. <b>2014</b> , 68, 247-58	28
1611	Straw- and slurry-associated prokaryotic communities differ during co-fermentation of straw and swine manure. <b>2014</b> , 98, 4771-80	49
1610	Native soil fungi associated with compostable plastics in three contrasting agricultural settings. <b>2014</b> , 98, 6467-85	28
1609	Salinity-dominated change in community structure and ecological function of Archaea from the lower Pearl River to coastal South China Sea. <b>2014</b> , 98, 7971-82	72
1608	Effect of haylage and monensin supplementation on ruminal bacterial communities of feedlot cattle. <b>2014</b> , 69, 169-75	8
1607	A molecular survey of protist diversity through the central Arctic Ocean. <b>2014</b> , 37, 1271-1287	34
1606	Bacterial diversity in snow on North Pole ice floes. <b>2014</b> , 18, 945-51	19
1605	Analyses of dryland biological soil crusts highlight lichens as an important regulator of microbial communities. <b>2014</b> , 23, 1735-1755	53
1604	Soil bacterial communities of different natural forest types in Northeast China. <b>2014</b> , 383, 203-216	57
1603	An improved dual-indexing approach for multiplexed 16S rRNA gene sequencing on the Illumina MiSeq platform. <b>2014</b> , 2, 6	930
1602	Strong functional stability of soil microbial communities under semiarid Mediterranean conditions and subjected to long-term shifts in baseline precipitation. <b>2014</b> , 69, 223-233	83
1601	Influence of environmental variation on symbiotic bacterial communities of two temperate sponges. <b>2014</b> , 88, 516-27	47
1600	Long-term changes in soil microbial communities during primary succession. <b>2014</b> , 69, 359-370	46
1599	Bacterial community structures in rhizosphere microsites of ryegrass ( <i>Lolium perenne</i> var. Nui) as revealed by pyrosequencing. <b>2014</b> , 50, 1253-1266	22
1598	Influence of DNA extraction method, 16S rRNA targeted hypervariable regions, and sample origin on microbial diversity detected by 454 pyrosequencing in marine chemosynthetic ecosystems. <b>2014</b> , 80, 4626-39	61

1597	The effect of PPI use on human gut microbiota and weight loss in patients undergoing laparoscopic Roux-en-Y gastric bypass. <b>2014</b> , 24, 1567-71	35
1596	Regional effects on chimera formation in 454 pyrosequenced amplicons from a mock community. <b>2014</b> , 52, 566-73	10
1595	Identifying airborne fungi in Seoul, Korea using metagenomics. <b>2014</b> , 52, 465-72	35
1594	Fungal diversity in the Antarctic active layer. <b>2014</b> , 83, 94-101	19
1593	The fecal microbiota of semi-free-ranging wood bison ( <i>Bison bison athabasca</i> ). <b>2014</b> , 10, 120	6
1592	Pyrosequencing analysis of microbiota reveals that lactic acid bacteria are dominant in Korean flat fish fermented food, <i>gajami-sikhae</i> . <b>2014</b> , 78, 1611-8	10
1591	Microbial community dynamics during fermentation of <i>doenjang-meju</i> , traditional Korean fermented soybean. <b>2014</b> , 185, 112-20	86
1590	Forensic soil DNA analysis using high-throughput sequencing: a comparison of four molecular markers. <b>2014</b> , 13, 176-84	42
1589	Temporal changes in microbial ecology and geochemistry in produced water from hydraulically fractured Marcellus shale gas wells. <b>2014</b> , 48, 6508-17	181
1588	Investigating microbial eukaryotic diversity from a global census: insights from a comparison of pyrotag and full-length sequences of 18S rRNA genes. <b>2014</b> , 80, 4363-73	58
1587	To pool or not to pool? Impact of the use of individual and pooled fecal samples for in vitro fermentation studies. <b>2014</b> , 107, 1-7	56
1586	Release of arsenite, arsenate and methyl-arsenic species from streambed sediment affected by acid mine drainage: a microcosm study. <b>2014</b> , 11, 514	13
1585	Wastewater irrigation increases the abundance of potentially harmful gammaproteobacteria in soils in Mezquital Valley, Mexico. <b>2014</b> , 80, 5282-91	51
1584	Alteration of the murine gastrointestinal microbiota by tigecycline leads to increased susceptibility to <i>Clostridium difficile</i> infection. <b>2014</b> , 58, 2767-74	53
1583	Critical review of NGS analyses for de novo genotyping multigene families. <b>2014</b> , 23, 3957-72	46
1582	Analysis of microbial community adaptation in mesophilic hydrogen fermentation from food waste by tagged 16S rRNA gene pyrosequencing. <b>2014</b> , 144, 143-51	31
1581	Carbon dioxide and hydrogen sulfide associations with regional bacterial diversity patterns in microbially induced concrete corrosion. <b>2014</b> , 48, 7357-64	28
1580	Effects of long-term differential fertilization on eukaryotic microbial communities in an arable soil: a multiple barcoding approach. <b>2014</b> , 23, 3341-55	117

1579	The effect of ecological and temporal factors on the composition of Bartonella infection in rodents and their fleas. <b>2014</b> , 8, 1598-608	28
1578	Analyzing the human microbiome: a "how to" guide for physicians. <b>2014</b> , 109, 983-93	57
1577	Correlating microbial diversity patterns with geochemistry in an extreme and heterogeneous environment of mine tailings. <b>2014</b> , 80, 3677-86	117
1576	Targeted 16S rRNA high-throughput sequencing to characterize microbial communities during composting of livestock mortalities. <b>2014</b> , 116, 1181-94	39
1575	Diversity of bacterial symbionts in populations of Sitobion miscanthi (Hemiptera: Aphididae) in China. <b>2014</b> , 43, 605-11	9
1574	Bacterial community dynamics during industrial malting, with an emphasis on lactic acid bacteria. <b>2014</b> , 39, 39-46	31
1573	Long-term batch brewing accumulates adaptive microbes, which comprehensively produce more flavorful Chinese liquors. <b>2014</b> , 62, 894-901	31
1572	Impact of sampler selection on the characterization of the indoor microbiome via high-throughput sequencing. <b>2014</b> , 80, 274-282	41
1571	Spatial variability of winter bacterioplankton community composition in the Gulf of Finland (the Baltic Sea). <b>2014</b> , 129, 127-134	12
1570	Two necrotic enteritis predisposing factors, dietary fishmeal and Eimeria infection, induce large changes in the caecal microbiota of broiler chickens. <b>2014</b> , 169, 188-97	117
1569	Distributions and assemblages of microbial communities along a sediment core retrieved from a potential hydrate-bearing region offshore southwestern Taiwan. <b>2014</b> , 92, 276-292	13
1568	Variations in 16S rRNA-based microbiome profiling between pyrosequencing runs and between pyrosequencing facilities. <b>2014</b> , 52, 355-65	25
1567	Bacterial targets as potential indicators of diesel fuel toxicity in subantarctic soils. <b>2014</b> , 80, 4021-33	52
1566	Microbial diversities (16S and 18S rRNA gene pyrosequencing) and environmental pathogens within drinking water biofilms grown on the common premise plumbing materials unplasticized polyvinylchloride and copper. <b>2014</b> , 88, 280-95	55
1565	Coexisting orchid species have distinct mycorrhizal communities and display strong spatial segregation. <b>2014</b> , 202, 616-627	71
1564	Human milk oligosaccharides shorten rotavirus-induced diarrhea and modulate piglet mucosal immunity and colonic microbiota. <b>2014</b> , 8, 1609-20	93
1563	Effects of light and prey availability on Arctic freshwater protist communities examined by high-throughput DNA and RNA sequencing. <b>2014</b> , 88, 550-64	38
1562	Spatial and temporal structuring of arbuscular mycorrhizal communities is differentially influenced by abiotic factors and host crop in a semi-arid prairie agroecosystem. <b>2014</b> , 88, 333-44	101

1561	Unraveling the outcome of 16S rDNA-based taxonomy analysis through mock data and simulations. <i>Bioinformatics</i> , <b>2014</b> , 30, 1530-8	7.2	27
1560	Distinct signatures of host-microbial meta-metabolome and gut microbiome in two C57BL/6 strains under high-fat diet. <b>2014</b> , 8, 2380-96		87
1559	Assessing effects of the fungicide tebuconazole to heterotrophic microbes in aquatic microcosms. <b>2014</b> , 490, 1002-11		45
1558	Indications for algae-degrading benthic microbial communities in deep-sea sediments along the Antarctic Polar Front. <b>2014</b> , 108, 6-16		41
1557	Comparison of root-associated communities of native and non-native ectomycorrhizal hosts in an urban landscape. <b>2014</b> , 24, 267-80		18
1556	High-throughput sequencing shows inconsistent results with a microscope-based analysis of the soil prokaryotic community. <b>2014</b> , 76, 53-56		13
1555	Characterization of rhizosphere and endophytic bacterial communities from leaves, stems and roots of medicinal <i>Stellera chamaejasme</i> L. <b>2014</b> , 37, 376-85		71
1554	Surface soil fungal and bacterial communities in aspen stands are resilient to eleven years of elevated CO <sub>2</sub> and O <sub>3</sub> . <b>2014</b> , 76, 227-234		21
1553	A first comprehensive census of fungi in soil reveals both hyperdiversity and fine-scale niche partitioning. <b>2014</b> , 84, 3-20		223
1552	Metatranscriptomics reveals overall active bacterial composition in caries lesions. <b>2014</b> , 6, 25443		83
1551	Library construction for next-generation sequencing: overviews and challenges. <b>2014</b> , 56, 61-4, 66, 68, passim		370
1550	Bacteria and bacterial DNA in atherosclerotic plaque and aneurysmal wall biopsies from patients with and without periodontitis. <b>2014</b> , 6,		58
1549	Purifying the impure: sequencing metagenomes and metatranscriptomes from complex animal-associated samples. <b>2014</b> ,		18
1548	An experimental and bioinformatics protocol for RNA-Seq analyses of photoperiodic diapause in the Asian tiger mosquito, <i>Aedes albopictus</i> . <b>2014</b> , e51961		5
1547	BOTUX: bayesian-like operational taxonomic unit examiner. <b>2014</b> , 7, 130-45		1
1546	Next-generation environmental diversity surveys of foraminifera: preparing the future. <b>2014</b> , 227, 93-106		50
1545	Multiple approaches to microbial source tracking in tropical northern Australia. <b>2014</b> , 3, 860-74		31
1544	Molecular analysis of the benthos microbial community in Zavarzin thermal spring (Uzon Caldera, Kamchatka, Russia). <b>2014</b> , 15 Suppl 12, S12		32

1543	Characterization and quantification of the fungal microbiome in serial samples from individuals with cystic fibrosis. <b>2014</b> , 2, 40	103
1542	Impacts of Shallow Geothermal Energy on Groundwater Quality. <b>2014</b> , 13,	10
1541	DNA metabarcoding of insects and allies: an evaluation of primers and pipelines. <b>2015</b> , 105, 717-27	90
1540	Tracking year-to-year changes in intestinal nematode communities of rufous mouse lemurs ( <i>Microcebus rufus</i> ). <b>2015</b> , 142, 1095-107	12
1539	What is living on your dog's skin? Characterization of the canine cutaneous mycobiota and fungal dysbiosis in canine allergic dermatitis. <b>2015</b> , 91,	45
1538	Microbiome structure of the fungid coral <i>Ctenactis echinata</i> aligns with environmental differences. <b>2015</b> , 24, 3501-11	84
1537	Divergence thresholds and divergent biodiversity estimates: can metabarcoding reliably describe zooplankton communities?. <b>2015</b> , 5, 2234-51	80
1536	Molecular study of bacterial diversity within the trophosome of the vestimentiferan tubeworm <i>Ridgeia piscesae</i> . <b>2015</b> , 36, 35-44	8
1535	The stool microbiota of insulin resistant women with recent gestational diabetes, a high risk group for type 2 diabetes. <b>2015</b> , 5, 13212	75
1534	Bacterial community analysis of drinking water biofilms in southern Sweden. <b>2015</b> , 30, 99-107	39
1533	Bacterial Community Composition in Oligosaline Lake Bosten: Low Overlap of Betaproteobacteria and Bacteroidetes with Freshwater Ecosystems. <b>2015</b> , 30, 180-8	15
1532	River bacterioplankton community responses to a high inflow event. <b>2015</b> , 75, 187-205	16
1531	Minor revision to V4 region SSU rRNA 806R gene primer greatly increases detection of SAR11 bacterioplankton. <b>2015</b> , 75, 129-137	790
1530	Microbial ecology and geoelectric responses across a groundwater plume. <b>2015</b> , 3, SAB9-SAB21	2
1529	Impact of a wastewater treatment plant on microbial community composition and function in a hyporheic zone of a eutrophic river. <b>2015</b> , 5, 17284	50
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1527	Combined DNA, toxicological and heavy metal analyses provides an auditing toolkit to improve pharmacovigilance of traditional Chinese medicine (TCM). <b>2015</b> , 5, 17475	67
1526	High-throughput sequencing and morphology perform equally well for benthic monitoring of marine ecosystems. <b>2015</b> , 5, 13932	132

1525	Deterministic processes vary during community assembly for ecologically dissimilar taxa. <b>2015</b> , 6, 8444	139
1524	Insights into the distribution and abundance of the ubiquitous candidatus Saccharibacteria phylum following tag pyrosequencing. <b>2014</b> , 4, 3957	48
1523	Roles of Oligotrophic Acidophiles (Alicyclobacillus) in Chalcopyrite Bioleaching System: Shake Flask Evaluation. <b>2015</b> , 1130, 410-413	1
1522	The hidden 'mycobacteriome' of the human healthy oral cavity and upper respiratory tract. <b>2015</b> , 7, 26094	24
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1520	Using Bayesian modelling to investigate factors governing antibiotic-induced <i>Candida albicans</i> colonization of the GI tract. <b>2015</b> , 5, 8131	27
1519	Niche differentiation of bacterial communities at a millimeter scale in Shark Bay microbial mats. <b>2015</b> , 5, 15607	71
1518	A Comprehensive, Automatically Updated Fungal ITS Sequence Dataset for Reference-Based Chimera Control in Environmental Sequencing Efforts. <b>2015</b> , 30, 145-50	144
1517	MICCA: a complete and accurate software for taxonomic profiling of metagenomic data. <b>2015</b> , 5, 9743	158
1516	Potential applications of next generation DNA sequencing of 16S rRNA gene amplicons in microbial water quality monitoring. <b>2015</b> , 72, 1962-72	40
1515	Aboveground-belowground biodiversity linkages differ in early and late successional temperate forests. <b>2015</b> , 5, 12234	16
1514	Probiotic <i>Bifidobacterium longum</i> alters gut luminal metabolism through modification of the gut microbial community. <b>2015</b> , 5, 13548	95
1513	<i>Plasmodium berghei</i> ANKA causes intestinal malaria associated with dysbiosis. <b>2015</b> , 5, 15699	40
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1511	Micelle PCR reduces chimera formation in 16S rRNA profiling of complex microbial DNA mixtures. <b>2015</b> , 5, 14181	23
1510	Abundance, viability and diversity of the indigenous microbial populations at different depths of the NEEM Greenland ice core. <b>2015</b> , 34, 25057	11
1509	In vitro characterisation of the fermentation profile and prebiotic capacity of gold-fleshed kiwifruit. <b>2015</b> , 6, 829-39	9
1508	Molecular-based approaches to characterize coastal microbial community and their potential relation to the trophic state of Red Sea. <b>2015</b> , 5, 9001	21



1507	Robust species taxonomy assignment algorithm for 16S rRNA NGS reads: application to oral carcinoma samples. <b>2015</b> , 7, 28934	64
1506	Pyridine-type alkaloid composition affects bacterial community composition of floral nectar. <b>2015</b> , 5, 11536	25
1505	Evidence of bacterioplankton community adaptation in response to long-term mariculture disturbance. <b>2015</b> , 5, 15274	31
1504	Surveying the endomicrobiome and ectomicrobiome of bark beetles: The case of <i>Dendroctonus simplex</i> . <b>2015</b> , 5, 17190	29
1503	Systemic immunity shapes the oral microbiome and susceptibility to bisphosphonate-associated osteonecrosis of the jaw. <b>2015</b> , 13, 212	26
1502	Microbiomes of the dust particles collected from the International Space Station and Spacecraft Assembly Facilities. <b>2015</b> , 3, 50	113
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1499	Microenvironment and phylogenetic diversity of <i>Prochloron</i> inhabiting the surface of crustose didemnid ascidians. <b>2015</b> , 17, 4121-32	5
1498	Source Tracking and Succession of Kimchi Lactic Acid Bacteria during Fermentation. <b>2015</b> , 80, M1871-7	57
1497	Rearing and foraging affects bumblebee ( <i>Bombus terrestris</i> ) gut microbiota. <b>2015</b> , 7, 634-41	7
1496	The rise and fall of arbuscular mycorrhizal fungal diversity during ecosystem retrogression. <b>2015</b> , 24, 4912-30	39
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1494	Improved taxonomic assignment of human intestinal 16S rRNA sequences by a dedicated reference database. <b>2015</b> , 16, 1056	87
1493	Longitudinal study of the early-life fecal and nasal microbiotas of the domestic pig. <b>2015</b> , 15, 184	83
1492	Faecal microbiota characterisation of horses using 16 rdna barcoded pyrosequencing, and carriage rate of <i>clostridium difficile</i> at hospital admission. <b>2015</b> , 15, 181	53
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1489	Xander: employing a novel method for efficient gene-targeted metagenomic assembly. <b>2015</b> , 3, 32	67
1488	Amplicon sequencing for the quantification of spoilage microbiota in complex foods including bacterial spores. <b>2015</b> , 3, 30	16
1487	An accurate and efficient experimental approach for characterization of the complex oral microbiota. <b>2015</b> , 3, 48	63
1486	Microbial aerosol liberation from soiled textiles isolated during routine residuals handling in a modern health care setting. <b>2015</b> , 3, 72	24
1485	Barite encrustation of benthic sulfur-oxidizing bacteria at a marine cold seep. <b>2015</b> , 13, 588-603	28
1484	Seasonal assemblages and short-lived blooms in coastal north-west Atlantic Ocean bacterioplankton. <b>2015</b> , 17, 3642-61	30
1483	Mycorrhizal diversity, seed germination and long-term changes in population size across nine populations of the terrestrial orchid <i>Neottia ovata</i> . <b>2015</b> , 24, 3269-80	45
1482	Resistivity and induced polarization monitoring of biogas combined with microbial ecology at a brownfield site. <b>2015</b> , 3, SAB43-SAB56	2
1481	Gut metabolites and bacterial community networks during a pilot intervention study with flaxseeds in healthy adult men. <b>2015</b> , 59, 1614-28	65
1480	Atmospheric N deposition alters connectance, but not functional potential among saprotrophic bacterial communities. <b>2015</b> , 24, 3170-80	31
1479	Microbial communities and nutrient dynamics in experimental microcosms are altered after the application of a high dose of Bti. <b>2015</b> , 52, 763-773	12
1478	Marine protist diversity in European coastal waters and sediments as revealed by high-throughput sequencing. <b>2015</b> , 17, 4035-49	239
1477	Bacterial Diversity Analysis during the Fermentation Processing of Traditional Chinese Yellow Rice Wine Revealed by 16S rDNA 454 Pyrosequencing. <b>2015</b> , 80, M2265-71	24
1476	Characterisation of the faecal metabolome and microbiome of Thoroughbred racehorses. <b>2015</b> , 47, 580-6	37
1475	Development and application of primers for the class Dehalococcoidia (phylum Chloroflexi) enables deep insights into diversity and stratification of subgroups in the marine subsurface. <b>2015</b> , 17, 3540-56	13
1474	Bacterial community dynamics during polysaccharide degradation at contrasting sites in the Southern and Atlantic Oceans. <b>2015</b> , 17, 3822-31	54
1473	High-throughput monitoring of wild bee diversity and abundance via mitogenomics. <b>2015</b> , 6, 1034-1043	97
1472	The coral immune response facilitates protection against microbes during tissue regeneration. <b>2015</b> , 24, 3390-404	46

1471	Sinus culture poorly predicts resident microbiota. <b>2015</b> , 5, 3-9	51
1470	Temporal dynamics of plant-soil feedback and root-associated fungal communities over 100 years of invasion by a non-native plant. <b>2015</b> , 103, 1557-1569	19
1469	Changes in the faecal microbiota of mares precede the development of post partum colic. <b>2015</b> , 47, 641-9	77
1468	Initial colonization, community assembly and ecosystem function: fungal colonist traits and litter biochemistry mediate decay rate. <b>2015</b> , 24, 5045-58	30
1467	High-throughput functional screening reveals low frequency of antibiotic resistance genes in DNA recovered from the Upper Mississippi River. <b>2015</b> , 13, 693-703	9
1466	Bacterial biogeography in the coastal waters of northern Zhejiang, East China Sea is highly controlled by spatially structured environmental gradients. <b>2015</b> , 17, 3898-913	56
1465	The Quantification of Representative Sequences pipeline for amplicon sequencing: case study on within-population ITS1 sequence variation in a microparasite infecting Daphnia. <b>2015</b> , 15, 1385-95	7
1464	Petroleum Hydrocarbon Spills in the Environment and Abundance of Microbial Community Capable of Biosurfactant Production. <b>2015</b> , 06,	3
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1462	Diazotroph community succession during the VAHINE mesocosm experiment (New Caledonia lagoon). <b>2015</b> , 12, 7435-7452	42
1461	Comparison of the gut microbiota profile in breast-fed and formula-fed Korean infants using pyrosequencing. <b>2015</b> , 9, 242-8	68
1460	A Comparison of Three Bioinformatics Pipelines for the Analysis of Preterm Gut Microbiota using 16S rRNA Gene Sequencing Data. <b>2015</b> , 8,	70
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1456	Molecular Analysis of Bacterial Microbiota on Brazilian Currency Note Surfaces. <b>2015</b> , 12, 13276-88	15
1455	Avoidance and Potential Remedy Solutions of Chimeras in Reconstructing the Phylogeny of Aphids Using the 16S rRNA Gene of Buchnera: A Case in Lachninae (Hemiptera). <b>2015</b> , 16, 20152-67	4
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1453	Microbial communities associated with benthic faunal assemblages at cold seep sediments of the Sonora Margin, Guaymas Basin. <b>2015</b> , 2,	9
1452	Microbial communities of the Lemon Creek Glacier show subtle structural variation yet stable phylogenetic composition over space and time. <b>2015</b> , 6, 495	20
1451	Distribution of iron- and sulfate-reducing bacteria across a coastal acid sulfate soil (CASS) environment: implications for passive bioremediation by tidal inundation. <b>2015</b> , 6, 624	15
1450	High resolution depth distribution of Bacteria, Archaea, methanotrophs, and methanogens in the bulk and rhizosphere soils of a flooded rice paddy. <b>2015</b> , 6, 639	85
1449	Functional gene pyrosequencing reveals core proteobacterial denitrifiers in boreal lakes. <b>2015</b> , 6, 674	38
1448	Legacy effects of anaerobic soil disinfestation on soil bacterial community composition and production of pathogen-suppressing volatiles. <b>2015</b> , 6, 701	49
1447	The effect of carbon subsidies on marine planktonic niche partitioning and recruitment during biofilm assembly. <b>2015</b> , 6, 703	12
1446	Bacterial diversity differences along an epigenic cave stream reveal evidence of community dynamics, succession, and stability. <b>2015</b> , 6, 729	14
1445	Reutericyclin producing <i>Lactobacillus reuteri</i> modulates development of fecal microbiota in weanling pigs. <b>2015</b> , 6, 762	24
1444	Primer and platform effects on 16S rRNA tag sequencing. <b>2015</b> , 6, 771	314
1443	The green impact: bacterioplankton response toward a phytoplankton spring bloom in the southern North Sea assessed by comparative metagenomic and metatranscriptomic approaches. <b>2015</b> , 6, 805	52
1442	Response of leaf endophytic bacterial community to elevated CO <sub>2</sub> at different growth stages of rice plant. <b>2015</b> , 6, 855	20
1441	Microbial mineral colonization across a subsurface redox transition zone. <b>2015</b> , 6, 858	15
1440	Soil bacterial and fungal community responses to nitrogen addition across soil depth and microhabitat in an arid shrubland. <b>2015</b> , 6, 891	60
1439	Wine fermentation microbiome: a landscape from different Portuguese wine appellations. <b>2015</b> , 6, 905	114
1438	The large-scale distribution of ammonia oxidizers in paddy soils is driven by soil pH, geographic distance, and climatic factors. <b>2015</b> , 6, 938	38
1437	Co-occurrence of <i>Methanosarcina mazei</i> and Geobacteraceae in an iron (III)-reducing enrichment culture. <b>2015</b> , 6, 941	29
1436	Bacterial endophyte communities in the foliage of coast redwood and giant sequoia. <b>2015</b> , 6, 1008	36

1435	Responses of soil microeukaryotic communities to short-term fumigation-incubation revealed by MiSeq amplicon sequencing. <b>2015</b> , 6, 1149	16
1434	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. <b>2015</b> , 6, 1205	50
1433	Hunting Down Frame Shifts: Ecological Analysis of Diverse Functional Gene Sequences. <b>2015</b> , 6, 1267	3
1432	Forest Management Type Influences Diversity and Community Composition of Soil Fungi across Temperate Forest Ecosystems. <b>2015</b> , 6, 1300	93
1431	Natural Sunlight Shapes Crude Oil-Degrading Bacterial Communities in Northern Gulf of Mexico Surface Waters. <b>2015</b> , 6, 1325	58
1430	Substrate Type and Free Ammonia Determine Bacterial Community Structure in Full-Scale Mesophilic Anaerobic Digesters Treating Cattle or Swine Manure. <b>2015</b> , 6, 1337	57
1429	Impact of Lowland Rainforest Transformation on Diversity and Composition of Soil Prokaryotic Communities in Sumatra (Indonesia). <b>2015</b> , 6, 1339	62
1428	The Scion/Rootstock Genotypes and Habitats Affect Arbuscular Mycorrhizal Fungal Community in Citrus. <b>2015</b> , 6, 1372	15
1427	Bacterial Exchange in Household Washing Machines. <b>2015</b> , 6, 1381	41
1426	Intestinal Microbiota Signatures Associated with Inflammation History in Mice Experiencing Recurring Colitis. <b>2015</b> , 6, 1408	67
1425	Microbial Communities on Seafloor Basalts at Dorado Outcrop Reflect Level of Alteration and Highlight Global Lithic Clades. <b>2015</b> , 6, 1470	30
1424	The vaginal microbiota over an 8- to 10-year period in a cohort of HIV-infected and HIV-uninfected women. <b>2015</b> , 10, e0116894	22
1423	Endosymbiont dominated bacterial communities in a dwarf spider. <b>2015</b> , 10, e0117297	28
1422	Microbial iron mats at the Mid-Atlantic Ridge and evidence that Zetaproteobacteria may be restricted to iron-oxidizing marine systems. <b>2015</b> , 10, e0119284	48
1421	The unique chemistry of Eastern Mediterranean water masses selects for distinct microbial communities by depth. <b>2015</b> , 10, e0120605	40
1420	Redox-specialized bacterioplankton metacommunity in a temperate estuary. <b>2015</b> , 10, e0122304	9
1419	Soil bacterial community structure responses to precipitation reduction and forest management in forest ecosystems across Germany. <b>2015</b> , 10, e0122539	24
1418	The gut microbiota composition in dichorionic triplet sets suggests a role for host genetic factors. <b>2015</b> , 10, e0122561	27

1417	From benchtop to desktop: important considerations when designing amplicon sequencing workflows. <b>2015</b> , 10, e0124671	111
1416	Microbial diversity in a permanently cold and alkaline environment in Greenland. <b>2015</b> , 10, e0124863	28
1415	16S rRNA Amplicon Sequencing Demonstrates that Indoor-Reared Bumblebees ( <i>Bombus terrestris</i> ) Harbor a Core Subset of Bacteria Normally Associated with the Wild Host. <b>2015</b> , 10, e0125152	31
1414	Contrasting diversity and host association of ectomycorrhizal basidiomycetes versus root-associated ascomycetes in a dipterocarp rainforest. <b>2015</b> , 10, e0125550	19
1413	Metagenomic insights into the bioaerosols in the indoor and outdoor environments of childcare facilities. <b>2015</b> , 10, e0126960	54
1412	Patterns in species persistence and biomass production in soil microcosms recovering from a disturbance reject a neutral hypothesis for bacterial community assembly. <b>2015</b> , 10, e0126962	6
1411	Pyrosequencing characterization of the microbiota from Atlantic intertidal marine sponges reveals high microbial diversity and the lack of co-occurrence patterns. <b>2015</b> , 10, e0127455	25
1410	Comparison of Fecal Microbiota in Children with Autism Spectrum Disorders and Neurotypical Siblings in the Simons Simplex Collection. <b>2015</b> , 10, e0137725	125
1409	Bacterial communities associated with host-adapted populations of pea aphids revealed by deep sequencing of 16S ribosomal DNA. <b>2015</b> , 10, e0120664	89
1408	Determining Microeukaryotic Plankton Community around Xiamen Island, Southeast China, Using Illumina MiSeq and PCR-DGGE Techniques. <b>2015</b> , 10, e0127721	23
1407	Bioinformatic Amplicon Read Processing Strategies Strongly Affect Eukaryotic Diversity and the Taxonomic Composition of Communities. <b>2015</b> , 10, e0130035	48
1406	Sputum Bacterial and Fungal Dynamics during Exacerbations of Severe COPD. <b>2015</b> , 10, e0130736	36
1405	The Microbiota and Abundance of the Class 1 Integron-Integrase Gene in Tropical Sewage Treatment Plant Influent and Activated Sludge. <b>2015</b> , 10, e0131532	10
1404	Evidences on the Ability of Mycorrhizal Genus <i>Piloderma</i> to Use Organic Nitrogen and Deliver It to Scots Pine. <b>2015</b> , 10, e0131561	17
1403	Inter-Individual Differences in the Oral Bacteriome Are Greater than Intra-Day Fluctuations in Individuals. <b>2015</b> , 10, e0131607	38
1402	Perilipin-2 Modulates Lipid Absorption and Microbiome Responses in the Mouse Intestine. <b>2015</b> , 10, e0131944	33
1401	Effects of Host Phylogeny and Habitats on Gut Microbiomes of Oriental River Prawn ( <i>Macrobrachium nipponense</i> ). <b>2015</b> , 10, e0132860	42
1400	Assessment of Zooplankton Community Composition along a Depth Profile in the Central Red Sea. <b>2015</b> , 10, e0133487	24

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1396	Bacterial Landscape of Bloodstream Infections in Neutropenic Patients via High Throughput Sequencing. <b>2015</b> , 10, e0135756	26
1395	Molecular Fingerprint and Dominant Environmental Factors of Nitrite-Dependent Anaerobic Methane-Oxidizing Bacteria in Sediments from the Yellow River Estuary, China. <b>2015</b> , 10, e0137996	24
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1382	Comparison of microbiomes from different niches of upper and lower airways in children and adolescents with cystic fibrosis. <b>2015</b> , 10, e0116029	101

1381	Context dependency and saturating effects of loss of rare soil microbes on plant productivity. <b>2015</b> , 6, 485	35
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1378	Variations of Tongue Coating Microbiota in Patients with Gastric Cancer. <b>2015</b> , 2015, 173729	34
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1352	Microbial community composition of a household sand filter used for arsenic, iron, and manganese removal from groundwater in Vietnam. <b>2015</b> , 138, 47-59	59
1351	Bacterial diversity of Drass, cold desert in Western Himalaya, and its comparison with Antarctic and Arctic. <b>2015</b> , 197, 851-60	20
1350	Polymerase matters: non-proofreading enzymes inflate fungal community richness estimates by up to 15%. <b>2015</b> , 15, 86-89	60
1349	Illumina-based analysis of bacterial community in Khuangcherapuk cave of Mizoram, Northeast India. <b>2015</b> , 5, 13-4	10
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1322	Gut Microbiome Diversity among Cheyenne and Arapaho Individuals from Western Oklahoma. <b>2015</b> , 25, 3161-9	39
1321	Metagenome Sequencing Reveals Rhodococcus Dominance in Farpuk Cave, Mizoram, India, an Eastern Himalayan Biodiversity Hot Spot Region. <b>2015</b> , 3,	9
1320	Electrolytic extraction drives volatile fatty acid chain elongation through lactic acid and replaces chemical pH control in thin stillage fermentation. <b>2015</b> , 8, 221	77
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1292	Directed shift of vaginal microbiota induced by vaginal application of sucrose gel in rhesus macaques. <b>2015</b> , 33, 32-6	11

1291	Bacterial communities associated with surfaces of leafy greens: shift in composition and decrease in richness over time. <b>2015</b> , 81, 1530-9	69
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1289	Bacterial structure of aerobic granules is determined by aeration mode and nitrogen load in the reactor cycle. <b>2015</b> , 181, 312-20	52
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1279	Novel basal, fungal lineages from freshwater phytoplankton and lake samples. <b>2015</b> , 7, 435-41	42
1278	High-throughput sequencing of fecal DNA to identify insects consumed by wild Weddell's saddleback tamarins ( <i>Saguinus weddelli</i> , Cebidae, Primates) in Bolivia. <b>2015</b> , 156, 474-81	21
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1275	Improved pipeline for reducing erroneous identification by 16S rRNA sequences using the Illumina MiSeq platform. <b>2015</b> , 53, 60-9	30
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1269	Bacterial community dynamics during cold storage of minced meat packaged under modified atmosphere and supplemented with different preservatives. <b>2015</b> , 48, 192-9	56
1268	Environmental genes and genomes: understanding the differences and challenges in the approaches and software for their analyses. <b>2015</b> , 16, 745-58	44
1267	Composition of fungal and bacterial communities in forest litter and soil is largely determined by dominant trees. <b>2015</b> , 84, 53-64	317
1266	Profiling microbial communities in manganese remediation systems treating coal mine drainage. <b>2015</b> , 81, 2189-98	30
1265	Bacterial communities associated with aerobic degradation of polybrominated diphenyl ethers from river sediments. <b>2015</b> , 22, 3810-9	21
1264	Intraindividual variation in core microbiota in peri-implantitis and periodontitis. <b>2014</b> , 4, 6602	91
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1066	Non-random expression of ribosomal DNA units in a grasshopper showing high intragenomic variation for the ITS2 region. <b>2015</b> , 24, 319-30	2
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1064	Community assembly of a euryhaline fish microbiome during salinity acclimation. <b>2015</b> , 24, 2537-50	128
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1056	Nonproteinogenic D-amino acids at millimolar concentrations are a toxin for anaerobic microorganisms relevant to early Earth and other anoxic planets. <b>2015</b> , 15, 238-46	5
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1051	The levonorgestrel-releasing intrauterine system is associated with delayed endocervical clearance of <i>Chlamydia trachomatis</i> without alterations in vaginal microbiota. <b>2015</b> , 73, ftv070	7
1050	Comparison of bacterial diversity in full scale anammox bioreactors operated under different conditions. <b>2015</b> , 31, 1464-72	52
1049	FUNGAL SYMBIONTS. Global assessment of arbuscular mycorrhizal fungus diversity reveals very low endemism. <b>2015</b> , 349, 970-3	454
1048	Housefly Larva Vermicomposting Efficiently Attenuates Antibiotic Resistance Genes in Swine Manure, with Concomitant Bacterial Population Changes. <b>2015</b> , 81, 7668-79	32
1047	The complicated substrates enhance the microbial diversity and zinc leaching efficiency in sphalerite bioleaching system. <b>2015</b> , 99, 10311-22	23
1046	Collection media and delayed freezing effects on microbial composition of human stool. <b>2015</b> , 3, 33	87
1045	Diversity and distribution of bacterial community in the coastal sediments of Bohai Bay, China. <b>2015</b> , 34, 122-131	11
1044	Classifying the bacterial gut microbiota of termites and cockroaches: A curated phylogenetic reference database (DictDb). <b>2015</b> , 38, 472-82	61
1043	The female urinary microbiome in urgency urinary incontinence. <b>2015</b> , 213, 347.e1-11	166
1042	Potential for using a hermetically-sealed, positive-pressured isocage system for studies involving germ-free mice outside a flexible-film isolator. <b>2015</b> , 6, 255-65	26
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1040	Comparative analysis of oligonucleotide primers for high-throughput screening of genes encoding adenylation domains of nonribosomal peptide synthetases in actinomycetes. <b>2015</b> , 108, 1267-74	1

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1038	A new step aeration approach towards the improvement of nitrogen removal in a full scale Carrousel oxidation ditch. <b>2015</b> , 198, 23-30	13
1037	Woody plant encroachment, and its removal, impact bacterial and fungal communities across stream and terrestrial habitats in a tallgrass prairie ecosystem. <b>2015</b> , 91,	16
1036	Differential responses of total and active soil microbial communities to long-term experimental N deposition. <b>2015</b> , 90, 275-282	83
1035	The links between ecosystem multifunctionality and above- and belowground biodiversity are mediated by climate. <b>2015</b> , 6, 8159	243
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1033	Microbial diversity in deep-sea sediments from the Menez Gwen hydrothermal vent system of the Mid-Atlantic Ridge. <b>2015</b> , 24 Pt 3, 343-55	25
1032	Metagenomics study of endophytic bacteria in Aloe vera using next-generation technology. <b>2015</b> , 6, 159-63	106
1031	The microbiome of otitis media with effusion in Indigenous Australian children. <b>2015</b> , 79, 1548-55	40
1030	Surveying wood-inhabiting fungi: Most molecularly detected polypore species form fruit-bodies within short distances. <b>2015</b> , 18, 93-99	33
1029	Landscape position influences microbial composition and function via redistribution of soil water across a watershed. <b>2015</b> , 81, 8457-68	19
1028	The African buffalo parasite <i>Theileria</i> . sp. (buffalo) can infect and immortalize cattle leukocytes and encodes divergent orthologues of <i>Theileria parva</i> antigen genes. <b>2015</b> , 4, 333-42	26
1027	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <b>2015</b> , 528, 262-266	1107
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1025	Effect of CH <sub>4</sub> /O <sub>2</sub> ratio on fatty acid profile and polyhydroxybutyrate content in a heterotrophic-methanotrophic consortium. <b>2015</b> , 141, 235-42	21
1024	Communities of wood-inhabiting fungi in dead pine logs along a geographical gradient in Japan. <b>2015</b> , 18, 75-82	23
1023	The rectal microbiota of cats infected with feline immunodeficiency virus infection and uninfected controls. <b>2015</b> , 180, 96-102	8
1022	The effects of entombment on water chemistry and bacterial assemblages in closed cryoconite holes on Antarctic glaciers. <b>2015</b> , 91,	22

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1020	Relocation, high-latitude warming and host genetic identity shape the foliar fungal microbiome of poplars. <b>2015</b> , 24, 235-48	88
1019	An improved method to set significance thresholds for $\alpha$ diversity testing in microbial community comparisons. <b>2015</b> , 17, 3154-67	4
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1017	Bacterial community structure of a lab-scale anammox membrane bioreactor. <b>2015</b> , 31, 186-93	33
1016	Shifts of tundra bacterial and archaeal communities along a permafrost thaw gradient in Alaska. <b>2015</b> , 24, 222-34	76
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1005	Ammonia-oxidizing microbial communities in reactors with efficient nitrification at low-dissolved oxygen. <b>2015</b> , 70, 38-51	158
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890	Identification of Free-Living and Particle-Associated Microbial Communities Present in Hadal Regions of the Mariana Trench. <b>2016</b> , 7, 665	56
889	Superimposed Pristine Limestone Aquifers with Marked Hydrochemical Differences Exhibit Distinct Fungal Communities. <b>2016</b> , 7, 666	19
888	The Ability of Microbial Community of Lake Baikal Bottom Sediments Associated with Gas Discharge to Carry Out the Transformation of Organic Matter under Thermobaric Conditions. <b>2016</b> , 7, 690	9
887	Comparison of Microbial Communities Isolated from Feces of Asymptomatic Salmonella-Shedding and Non-Salmonella Shedding Dairy Cows. <b>2016</b> , 7, 691	5
886	Induction of Subacute Ruminal Acidosis Affects the Ruminal Microbiome and Epithelium. <b>2016</b> , 7, 701	77
885	Low Fermentation pH Is a Trigger to Alcohol Production, but a Killer to Chain Elongation. <b>2016</b> , 7, 702	70
884	Tracking Strains in the Microbiome: Insights from Metagenomics and Models. <b>2016</b> , 7, 712	37
883	Aurelia aurita Ephyrae Reshape a Coastal Microbial Community. <b>2016</b> , 7, 749	9
882	Isolation and Characterization of Electrochemically Active Subsurface Delftia and Azonexus Species. <b>2016</b> , 7, 756	39
881	Pika Population Density Is Associated with the Composition and Diversity of Gut Microbiota. <b>2016</b> , 7, 758	47
880	In Situ Microbial Community Succession on Mild Steel in Estuarine and Marine Environments: Exploring the Role of Iron-Oxidizing Bacteria. <b>2016</b> , 7, 767	43
879	Size Matters: Assessing Optimum Soil Sample Size for Fungal and Bacterial Community Structure Analyses Using High Throughput Sequencing of rRNA Gene Amplicons. <b>2016</b> , 7, 824	42
878	Functional Characterization of Bacterial Communities Responsible for Fermentation of Doenjang: A Traditional Korean Fermented Soybean Paste. <b>2016</b> , 7, 827	57

877	Bacterial Dormancy Is More Prevalent in Freshwater than Hypersaline Lakes. <b>2016, 7, 853</b>	29
876	Responses of Aquatic Bacteria to Terrestrial Runoff: Effects on Community Structure and Key Taxonomic Groups. <b>2016, 7, 889</b>	7
875	Microbiomes of <i>Muricea californica</i> and <i>M. fruticosa</i> : Comparative Analyses of Two Co-occurring Eastern Pacific Octocorals. <b>2016, 7, 917</b>	26
874	Diversity and Distribution of Prokaryotes within a Shallow-Water Pockmark Field. <b>2016, 7, 941</b>	17
873	A Modified SDS-Based DNA Extraction Method for High Quality Environmental DNA from Seafloor Environments. <b>2016, 7, 986</b>	37
872	Taxonomic Assessment of Rumen Microbiota Using Total RNA and Targeted Amplicon Sequencing Approaches. <b>2016, 7, 987</b>	42
871	Insights into Abundant Rumen Ureolytic Bacterial Community Using Rumen Simulation System. <b>2016, 7, 1006</b>	30
870	Distribution and Composition of Thiotrophic Mats in the Hypoxic Zone of the Black Sea (150-170 m Water Depth, Crimea Margin). <b>2016, 7, 1011</b>	15
869	Effects of Short-Term Warming and Altered Precipitation on Soil Microbial Communities in Alpine Grassland of the Tibetan Plateau. <b>2016, 7, 1032</b>	50
868	Characterization of Chemosynthetic Microbial Mats Associated with Intertidal Hydrothermal Sulfur Vents in White Point, San Pedro, CA, USA. <b>2016, 7, 1163</b>	7
867	Diet Diversity Is Associated with Beta but not Alpha Diversity of Pika Gut Microbiota. <b>2016, 7, 1169</b>	71
866	Diversity and Composition of Bacterial Community in Soils and Lake Sediments from an Arctic Lake Area. <b>2016, 7, 1170</b>	43
865	A Metaproteomic Analysis of the Response of a Freshwater Microbial Community under Nutrient Enrichment. <b>2016, 7, 1172</b>	17
864	Rumen Bacterial Community Composition in Holstein and Jersey Cows Is Different under Same Dietary Condition and Is Not Affected by Sampling Method. <b>2016, 7, 1206</b>	86
863	The Salivary Microbiome in Polycystic Ovary Syndrome (PCOS) and Its Association with Disease-Related Parameters: A Pilot Study. <b>2016, 7, 1270</b>	20
862	Aboveground Whitefly Infestation-Mediated Reshaping of the Root Microbiota. <b>2016, 7, 1314</b>	39
861	Fungal Assemblages in Different Habitats in an Erman's Birch Forest. <b>2016, 7, 1368</b>	14
860	Unexpectedly High Beta-Diversity of Root-Associated Fungal Communities in the Bolivian Andes. <b>2016, 7, 1377</b>	21

859	The Probiotic Reduces Feed Conversion and Protects from Potentially Harmful Intestinal Microorganisms and Necrotic Enteritis in Broilers. <b>2016</b> , 7, 1416	56
858	Mineral vs. Organic Amendments: Microbial Community Structure, Activity and Abundance of Agriculturally Relevant Microbes Are Driven by Long-Term Fertilization Strategies. <b>2016</b> , 7, 1446	266
857	Microbial Community Structure of Subglacial Lake Whillans, West Antarctica. <b>2016</b> , 7, 1457	56
856	Upstream Freshwater and Terrestrial Sources Are Differentially Reflected in the Bacterial Community Structure along a Small Arctic River and Its Estuary. <b>2016</b> , 7, 1474	24
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854	Differences in the Composition of Archaeal Communities in Sediments from Contrasting Zones of Lake Taihu. <b>2016</b> , 7, 1510	21
853	Response of Core Microbial Consortia to Chronic Hydrocarbon Contaminations in Coastal Sediment Habitats. <b>2016</b> , 7, 1637	44
852	Taxonomic and Functional Diversity of Soil and Hypolithic Microbial Communities in Miers Valley, McMurdo Dry Valleys, Antarctica. <b>2016</b> , 7, 1642	40
851	Assessing Marine Microbial Induced Corrosion at Santa Catalina Island, California. <b>2016</b> , 7, 1679	26
850	Different Flour Microbial Communities Drive to Sourdoughs Characterized by Diverse Bacterial Strains and Free Amino Acid Profiles. <b>2016</b> , 7, 1770	17
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848	Insights into the Regulation of Rhizosphere Bacterial Communities by Application of Bio-organic Fertilizer in Monoculture Regime. <b>2016</b> , 7, 1788	21
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844	Local and Regional Diversity Reveals Dispersal Limitation and Drift as Drivers for Groundwater Bacterial Communities from a Fractured Granite Formation. <b>2016</b> , 7, 1933	13
843	The Relationship between pH and Bacterial Communities in a Single Karst Ecosystem and Its Implication for Soil Acidification. <b>2016</b> , 7, 1955	75
842	Diversity of Phototrophic Genes Suggests Multiple Bacteria May Be Able to Exploit Sunlight in Exposed Soils from the Sør Rondane Mountains, East Antarctica. <b>2016</b> , 7, 2026	13

841	Trace Elements Induce Predominance among Methanogenic Activity in Anaerobic Digestion. <b>2016</b> , 7, 2034	48
840	Dynamics in the Strawberry Rhizosphere Microbiome in Response to Biochar and Leaf Infection. <b>2016</b> , 7, 2062	31
839	Fine Spatial Scale Variation of Soil Microbial Communities under European Beech and Norway Spruce. <b>2016</b> , 7, 2067	48
838	Early Recovery of from Food Using a 6-Hour Non-selective Pre-enrichment and Reformulation of Tetrathionate Broth. <b>2016</b> , 7, 2103	24
837	Considerations For Optimizing Microbiome Analysis Using a Marker Gene. <b>2016</b> , 3, 26	18
836	Diversity of Bacterial Communities on Four Frequently Used Surfaces in a Large Brazilian Teaching Hospital. <b>2016</b> , 13, 152	14
835	Pine Defensive Monoterpene $\beta$ -Pinene Influences the Feeding Behavior of <i>Dendroctonus valens</i> and Its Gut Bacterial Community Structure. <b>2016</b> , 17,	27
834	Longitudinal survey of <i>Clostridium difficile</i> presence and gut microbiota composition in a Belgian nursing home. <b>2016</b> , 16, 229	28
833	Trophic and Non-Trophic Interactions in a Biodiversity Experiment Assessed by Next-Generation Sequencing. <b>2016</b> , 11, e0148781	16
832	The Potential of Class II Bacteriocins to Modify Gut Microbiota to Improve Host Health. <b>2016</b> , 11, e0164036	68
831	Bacterial Communities of Three Saline Meromictic Lakes in Central Asia. <b>2016</b> , 11, e0150847	35
830	Microbiota in Breast Milk of Chinese Lactating Mothers. <b>2016</b> , 11, e0160856	61
829	Effect of <i>Saccharomyces boulardii</i> and Mode of Delivery on the Early Development of the Gut Microbial Community in Preterm Infants. <b>2016</b> , 11, e0150306	22
828	Influence of Endogenous and Exogenous Estrogenic Endocrine on Intestinal Microbiota in Zebrafish. <b>2016</b> , 11, e0163895	31
827	The Effect of Dietary Replacement of Ordinary Rice with Red Yeast Rice on Nutrient Utilization, Enteric Methane Emission and Rumen Archaeal Diversity in Goats. <b>2016</b> , 11, e0160198	10
826	Influences of Plant Species, Season and Location on Leaf Endophytic Bacterial Communities of Non-Cultivated Plants. <b>2016</b> , 11, e0150895	50
825	New Primers for Discovering Fungal Diversity Using Nuclear Large Ribosomal DNA. <b>2016</b> , 11, e0159043	30
824	Beneficial Effect of <i>Bidens pilosa</i> on Body Weight Gain, Food Conversion Ratio, Gut Bacteria and Coccidiosis in Chickens. <b>2016</b> , 11, e0146141	32

823	Assessing Bacterial Diversity in the Rhizosphere of <i>Thymus zygis</i> Growing in the Sierra Nevada National Park (Spain) through Culture-Dependent and Independent Approaches. <b>2016</b> , 11, e0146558	40
822	Exploration of Human Salivary Microbiomes—Insights into the Novel Characteristics of Microbial Community Structure in Caries and Caries-Free Subjects. <b>2016</b> , 11, e0147039	28
821	Biogeography and Photosynthetic Biomass of Arctic Marine Pico-Eukaryotes during Summer of the Record Sea Ice Minimum 2012. <b>2016</b> , 11, e0148512	49
820	Chronic Psychological Stress Disrupted the Composition of the Murine Colonic Microbiota and Accelerated a Murine Model of Inflammatory Bowel Disease. <b>2016</b> , 11, e0150559	19
819	Soil Respiration and Bacterial Structure and Function after 17 Years of a Reciprocal Soil Transplant Experiment. <b>2016</b> , 11, e0150599	33
818	Age-Related Differences in the Gastrointestinal Microbiota of Chinstrap Penguins ( <i>Pygoscelis antarctica</i> ). <b>2016</b> , 11, e0153215	47
817	Characterisation of <i>Candida</i> within the Mycobiome/Microbiome of the Lower Respiratory Tract of ICU Patients. <b>2016</b> , 11, e0155033	36
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815	Effect of Co-Composting Cattle Manure with Construction and Demolition Waste on the Archaeal, Bacterial, and Fungal Microbiota, and on Antimicrobial Resistance Determinants. <b>2016</b> , 11, e0157539	37
814	Factors Influencing Bacterial Diversity and Community Composition in Municipal Drinking Waters in the Ohio River Basin, USA. <b>2016</b> , 11, e0157966	42
813	Spatial Heterogeneity of Gut Microbial Composition along the Gastrointestinal Tract in Natural Populations of House Mice. <b>2016</b> , 11, e0163720	50
812	Mycorrhizal Fungal Diversity and Community Composition in Two Closely Related <i>Platanthera</i> (Orchidaceae) Species. <b>2016</b> , 11, e0164108	17
811	Networks Depicting the Fine-Scale Co-Occurrences of Fungi in Soil Horizons. <b>2016</b> , 11, e0165987	48
810	Vertical Structure of Phyllosphere Fungal Communities in a Tropical Forest in Thailand Uncovered by High-Throughput Sequencing. <b>2016</b> , 11, e0166669	19
809	Environmental and Geographical Factors Structure Soil Microbial Diversity in New Caledonian Ultramafic Substrates: A Metagenomic Approach. <b>2016</b> , 11, e0167405	35
808	Airway Microbiota in Bronchoalveolar Lavage Fluid from Clinically Well Infants with Cystic Fibrosis. <b>2016</b> , 11, e0167649	39
807	Patchiness of Ciliate Communities Sampled at Varying Spatial Scales along the New England Shelf. <b>2016</b> , 11, e0167659	9
806	Characterization of Soil Suppressiveness to Root-Knot Nematodes in Organic Horticulture in Plastic Greenhouse. <b>2016</b> , 7, 164	35

805	454-Pyrosequencing Reveals Variable Fungal Diversity Across Farming Systems. <b>2016</b> , 7, 314	16
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801	Individual-specific changes in the human gut microbiota after challenge with enterotoxigenic <i>Escherichia coli</i> and subsequent ciprofloxacin treatment. <b>2016</b> , 17, 440	38
800	Effect of Vitamin E With Therapeutic Iron Supplementation on Iron Repletion and Gut Microbiome in US Iron Deficient Infants and Toddlers. <b>2016</b> , 63, 379-85	24
799	Bacterial communities in Arctic first-year drift ice during the winter/spring transition. <b>2016</b> , 8, 527-35	8
798	Influences of plant type on bacterial and archaeal communities in constructed wetland treating polluted river water. <b>2016</b> , 23, 19570-9	28
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795	Fungal compositions and diversities on indoor surfaces with visible mold growths in residential buildings in the Seoul Capital Area of South Korea. <b>2016</b> , 26, 714-23	19
794	A comparison of the gut microbiome between long-term users and non-users of proton pump inhibitors. <b>2016</b> , 43, 974-84	101
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792	Coexisting cryptic species of the <i>Litoditis marina</i> complex (Nematoda) show differential resource use and have distinct microbiomes with high intraspecific variability. <b>2016</b> , 25, 2093-110	57
791	Temporal dynamics of sediment bacterial communities in monospecific stands of <i>Juncus maritimus</i> and <i>Spartina maritima</i> . <b>2016</b> , 18, 824-34	10
790	The Root-Associated Microbial Community of the World's Highest Growing Vascular Plants. <b>2016</b> , 72, 394-406	51
789	Fire severity influences the response of soil microbes to a boreal forest fire. <b>2016</b> , 11, 035004	52
788	Development, diet and dynamism: longitudinal and cross-sectional predictors of gut microbial communities in wild baboons. <b>2016</b> , 18, 1312-25	41



787	Every base matters: assessing small subunit rRNA primers for marine microbiomes with mock communities, time series and global field samples. <b>2016</b> , 18, 1403-14	1190
786	Analysis of single root tip microbiomes suggests that distinctive bacterial communities are selected by <i>Pinus sylvestris</i> roots colonized by different ectomycorrhizal fungi. <b>2016</b> , 18, 1470-83	57
785	Chytrids dominate arctic marine fungal communities. <b>2016</b> , 18, 2001-9	93
784	Effects of land use on the structure and function of leaf-litter microbial communities in boreal streams. <b>2016</b> , 61, 1049-1061	9
783	Carbon content and climate variability drive global soil bacterial diversity patterns. <b>2016</b> , 86, 373-390	97
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781	Modulatory effects of condensed tannin fractions of different molecular weights from a <i>Leucaena leucocephala</i> hybrid on the bovine rumen bacterial community in vitro. <b>2016</b> , 96, 4565-74	12
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777	Development of the faecal microbiota in foals. <b>2016</b> , 48, 681-688	47
776	Characterizing the bacterial communities in retail stores in the United States. <b>2016</b> , 26, 857-868	22
775	Sequence variation in nuclear ribosomal small subunit, internal transcribed spacer and large subunit regions of <i>Rhizophagus irregularis</i> and <i>Gigaspora margarita</i> is high and isolate-dependent. <b>2016</b> , 25, 2816-32	41
774	Ericaceous plant-fungus network in a harsh alpine-subalpine environment. <b>2016</b> , 25, 3242-57	63
773	Changes in bacterial composition of biofilm in a metropolitan drinking water distribution system. <b>2016</b> , 121, 294-305	35
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771	Simultaneous purification of DNA and RNA from microbiota in a single colonic mucosal biopsy. <b>2016</b> , 9, 328	15
770	Structural Change in Microbiota by a Probiotic Cocktail Enhances the Gut Barrier and Reduces Cancer via TLR2 Signaling in a Rat Model of Colon Cancer. <b>2016</b> , 61, 2908-2920	82

769	Isolation of Marine <i>Paracoccus</i> sp. Ss63 from the Sponge <i>Sarcotragus</i> sp. and Characterization of its Quorum-Sensing Chemical-Signaling Molecules by LC-MS/MS Analysis. <b>2016</b> , 56, 330-340	12
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766	Chronic cigarette smoke exposure induces microbial and inflammatory shifts and mucin changes in the murine gut. <b>2016</b> , 18, 1352-63	107
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754	A framework for inferring biological communities from environmental DNA. <b>2016</b> , 26, 1645-1659	45
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749	Alterations of the gut microbiome of largemouth bronze gudgeon ( <i>Coreius guichenoti</i> ) suffering from furunculosis. <b>2016</b> , 6, 30606	54
748	Temporal Development of Gut Microbiota in Triclocarban Exposed Pregnant and Neonatal Rats. <b>2016</b> , 6, 33430	18
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745	An Improved Methodology to Overcome Key Issues in Human Fecal Metagenomic DNA Extraction. <b>2016</b> , 14, 371-378	25
744	<i>Bacillus</i> as a potential diagnostic marker for yellow tongue coating. <b>2016</b> , 6, 32496	24
743	Characterizing human lung tissue microbiota and its relationship to epidemiological and clinical features. <b>2016</b> , 17, 163	163
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739	Improvement of physical, chemical, and biological properties of aridisol from Botswana by the incorporation of torrefied biomass. <b>2016</b> , 6, 28011	29
738	Microbial succession in response to pollutants in batch-enrichment culture. <b>2016</b> , 6, 21791	63
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736	Dysfunctional gut microbiota and relative co-abundance network in infantile eczema. <b>2016</b> , 8, 36	24
735	Olfactory epithelium changes in germfree mice. <b>2016</b> , 6, 24687	34
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724	Probiotic treatment reduces appetite and glucose level in the zebrafish model. <b>2016</b> , 6, 18061	61
723	Enrichment dynamics of <i>Listeria monocytogenes</i> and the associated microbiome from naturally contaminated ice cream linked to a listeriosis outbreak. <b>2016</b> , 16, 275	83
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719	Exploring the methanogen and bacterial communities of rumen environments: solid adherent, fluid and epimural. <b>2017</b> , 93,	34
718	Multi-Body-Site Microbiome and Culture Profiling of Military Trainees Suffering from Skin and Soft Tissue Infections at Fort Benning, Georgia. <b>2016</b> , 1,	17
717	The human milk oligosaccharide 2'-fucosyllactose attenuates the severity of experimental necrotising enterocolitis by enhancing mesenteric perfusion in the neonatal intestine. <b>2016</b> , 116, 1175-1187	106
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711	Species-specific control of external superoxide levels by the coral holobiont during a natural bleaching event. <b>2016</b> , 7, 13801	41
710	Oral supplementation of healthy adults with 2'-O-fucosyllactose and lacto-N-neotetraose is well tolerated and shifts the intestinal microbiota. <b>2016</b> , 116, 1356-1368	97
709	MHC-dependent mate choice is linked to a trace-amine-associated receptor gene in a mammal. <b>2016</b> , 6, 38490	26
708	Strong Linkage Between Symbiotic Bacterial Community and Host Age and Morph in a Hemipteran Social Insect.	0
707	Characteristics of lower respiratory tract microbiota in the patients with post-hematopoietic stem cell transplantation pneumonia. 12,	0
706	Comparison of Gut Bacterial Communities of <i>Locusta migratoria manilensis</i> (Meyen) Reared on Different Food Plants. <b>2022</b> , 11, 1347	0
705	Effects of sodium humate and probiotics on growth performance enzyme activity and microbial environment of <i>Litopenaeus vannamei</i> in high-density zero-water exchange systems. 9,	0
704	<i>Strongyloides stercoralis</i> infection induces gut dysbiosis in chronic kidney disease patients. <b>2022</b> , 16, e0010302	0
703	Effect of continuous cropping of konjac ( <i>Amorphophallus konjac</i> ) on soil bacterial communities as evaluated by Illumina high-throughput sequencing. 1-15	0
702	Response of the plant core microbiome to <i>Fusarium oxysporum</i> infection and identification of the pathobiome.	1
701	Residues from black soldier fly ( <i>Hermetia illucens</i> ) larvae rearing influence the plant-associated soil microbiome in the short term. 13,	0
700	Fellfields of the Kerguelen Islands harbour specific soil microbiomes and rhizomicrobiomes of an endemic plant facing necrosis. 2,	0
699	Correlation between postmortem microbial signatures and substance abuse disorders. <b>2022</b> , 17, e0274401	0
698	Effects of Water Loss Stress under Tidal Effects on the Epiphytic Bacterial Community of <i>Sargassum thunbergii</i> in the Intertidal Zone.	0

- 697 Long-term cultivation alter soil bacterial community in a forest-grassland transition zone. 13, 1
- 696 Sediment microbial community structure, enzymatic activities and functional gene abundance in the coastal hypersaline habitats. 0
- 695 Increased diversity of a cervical microbiome associates with cervical cancer. 12, 0
- 694 The study on the feasibility of dietary supplementation with dimethyl silicone oil to prevent frothy rumen bloat in goats fed with high concentrate diets. 1-11 0
- 693 The response of sugar beet rhizosphere micro-ecological environment to continuous cropping. 13, 0
- 692 Dietary Antimicrobial Peptides Improve Intestinal Function, Microbial Composition and Oxidative Stress Induced by *Aeromonas hydrophila* in Pengze Crucian Carp (*Carassius auratus* var. Pengze). **2022**, 11, 1756 0
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- 685 Effects of continuous and rotational cropping practices on soil fungal communities in pineapple cultivation. 10, e13937 0
- 684 Evolution of the Gut Microbiome in HIV-Exposed Uninfected and Unexposed Infants during the First Year of Life. 1
- 683 Mitigation of cadmium toxicity in Thai rice cultivar (PSL2) using biofertilizer containing indigenous cadmium-resistant microbial consortia. 0
- 682 Diversity, antibacterial activity and chemical analyses of gut-associated fungi isolated from the *Crocothemis servilia*. 13, 0
- 681 Metagenomic Analysis for Indigenous Microbial Diversity in Soaking Process of making Tempeh Jack beans (*Canavalia ensiformis*). **2022**, 10, 620-632 1
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- 674 Microbial community structure and shift pattern of industry brine after a long-term static storage in closed tank. 13, 0
- 673 Isolation of *Pseudomonas aromaticivorans* sp. nov from a hydrocarbon-contaminated groundwater capable of degrading benzene-, toluene-, m- and p-xylene under microaerobic conditions. 13, 2
- 672 Meat and bone meal stimulates microbial diversity and suppresses plant pathogens in asparagus straw composting. 13, 2
- 671 Freshwater mussels and host fish gut microbe community composition shifts after agricultural contaminant exposure. 2
- 670 Short- and Long-Term Effects of a Prebiotic Intervention with Polyphenols Extracted from European Black Elderberry Sustained Expansion of *Akkermansia* spp.. **2022**, 12, 1479 1
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- 668 Bone appetite: DNA metabarcoding as a non-lethal alternative to morphological dietary assessment in Atlantic bonefish (*Albula vulpes*). 0
- 667 Disentangling arthropod and plant resources consumed by *Orius* spp. in peach and alfalfa crops by metagenomic analysis. **2022**, 95, 1543-1556 0
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- 663 Influence of Sharklet-inspired Micropatterned Polymers on Spatio-temporal Variations of Marine Biofouling. 2200304 1
- 662 Changes in the gut microbiota of forest musk deer (*Moschus berezovskii*) during ex situ conservation. 13, 1

661	Bacterial diversity in surface sediments of collapsed lakes in Huaibei, China. <b>2022</b> , 12,	1
660	Snow Exclusion Does Not Affect Soil Ammonia-Oxidizing Bacteria and Archaea Communities. <b>2022</b> , 13, 1483	0
659	Effect of Autolyzed <i>Yarrowia lipolytica</i> on the Growth Performance, Antioxidant Capacity, Intestinal Histology, Microbiota, and Transcriptome Profile of Juvenile Largemouth Bass ( <i>Micropterus salmoides</i> ). <b>2022</b> , 23, 10780	1
658	Exploration of acupuncture therapy in the treatment of mild cognitive impairment based on the brain-gut axis theory. 16,	0
657	Metabarcoding and Metabolome Analyses Reveal Mechanisms of <i>Leymus chinensis</i> Growth Promotion by Fairy Ring of <i>Leucocalocybe mongolica</i> . <b>2022</b> , 8, 944	1
656	Early season soil microbiome best predicts wheat grain quality.	0
655	Crop Rotation with Marigold Promotes Soil Bacterial Structure to Assist in Mitigating Clubroot Incidence in Chinese Cabbage. <b>2022</b> , 11, 2295	1
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653	Alterations of gut microbiota in cirrhotic patients with spontaneous bacterial peritonitis: A distinctive diagnostic feature. 12,	2
652	Enrichment and application of bacterial sialic acids containing polymers from the extracellular polymeric substances of <i>Candidatus Accumulibacter</i>	0
651	Long-term D-Allose Administration Favorably Alters the Intestinal Environment in Aged Male Mice. <b>2022</b> ,	0
650	Effects of feed transition on digestive tract digestive enzyme, morphology and intestinal community in cuttlefish ( <i>Sepia pharaonis</i> ). 9,	0
649	Unexpected diversity found within benthic microbial mats at hydrothermal springs in Crater Lake, Oregon. 13,	0
648	Temperature sensitivity of dark CO <sub>2</sub> fixation in temperate forest soils. <b>2022</b> , 19, 4011-4028	0
647	Microbial community starters affect the profiles of volatile compounds in traditional Chinese Xiaoqu rice wine: Assesment via high-throughput sequencing and gas chromatography-ion mobility spectrometry. <b>2022</b> , 114000	0
646	Environmental DNA Metabarcoding Reflects Fish DNA Dynamics in Lentic Ecosystems: A Case Study of Freshwater Ponds. <b>2022</b> , 7, 257	0
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644	A Preliminary Study of Bacterioplankton Community Structure in the Taiyangshan Wetland in Ningxia and Its Driving Factors. <b>2022</b> , 19, 12224	0



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- 637 Prevalence and genetic characterisation of *Giardia duodenalis* in river water and riverbed sediment using next-generation sequencing. ○
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- 635 Insights into the microbial life in silica-rich subterranean environments: microbial communities and ecological interactions in an orthoquartzite cave (Imawarí Yeuta, Auyan Tepui, Venezuela). 13, ○
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- 633 Catch me if you can: Capturing extracellular DNA transformation in mixed cultures via Hi-C sequencing. ○
- 632 Characterization of Foliar Fungal Endophyte Communities from White Pine Blister Rust Resistant and Susceptible *Pinus flexilis* in Natural Stands in the Southern Rocky Mountains. ○
- 631 Seasonal variations in gut microbiota of semiprovisioned rhesus macaques (*Macaca mulatta*) living in a limestone forest of Guangxi, China. 13, ○
- 630 Bacterial and archaeal communities within the alkaline soda Langaco Lake in the Qinghai-Tibet Plateau. **2022**, 72, ○
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- 627 Fecal Bile Acids and Neutral Sterols Are Associated with Latent Microbial Subgroups in the Human Gut. **2022**, 12, 846 1
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- 617 Supplementation with paraformic acid in the diet improved intestinal development through modulating intestinal inflammation and microbiota in broiler chickens. 13, ○
- 616 Effect of Probiotic *Lactobacillus plantarum* Dad-13 on Metabolic Profiles and Gut Microbiota in Type 2 Diabetic Women: A Randomized Double-Blind Controlled Trial. **2022**, 10, 1806 ○
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- 614 Microbial community structure and niche differentiation under different health statuses of *Pinus bungeana* in the Xiong'an New Area in China. 13, ○
- 613 Management-induced shifts in rhizosphere bacterial communities contribute to the control of pathogen causing citrus greening disease. ○
- 612 Leaf endophytic microbiomes of different almond cultivars grafted to the same rootstock. ○
- 611 Soil microbial diversity and functional capacity associated with the production of edible mushroom *Stropharia rugosoannulata* in croplands. 10, e14130 1
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606	Differences in the microbiota of oral rinse, lesion, and normal site samples from patients with mucosal abnormalities on the tongue. <b>2022, 12,</b>	0
605	Transcriptome and 16S rRNA analysis revealed the response of largemouth bass ( <i>Micropterus salmoides</i> ) to Rhabdovirus infection. 13,	1
604	Effects of close-to-nature management of plantation on the structure and ecological functions of soil microorganisms with different habitat specialization.	0
603	Connectivity and divergence of symbiotic bacteria of deep-sea hydrothermal vent mussels in relation to the structure and dynamics of mid-ocean ridges. 9,	0
602	Analysis of the gut microbiota of healthy CARI-Nirbheek (Aseel cross) Chickens: A Metagenomic Approaches. <b>2022, 100304</b>	0
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600	Core members and differential abundance of chrysomelid microbiota in the life stages of <i>Podontia affinis</i> (Galerucinae) and adult <i>Silana farinosa</i> (Cassidinae, Coleoptera). 10,	0
599	Convergent evolution of the gut microbiome in marine carnivores. <b>2022, 12,</b>	1
598	Sustainable management of the potato cyst nematode, <i>Globodera rostochiensis</i> , with two microbial fermentation products. 13,	0
597	Sorghum flour BRS 305 hybrid has the potential to modulate the intestinal microbiota of rats fed with a high-fat high-fructose diet.	0
596	Peanut/sorghum intercropping drives specific variation in peanut rhizosphere soil properties and microbiomes under salt stress.	0
595	Response of soil microbial communities to natural radionuclides along specific-activity gradients. <b>2022, 246, 114156</b>	0
594	Changes in the population and functional profile of bacteria and fungi in the rhizosphere of <i>Suaeda salsa</i> is driven by invasion of <i>Spartina alterniflora</i> . <b>2022, 144, 109516</b>	1
593	Changes in community assembly processes and co-occurrence networks of soil diazotrophs along an elevational gradient in Tibetan alpine meadows. <b>2022, 113, 103445</b>	0
592	Analysis on the soil physical, chemical, and microbial community properties of different alpine meadow patches in the Source Zone of the Yellow River, West China. <b>2022, 144, 109531</b>	1
591	Microbiome and metabolome dysbiosis of the gut-lung axis in pulmonary hypertension. <b>2022, 265, 127205</b>	0
590	Cholesterol supplementation improved growth performance, cholesterol metabolism, and intestinal health of Pacific white shrimp ( <i>Litopenaeus vannamei</i> ) fed a low fishmeal diet. <b>2022, 27, 101351</b>	0

589	Diversity-triggered bottom-up trophic interactions impair key soil functions under lindane pollution stress. <b>2022</b> , 314, 120293	0
588	Applying meta-data of soybean grain in origin trace and quarantine inspection. <b>2022</b> , 162, 111998	0
587	Correlation between microbial communities changes and physicochemical indexes of Dazu Dongcai during different fermentation periods. 42,	1
586	Analysis of microbial diversity in the root of Astragalus mongholicus. 82,	0
585	Genistein improves glucose metabolism and promotes adipose tissue browning through modulating gut microbiota in mice.	0
584	Molecular characterization of Deciphering Fungal Community structure in Zea mays L. and Triticum Aestivum L. <b>2022</b> , 4, 727-737	1
583	Identification of Gut Microbiota Affecting Fiber Digestibility in Pigs. <b>2022</b> , 44, 4557-4569	1
582	Epidemic Identification of Fungal Diseases in Morchella Cultivation across China. <b>2022</b> , 8, 1107	2
581	Cysteamine-supplemented diet for cashmere goats: A potential strategy to inhibit rumen biohydrogenation and enhance plasma antioxidant capacity. 9,	0
580	Effect of Environmental Heterogeneity and Trophic Status in Sampling Strategy on Estimation of Small-Scale Regional Biodiversity of Microorganisms. <b>2022</b> , 10, 2119	0
579	The Impact of Selective Dry Cow Therapy Adopted in a Brazilian Farm on Bacterial Diversity and the Abundance of Quarter Milk. <b>2022</b> , 9, 550	0
578	Dynamics of species-rich predator-prey networks and seasonal alternations of keystone species.	0
577	Baseline gut microbial profiles are associated with the efficacy of Bacillus subtilis and Enterococcus faecium in IBS-D. 1-10	0
576	Combination effect between gut microbiota and traditional potentially modifiable risk factors for first-ever ischemic stroke in Tujia, Miao and Han populations in China. 15,	0
575	The intestinal clock drives the microbiome to maintain gastrointestinal homeostasis. <b>2022</b> , 13,	4
574	Identification of Human Gut Microbiome Associated with Enterolignan Production. <b>2022</b> , 10, 2169	0
573	Tripartite Symbiotic Digestion of Lignocellulose in the Digestive System of a Fungus-Growing Termite.	0
572	Microbial Communities of Ferromanganese Sedimentary Layers and Nodules of Lake Baikal (Bolshoy Ushkany Island). <b>2022</b> , 14, 868	0

571	Differential Influences of Wind-Blown Sand Burial on Bacterial and Fungal Communities Inhabiting Biological Soil Crusts in a Temperate Desert, China. <b>2022</b> , 10, 2010	0
570	Melatonin and dopamine enhance waterlogging tolerance by modulating ROS scavenging, nitrogen uptake, and the rhizosphere microbial community in <i>Malus hupehensis</i> .	0
569	Sexual Dimorphism of the Gut Microbiota in the Chinese Alligator and Its Convergence in the Wild Environment. <b>2022</b> , 23, 12140	0
568	Core rhizosphere microbiome of <i>Panax notoginseng</i> and its associations with belowground biomass and saponin contents.	0
567	Sex-based metabolic and microbiota differences in roots and rhizosphere soils of dioecious papaya ( <i>Carica papaya</i> L.). 13,	1
566	Gut microbiota modulation by plant polyphenols in koi carp ( <i>Cyprinus carpio</i> L.). 13,	0
565	A Study on the Possibility of Early Warning for <i>Cochlodinium polykrikoides</i> Blooms, Using Molecular Methods. <b>2022</b> , 14, 3115	0
564	Effect of methionine hydroxy analog feed supplements: Significant alteration and enrichment of rumen microbiota and metabolome in Hu sheep. 9,	0
563	Early immunomodulatory program triggered by pro-tolerogenic <i>Bifidobacterium pseudolongum</i> drives cardiac transplant outcomes.	0
562	Effects of autochthonous strains mixture on gut microbiota and metabolic profile in cobia ( <i>Rachycentron canadum</i> ). <b>2022</b> , 12,	0
561	Maternal supplementation with a casein hydrolysate and yeast beta-glucan from late gestation through lactation improves gastrointestinal health of piglets at weaning. <b>2022</b> , 12,	0
560	Prophylactic effect of pectic oligosaccharides against poly I: C- induced virus-like infection in BALB/c mice.	0
559	Effects of Preservation and Propagation Methodology on Microcosms Derived from the Oral Microbiome. <b>2022</b> , 10, 2146	0
558	Single-cell Raman-activated sorting and cultivation (scRACS-Culture) for assessing and mining in situ phosphate-solubilizing microbes from nature. <b>2022</b> , 2,	0
557	Black corn ( <i>Zea mays</i> L.) flour has the potential to improve the gut microbiota composition and goblet cell proliferation in mice fed a high-fat diet. <b>2022</b> ,	0
556	Transmission of tetracycline resistance genes and microbiomes from manure-borne black soldier fly larvae frass to rhizosphere soil and pakchoi endophytes. 13,	1
555	Contrasting effect of irrigation practices on the cotton rhizosphere microbiota and soil functionality in fields. 13,	0
554	Evolution of the Piauí Laterite, Brazil: Mineralogical, Geochemical and Geomicrobiological Mechanisms for Cobalt and Nickel Enrichment. <b>2022</b> , 12, 1298	0

553	The Endophytic Fungi Diversity, Community Structure, and Ecological Function Prediction of <i>Sophora alopecuroides</i> in Ningxia, China. <b>2022</b> , 10, 2099	1
552	Association between Gut Microbiota and Emotional-Behavioral Symptoms in Children with Attention-Deficit/Hyperactivity Disorder. <b>2022</b> , 12, 1634	0
551	Microbial assemblages of Schisandraceae plants and the correlations between endophytic species and the accumulation of secondary metabolites.	0
550	Microbiome landscape of lesions and adjacent normal mucosal areas in oral lichen planus patient. 13,	0
549	Effects of Plant Growth-Promoting Rhizobacteria on the Growth and Soil Microbial Community of <i>Carya illinoensis</i> . <b>2022</b> , 79,	0
548	Unravelling the Portuguese Coastal and Transitional Waters Microbial Resistome as a Biomarker of Differential Anthropogenic Impact. <b>2022</b> , 10, 613	1
547	Genomic insights into the physiology of <i>Quinella</i> , an iconic uncultured rumen bacterium. <b>2022</b> , 13,	0
546	Effects of Lysophosphatidylcholine on Intestinal Health of Turbot Fed High-Lipid Diets. <b>2022</b> , 14, 4398	1
545	High-Density Lipoprotein Cholesterol as a Potential Medium between Depletion of Lachnospiraceae Genera and Hypertension under a High-Calorie Diet.	1
544	Cellular microbiota: an inherent inhabitant of cells.	0
543	Shifts in soil prokaryotic and microeukaryotic communities following a translocation of wet meadows to derelict land.	0
542	Saline soil reclamation by halophytes increased soil multifunctionality through modulation of soil microbial communities.	0
541	Investigating fecal microbial transplant as a novel therapy in dogs with inflammatory bowel disease: A preliminary study. <b>2022</b> , 17, e0276295	0
540	<i>Lactobacillus</i> (LA-1) and butyrate inhibit osteoarthritis by controlling autophagy and inflammatory cell death of chondrocytes. 13,	0
539	An automated workflow to assess completeness and curate GenBank for eDNA metabarcoding: the marine fish assemblage as case study.	0
538	Assessing the relationship between physical activity and the gut microbiome in a large, population-based sample of Wisconsin adults. <b>2022</b> , 17, e0276684	1
537	Electrochemical Responses and Microbial Community Shift of Electroactive Biofilm to Acidity Stress in Microbial Fuel Cells. <b>2022</b> , 12, 1268	0
536	Selection of Multidrug-Resistant Enterobacteria in Weaned Pigs and Its Association With In-feed Subtherapeutic Combination of Colistin and Tylosin. <b>2022</b> , 79,	0

535	Pretreatment with probiotics <i>Enterococcus faecium</i> NCIMB 11181 attenuated <i>Salmonella</i> Typhimurium-induced gut injury through modulating intestinal microbiome and immune responses with barrier function in broiler chickens. <b>2022</b> , 13,	0
534	Exploratory studies of oral and fecal microbiome in healthy human aging. 3,	0
533	Effects of Variety, Plant Location, and Season on the Phyllosphere Bacterial Community Structure of Alfalfa ( <i>Medicago sativa</i> L.). <b>2022</b> , 10, <b>2023</b>	0
532	Hyperbaric oxygen improves depression-like behaviors in chronic stress model mice by remodeling gut microbiota and regulating host metabolism.	1
531	Correlation between fine root traits and pathogen richness depends on plant mycorrhizal types.	0
530	Trophic ecology of <i>Octopus vulgaris</i> paralarvae along the Iberian Canary current eastern boundary upwelling system.	0
529	Rice growth stages modulate rhizosphere bacteria and archaea co-occurrence and sensitivity to long-term inorganic fertilization.	0
528	Gut microbiota assemblages of generalist predators are driven by local- and landscape-scale factors.	0
527	Proportions of Pacific white shrimp, <i>Litopenaeus vannamei</i> , gut microbiota from ambient microbiota increased with aquaculture process.	0
526	Metagenomics analysis on the microbiota of chicken manure anaerobic digestion materials in biogas production.	0
525	Gut microbiota diversity and specific composition during immunotherapy in responders with non-small cell lung cancer. 9,	0
524	Effects of heat stress on 16S rDNA, metagenome and metabolome in Holstein cows at different growth stages. <b>2022</b> , 9,	0
523	Uncovering the Fungal Diversity Colonizing Limestone Walls of a Forgotten Monument in the Central Region of Portugal by High-Throughput Sequencing and Culture-Based Methods. <b>2022</b> , 12, 10650	1
522	Effects of <i>Rhizophagus intraradices</i> on soybean yield and the composition of microbial communities in the rhizosphere soil of continuous cropping soybean. <b>2022</b> , 12,	0
521	Community composition and trophic mode diversity of fungi associated with fruiting body of medicinal <i>Sanguangporus vaninii</i> . <b>2022</b> , 22,	0
520	Spatial pattern and co-occurrence network of microbial community in response to extreme environment of salt lakes on the Qinghai-Tibet Plateau.	0
519	Sodium humate alters the intestinal microbiome, short-chain fatty acids, eggshell ultrastructure, and egg performance of old laying hens. 9,	0
518	Effects of combined aerobic and resistance training on gut microbiota and cardiovascular risk factors in physically active elderly women: A randomized controlled trial. 13,	1

- 517 Distributional Pattern of Bacteria, Protists, and Diatoms in Ocean according to Water Depth in the Northern South China Sea. ○
- 516 The role of farming practice in nutrient assimilation in small-scale tilapia farming. **2022**, 739005 ○
- 515 Effect of Astaxanthin on the Antioxidant Capacity and Intestinal Microbiota of Tsinling Lenok Trout (*Brachymystax lenok tsinlingensis*). ○
- 514 Long-Read Sequencing Analysis Revealed the Impact of Forest Conversion on Soil Fungal Diversity in Limu Mountain, Hainan. ○
- 513 Bacterial Community Dynamics along a River-Wetland-Lake System. **2022**, 14, 3519 ○
- 512 Effect of Diet on the Midgut Microbial Composition and Host Immunity of the Fall Armyworm, *Spodoptera frugiperda*. **2022**, 11, 1602 ○
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- 510 Metagenomics Analysis of the Polymeric and Monomeric Phenolic Dynamic Changes Related to the Indigenous Bacteria of Black Tea Spontaneous Fermentation. **2022**, e00774 ○
- 509 Environmental Response to Root Secondary Metabolite Accumulation in *Paeonia lactiflora*: Insights from Rhizosphere Metabolism and Root-Associated Microbial Communities. ○
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352	Differentially enriched fungal communities in root rot resistant and susceptible varieties of tobacco ( <i>Nicotiana tabacum</i> L.) under continuous monoculture cropping. 13,	○
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- 283 Response of Microbial Communities on Cathode with Different Potentials in a Single-Chamber Reactor. **2023**, 80, ○
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- 155 Responses of Soil Bacterial Communities and Enzyme Activities to Straw Return and Potassium Fertilization with Two Soils Under Soil Potassium Balance Condition in Rice-Wheat System. ○
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