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QIIME allows analysis of high-throughput community sequencing data

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2215	Loss of deep roots limits biogenic agents of soil development that are only partially restored by decades of forest regeneration. <b>2018</b> , 6,	
2214	Abstract.	
2213	The Virtues of Nonsimulation Games. <b>1970</b> , 1, 319-326	12
2212	A Nonextensive Entropy Approach to Solar Wind Intermittency. <b>2005</b> , 618, 547-555	98
2211	arrayQualityMetrics--a bioconductor package for quality assessment of microarray data. <b>2009</b> , 25, 415-6	635
2210	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 10. <b>2010</b> , 3, 225-31	7
2209	Introducing W.A.T.E.R.S.: a workflow for the alignment, taxonomy, and ecology of ribosomal sequences. <b>2010</b> , 11, 317	26
2208	Sampling and pyrosequencing methods for characterizing bacterial communities in the human gut using 16S sequence tags. <b>2010</b> , 10, 206	283
2207	Soil bacterial and fungal communities across a pH gradient in an arable soil. <b>2010</b> , 4, 1340-51	2148
2206	Postprandial remodeling of the gut microbiota in Burmese pythons. <b>2010</b> , 4, 1375-85	181
2205	Viruses in the faecal microbiota of monozygotic twins and their mothers. <b>2010</b> , 466, 334-8	840
2204	Rapidly denoising pyrosequencing amplicon reads by exploiting rank-abundance distributions. <i>Nature Methods</i> , <b>2010</b> , 7, 668-9	21.6 590
2203	Adaptation to herbivory by the Tammar wallaby includes bacterial and glycoside hydrolase profiles different from other herbivores. <b>2010</b> , 107, 14793-8	163
2202	PlutoFâ Web Based Workbench for Ecological and Taxonomic Research, with an Online Implementation for Fungal ITS Sequences. <b>2010</b> , 6, EBO.S6271	144
2201	Novel approaches for analysing gut microbes and dietary polyphenols: challenges and opportunities. <b>2010</b> , 156, 3224-3231	146

2200	From structure to function: the ecology of host-associated microbial communities. <b>2010</b> , 74, 453-76	251
2199	The human gut virome: inter-individual variation and dynamic response to diet. <b>2011</b> , 21, 1616-25	637
2198	An Open-source Collaboration Environment for Metagenomics Research. <b>2011</b> ,	1
2197	Visual exploration of microbial populations. <b>2011</b> ,	5
2196	Hydrocarbon-degrading bacteria and the bacterial community response in gulf of Mexico beach sands impacted by the deepwater horizon oil spill. <b>2011</b> , 77, 7962-74	609
2195	Topographical continuity of bacterial populations in the healthy human respiratory tract. <b>2011</b> , 184, 957-63	693
2194	Bacteria on Human Skin. <b>2011</b> , 2, 25-34	
2193	Diet drives convergence in gut microbiome functions across mammalian phylogeny and within humans. <b>2011</b> , 332, 970-4	1215
2192	Parallel-META: A high-performance computational pipeline for metagenomic data analysis. <b>2011</b> ,	1
2191	Gastrointestinal microbiome signatures of pediatric patients with irritable bowel syndrome. <b>2011</b> , 141, 1782-91	464
2190	Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. <b>2011</b> , 108 Suppl 1, 4516-22	4742
2189	Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons. <b>2011</b> , 21, 494-504	2174
2188	Barcoded primers used in multiplex amplicon pyrosequencing bias amplification. <b>2011</b> , 77, 7846-9	377
2187	The impact of a consortium of fermented milk strains on the gut microbiome of gnotobiotic mice and monozygotic twins. <b>2011</b> , 3, 106ra106	384
2186	The Use of rRNA Gene Sequence Data in the Classification and Identification of Prokaryotes. <b>2011</b> , 349-384	4
2185	NLRP6 inflammasome regulates colonic microbial ecology and risk for colitis. <b>2011</b> , 145, 745-57	1401
2184	Hydrogen-isotopic variability in fatty acids from Yellowstone National Park hot spring microbial communities. <b>2011</b> , 75, 4830-4845	47
2183	Bacterial communities associated with the lichen symbiosis. <b>2011</b> , 77, 1309-14	238

2182	Integrative analysis of environmental sequences using MEGAN4. <b>2011</b> , 21, 1552-60	1019
2181	Skin microbiome: genomics-based insights into the diversity and role of skin microbes. <b>2011</b> , 17, 320-8	176
2180	A novel method for determining microflora composition using dynamic phylogenetic analysis of 16S ribosomal RNA deep sequencing data. <b>2011</b> , 98, 253-9	9
2179	Combined phylogenetic and genomic approaches for the high-throughput study of microbial habitat adaptation. <b>2011</b> , 19, 472-82	22
2178	Extensive personal human gut microbiota culture collections characterized and manipulated in gnotobiotic mice. <b>2011</b> , 108, 6252-7	499
2177	Trends and Developments in Bioinformatics in 2010: Prospects and Perspectives. <b>2011</b> , 20, 146-155	
2176	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing â&#x2013;standard operating procedure, version1.0. <b>2011</b> ,	3
2175	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing â&#x2013;standard operating procedure, version 1.0. <b>2011</b> ,	
2174	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing â&#x2013;standard operating procedure, version 1.0. <b>2011</b> ,	3
2173	The effect of resource history on the functioning of soil microbial communities is maintained across time. <b>2011</b> , 8, 1477-1486	80
2172	Microbial eukaryotes in the human microbiome: ecology, evolution, and future directions. <b>2011</b> , 2, 153	142
2171	Coccolithophores: functional biodiversity, enzymes and bioprospecting. <b>2011</b> , 9, 586-602	6
2170	CORE: a phylogenetically-curated 16S rDNA database of the core oral microbiome. <b>2011</b> , 6, e19051	132
2169	Fecal microbiota in premature infants prior to necrotizing enterocolitis. <b>2011</b> , 6, e20647	359
2168	Desert farming benefits from microbial potential in arid soils and promotes diversity and plant health. <b>2011</b> , 6, e24452	163
2167	CDinFusion--submission-ready, on-line integration of sequence and contextual data. <b>2011</b> , 6, e24797	6
2166	Branched chain fatty acids reduce the incidence of necrotizing enterocolitis and alter gastrointestinal microbial ecology in a neonatal rat model. <b>2011</b> , 6, e29032	113
2165	Microbial diversity associated with four functional groups of benthic reef algae and the reef-building coral <i>Montastraea annularis</i> . <b>2011</b> , 13, 1192-204	158

2164	Hot spring siliceous stromatolites from Yellowstone National Park: assessing growth rate and laminae formation. <b>2011</b> , 9, 411-24	44
2163	V-REVCOMP: automated high-throughput detection of reverse complementary 16S rRNA gene sequences in large environmental and taxonomic datasets. <b>2011</b> , 319, 140-5	10
2162	Supervised classification of human microbiota. <b>2011</b> , 35, 343-59	279
2161	Soil-specific limitations for access and analysis of soil microbial communities by metagenomics. <b>2011</b> , 78, 31-49	145
2160	UniFrac: an effective distance metric for microbial community comparison. <b>2011</b> , 5, 169-72	1474
2159	Supervised classification of microbiota mitigates mislabeling errors. <b>2011</b> , 5, 570-3	36
2158	Spatial variability in airborne bacterial communities across land-use types and their relationship to the bacterial communities of potential source environments. <b>2011</b> , 5, 601-12	288
2157	Examining the global distribution of dominant archaeal populations in soil. <b>2011</b> , 5, 908-17	822
2156	Numerical ecology validates a biogeographical distribution and gender-based effect on mucosa-associated bacteria along the human colon. <b>2011</b> , 5, 801-9	63
2155	Evidence for a core gut microbiota in the zebrafish. <b>2011</b> , 5, 1595-608	659
2154	Oligonucleotide primers, probes and molecular methods for the environmental monitoring of methanogenic archaea. <b>2011</b> , 4, 585-602	52
2153	The under-recognized dominance of Verrucomicrobia in soil bacterial communities. <b>2011</b> , 43, 1450-1455	440
2152	Removing noise from pyrosequenced amplicons. <b>2011</b> , 12, 38	1088
2151	Generation of multimillion-sequence 16S rRNA gene libraries from complex microbial communities by assembling paired-end illumina reads. <b>2011</b> , 77, 3846-52	560
2150	The antibacterial lectin RegIIIgamma promotes the spatial segregation of microbiota and host in the intestine. <b>2011</b> , 334, 255-8	948
2149	Comparative analysis of microbial diversity in Longitarsus flea beetles (Coleoptera: Chrysomelidae). <b>2011</b> , 139, 541-50	30
2148	The effects from DNA extraction methods on the evaluation of microbial diversity associated with human colonic tissue. <b>2011</b> , 61, 353-62	47
2147	Transition of microbial communities during the adaption to anaerobic digestion of carrot waste. <b>2011</b> , 102, 7249-56	52

2146	Current concepts of the intestinal microbiota and the pathogenesis of infection. <b>2011</b> , 13, 28-34	79
2145	CLOTU: an online pipeline for processing and clustering of 454 amplicon reads into OTUs followed by taxonomic annotation. <b>2011</b> , 12, 182	57
2144	CloVR: a virtual machine for automated and portable sequence analysis from the desktop using cloud computing. <b>2011</b> , 12, 356	220
2143	Estimation of bacterial diversity using next generation sequencing of 16S rDNA: a comparison of different workflows. <b>2011</b> , 12, 473	47
2142	Flexible taxonomic assignment of ambiguous sequencing reads. <b>2011</b> , 12, 8	20
2141	WebMGA: a customizable web server for fast metagenomic sequence analysis. <b>2011</b> , 12, 444	440
2140	Analysis of 16S rRNA environmental sequences using MEGAN. <b>2011</b> , 12 Suppl 3, S17	59
2139	Bacterial community diversity and variation in spray water sources and the tomato fruit surface. <b>2011</b> , 11, 81	55
2138	Caspase deficiency alters the murine gut microbiome. <b>2011</b> , 2, e220	54
2137	Bayesian community-wide culture-independent microbial source tracking. <i>Nature Methods</i> , <b>2011</b> , 8, 761-31.6	777
2136	Human oral, gut, and plaque microbiota in patients with atherosclerosis. <b>2011</b> , 108 Suppl 1, 4592-8	679
2135	Bacterial biogeography of the human digestive tract. <b>2011</b> , 1, 170	268
2134	OTUbase: an R infrastructure package for operational taxonomic unit data. <b>2011</b> , 27, 1700-1	15
2133	Sources of bacteria in outdoor air across cities in the midwestern United States. <b>2011</b> , 77, 6350-6	195
2132	Target region selection is a critical determinant of community fingerprints generated by 16S pyrosequencing. <b>2011</b> , 6, e20956	174
2131	Strategy for modular tagged high-throughput amplicon sequencing. <b>2011</b> , 77, 6310-2	19
2130	Pan-genome of the dominant human gut-associated archaeon, <i>Methanobrevibacter smithii</i> , studied in twins. <b>2011</b> , 108 Suppl 1, 4599-606	165
2129	Bacterial communities of two parthenogenetic aphid species cocolonizing two host plants across the Hawaiian Islands. <b>2011</b> , 77, 8345-9	49



2128	Flower: extracting information from pyrosequencing data. <b>2011</b> , 27, 1041-2	6
2127	Comparison of the gut microbiotas of healthy adult twins living in South Korea and the United States. <b>2011</b> , 77, 7433-7	63
2126	Evaluation of subsampling-based normalization strategies for tagged high-throughput sequencing data sets from gut microbiomes. <b>2011</b> , 77, 8795-8	80
2125	Tobacco smoking affects bacterial acquisition and colonization in oral biofilms. <b>2011</b> , 79, 4730-8	156
2124	Soil rotifer communities are extremely diverse globally but spatially autocorrelated locally. <b>2011</b> , 108, 4406-10	72
2123	Pyrosequencing-based assessment of bacterial community structure along different management types in German forest and grassland soils. <b>2011</b> , 6, e17000	370
2122	Host-associated and free-living phage communities differ profoundly in phylogenetic composition. <b>2011</b> , 6, e16900	21
2121	Computational challenges of sequence classification in microbiomic data. <b>2011</b> , 12, 614-25	11
2120	Strain-resolved community genomic analysis of gut microbial colonization in a premature infant. <b>2011</b> , 108, 1128-33	201
2119	TopiaryExplorer: visualizing large phylogenetic trees with environmental metadata. <b>2011</b> , 27, 3067-9	15
2118	Bacterial community structures are unique and resilient in full-scale bioenergy systems. <b>2011</b> , 108, 4158-63	325
2117	JAGUC--a software package for environmental diversity analyses. <b>2011</b> , 9, 749-73	40
2116	Sparse distance-based learning for simultaneous multiclass classification and feature selection of metagenomic data. <b>2011</b> , 27, 3242-9	42
2115	ESPRIT-Tree: hierarchical clustering analysis of millions of 16S rRNA pyrosequences in quasilinear computational time. <b>2011</b> , 39, e95	105
2114	Deep sequencing of plant and animal DNA contained within traditional Chinese medicines reveals legality issues and health safety concerns. <b>2012</b> , 8, e1002657	180
2113	Incorporating 16S gene copy number information improves estimates of microbial diversity and abundance. <b>2012</b> , 8, e1002743	303
2112	Spatial distribution of microbial communities in the cystic fibrosis lung. <b>2012</b> , 6, 471-4	135
2111	Targeted recovery of novel phylogenetic diversity from next-generation sequence data. <b>2012</b> , 6, 2067-77	42

2110	A platform-independent method for detecting errors in metagenomic sequencing data: DRISSE. <b>2012</b> , 8, e1002541	49
2109	Chapter 12: Human microbiome analysis. <b>2012</b> , 8, e1002808	310
2108	Therapeutic helminth infection of macaques with idiopathic chronic diarrhea alters the inflammatory signature and mucosal microbiota of the colon. <b>2012</b> , 8, e1003000	157
2107	Bioinformatics for the Human Microbiome Project. <b>2012</b> , 8, e1002779	54
2106	Structural changes of gut microbiota during berberine-mediated prevention of obesity and insulin resistance in high-fat diet-fed rats. <b>2012</b> , 7, e42529	339
2105	The great obstetrical syndromes and the human microbiome-a new frontier. <b>2012</b> , 3, e0009	7
2104	Microbial community structure and activity linked to contrasting biogeochemical gradients in bog and fen environments of the Glacial Lake Agassiz Peatland. <b>2012</b> , 78, 7023-31	102
2103	Grinder: a versatile amplicon and shotgun sequence simulator. <b>2012</b> , 40, e94	137
2102	METAGENassist: a comprehensive web server for comparative metagenomics. <b>2012</b> , 40, W88-95	267
2101	Identifying genomic and metabolic features that can underlie early successional and opportunistic lifestyles of human gut symbionts. <b>2012</b> , 22, 1974-84	97
2100	Nurture trumps nature in a longitudinal survey of salivary bacterial communities in twins from early adolescence to early adulthood. <b>2012</b> , 22, 2146-52	131
2099	Specific detection of naturally occurring hepatitis C virus mutants with resistance to telaprevir and boceprevir (protease inhibitors) among treatment-naïve infected individuals. <b>2012</b> , 50, 281-7	45
2098	Culture-dependent and -independent investigations of microbial diversity on urinary catheters. <b>2012</b> , 50, 3901-8	31
2097	Yeast communities of diverse Drosophila species: comparison of two symbiont groups in the same hosts. <b>2012</b> , 78, 7327-36	109
2096	Maternal micronutrients can modify colonic mucosal microbiota maturation in murine offspring. <b>2012</b> , 3, 426-33	22
2095	. <b>2012</b> ,	4
2094	Interleukin-1 $\beta$ (IL-1 $\beta$ ) promotes susceptibility of Toll-like receptor 5 (TLR5) deficient mice to colitis. <b>2012</b> , 61, 373-84	59
2093	Rapid and Robust Denoising of Pyrosequenced Amplicons for Metagenomics. <b>2012</b> ,	1

2092	Lake microbial communities are resilient after a whole-ecosystem disturbance. <b>2012</b> , 6, 2153-67	143
2091	Consumption of different soymilk formulations differentially affects the gut microbiomes of overweight and obese men. <b>2012</b> , 3, 490-500	44
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2089	Abiotic factors shape microbial diversity in Sonoran Desert soils. <b>2012</b> , 78, 7527-37	137
2088	Architectural design influences the diversity and structure of the built environment microbiome. <b>2012</b> , 6, 1469-79	302
2087	Co-habiting amphibian species harbor unique skin bacterial communities in wild populations. <b>2012</b> , 6, 588-96	188
2086	Microbial community dynamics of an urban drinking water distribution system subjected to phases of chloramination and chlorination treatments. <b>2012</b> , 78, 7856-65	105
2085	Characterization of geographically distinct bacterial communities associated with coral mucus produced by <i>Acropora</i> spp. and <i>Porites</i> spp. <b>2012</b> , 78, 5229-37	49
2084	Probiotics stimulate enterocyte migration and microbial diversity in the neonatal mouse intestine. <b>2012</b> , 26, 1960-9	78
2083	High-throughput sequencing for detection of subpopulations of bacteria not previously associated with artisanal cheeses. <b>2012</b> , 78, 5717-23	191
2082	Fungal endophyte communities reflect environmental structuring across a Hawaiian landscape. <b>2012</b> , 109, 13022-7	227
2081	Impact of training sets on classification of high-throughput bacterial 16s rRNA gene surveys. <b>2012</b> , 6, 94-103	385
2080	Banana-associated microbial communities in Uganda are highly diverse but dominated by Enterobacteriaceae. <b>2012</b> , 78, 4933-41	32
2079	Fecal lactic acid bacteria increased in adolescents randomized to whole-grain but not refined-grain foods, whereas inflammatory cytokine production decreased equally with both interventions. <b>2012</b> , 142, 2025-32	26
2078	Bacterial Community Structure in the Hindgut of Wild and Captive Dugongs ( <i>Dugong dugon</i> ). <b>2012</b> , 38, 402-411	30
2077	Pulmonary bacterial communities in surgically resected noncystic fibrosis bronchiectasis lungs are similar to those in cystic fibrosis. <b>2012</b> , 2012, 746358	15
2076	Novel high-rank phylogenetic lineages within a sulfur spring (Zodletone Spring, Oklahoma), revealed using a combined pyrosequencing-sanger approach. <b>2012</b> , 78, 2677-88	29
2075	Direct sampling of cystic fibrosis lungs indicates that DNA-based analyses of upper-airway specimens can misrepresent lung microbiota. <b>2012</b> , 109, 13769-74	200

2074	The fecal microbiome in dogs with acute diarrhea and idiopathic inflammatory bowel disease. <b>2012</b> , 7, e51907	237
2073	SitePainter: a tool for exploring biogeographical patterns. <b>2012</b> , 28, 436-8	18
2072	MyD88-deficient Hydra reveal an ancient function of TLR signaling in sensing bacterial colonizers. <b>2012</b> , 109, 19374-9	112
2071	Bacterial associates of two Caribbean coral species reveal species-specific distribution and geographic variability. <b>2012</b> , 78, 6438-49	160
2070	Dissolved organic carbon influences microbial community composition and diversity in managed aquifer recharge systems. <b>2012</b> , 78, 6819-28	92
2069	Changes in bowel microbiota induced by feeding weanlings resistant starch stimulate transcriptomic and physiological responses. <b>2012</b> , 78, 6656-64	24
2068	Analysis of the cystic fibrosis lung microbiota via serial Illumina sequencing of bacterial 16S rRNA hypervariable regions. <b>2012</b> , 7, e45791	40
2067	VIROME: a standard operating procedure for analysis of viral metagenome sequences. <b>2012</b> , 6, 427-39	132
2066	Report of the 13(th) Genomic Standards Consortium Meeting, Shenzhen, China, March 4-7, 2012. <b>2012</b> , 6, 276-86	1
2065	Gut microbiota in children vaccinated with rotavirus vaccine. <b>2012</b> , 31, 1300-2	15
2064	Stimulated bacterioplankton growth and selection for certain bacterial taxa in the vicinity of the ctenophore <i>Mnemiopsis leidyi</i> . <b>2012</b> , 3, 302	29
2063	Microbial diversity in deep-sea methane seep sediments presented by SSU rRNA gene tag sequencing. <b>2012</b> , 27, 382-90	79
2062	Molecular analysis of bacterial communities in biofilms of a drinking water clearwell. <b>2012</b> , 27, 443-8	48
2061	Use of direct gradient analysis to uncover biological hypotheses in 16s survey data and beyond. <b>2012</b> , 2, 774	6
2060	Microbes en masse: The sequencing machine. <b>2012</b> , 487, 156-8	4
2059	The microbiota of the vagina and its influence on women's health and disease. <b>2012</b> , 343, 2-9	154
2058	Factors associated with the diversification of the gut microbial communities within chimpanzees from Gombe National Park. <b>2012</b> , 109, 13034-9	123
2057	Molecular methods to measure intestinal bacteria: a review. <b>2012</b> , 95, 5-23	39

2056	Defining the human microbiome. <b>2012</b> , 70 Suppl 1, S38-44	471
2055	Geographical and ecological stability of the symbiotic mid-gut microbiota in European firebugs, <i>Pyrrhocoris apterus</i> (Hemiptera, Pyrrhocoridae). <b>2012</b> , 21, 6134-51	96
2054	Asexual reproduction in introduced and native populations of the ant <i>Cerapachys biroi</i> . <b>2012</b> , 21, 5221-35	44
2053	Comparing clustering and pre-processing in taxonomy analysis. <b>2012</b> , 28, 2891-7	65
2052	Chimpanzees and humans harbour compositionally similar gut enterotypes. <b>2012</b> , 3, 1179	91
2051	Deep sequencing reveals extensive variation in the gut microbiota of wild mosquitoes from Kenya. <b>2012</b> , 21, 5138-50	189
2050	The composition of phyllosphere fungal assemblages of European beech ( <i>Fagus sylvatica</i> ) varies significantly along an elevation gradient. <b>2012</b> , 196, 510-519	116
2049	Cross-biome metagenomic analyses of soil microbial communities and their functional attributes. <b>2012</b> , 109, 21390-5	956
2048	Intestinal microbiota associated with differential feed conversion efficiency in chickens. <b>2012</b> , 96, 1361-9	179
2047	Modeling microbial communities: current, developing, and future technologies for predicting microbial community interaction. <b>2012</b> , 160, 17-24	40
2046	Microbiome dynamics of human epidermis following skin barrier disruption. <b>2012</b> , 13, R101	153
2045	A tool kit for quantifying eukaryotic rRNA gene sequences from human microbiome samples. <b>2012</b> , 13, R60	92
2044	Molecular characterisation of gastrointestinal microbiota of children with autism (with and without gastrointestinal dysfunction) and their neurotypical siblings. <b>2012</b> , 5, 419-27	128
2043	Host remodeling of the gut microbiome and metabolic changes during pregnancy. <b>2012</b> , 150, 470-80	1117
2042	Advances in the methods for studying gut microbiota and their relevance to the research of dietary fiber functions. <b>2012</b> , 48, 916-929	38
2041	Profiling of the metabolically active community from a production-scale biogas plant by means of high-throughput metatranscriptome sequencing. <b>2012</b> , 158, 248-58	170
2040	Translational research in infectious disease: current paradigms and challenges ahead. <b>2012</b> , 159, 430-53	34
2039	The human gut microbiome: current knowledge, challenges, and future directions. <b>2012</b> , 160, 246-57	178

2038	Changes in the caecal microflora of chickens following <i>Clostridium perfringens</i> challenge to induce necrotic enteritis. <b>2012</b> , 159, 155-62	99
2037	Structure, function and diversity of the healthy human microbiome. <b>2012</b> , 486, 207-14	6938
2036	Nucleic acid-based methods to assess the composition and function of the bowel microbiota. <b>2012</b> , 41, 855-68	5
2035	N3phele: Open Science-as-a-Service Workbench for Cloud-based Scientific Computing. <b>2012</b> ,	1
2034	GPU Acceleration of Pyrosequencing Noise Removal. <b>2012</b> ,	2
2033	Shaping reactor microbiomes to produce the fuel precursor n-butyrate from pretreated cellulosic hydrolysates. <b>2012</b> , 46, 10229-38	41
2032	Establishment of characteristic gut bacteria during development of the honeybee worker. <b>2012</b> , 78, 2830-40	305
2031	Dysbiosis in Epizootic Shell Disease of the American Lobster ( <i>Homarus americanus</i> ). <b>2012</b> , 31, 463-472	38
2030	Contrasting effects of <i>Bifidobacterium breve</i> NCIMB 702258 and <i>Bifidobacterium breve</i> DPC 6330 on the composition of murine brain fatty acids and gut microbiota. <b>2012</b> , 95, 1278-87	94
2029	The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. <b>2013</b> , 41, D590-6	11640
2028	Measuring the microbiome: perspectives on advances in DNA-based techniques for exploring microbial life. <b>2012</b> , 13, 420-9	31
2027	"Remake" by high-throughput sequencing of the microbiota involved in the production of water buffalo mozzarella cheese. <b>2012</b> , 78, 8142-5	142
2026	Sphagnum mosses harbour highly specific bacterial diversity during their whole lifecycle. <b>2012</b> , 6, 802-13	119
2025	Duty cycling influences current generation in multi-anode environmental microbial fuel cells. <b>2012</b> , 46, 5222-9	43
2024	Using network analysis to explore co-occurrence patterns in soil microbial communities. <b>2012</b> , 6, 343-51	1211
2023	A framework for human microbiome research. <b>2012</b> , 486, 215-21	1722
2022	Long-term balanced fertilization decreases arbuscular mycorrhizal fungal diversity in an arable soil in North China revealed by 454 pyrosequencing. <b>2012</b> , 46, 5764-71	193
2021	Ultrafast clustering algorithms for metagenomic sequence analysis. <b>2012</b> , 13, 656-68	294

2020	Spatial and species variations in bacterial communities associated with corals from the Red Sea as revealed by pyrosequencing. <b>2012</b> , 78, 7173-84	79
2019	Integrated online system for a pyrosequencing-based microbial source tracking method that targets Bacteroidetes 16S rDNA. <b>2012</b> , 46, 93-8	33
2018	Novel techniques and findings in the study of plant microbiota: search for plant probiotics. <b>2012</b> , 193-194, 96-102	89
2017	Saliva microbiomes distinguish caries-active from healthy human populations. <b>2012</b> , 6, 1-10	245
2016	Antibiotics in early life alter the murine colonic microbiome and adiposity. <b>2012</b> , 488, 621-6	1095
2015	Interactions between commensal fungi and the C-type lectin receptor Dectin-1 influence colitis. <b>2012</b> , 336, 1314-7	708
2014	Associating microbiome composition with environmental covariates using generalized UniFrac distances. <b>2012</b> , 28, 2106-13	520
2013	Testing potential effects of maize expressing the <i>Bacillus thuringiensis</i> Cry1Ab endotoxin (Bt maize) on mycorrhizal fungal communities via DNA- and RNA-based pyrosequencing and molecular fingerprinting. <b>2012</b> , 78, 7384-92	46
2012	Phenazine content in the cystic fibrosis respiratory tract negatively correlates with lung function and microbial complexity. <b>2012</b> , 47, 738-45	140
2011	Particle-size distributions and seasonal diversity of allergenic and pathogenic fungi in outdoor air. <b>2012</b> , 6, 1801-11	169
2010	Lung-enriched organisms and aberrant bacterial and fungal respiratory microbiota after lung transplant. <b>2012</b> , 186, 536-45	216
2009	Quantitative profiling of gut microbiota of children with diarrhea-predominant irritable bowel syndrome. <b>2012</b> , 107, 1740-51	131
2008	Innate lymphoid cells promote anatomical containment of lymphoid-resident commensal bacteria. <b>2012</b> , 336, 1321-5	542
2007	Spatial and temporal variability of the human microbiota. <b>2012</b> , 18 Suppl 4, 8-11	42
2006	Seasonal trends in the biomass and structure of bryophyte-associated fungal communities explored by 454 pyrosequencing. <b>2012</b> , 195, 844-856	70
2005	Measuring community similarity with phylogenetic networks. <b>2012</b> , 29, 3947-58	19
2004	Improving oligonucleotide fingerprinting of rRNA genes by implementation of polony microarray technology. <b>2012</b> , 90, 235-40	1
2003	The impact of the gut microbiota on human health: an integrative view. <b>2012</b> , 148, 1258-70	2117

2002	Gut immune maturation depends on colonization with a host-specific microbiota. <b>2012</b> , 149, 1578-93	778
2001	Detection of diverse aquatic microbes in blood and organs of drowning victims: first metagenomic approach using high-throughput 454-pyrosequencing. <b>2012</b> , 220, 135-46	43
2000	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. <b>2012</b> , 6, 1715-27	420
1999	Stochastic and deterministic assembly processes in subsurface microbial communities. <b>2012</b> , 6, 1653-64	651
1998	Sequencing our way towards understanding global eukaryotic biodiversity. <b>2012</b> , 27, 233-43	322
1997	Metagenomic analysis reveals a functional signature for biomass degradation by cecal microbiota in the leaf-eating flying squirrel ( <i>Petaurista alborufus lena</i> ). <b>2012</b> , 13, 466	19
1996	Storage conditions of intestinal microbiota matter in metagenomic analysis. <b>2012</b> , 12, 158	161
1995	Influence of wet distillers grains diets on beef cattle fecal bacterial community structure. <b>2012</b> , 12, 25	34
1994	Characterization of microflora in Latin-style cheeses by next-generation sequencing technology. <b>2012</b> , 12, 254	47
1993	Fecal microbial determinants of fecal and systemic estrogens and estrogen metabolites: a cross-sectional study. <b>2012</b> , 10, 253	234
1992	Pyrosequencing of 16S rRNA genes in fecal samples reveals high diversity of hindgut microflora in horses and potential links to chronic laminitis. <b>2012</b> , 8, 231	99
1991	Using metagenomic analyses to estimate the consequences of enrichment bias for pathogen detection. <b>2012</b> , 5, 378	25
1990	High throughput DNA sequencing to detect differences in the subgingival plaque microbiome in elderly subjects with and without dementia. <b>2012</b> , 3, 19	29
1989	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. <b>2012</b> , 1, 7	484
1988	Environmental and Evolutionary Genomics of Microbial Algae: Power and Challenges of Metagenomics. <b>2012</b> , 64, 383-427	10
1987	Diversity of bifidobacteria within the infant gut microbiota. <b>2012</b> , 7, e36957	415
1986	MALINA: a web service for visual analytics of human gut microbiota whole-genome metagenomic reads. <b>2012</b> , 7, 13	3
1985	Data mining the human gut microbiota for therapeutic targets. <b>2012</b> , 13, 751-68	14



1984	Nitrogen metabolism and rumen microbial enumeration in lactating cows with divergent residual feed intake fed high-digestibility pasture. <b>2012</b> , 95, 5024-5034	89
1983	Evidence of a robust resident bacteriophage population revealed through analysis of the human salivary virome. <b>2012</b> , 6, 915-26	211
1982	Defining the core <i>Arabidopsis thaliana</i> root microbiome. <b>2012</b> , 488, 86-90	1613
1981	Millimeter-scale patterns of phylogenetic and trait diversity in a salt marsh microbial mat. <b>2012</b> , 3, 293	34
1980	The interpersonal and intrapersonal diversity of human-associated microbiota in key body sites. <b>2012</b> , 129, 1204-8	207
1979	Soil bacterial community abundance and diversity in ice-free areas of Keller Peninsula, Antarctica. <b>2012</b> , 61, 7-15	19
1978	Integrated and novel survey methods for rhinoceros populations confirm the extinction of <i>Rhinoceros sondaicus annamiticus</i> from Vietnam. <b>2012</b> , 155, 59-67	31
1977	Systems biology approach to bioremediation. <b>2012</b> , 23, 483-90	115
1976	Spatial variability of phyllosphere fungal assemblages: genetic distance predominates over geographic distance in a European beech stand ( <i>Fagus sylvatica</i> ). <b>2012</b> , 5, 509-520	98
1975	Don't make a mista(g)ke: is tag switching an overlooked source of error in amplicon pyrosequencing studies?. <b>2012</b> , 5, 747-749	132
1974	Microbial 16S rRNA Ion Tag and community metagenome sequencing using the Ion Torrent (PGM) Platform. <b>2012</b> , 91, 80-8	143
1973	Reconstruction of ribosomal RNA genes from metagenomic data. <b>2012</b> , 7, e39948	48
1972	Massively Parallel Tag Sequencing Unveils the Complexity of Marine Protistan Communities in Oxygen-Depleted Habitats. <b>2012</b> , 171-183	1
1971	Inflammasome-mediated dysbiosis regulates progression of NAFLD and obesity. <b>2012</b> , 482, 179-85	1651
1970	Comparative metagenomic, phylogenetic and physiological analyses of soil microbial communities across nitrogen gradients. <b>2012</b> , 6, 1007-17	952
1969	Spatial variability overwhelms seasonal patterns in bacterioplankton communities across a river to ocean gradient. <b>2012</b> , 6, 554-63	179
1968	Analysis of gut microbial regulation of host gene expression along the length of the gut and regulation of gut microbial ecology through MyD88. <b>2012</b> , 61, 1124-31	261
1967	Identification of soil bacteria susceptible to TiO <sub>2</sub> and ZnO nanoparticles. <b>2012</b> , 78, 6749-58	195

1966	Insights into the bovine rumen plasmidome. <b>2012</b> , 109, 5452-7	96
1965	A large-scale benchmark study of existing algorithms for taxonomy-independent microbial community analysis. <b>2012</b> , 13, 107-21	119
1964	High-Throughput Characterization and Comparison of Microbial Communities. <b>2012</b> , 37-57	
1963	'Self-healing' dyes: intramolecular stabilization of organic fluorophores. <i>Nature Methods</i> , <b>2012</b> , 9, 426-7; author reply 427-8	21.6 59
1962	Bacterial flora of dental periradicular lesions analyzed by the 454-pyrosequencing technology. <b>2012</b> , 38, 1484-8	33
1961	Metaproteome analysis and molecular genetics of rat intestinal microbiota reveals section and localization resolved species distribution and enzymatic functionalities. <b>2012</b> , 11, 5406-17	51
1960	Microbial and geochemical assessment of bauxitic un-mined and post-mined chronosequence soils from Mocho Mountains, Jamaica. <b>2012</b> , 64, 738-49	14
1959	Mycangia of ambrosia beetles host communities of bacteria. <b>2012</b> , 64, 784-93	47
1958	Traumatic wound microbiome workshop. <b>2012</b> , 64, 837-50	1
1957	The Genboree Microbiome Toolset and the analysis of 16S rRNA microbial sequences. <b>2012</b> , 13 Suppl 13, S11	35
1956	Species-level classification of the vaginal microbiome. <b>2012</b> , 13 Suppl 8, S17	114
1955	PyroTRF-ID: a novel bioinformatics methodology for the affiliation of terminal-restriction fragments using 16S rRNA gene pyrosequencing data. <b>2012</b> , 12, 306	13
1954	Ray Meta: scalable de novo metagenome assembly and profiling. <b>2012</b> , 13, R122	420
1953	A format for phylogenetic placements. <b>2012</b> , 7, e31009	36
1952	Effect of <i>Lactobacillus salivarius</i> bacteriocin Abp118 on the mouse and pig intestinal microbiota. <b>2012</b> , 7, e31113	101
1951	Comparison of DNA extraction methods for microbial community profiling with an application to pediatric bronchoalveolar lavage samples. <b>2012</b> , 7, e34605	104
1950	A proposed taxonomy of anaerobic fungi (class neocallimastigomycetes) suitable for large-scale sequence-based community structure analysis. <b>2012</b> , 7, e36866	73
1949	Comparison of storage conditions for human vaginal microbiome studies. <b>2012</b> , 7, e36934	50

1948	Bacterial communities in the sediments of Dianchi Lake, a partitioned eutrophic waterbody in China. <b>2012</b> , 7, e37796	98
1947	High-throughput sequencing of 16S rRNA gene amplicons: effects of extraction procedure, primer length and annealing temperature. <b>2012</b> , 7, e38094	56
1946	Pyrosequencing of bacterial symbionts within <i>Axinella corrugata</i> sponges: diversity and seasonal variability. <b>2012</b> , 7, e38204	65
1945	Murine gut microbiota is defined by host genetics and modulates variation of metabolic traits. <b>2012</b> , 7, e39191	152
1944	16S rRNA gene pyrosequencing reveals bacterial dysbiosis in the duodenum of dogs with idiopathic inflammatory bowel disease. <b>2012</b> , 7, e39333	137
1943	Microbial diversity and potential pathogens in ornamental fish aquarium water. <b>2012</b> , 7, e39971	40
1942	Genometa--a fast and accurate classifier for short metagenomic shotgun reads. <b>2012</b> , 7, e41224	29
1941	The relation between oral <i>Candida</i> load and bacterial microbiome profiles in Dutch older adults. <b>2012</b> , 7, e42770	86
1940	Expression of human paraoxonase 1 decreases superoxide levels and alters bacterial colonization in the gut of <i>Drosophila melanogaster</i> . <b>2012</b> , 7, e43777	11
1939	Correlations between root-associated microorganisms and peach replant disease symptoms in a California soil. <b>2012</b> , 7, e46420	48
1938	Brewhouse-resident microbiota are responsible for multi-stage fermentation of American coolship ale. <b>2012</b> , 7, e35507	128
1937	A direct PCR approach to accelerate analyses of human-associated microbial communities. <b>2012</b> , 7, e44563	52
1936	Improved detection of bifidobacteria with optimised 16S rRNA-gene based pyrosequencing. <b>2012</b> , 7, e32543	143
1935	Next-generation sequencing reveals significant bacterial diversity of botrytized wine. <b>2012</b> , 7, e36357	162
1934	Analysis of the gut microbiota in the old order Amish and its relation to the metabolic syndrome. <b>2012</b> , 7, e43052	161
1933	Succession in the gut microbiome following antibiotic and antibody therapies for <i>Clostridium difficile</i> . <b>2012</b> , 7, e46966	67
1932	Routine habitat change: a source of unrecognized transient alteration of intestinal microbiota in laboratory mice. <b>2012</b> , 7, e47416	42
1931	Functional similarities between pigeon 'milk' and mammalian milk: induction of immune gene expression and modification of the microbiota. <b>2012</b> , 7, e48363	22

1930	Statistical object data analysis of taxonomic trees from human microbiome data. <b>2012</b> , 7, e48996	12
1929	CREST--classification resources for environmental sequence tags. <b>2012</b> , 7, e49334	167
1928	Commensal bacteria and MAMPs are necessary for stress-induced increases in IL-1 $\beta$ and IL-18 but not IL-6, IL-10 or MCP-1. <b>2012</b> , 7, e50636	56
1927	Insights from characterizing extinct human gut microbiomes. <b>2012</b> , 7, e51146	141
1926	Diversity and succession of bacterial communities in the uterine fluid of postpartum metritic, endometritic and healthy dairy cows. <b>2012</b> , 7, e53048	98
1925	A Canadian Working Group report on fecal microbial therapy: microbial ecosystems therapeutics. <b>2012</b> , 26, 457-62	50
1924	RNA-based assessment of diversity and composition of active archaeal communities in the German Bight. <b>2012</b> , 2012, 695826	32
1923	Pyrosequencing reveals bacteria carried in different wind-eroded sediments. <b>2012</b> , 41, 744-53	23
1922	Similar diversity of alphaproteobacteria and nitrogenase gene amplicons on two related sphagnum mosses. <b>2011</b> , 2, 275	49
1921	Carbon, metals, and grain size correlate with bacterial community structure in sediments of a high arsenic aquifer. <b>2012</b> , 3, 82	19
1920	Detection of autotrophic verrucomicrobial methanotrophs in a geothermal environment using stable isotope probing. <b>2012</b> , 3, 303	49
1919	Microbial biogeography of arctic streams: exploring influences of lithology and habitat. <b>2012</b> , 3, 309	25
1918	Bacterial Selection during the Formation of Early-Stage Aerobic Granules in Wastewater Treatment Systems Operated Under Wash-Out Dynamics. <b>2012</b> , 3, 332	57
1917	Microbial communities associated with wet flue gas desulfurization systems. <b>2012</b> , 3, 412	7
1916	CHANGES IN THE HUMAN SKIN MICROBIOME OVER ONE YEAR'S TIME. <b>2012</b> , 3, 18-30	1
1915	Computational methods for the analysis of tag sequences in metagenomics studies. <b>2012</b> , 4, 1333-43	2
1914	Human gut microbiome viewed across age and geography. <b>2012</b> , 486, 222-7	4616
1913	Computational Challenges in Characterization of Bacteria and Bacteria-Host Interactions Based on Genomic Data. <b>2012</b> , 27, 225-239	7

1912	Phylotype-level 16S rRNA analysis reveals new bacterial indicators of health state in acute murine colitis. <b>2012</b> , 6, 2091-106	208
1911	Microbes inside--from diversity to function: the case of Akkermansia. <b>2012</b> , 6, 1449-58	385
1910	miRNA data analysis: next-gen sequencing. <b>2012</b> , 822, 273-88	25
1909	Spatial and temporal dynamics of the microbial community in the Hanford unconfined aquifer. <b>2012</b> , 6, 1665-76	81
1908	Low sequencing efforts bias analyses of shared taxa in microbial communities. <b>2012</b> , 57, 409-13	25
1907	Global distribution and diversity of marine Verrucomicrobia. <b>2012</b> , 6, 1499-505	118
1906	Gut microbiota composition correlates with diet and health in the elderly. <b>2012</b> , 488, 178-84	1987
1905	Fast, accurate error-correction of amplicon pyrosequences using Acacia. <i>Nature Methods</i> , <b>2012</b> , 9, 425-6 21.6	268
1904	Temporal dynamics of the human vaginal microbiota. <b>2012</b> , 4, 132ra52	835
1903	Comprehensive analysis of the bacterial content of stool from patients with chronic pouchitis, normal pouches, or familial adenomatous polyposis pouches. <b>2012</b> , 18, 925-34	47
1902	Characterization of soil bacterial assemblies in Brazilian savanna-like vegetation reveals acidobacteria dominance. <b>2012</b> , 64, 760-70	66
1901	Unlocking the potential of metagenomics through replicated experimental design. <b>2012</b> , 30, 513-20	212
1900	The human microbiome: our second genome. <b>2012</b> , 13, 151-70	365
1899	Actinobacterial nitrate reducers and proteobacterial denitrifiers are abundant in N2O-metabolizing palsa peat. <b>2012</b> , 78, 5584-96	55
1898	The rare bacterial biosphere. <b>2012</b> , 4, 449-66	412
1897	Comparison of Illumina paired-end and single-direction sequencing for microbial 16S rRNA gene amplicon surveys. <b>2012</b> , 6, 1273-6	79
1896	Colonic microbiome is altered in alcoholism. <b>2012</b> , 302, G966-78	439
1895	Honor thy gut symbionts redux. <b>2012</b> , 336, 1251-3	145

1894	A preliminary survey of lichen associated eukaryotes using pyrosequencing. <b>2012</b> , 44, 137-146	54
1893	Assessing ectomycorrhizal fungal spore banks of truffle producing soils with pecan seedling trap-plants. <b>2012</b> , 356, 357-366	25
1892	Human microbiome and HIV/AIDS. <b>2012</b> , 9, 44-51	56
1891	Fungal community composition in neotropical rain forests: the influence of tree diversity and precipitation. <b>2012</b> , 63, 804-12	99
1890	The Effects of Soil Bacterial Community Structure on Decomposition in a Tropical Rain Forest. <b>2012</b> , 15, 284-298	43
1889	Soil microbial community response to drying and rewetting stress: does historical precipitation regime matter?. <b>2012</b> , 109, 101-116	276
1888	Beyond the Venn diagram: the hunt for a core microbiome. <b>2012</b> , 14, 4-12	581
1887	Consistent effects of nitrogen amendments on soil microbial communities and processes across biomes. <b>2012</b> , 18, 1918-1927	715
1886	Experimental and analytical tools for studying the human microbiome. <b>2011</b> , 13, 47-58	491
1885	Responses of gut microbiota to diet composition and weight loss in lean and obese mice. <b>2012</b> , 20, 738-47	287
1884	Effect of the proton pump inhibitor omeprazole on the gastrointestinal bacterial microbiota of healthy dogs. <b>2012</b> , 80, 624-36	86
1883	Pyrosequencing reveals unique microbial signatures associated with healthy and failing dental implants. <b>2012</b> , 39, 425-33	215
1882	Size-resolved emission rates of airborne bacteria and fungi in an occupied classroom. <b>2012</b> , 22, 339-51	245
1881	Advancing analytical algorithms and pipelines for billions of microbial sequences. <b>2012</b> , 23, 64-71	46
1880	Seasonal variability in airborne bacterial communities at a high-elevation site. <b>2012</b> , 50, 41-49	184
1879	Hydrogen and volatile fatty acid production during fermentation of cellulosic substrates by a thermophilic consortium at 50 and 60 °C. <b>2012</b> , 104, 424-31	27
1878	Effects of packing rates of cubic-shaped polyurethane foam carriers on the microbial community and the removal of organics and nitrogen in moving bed biofilm reactors. <b>2012</b> , 117, 201-7	79
1877	Ecology of the microbiome of the infected root canal system: a comparison between apical and coronal root segments. <b>2012</b> , 45, 530-41	83

1876	Phylogenetic clustering increases with elevation for microbes. <b>2012</b> , 4, 217-26	118
1875	Detection and diversity of pathogenic <i>Vibrio</i> from Fiji. <b>2012</b> , 4, 403-11	2
1874	Daily follow-up of bacterial communities in the human gut reveals stable composition and host-specific patterns of interaction. <b>2012</b> , 81, 427-37	20
1873	Spatial heterogeneity of eukaryotic microbial communities in an unstudied geothermal diatomaceous biological soil crust: Yellowstone National Park, WY, USA. <b>2012</b> , 82, 182-91	15
1872	Molecular methods for pathogen and microbial community detection and characterization: current and potential application in diagnostic microbiology. <b>2012</b> , 12, 505-21	104
1871	Bacterial community structure and function change in association with colonizer plants during early primary succession in a glacier forefield. <b>2012</b> , 46, 172-180	146
1870	Perennial plant species from semiarid gypsum soils support higher AMF diversity in roots than the annual <i>Bromus rubens</i> . <b>2012</b> , 49, 132-138	34
1869	Digging deeper to find unique microbial communities: The strong effect of depth on the structure of bacterial and archaeal communities in soil. <b>2012</b> , 50, 58-65	429
1868	Bacterial community structure of contrasting soils underlying Bornean rain forests: Inferences from microarray and next-generation sequencing methods. <b>2012</b> , 55, 48-59	32
1867	Assessment of the human faecal microbiota: II. Reproducibility and associations of 16S rRNA pyrosequences. <b>2012</b> , 42, 855-63	33
1866	Metagenetic community analysis of microbial eukaryotes illuminates biogeographic patterns in deep-sea and shallow water sediments. <b>2012</b> , 21, 1048-59	129
1865	Two decades of describing the unseen majority of aquatic microbial diversity. <b>2012</b> , 21, 1878-96	147
1864	Bioinformatic challenges for DNA metabarcoding of plants and animals. <b>2012</b> , 21, 1834-47	172
1863	Microbiome analysis among bats describes influences of host phylogeny, life history, physiology and geography. <b>2012</b> , 21, 2617-27	140
1862	Measuring ectomycorrhizal fungal dispersal: macroecological patterns driven by microscopic propagules. <b>2012</b> , 21, 4122-36	256
1861	Alterations in composition and diversity of the intestinal microbiota in patients with diarrhea-predominant irritable bowel syndrome. <b>2012</b> , 24, 521-30, e248	270
1860	Intestinal aganglionosis is associated with early and sustained disruption of the colonic microbiome. <b>2012</b> , 24, 874-e400	55
1859	The phylogenetic Kantorovich-Rubinstein metric for environmental sequence samples. <b>2012</b> , 74, 569-592	70

1858	Experience matters: prior exposure to plant toxins enhances diversity of gut microbes in herbivores. <b>2012</b> , 15, 1008-15	74
1857	amoA-based consensus phylogeny of ammonia-oxidizing archaea and deep sequencing of amoA genes from soils of four different geographic regions. <b>2012</b> , 14, 525-39	402
1856	Cyanobacterial construction of hot spring siliceous stromatolites in Yellowstone National Park. <b>2012</b> , 14, 1182-97	52
1855	Deep-sea bacteria enriched by oil and dispersant from the Deepwater Horizon spill. <b>2012</b> , 14, 2405-16	231
1854	Temporal variability in the diversity and composition of stream bacterioplankton communities. <b>2012</b> , 14, 2417-28	74
1853	Geographic distance and pH drive bacterial distribution in alkaline lake sediments across Tibetan Plateau. <b>2012</b> , 14, 2457-66	353
1852	Culturing captures members of the soil rare biosphere. <b>2012</b> , 14, 2247-52	140
1851	Biodiversity soup: metabarcoding of arthropods for rapid biodiversity assessment and biomonitoring. <b>2012</b> , 3, 613-623	414
1850	Parallel-META: efficient metagenomic data analysis based on high-performance computation. <b>2012</b> , 6 Suppl 1, S16	29
1849	A hump-backed trend in bacterial diversity with elevation on Mount Fuji, Japan. <b>2012</b> , 63, 429-37	115
1848	The dynamics of the vaginal microbiome during infertility therapy with in vitro fertilization-embryo transfer. <b>2012</b> , 29, 105-15	94
1847	MetAMOS: a modular and open source metagenomic assembly and analysis pipeline. <b>2013</b> , 14, R2	150
1846	Inflammation-associated enterotypes, host genotype, cage and inter-individual effects drive gut microbiota variation in common laboratory mice. <b>2013</b> , 14, R4	293
1845	Diversified pattern of the human colorectal cancer microbiome. <b>2013</b> , 5, 2	81
1844	Infant gut microbiota and the hygiene hypothesis of allergic disease: impact of household pets and siblings on microbiota composition and diversity. <b>2013</b> , 9, 15	172
1843	Infection with the carcinogenic liver fluke <i>Opisthorchis viverrini</i> modifies intestinal and biliary microbiome. <b>2013</b> , 27, 4572-84	95
1842	Large-scale survey of gut microbiota associated with MHE Via 16S rRNA-based pyrosequencing. <b>2013</b> , 108, 1601-11	104
1841	AXIOME: automated exploration of microbial diversity. <b>2013</b> , 2, 3	43



1840	Fluorescent epibiotic microbial community on the carapace of a Bahamian ostracod. <b>2013</b> , 195, 595-604	2
1839	Application of state-of-art sequencing technologies to indigenous food fermentations. <b>2013</b> , 24, 178-86	54
1838	Progressive and retrogressive ecosystem development coincide with soil bacterial community change in a dune system under lowland temperate rainforest in New Zealand. <b>2013</b> , 367, 235-247	17
1837	A unique signal distorts the perception of species richness and composition in high-throughput sequencing surveys of microbial communities: a case study of fungi in indoor dust. <b>2013</b> , 66, 735-41	46
1836	Pyrosequencing analysis of the bacterial community in drinking water wells. <b>2013</b> , 66, 19-29	73
1835	Deep sequencing of Myxilla (Ectyomyxilla) methanophila, an epibiotic sponge on cold-seep tubeworms, reveals methylotrophic, thiotrophic, and putative hydrocarbon-degrading microbial associations. <b>2013</b> , 65, 450-61	17
1834	Prokaryotic communities differ along a geothermal soil photic gradient. <b>2013</b> , 65, 171-9	
1833	Intergenerational transfer of specific bacteria in corals and possible implications for offspring fitness. <b>2013</b> , 65, 227-31	41
1832	Soil bacterial community succession during long-term ecosystem development. <b>2013</b> , 22, 3415-24	81
1831	Functional and compositional succession of bacterioplankton in response to a gradient in bioavailable dissolved organic carbon. <b>2013</b> , 15, 2616-28	37
1830	Anaerobic oxidation of methane coupled to nitrate reduction in a novel archaeal lineage. <b>2013</b> , 500, 567-70	750
1829	Changes in microbial dynamics during long-term decomposition in tropical forests. <b>2013</b> , 66, 60-68	42
1828	The gut microbiota and obesity: from correlation to causality. <b>2013</b> , 11, 639-47	478
1827	Comparison of direct boiling method with commercial kits for extracting fecal microbiome DNA by Illumina sequencing of 16S rRNA tags. <b>2013</b> , 95, 455-62	61
1826	Towards a unified paradigm for sequence-based identification of fungi. <b>2013</b> , 22, 5271-7	2019
1825	Stochastic changes over time and not founder effects drive cage effects in microbial community assembly in a mouse model. <b>2013</b> , 7, 2116-25	156
1824	Impacts of inundation and drought on eukaryote biodiversity in semi-arid floodplain soils. <b>2013</b> , 22, 1746-58	46
1823	Survival in hostile territory: the microbiota of the stomach. <b>2013</b> , 37, 736-61	99

1822	Methanotrophic bacteria in oilsands tailings ponds of northern Alberta. <b>2013</b> , 7, 908-21	79
1821	Termite hindguts and the ecology of microbial communities in the sequencing age. <b>2013</b> , 60, 421-8	7
1820	The Inflammasome. <b>2013</b> ,	4
1819	Contrasting circulating microbiome in cardiovascular disease patients and healthy individuals. <b>2013</b> , 168, 5118-20	40
1818	The NIH Human Microbiome Project. <b>2013</b> , 1-50	1
1817	Diversity, distribution and sources of bacteria in residential kitchens. <b>2013</b> , 15, 588-96	137
1816	FANTOM: Functional and taxonomic analysis of metagenomes. <b>2013</b> , 14, 38	32
1815	Baseline survey of the anatomical microbial ecology of an important food plant: <i>Solanum lycopersicum</i> (tomato). <b>2013</b> , 13, 114	152
1814	Influence of <i>Salmonella enterica</i> serovar Enteritidis infection on the composition of chicken cecal microbiota. <b>2013</b> , 9, 140	65
1813	Chicken faecal microbiota and disturbances induced by single or repeated therapy with tetracycline and streptomycin. <b>2013</b> , 9, 30	73
1812	Acidobacterial community responses to agricultural management of soybean in Amazon forest soils. <b>2013</b> , 83, 607-21	155
1811	High-resolution SAR11 ecotype dynamics at the Bermuda Atlantic Time-series Study site by phylogenetic placement of pyrosequences. <b>2013</b> , 7, 1322-32	121
1810	Land-use change and soil type are drivers of fungal and archaeal communities in the Pampa biome. <b>2013</b> , 29, 223-33	31
1809	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <b>2013</b> , 31, 814-21	5270
1808	Microeukaryote community composition assessed by pyrosequencing is associated with light availability and phytoplankton primary production along a lowland river. <b>2013</b> , 58, n/a-n/a	3
1807	Independent roles of ectomycorrhizal and saprotrophic communities in soil organic matter decomposition. <b>2013</b> , 57, 282-291	149
1806	Molecular investigation of bacterial communities on the inner and outer surfaces of peripheral venous catheters. <b>2013</b> , 32, 1083-90	16
1805	Microbiota-liberated host sugars facilitate post-antibiotic expansion of enteric pathogens. <b>2013</b> , 502, 96-9	630

1804	Practical innovations for high-throughput amplicon sequencing. <i>Nature Methods</i> , <b>2013</b> , 10, 999-1002	21.6	461
1803	Ecological Inferences from a deep screening of the Complex Bacterial Consortia associated with the coral, <i>Porites astreoides</i> . <b>2013</b> , 22, 4349-4362		43
1802	UPARSE: highly accurate OTU sequences from microbial amplicon reads. <i>Nature Methods</i> , <b>2013</b> , 10, 996-81.6	21.6	8067
1801	Characterization of bacterial and archaeal communities in air-cathode microbial fuel cells, open circuit and sealed-off reactors. <b>2013</b> , 97, 9885-95		79
1800	Structural modulation of gut microbiota in life-long calorie-restricted mice. <b>2013</b> , 4, 2163		305
1799	Investigating the diversity of <i>pseudomonas</i> spp. in soil using culture dependent and independent techniques. <b>2013</b> , 67, 423-30		16
1798	Composition of heterotrophic flagellates in coastal waters of different trophic status. <b>2013</b> , 67, 351-5		3
1797	Bacterial community structure and functional contributions to emergence of health or necrotizing enterocolitis in preterm infants. <b>2013</b> , 1, 20		110
1796	Enrichment of lung microbiome with supraglottic taxa is associated with increased pulmonary inflammation. <b>2013</b> , 1, 19		262
1795	Integrative analysis of the microbiome and metabolome of the human intestinal mucosal surface reveals exquisite inter-relationships. <b>2013</b> , 1, 17		175
1794	Early microbial and metabolomic signatures predict later onset of necrotizing enterocolitis in preterm infants. <b>2013</b> , 1, 13		213
1793	A comprehensive evaluation of multcategory classification methods for microbiomic data. <b>2013</b> , 1, 11		103
1792	Microbial phylogenetic profiling with the Pacific Biosciences sequencing platform. <b>2013</b> , 1, 10		107
1791	CloVR-ITS: Automated internal transcribed spacer amplicon sequence analysis pipeline for the characterization of fungal microbiota. <b>2013</b> , 1, 6		40
1790	Sequence-based analysis of the microbial composition of water kefir from multiple sources. <b>2013</b> , 348, 79-85		50
1789	Considerations for the development and application of control materials to improve metagenomic microbial community profiling. <b>2013</b> , 18, 77-83		15
1788	High abundance of heterotrophic prokaryotes in hydrothermal springs of the Azores as revealed by a network of 16S rRNA gene-based methods. <b>2013</b> , 17, 649-62		39
1787	Community-analyzer: a platform for visualizing and comparing microbial community structure across microbiomes. <b>2013</b> , 102, 409-18		18

1786	Analysis of microbiota alterations in inflammasome-deficient mice. <b>2013</b> , 1040, 185-94	23
1785	The inconstant gut microbiota of <i>Drosophila</i> species revealed by 16S rRNA gene analysis. <b>2013</b> , 7, 1922-32	205
1784	Hydrocarbon-degrading bacteria enriched by the Deepwater Horizon oil spill identified by cultivation and DNA-SIP. <b>2013</b> , 7, 2091-104	198
1783	Phoenix 2: a locally installable large-scale 16S rRNA gene sequence analysis pipeline with Web interface. <b>2013</b> , 167, 393-403	49
1782	Drivers of microbial community composition in mesophilic and thermophilic temperature-phased anaerobic digestion pre-treatment reactors. <b>2013</b> , 47, 7098-108	92
1781	Population dynamics during startup of thermophilic anaerobic digesters: the mixing factor. <b>2013</b> , 33, 2211-8	11
1780	Microbial community dynamics during acetate biostimulation of RDX-contaminated groundwater. <b>2013</b> , 47, 7672-8	30
1779	Diet, microbiota, and microbial metabolites in colon cancer risk in rural Africans and African Americans. <b>2013</b> , 98, 111-20	409
1778	Intestinal microbiota determines development of non-alcoholic fatty liver disease in mice. <b>2013</b> , 62, 1787-94	552
1777	SIV-induced instability of the chimpanzee gut microbiome. <b>2013</b> , 14, 340-5	62
1776	Pyrosequencing-based profiling of archaeal and bacterial 16S rRNA genes identifies a novel archaeon associated with black band disease in corals. <b>2013</b> , 15, 2994-3007	18
1775	Stage 0 sporulation gene A as a molecular marker to study diversity of endospore-forming Firmicutes. <b>2013</b> , 5, 911-24	31
1774	The core faecal bacterial microbiome of Irish Thoroughbred racehorses. <b>2013</b> , 57, 492-501	62
1773	Temporal bacterial community dynamics vary among ulcerative colitis patients after fecal microbiota transplantation. <b>2013</b> , 108, 1620-30	254
1772	The human mycobiome in health and disease. <b>2013</b> , 5, 63	204
1771	Microbial community analysis using MEGAN. <b>2013</b> , 531, 465-85	144
1770	High-throughput sequencing and metagenomics: moving forward in the culture-independent analysis of food microbial ecology. <b>2013</b> , 79, 3148-55	334
1769	Reconstructing the microbial diversity and function of pre-agricultural tallgrass prairie soils in the United States. <b>2013</b> , 342, 621-4	324

1768	Identification of trigger factors selecting for polyphosphate- and glycogen-accumulating organisms in aerobic granular sludge sequencing batch reactors. <b>2013</b> , 47, 7006-18	53
1767	Histone deacetylase 3 coordinates commensal-bacteria-dependent intestinal homeostasis. <b>2013</b> , 504, 153-7	154
1766	Nasal microenvironments and interspecific interactions influence nasal microbiota complexity and <i>S. aureus</i> carriage. <b>2013</b> , 14, 631-40	221
1765	Sequencing the human microbiome in health and disease. <b>2013</b> , 22, R88-94	89
1764	A comparison of two probiotic strains of bifidobacteria in premature infants. <b>2013</b> , 163, 1585-1591.e9	84
1763	The ignored diversity: complex bacterial communities in intensive care units revealed by 16S pyrosequencing. <b>2013</b> , 3, 1413	119
1762	The intestinal microbiota modulates the anticancer immune effects of cyclophosphamide. <b>2013</b> , 342, 971-6	1128
1761	Structure-constrained sparse canonical correlation analysis with an application to microbiome data analysis. <b>2013</b> , 14, 244-58	101
1760	Cell size distributions of soil bacterial and archaeal taxa. <b>2013</b> , 79, 7610-7	79
1759	Discovery and synthetic refactoring of tryptophan dimer gene clusters from the environment. <b>2013</b> , 135, 17906-12	37
1758	16S rRNA metagenome clustering and diversity estimation using locality sensitive hashing. <b>2013</b> , 7 Suppl 4, S11	9
1757	Methanosarcinaceae and acetate-oxidizing pathways dominate in high-rate thermophilic anaerobic digestion of waste-activated sludge. <b>2013</b> , 79, 6491-500	93
1756	Microbiota modulate behavioral and physiological abnormalities associated with neurodevelopmental disorders. <b>2013</b> , 155, 1451-63	1963
1755	Gut microbiota from twins discordant for obesity modulate metabolism in mice. <b>2013</b> , 341, 1241214	2251
1754	Fungal communities associated with the biodegradation of polyester polyurethane buried under compost at different temperatures. <b>2013</b> , 79, 7313-24	49
1753	Microbial communities associated with the degradation of oak wood in the Blanes submarine canyon and its adjacent open slope (NW Mediterranean). <b>2013</b> , 118, 137-143	16
1752	Human gut microbiome and risk for colorectal cancer. <b>2013</b> , 105, 1907-11	541
1751	Quikr: a method for rapid reconstruction of bacterial communities via compressive sensing. <b>2013</b> , 29, 2096-102	32

1750	Topics in Applied Statistics. <b>2013</b> ,	0
1749	A logistic normal multinomial regression model for microbiome compositional data analysis. <b>2013</b> , 69, 1053-63	68
1748	Characterization of the bacterial community of the chemically defended Hawaiian sacoglossan <i>Elysia rufescens</i> . <b>2013</b> , 79, 7073-81	27
1747	Data visualization in environmental proteomics. <b>2013</b> , 13, 2805-21	17
1746	Meta-analyses of studies of the human microbiota. <b>2013</b> , 23, 1704-14	289
1745	Use of bifidobacterial specific terminal restriction fragment length polymorphisms to complement next generation sequence profiling of infant gut communities. <b>2013</b> , 19, 62-9	18
1744	Characterization of gut microbiomes in nonalcoholic steatohepatitis (NASH) patients: a connection between endogenous alcohol and NASH. <b>2013</b> , 57, 601-9	904
1743	Comparison of microbial diversity determined with the same variable tag sequence extracted from two different PCR amplicons. <b>2013</b> , 13, 208	38
1742	Microbial community structure in a biogas digester utilizing the marine energy crop <i>Saccharina latissima</i> . <b>2013</b> , 3, 407-414	17
1741	mPUMA: a computational approach to microbiota analysis by de novo assembly of operational taxonomic units based on protein-coding barcode sequences. <b>2013</b> , 1, 23	25
1740	A comprehensive metatranscriptome analysis pipeline and its validation using human small intestine microbiota datasets. <b>2013</b> , 14, 530	92
1739	The PAMPA datasets: a metagenomic survey of microbial communities in Argentinean pampean soils. <b>2013</b> , 1, 21	16
1738	Genome resolved analysis of a premature infant gut microbial community reveals a <i>Varibaculum cambriense</i> genome and a shift towards fermentation-based metabolism during the third week of life. <b>2013</b> , 1, 30	39
1737	The murine lung microbiome in relation to the intestinal and vaginal bacterial communities. <b>2013</b> , 13, 303	82
1736	Community differentiation of the cutaneous microbiota in psoriasis. <b>2013</b> , 1, 31	245
1735	EMPeror: a tool for visualizing high-throughput microbial community data. <b>2013</b> , 2, 16	711
1734	Disturbance induced decoupling between host genetics and composition of the associated microbiome. <b>2013</b> , 13, 252	77
1733	Utilizing novel diversity estimators to quantify multiple dimensions of microbial biodiversity across domains. <b>2013</b> , 13, 259	9

1732	HIV Infection is associated with compositional and functional shifts in the rectal mucosal microbiota. <b>2013</b> , 1, 26	147
1731	Optimal operational conditions for biohydrogen production from sugar refinery wastewater in an ASBR. <b>2013</b> , 38, 13895-13906	27
1730	High throughput sequencing methods and analysis for microbiome research. <b>2013</b> , 95, 401-14	167
1729	Identification of chicken intestinal microbiota correlated with the efficiency of energy extraction from feed. <b>2013</b> , 164, 85-92	109
1728	Genome-wide mapping of gene-microbiota interactions in susceptibility to autoimmune skin blistering. <b>2013</b> , 4, 2462	62
1727	Advection shapes Southern Ocean microbial assemblages independent of distance and environment effects. <b>2013</b> , 4, 2457	87
1726	Human gut microbiota community structures in urban and rural populations in Russia. <b>2013</b> , 4, 2469	174
1725	The nonfermentable dietary fiber hydroxypropyl methylcellulose modulates intestinal microbiota. <b>2013</b> , 27, 692-702	59
1724	Determining indicator taxa across spatial and seasonal gradients in the Columbia River coastal margin. <b>2013</b> , 7, 1899-911	101
1723	Alterations in the gut microbiota associated with HIV-1 infection. <b>2013</b> , 14, 329-39	284
1722	Assessing the human gut microbiota in metabolic diseases. <b>2013</b> , 62, 3341-9	289
1721	Quantifying and identifying the active and damaged subsets of indigenous microbial communities. <b>2013</b> , 531, 91-107	8
1720	Quantifying community assembly processes and identifying features that impose them. <b>2013</b> , 7, 2069-79	624
1719	A metagenomics portal for a democratized sequencing world. <b>2013</b> , 531, 487-523	16
1718	A meta-analysis of changes in bacterial and archaeal communities with time. <b>2013</b> , 7, 1493-506	236
1717	A decentralized wastewater treatment system using microbial fuel cell techniques and its response to a copper shock load. <b>2013</b> , 143, 76-82	32
1716	Simultaneous pyrosequencing of the 16S rRNA, IncP-1 trfA, and merA genes. <b>2013</b> , 95, 280-4	5
1715	A user's guide to quantitative and comparative analysis of metagenomic datasets. <b>2013</b> , 531, 525-47	23

1714	Computational methods for high-throughput comparative analyses of natural microbial communities. <b>2013</b> , 531, 353-70	23
1713	Microbial characterization of basalt formation waters targeted for geological carbon sequestration. <b>2013</b> , 85, 62-73	21
1712	Differential abundance analysis for microbial marker-gene surveys. <i>Nature Methods</i> , <b>2013</b> , 10, 1200-2	21.6 1163
1711	Advancing our understanding of the human microbiome using QIIME. <b>2013</b> , 531, 371-444	373
1710	Diversity and population structure of Marine Group A bacteria in the Northeast subarctic Pacific Ocean. <b>2013</b> , 7, 256-68	52
1709	Host-compound foraging by intestinal microbiota revealed by single-cell stable isotope probing. <b>2013</b> , 110, 4720-5	147
1708	Improved selection of internal transcribed spacer-specific primers enables quantitative, ultra-high-throughput profiling of fungal communities. <b>2013</b> , 79, 2519-26	292
1707	Diversity and heritability of the maize rhizosphere microbiome under field conditions. <b>2013</b> , 110, 6548-53	1067
1706	Higher seasonal variation of actinobacterial communities than spatial heterogeneity in the surface sediments of Taihu Lake, China. <b>2013</b> , 59, 353-8	2
1705	Human Analysts at Superhuman Scales: What Has Friendly Software To Do?. <b>2013</b> , 1, 227-36	1
1704	Short communication: Evidence that microbial translocation occurs in HIV-infected children in the United Kingdom. <b>2013</b> , 29, 1589-93	14
1703	Coaggregation occurs amongst bacteria within and between biofilms in domestic showerheads. <b>2013</b> , 29, 53-68	32
1702	A high-throughput microfluidic dental plaque biofilm system to visualize and quantify the effect of antimicrobials. <b>2013</b> , 68, 2550-60	57
1701	Dynamics of cathode-associated microbial communities and metabolite profiles in a glycerol-fed bioelectrochemical system. <b>2013</b> , 79, 4008-14	53
1700	Coleoptera Collected from Rotting Fishhook Barrel Cacti ( <i>Ferocactus wislizeni</i> (Engelm.) Britton and Rose), with a Review of Nearctic Coleoptera Associated with Succulent Necrosis. <b>2013</b> , 67, 419-443	9
1699	Comparison of the compositions of the stool microbiotas of infants fed goat milk formula, cow milk-based formula, or breast milk. <b>2013</b> , 79, 3040-8	121
1698	The Paint Pots, Kootenay National Park, Canada – a natural acid spring analogue for Mars. <b>2013</b> , 50, 94-108	19
1697	Reactor performance in terms of COD and nitrogen removal and bacterial community structure of a three-stage rotating bioelectrochemical contactor. <b>2013</b> , 47, 881-94	69



1696	Soil microbe active community composition and capability of responding to litter addition after 12 years of no inputs. <b>2013</b> , 79, 1385-92		31
1695	Comparative metagenomic and rRNA microbial diversity characterization using archaeal and bacterial synthetic communities. <b>2013</b> , 15, 1882-99		147
1694	Xenobiotics shape the physiology and gene expression of the active human gut microbiome. <b>2013</b> , 152, 39-50		560
1693	Surveying the microbiome of ants: comparing 454 pyrosequencing with traditional methods to uncover bacterial diversity. <b>2013</b> , 79, 525-34		89
1692	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. <i>Nature Methods</i> , <b>2013</b> , 10, 57-9	21.6	2167
1691	Global biogeography of highly diverse protistan communities in soil. <b>2013</b> , 7, 652-9		302
1690	Metagenomics and Community Profiling: Culture-Independent Techniques in the Clinical Laboratory. <b>2013</b> , 35, 1-9		5
1689	Distinct cutaneous bacterial assemblages in a sampling of South American Amerindians and US residents. <b>2013</b> , 7, 85-95		80
1688	Influence of hydraulic regimes on bacterial community structure and composition in an experimental drinking water distribution system. <b>2013</b> , 47, 503-16		195
1687	Methanol oxidation by temperate soils and environmental determinants of associated methylotrophs. <b>2013</b> , 7, 1051-64		21
1686	Bifidobacterial succession and correlation networks in a large unselected cohort of mothers and their children. <b>2013</b> , 79, 497-507		59
1685	16S rRNA survey revealed complex bacterial communities and evidence of bacterial interference on human adenoids. <b>2013</b> , 15, 535-47		27
1684	Relationship between abundance and specific activity of bacterioplankton in open ocean surface waters. <b>2013</b> , 79, 177-84		102
1683	Biogeography of bacterial communities exposed to progressive long-term environmental change. <b>2013</b> , 7, 937-48		221
1682	Lineage-specific responses of microbial communities to environmental change. <b>2013</b> , 79, 39-47		17
1681	Diet-induced alterations of host cholesterol metabolism are likely to affect the gut microbiota composition in hamsters. <b>2013</b> , 79, 516-24		135
1680	Pre-exposure to drought increases the resistance of tropical forest soil bacterial communities to extended drought. <b>2013</b> , 7, 384-94		150
1679	Impact of different bioenergy crops on N-cycling bacterial and archaeal communities in soil. <b>2013</b> , 15, 928-42		57

1678	Bacteria and diatom co-occurrence patterns in microbial mats from polar desert streams. <b>2013</b> , 15, 1115-31	36
1677	The intestinal microbiota in aged mice is modulated by dietary resistant starch and correlated with improvements in host responses. <b>2013</b> , 83, 299-309	136
1676	Gut microbiome composition is linked to whole grain-induced immunological improvements. <b>2013</b> , 7, 269-80	357
1675	<i>Yersinia pestis</i> infection and laboratory conditions alter flea-associated bacterial communities. <b>2013</b> , 7, 224-8	13
1674	Comparing metabolic functionalities, community structures, and dynamics of herbicide-degrading communities cultivated with different substrate concentrations. <b>2013</b> , 79, 367-75	28
1673	Effects of OTU clustering and PCR artifacts on microbial diversity estimates. <b>2013</b> , 65, 709-19	39
1672	Evidence of the megavirome in humans. <b>2013</b> , 57, 191-200	85
1671	In vitro characterization of the impact of selected dietary fibers on fecal microbiota composition and short chain fatty acid production. <b>2013</b> , 23, 74-81	162
1670	Host- and tissue-specificity of moss-associated <i>Galerina</i> and <i>Mycena</i> determined from amplicon pyrosequencing data. <b>2013</b> , 6, 179-186	21
1669	Substrate induced emergence of different active bacterial and archaeal assemblages during biomethane production. <b>2013</b> , 148, 517-24	23
1668	Richness and composition of sediment bacterial assemblages in an Atlantic port environment. <b>2013</b> , 452-453, 172-80	15
1667	Redox effects on the microbial degradation of refractory organic matter in marine sediments. <b>2013</b> , 121, 582-598	35
1666	Characterization of cecal microbiota of the emu ( <i>Dromaius novaehollandiae</i> ). <b>2013</b> , 166, 304-10	27
1665	The hologenomic basis of speciation: gut bacteria cause hybrid lethality in the genus <i>Nasonia</i> . <b>2013</b> , 341, 667-9	256
1664	Patterns and processes of microbial community assembly. <b>2013</b> , 77, 342-56	798
1663	The scaling of many-task computing approaches in python on cluster supercomputers. <b>2013</b> ,	8
1662	Phylogenetic detection of novel Cryptomycota in an Iowa (United States) aquifer and from previously collected marine and freshwater targeted high-throughput sequencing sets. <b>2013</b> , 15, 2333-41	33
1661	Leaf litter is the main driver for changes in bacterial community structures in the rhizosphere of ash and beech. <b>2013</b> , 72, 150-160	33

1660	Operating aerobic wastewater treatment at very short sludge ages enables treatment and energy recovery through anaerobic sludge digestion. <b>2013</b> , 47, 6546-57	92
1659	The effect of coal oxidation on methane production and microbial community structure in Powder River Basin coal. <b>2013</b> , 115, 71-78	47
1658	Influence of pretreated activated sludge for electricity generation in microbial fuel cell application. <b>2013</b> , 145, 90-6	91
1657	Bacterial communities in soil mimic patterns of vegetative succession and ecosystem climax but are resilient to change between seasons. <b>2013</b> , 57, 749-757	64
1656	Bacterial community diversity in a low-permeability oil reservoir and its potential for enhancing oil recovery. <b>2013</b> , 147, 110-116	30
1655	Soil pH drives the spatial distribution of bacterial communities along elevation on Changbai Mountain. <b>2013</b> , 57, 204-211	529
1654	Innate and adaptive immunity interact to quench microbiome flagellar motility in the gut. <b>2013</b> , 14, 571-81	236
1653	Establishing a relationship between bacteria in the human gut and complex regional pain syndrome. <b>2013</b> , 29, 62-69	14
1652	Fecal microbiome and volatile organic compound metabolome in obese humans with nonalcoholic fatty liver disease. <b>2013</b> , 11, 868-75.e1-3	423
1651	Spatial uniformity of microbial diversity in a continuous bioelectrochemical system. <b>2013</b> , 129, 599-605	33
1650	CO <sub>2</sub> -induced shift in microbial activity affects carbon trapping and water quality in anoxic bioreactors. <b>2013</b> , 122, 198-208	19
1649	The microbial content of raw and pasteurized cow milk as determined by molecular approaches. <b>2013</b> , 96, 4928-37	108
1648	Investigation of the koala ( <i>Phascolarctos cinereus</i> ) hindgut microbiome via 16S pyrosequencing. <b>2013</b> , 167, 554-64	37
1647	Sequencing ancient calcified dental plaque shows changes in oral microbiota with dietary shifts of the Neolithic and Industrial revolutions. <b>2013</b> , 45, 450-5, 455e1	366
1646	Chronic N-amended soils exhibit an altered bacterial community structure in Harvard Forest, MA, USA. <b>2013</b> , 83, 478-93	64
1645	Stool substitute transplant therapy for the eradication of <i>Clostridium difficile</i> infection: 'RePOOPulating' the gut. <b>2013</b> , 1, 3	503
1644	Deep sequencing of subseafloor eukaryotic rRNA reveals active Fungi across marine subsurface provinces. <b>2013</b> , 8, e56335	180
1643	<i>Propionibacterium acnes</i> strain populations in the human skin microbiome associated with acne. <b>2013</b> , 133, 2152-60	391

1642	A cornucopia of human polyomaviruses. <b>2013</b> , 11, 264-76	236
1641	Shifts in soil bacterial community after eight years of land-use change. <b>2013</b> , 36, 137-44	73
1640	Amplicon-pyrosequencing-based detection of compositional shifts in bryophyte-associated fungal communities along an elevation gradient. <b>2013</b> , 22, 368-83	48
1639	Immune status, antibiotic medication and pH are associated with changes in the stomach fluid microbiota. <b>2013</b> , 7, 1354-66	99
1638	Complex interactions among diet, gastrointestinal transit, and gut microbiota in humanized mice. <b>2013</b> , 144, 967-77	281
1637	Structure and functions of the bacterial microbiota of plants. <b>2013</b> , 64, 807-38	1618
1636	Life in the dark: metagenomic evidence that a microbial slime community is driven by inorganic nitrogen metabolism. <b>2013</b> , 7, 1227-36	40
1635	Exploring the bovine rumen bacterial community from birth to adulthood. <b>2013</b> , 7, 1069-79	480
1634	Fecal microbiota diversity in survivors of adolescent/young adult Hodgkin lymphoma: a study of twins. <b>2013</b> , 108, 1163-7	34
1633	The Healthy Twin Study, Korea updates: resources for omics and genome epidemiology studies. <b>2013</b> , 16, 241-5	34
1632	Microbial community evolution during simulated managed aquifer recharge in response to different biodegradable dissolved organic carbon (BDOC) concentrations. <b>2013</b> , 47, 2421-30	75
1631	A microbiology-based multi-parametric approach towards assessing biological stability in drinking water distribution networks. <b>2013</b> , 47, 3015-25	115
1630	Loss in microbial diversity affects nitrogen cycling in soil. <b>2013</b> , 7, 1609-19	404
1629	The microbiome extends to subepidermal compartments of normal skin. <b>2013</b> , 4, 1431	280
1628	Temporal variability in soil microbial communities across land-use types. <b>2013</b> , 7, 1641-50	299
1627	Association between living environment and human oral viral ecology. <b>2013</b> , 7, 1710-24	73
1626	Sediment microbial communities in Great Boiling Spring are controlled by temperature and distinct from water communities. <b>2013</b> , 7, 718-29	106
1625	The dynamic bacterial communities of a melting High Arctic glacier snowpack. <b>2013</b> , 7, 1814-26	104

1624	Molecular indicators of microbial diversity in oolitic sands of Highborne Cay, Bahamas. <b>2013</b> , 11, 234-51	33
1623	Low acetate concentrations favor polyphosphate-accumulating organisms over glycogen-accumulating organisms in enhanced biological phosphorus removal from wastewater. <b>2013</b> , 47, 3816-24	61
1622	Compression-based distance (CBD): a simple, rapid, and accurate method for microbiota composition comparison. <b>2013</b> , 14, 136	4
1621	Strong coupling of plant and fungal community structure across western Amazonian rainforests. <b>2013</b> , 7, 1852-61	235
1620	Testing three pipelines for 18S rDNA-based metabarcoding of soil faunal diversity. <b>2013</b> , 56, 73-81	20
1619	Phylogenetic beta diversity in bacterial assemblages across ecosystems: deterministic versus stochastic processes. <b>2013</b> , 7, 1310-21	352
1618	Phylogenetic analysis of nitrate- and sulfate-reducing bacteria in a hydrogen-fed biofilm. <b>2013</b> , 85, 158-67	35
1617	Quantifying sequence proportions in a DNA-based diet study using Ion Torrent amplicon sequencing: which counts count?. <b>2013</b> , 13, 620-33	142
1616	An altered gut microbiome profile in a child affected by Crohn's disease normalized after nutritional therapy. <b>2013</b> , 108, 851-2	49
1615	Ca. Nitrososphaera and Bradyrhizobium are inversely correlated and related to agricultural practices in long-term field experiments. <b>2013</b> , 4, 104	58
1614	Arsenite modifies structure of soil microbial communities and arsenite oxidization potential. <b>2013</b> , 84, 270-9	22
1613	The effect of chlortetracycline on faecal microbial populations in growing swine. <b>2013</b> , 1, 171-174	13
1612	Effects of multiple electron acceptors on microbial interactions in a hydrogen-based biofilm. <b>2013</b> , 47, 7396-403	43
1611	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
1610	Community transcriptomic assembly reveals microbes that contribute to deep-sea carbon and nitrogen cycling. <b>2013</b> , 7, 1962-73	82
1609	Diversity of human small intestinal Streptococcus and Veillonella populations. <b>2013</b> , 85, 376-88	90
1608	Changes in assembly processes in soil bacterial communities following a wildfire disturbance. <b>2013</b> , 7, 1102-11	239
1607	Bacterial community structure on two alpine debris-covered glaciers and biogeography of Polaromonas phylotypes. <b>2013</b> , 7, 1483-92	49

1606	Coral reef invertebrate microbiomes correlate with the presence of photosymbionts. <b>2013</b> , 7, 1452-8	105
1605	Impact of organosulfur content on diesel fuel stability and implications for carbon steel corrosion. <b>2013</b> , 47, 6052-62	21
1604	Innate lymphoid cells regulate CD4+ T-cell responses to intestinal commensal bacteria. <b>2013</b> , 498, 113-7	508
1603	Ancient T-independence of mucosal IgX/A: gut microbiota unaffected by larval thymectomy in <i>Xenopus laevis</i> . <b>2013</b> , 6, 358-68	39
1602	Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes. <b>2013</b> , 31, 533-8	869
1601	Phylogenetic and functional changes in the microbial community of long-term restored soils under semiarid climate. <b>2013</b> , 65, 12-21	68
1600	Severe plant invasions can increase mycorrhizal fungal abundance and diversity. <b>2013</b> , 7, 1424-33	136
1599	In situ chemistry and microbial community compositions in five deep-sea hydrothermal fluid samples from Irina II in the Logatchev field. <b>2013</b> , 15, 1551-60	36
1598	Bacterial abundance and composition in marine sediments beneath the Ross Ice Shelf, Antarctica. <b>2013</b> , 11, 377-95	30
1597	Impact of Mangrove Roots on Bacterial Composition. <b>2013</b> , 1081-1088	
1596	Bacterial communities established in bauxite residues with different restoration histories. <b>2013</b> , 47, 7110-9	52
1595	The discovery of stromatolites developing at 3570 m above sea level in a high-altitude volcanic lake Socompa, Argentinean Andes. <b>2013</b> , 8, e53497	89
1594	Life in the "plastisphere": microbial communities on plastic marine debris. <b>2013</b> , 47, 7137-46	1232
1593	Nutrient enrichment increased species richness of leaf litter fungal assemblages in a tropical forest. <b>2013</b> , 22, 2827-38	44
1592	Relative impacts of tillage, residue management and crop-rotation on soil bacterial communities in a semi-arid agroecosystem. <b>2013</b> , 65, 86-95	161
1591	Phylogenetic stratigraphy in the Guerrero Negro hypersaline microbial mat. <b>2013</b> , 7, 50-60	147
1590	Study of the viral and microbial communities associated with Crohn's disease: a metagenomic approach. <b>2013</b> , 4, e36	87
1589	Testing evolutionary models to explain the process of nucleotide substitution in gut bacterial 16S rRNA gene sequences. <b>2013</b> , 346, 97-104	3

1588	Fusobacterium is associated with colorectal adenomas. <b>2013</b> , 8, e53653	338
1587	A guide to enterotypes across the human body: meta-analysis of microbial community structures in human microbiome datasets. <b>2013</b> , 9, e1002863	359
1586	Changes in diversity, abundance, and structure of soil bacterial communities in Brazilian Savanna under different land use systems. <b>2013</b> , 66, 593-607	69
1585	Quantitatively different, yet qualitatively alike: a meta-analysis of the mouse core gut microbiome with a view towards the human gut microbiome. <b>2013</b> , 8, e62578	136
1584	Arabidopsis thaliana as Model for Studies on the Bacterial Root Microbiota. <b>2013</b> , 243-256	5
1583	Early diet impacts infant rhesus gut microbiome, immunity, and metabolism. <b>2013</b> , 12, 2833-45	72
1582	Bacterial colonization of Hydra hatchlings follows a robust temporal pattern. <b>2013</b> , 7, 781-90	71
1581	Microbial community adaptation to quaternary ammonium biocides as revealed by metagenomics. <b>2013</b> , 15, 2850-64	60
1580	Probiotic administration in congenital heart disease: a pilot study. <b>2013</b> , 33, 691-7	14
1579	454 pyrosequencing analyses of bacterial and archaeal richness in 21 full-scale biogas digesters. <b>2013</b> , 85, 612-26	478
1578	A metabolomic view of how the human gut microbiota impacts the host metabolome using humanized and gnotobiotic mice. <b>2013</b> , 7, 1933-43	222
1577	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
1576	Differences between aerobic and anaerobic degradation of microphytobenthic biofilm-derived organic matter within intertidal sediments. <b>2013</b> , 84, 495-509	46
1575	Uncovering symbiont-driven genetic diversity across North American pea aphids. <b>2013</b> , 22, 2045-59	151
1574	Improving diversity in cultures of bacteria from an extreme environment. <b>2013</b> , 59, 581-6	9
1573	Alterations in intestinal microbiota of elderly Irish subjects post-antibiotic therapy. <b>2013</b> , 68, 214-21	60
1572	Reliable, verifiable and efficient monitoring of biodiversity via metabarcoding. <b>2013</b> , 16, 1245-57	369
1571	Association of gut microbiota with post-operative clinical course in Crohn's disease. <b>2013</b> , 13, 131	63

1570	Bacterial diversity of the rock-water interface in an East Antarctic freshwater ecosystem, Lake Tawani(P)â 2013, 9, 4	19
1569	Changes in Soil Fungal Communities, Extracellular Enzyme Activities, and Litter Decomposition Across a Fire Chronosequence in Alaskan Boreal Forests. 2013, 16, 34-46	107
1568	The relative contribution of methanotrophs to microbial communities and carbon cycling in soil overlying a coal-bed methane seep. 2013, 84, 474-94	17
1567	Fungal community analysis by high-throughput sequencing of amplified markers--a user's guide. 2013, 199, 288-299	601
1566	Encyclopedia of Metagenomics. 2013, 1-11	1
1565	Transcriptional response of bathypelagic marine bacterioplankton to the Deepwater Horizon oil spill. 2013, 7, 2315-29	118
1564	Contemporary environmental variation determines microbial diversity patterns in acid mine drainage. 2013, 7, 1038-50	235
1563	Changes in bacterial diversity in response to dissolved organic matter supply in a continuous culture experiment. 2013, 69, 157-168	60
1562	Bacteriohopanepolyols in a stratified cyanobacterial mat from Kiritimati (Christmas Island, Kiribati). 2013, 55, 55-62	12
1561	Suppression of methanogenesis in cellulose-fed microbial fuel cells in relation to performance, metabolite formation, and microbial population. 2013, 129, 281-8	61
1560	Sterile paper points as a bacterial DNA-contamination source in microbiome profiles of clinical samples. 2013, 41, 1297-301	28
1559	Patient-specific analysis of periodontal and peri-implant microbiomes. 2013, 92, 168S-75S	117
1558	A single betaproteobacterium dominates the microbial community of the crambescidine-containing sponge <i>Crambe crambe</i> . 2013, 3, 2583	45
1557	Symbiotic prokaryotic communities from different populations of the giant barrel sponge, <i>Xestospongia muta</i> . 2013, 2, 938-52	31
1556	Gut microbiomes of Malawian twin pairs discordant for kwashiorkor. 2013, 339, 548-54	810
1555	Seasonal variability in bacterial and fungal diversity of the near-surface atmosphere. 2013, 47, 12097-106	269
1554	Probiotic dosing of <i>Ruminococcus flavefaciens</i> affects rumen microbiome structure and function in reindeer. 2013, 66, 840-9	13
1553	Outgrowth of the bacterial airway microbiome after rhinovirus exacerbation of chronic obstructive pulmonary disease. 2013, 188, 1224-31	262



1552	Gut microbiome perturbations induced by bacterial infection affect arsenic biotransformation. <b>2013</b> , 26, 1893-903	57
1551	Ocean acidification and rising temperatures may increase biofilm primary productivity but decrease grazer consumption. <b>2013</b> , 368, 20120438	67
1550	Using a two-stage hydrogen-based membrane biofilm reactor (MBfR) to achieve complete perchlorate reduction in the presence of nitrate and sulfate. <b>2013</b> , 47, 1565-72	66
1549	Abundance and Diversity of Ammonia-Oxidizing Bacteria and Archaea in Cold Springs on the Qinghai-Tibet Plateau. <b>2013</b> , 30, 530-539	7
1548	High-performance computing and the cloud. <b>2013</b> , 19, 52-57	3
1547	Monotonous diets protect against acute colitis in mice: epidemiologic and therapeutic implications. <b>2013</b> , 56, 544-50	15
1546	Standard methods for research on <i>Apis mellifera</i> gut symbionts. <b>2013</b> , 52, 1-24	62
1545	Widespread colonization of the lung by <i>Tropheryma whippelii</i> in HIV infection. <b>2013</b> , 187, 1110-7	140
1544	Male circumcision significantly reduces prevalence and load of genital anaerobic bacteria. <b>2013</b> , 4, e00076	81
1543	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
1542	Impact of <i>Azospirillum</i> sp. B510 inoculation on rice-associated bacterial communities in a paddy field. <b>2013</b> , 28, 487-90	21
1541	Bacterial community response to petroleum hydrocarbon amendments in freshwater, marine, and hypersaline water-containing microcosms. <b>2013</b> , 79, 5927-35	75
1540	Elevated ground-level O <sub>3</sub> negatively influences paddy methanogenic archaeal community. <b>2013</b> , 3, 3193	27
1539	454 Pyrosequencing Analysis of Fungal Assemblages from Geographically Distant, Disparate Soils Reveals Spatial Patterning and a Core Mycobiome. <b>2013</b> , 5, 73-98	58
1538	Seasonal restructuring of the ground squirrel gut microbiota over the annual hibernation cycle. <b>2013</b> , 304, R33-42	103
1537	Insights into fungal communities in composts revealed by 454-pyrosequencing: implications for human health and safety. <b>2013</b> , 4, 164	60
1536	Analyzing spatial patterns linked to the ecology of herbivores and their natural enemies in the soil. <b>2013</b> , 4, 378	16
1535	FunFrame: functional gene ecological analysis pipeline. <b>2013</b> , 29, 1212-4	10

1534	Potentiostatically Poised Electrodes Mimic Iron Oxide and Interact with Soil Microbial Communities to Alter the Biogeochemistry of Arctic Peat Soils. <b>2013</b> , 3, 318-336	8
1533	The role of microbial communities in parturition: is there evidence of association with preterm birth and perinatal morbidity and mortality?. <b>2013</b> , 30, 613-24	28
1532	Smoking cessation induces profound changes in the composition of the intestinal microbiota in humans. <b>2013</b> , 8, e59260	245
1531	Effects of diet on resource utilization by a model human gut microbiota containing <i>Bacteroides cellulosilyticus</i> WH2, a symbiont with an extensive glycobiome. <b>2013</b> , 11, e1001637	184
1530	Laxative treatment with polyethylene glycol decreases microbial primary bile salt dehydroxylation and lipid metabolism in the intestine of rats. <b>2013</b> , 305, G474-82	8
1529	Scrapheap challenge: a novel bulk-bone metabarcoding method to investigate ancient DNA in faunal assemblages. <b>2013</b> , 3, 3371	53
1528	The individual-specific and diverse nature of the preterm infant microbiota. <b>2013</b> , 98, F334-40	83
1527	Surface microbes in the neonatal intensive care unit: changes with routine cleaning and over time. <b>2013</b> , 51, 2617-24	55
1526	Molecular diversity of Bacteroidales in fecal and environmental samples and swine-associated subpopulations. <b>2013</b> , 79, 816-24	7
1525	Abundant DNase I-sensitive bacterial DNA in healthy porcine lungs and its implications for the lung microbiome. <b>2013</b> , 79, 5936-41	33
1524	Conserved shifts in the gut microbiota due to gastric bypass reduce host weight and adiposity. <b>2013</b> , 5, 178ra41	686
1523	Quantitation and composition of cutaneous microbiota in diabetic and nondiabetic men. <b>2013</b> , 207, 1105-14	63
1522	Impact of long-term diesel contamination on soil microbial community structure. <b>2013</b> , 79, 619-30	238
1521	Improved inference of taxonomic richness from environmental DNA. <b>2013</b> , 8, e71974	30
1520	Insights into foraminiferal influences on microfabrics of microbialites at Highborne Cay, Bahamas. <b>2013</b> , 110, 9830-4	32
1519	Quality-based guidance for exploratory dimensionality reduction. <b>2013</b> , 12, 44-64	13
1518	Microbial ecology dynamics during rye and wheat sourdough preparation. <b>2013</b> , 79, 7827-36	136
1517	Sympatric chimpanzees and gorillas harbor convergent gut microbial communities. <b>2013</b> , 23, 1715-20	106

1516	Simultaneous amplicon sequencing to explore co-occurrence patterns of bacterial, archaeal and eukaryotic microorganisms in rumen microbial communities. <b>2013</b> , 8, e47879	233
1515	Atomic emission spectroscopic characteristics of argon plasma in a pulsed discharge nozzle ion source. <b>2013</b> , T156, 014076	1
1514	Large cryoconite aggregates on a Svalbard glacier support a diverse microbial community including ammonia-oxidizing archaea. <b>2013</b> , 8, 035044	40
1513	Forest Age and Plant Species Composition Determine the Soil Fungal Community Composition in a Chinese Subtropical Forest. <b>2013</b> , 8, e66829	37
1512	Analytical tools and databases for metagenomics in the next-generation sequencing era. <b>2013</b> , 11, 102-13	98
1511	Species identification and profiling of complex microbial communities using shotgun Illumina sequencing of 16S rRNA amplicon sequences. <b>2013</b> , 8, e60811	72
1510	Human gut microbiota changes reveal the progression of glucose intolerance. <b>2013</b> , 8, e71108	448
1509	FunGene: the functional gene pipeline and repository. <b>2013</b> , 4, 291	368
1508	Linking microbial community structure to function in representative simulated systems. <b>2013</b> , 79, 2552-9	15
1507	Microbial diversity and structure are drivers of the biological barrier effect against <i>Listeria monocytogenes</i> in soil. <b>2013</b> , 8, e76991	64
1506	Ion Torrent PGM as tool for fungal community analysis: a case study of endophytes in <i>Eucalyptus grandis</i> reveals high taxonomic diversity. <b>2013</b> , 8, e81718	69
1505	Distinct distal gut microbiome diversity and composition in healthy children from Bangladesh and the United States. <b>2013</b> , 8, e53838	224
1504	Fungi of the murine gut: episodic variation and proliferation during antibiotic treatment. <b>2013</b> , 8, e71806	143
1503	Intestinal microbial ecology and environmental factors affecting necrotizing enterocolitis. <b>2013</b> , 8, e83304	125
1502	Structural and functional variation in soil fungal communities associated with litter bags containing maize leaf. <b>2013</b> , 84, 519-31	48
1501	Intestinal bacteria modify lymphoma incidence and latency by affecting systemic inflammatory state, oxidative stress, and leukocyte genotoxicity. <b>2013</b> , 73, 4222-32	48
1500	Unexpected diversity during community succession in the apple flower microbiome. <b>2013</b> , 4,	157
1499	Facility-specific "house" microbiome drives microbial landscapes of artisan cheesemaking plants. <b>2013</b> , 79, 5214-23	170

1498	Quantification of endospore-forming firmicutes by quantitative PCR with the functional gene spo0A. <b>2013</b> , 79, 5302-12	32
1497	Bacterial Infections across the Ants: Frequency and Prevalence of Wolbachia, Spiroplasma, and Asaia. <b>2013</b> , 2013, 1-11	32
1496	IL-22 deficiency alters colonic microbiota to be transmissible and colitogenic. <b>2013</b> , 190, 5306-12	171
1495	Mineralogical Study of a Biologically-Based Treatment System That Removes Arsenic, Zinc and Copper from Landfill Leachate. <b>2013</b> , 3, 427-449	9
1494	Distribution-based clustering: using ecology to refine the operational taxonomic unit. <b>2013</b> , 79, 6593-603	102
1493	Heterotrophic protists in hypersaline microbial mats and deep hypersaline basin water columns. <b>2013</b> , 3, 346-62	18
1492	Unique vaginal microbiota that includes an unknown Mycoplasma-like organism is associated with Trichomonas vaginalis infection. <b>2013</b> , 207, 1922-31	53
1491	Genomic and physiological characterization of the chromate-reducing, aquifer-derived Firmicute Pelosinus sp. strain HCF1. <b>2013</b> , 79, 63-73	39
1490	Dietary format alters fecal bacterial populations in the domestic cat (Felis catus). <b>2013</b> , 2, 173-81	45
1489	Land coverage influences the bacterial community composition in the critical zone of a sub-Arctic basaltic environment. <b>2013</b> , 86, 381-93	14
1488	Effects of amoxicillin treatment on the salivary microbiota in children with acute otitis media. <b>2013</b> , 19, E335-42	27
1487	Altered enteric microbiota ecology in interleukin 10-deficient mice during development and progression of intestinal inflammation. <b>2013</b> , 4, 316-24	91
1486	Habitat- and host-related variation in sponge bacterial symbiont communities in Indonesian waters. <b>2013</b> , 85, 465-82	73
1485	Analysis of the bacterial communities associated with two ant-plant symbioses. <b>2013</b> , 2, 276-83	28
1484	A novel nonwoven hybrid bioreactor (NWHBR) for enhancing simultaneous nitrification and denitrification. <b>2013</b> , 110, 1903-12	18
1483	Restructuring of the amphibian gut microbiota through metamorphosis. <b>2013</b> , 5, 899-903	87
1482	Minor impact of ocean acidification to the composition of the active microbial community in an Arctic sediment. <b>2013</b> , 5, 851-60	19
1481	Complement modulates the cutaneous microbiome and inflammatory milieu. <b>2013</b> , 110, 15061-6	100

1480	Streptomycin application has no detectable effect on bacterial community structure in apple orchard soil. <b>2013</b> , 79, 6617-25	27
1479	Future reef decalcification under a business-as-usual CO2 emission scenario. <b>2013</b> , 110, 15342-7	131
1478	Actinobacteria as essential symbionts in firebugs and cotton stainers (Hemiptera, Pyrrhocoridae). <b>2013</b> , 15, 1956-68	85
1477	Exploring the maize rhizosphere microbiome in the field: A glimpse into a highly complex system. <b>2013</b> , 6, e25177	21
1476	Gut microbial diversity is reduced and is associated with colonic inflammation in a piglet model of short bowel syndrome. <b>2013</b> , 4, 212-21	65
1475	Microbiome of the upper troposphere: species composition and prevalence, effects of tropical storms, and atmospheric implications. <b>2013</b> , 110, 2575-80	297
1474	Evidence for hydrogen oxidation and metabolic plasticity in widespread deep-sea sulfur-oxidizing bacteria. <b>2013</b> , 110, 330-5	130
1473	Oligotyping: Differentiating between closely related microbial taxa using 16S rRNA gene data. <b>2013</b> , 4, 1111	407
1472	Culture-dependent and independent approaches for identifying novel halogenases encoded by <i>Crambe crambe</i> (marine sponge) microbiota. <b>2013</b> , 3, 2780	31
1471	Metatranscriptomics reveal differences in in situ energy and nitrogen metabolism among hydrothermal vent snail symbionts. <b>2013</b> , 7, 1556-67	53
1470	Surprisingly extensive mixed phylogenetic and ecological signals among bacterial Operational Taxonomic Units. <b>2013</b> , 41, 5175-88	81
1469	Collaborative cloud-enabled tools allow rapid, reproducible biological insights. <b>2013</b> , 7, 461-4	14
1468	Biphasic assembly of the murine intestinal microbiota during early development. <b>2013</b> , 7, 1112-5	100
1467	Distinctive microbial community structure in highly stratified deep-sea brine water columns. <b>2013</b> , 79, 3425-37	45
1466	Medical therapy reduces microbiota diversity and evenness in surgically recalcitrant chronic rhinosinusitis. <b>2013</b> , 3, 775-81	58
1465	Evidence for a persistent microbial seed bank throughout the global ocean. <b>2013</b> , 110, 4651-5	158
1464	Distinct antimicrobial peptide expression determines host species-specific bacterial associations. <b>2013</b> , 110, E3730-8	212
1463	Microbiome assembly across multiple body sites in low-birthweight infants. <b>2013</b> , 4, e00782-13	103

1462	Aquacultured rainbow trout ( <i>Oncorhynchus mykiss</i> ) possess a large core intestinal microbiota that is resistant to variation in diet and rearing density. <b>2013</b> , 79, 4974-84	137
1461	Impact of chloramination on the development of laboratory-grown biofilms fed with filter-pretreated groundwater. <b>2013</b> , 28, 50-7	21
1460	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
1459	VARIABLE SELECTION FOR SPARSE DIRICHLET-MULTINOMIAL REGRESSION WITH AN APPLICATION TO MICROBIOME DATA ANALYSIS. <b>2013</b> , 7,	129
1458	Identification of Norovirus in Sewage by Using Pyrosequencing. <b>2013</b> , 69, III_639-III_646	
1457	Different bacterial communities in ectomycorrhizae and surrounding soil. <b>2013</b> , 3, 3471	62
1456	Gut microbiota dysbiosis and bacterial community assembly associated with cholesterol gallstones in large-scale study. <b>2013</b> , 14, 669	99
1455	Alteration of intestinal dysbiosis by fecal microbiota transplantation does not induce remission in patients with chronic active ulcerative colitis. <b>2013</b> , 19, 2155-65	183
1454	Histamine-2 receptor blockers alter the fecal microbiota in premature infants. <b>2013</b> , 56, 397-400	80
1453	Metabolomic phenotyping validates the infant rhesus monkey as a model of human infant metabolism. <b>2013</b> , 56, 355-63	46
1452	Deciphering the presence and activity of fungal communities in marine sediments using a model estuarine system. <b>2013</b> , 70, 45-62	40
1451	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
1450	Sputum microbiota associated with new, recurrent and treatment failure tuberculosis. <b>2013</b> , 8, e83445	63
1449	Identification of differential duodenal gene expression levels and microbiota abundance correlated with differences in energy utilisation in chickens. <b>2013</b> , 53, 1269	17
1448	Bacterial community structure in High-Arctic snow and freshwater as revealed by pyrosequencing of 16S rRNA genes and cultivation. <b>2013</b> , 32, 17390	55
1447	Colonization patterns of soil microbial communities in the Atacama Desert. <b>2013</b> , 1, 28	132
1446	Bacterial population dynamics in a laboratory activated sludge reactor monitored by pyrosequencing of 16S rRNA. <b>2013</b> , 28, 65-70	23
1445	Comprehensive phylogenetic diversity of [FeFe]-hydrogenase genes in termite gut microbiota. <b>2013</b> , 28, 491-4	7

1444	Soil bacterial community structure in five tropical forests in Malaysia and one temperate forest in Japan revealed by pyrosequencing analyses of 16S rRNA gene sequence variation. <b>2013</b> , 88, 93-103	26
1443	Up to Species-level Community Analysis of Human Gut Microbiota by 16S rRNA Amplicon Pyrosequencing. <b>2013</b> , 32, 69-76	12
1442	Culture-independence for surveillance and epidemiology. <b>2013</b> , 2, 556-70	4
1441	Assessment of Fungal Diversity in the Environment using Metagenomics:a Decade in Review. <b>2013</b> , 03,	18
1440	Arctic gypsum endoliths: a biogeochemical characterization of a viable and active microbial community. <b>2013</b> , 10, 7661-7675	19
1439	Targeting the microbiota to address diet-induced obesity: a time dependent challenge. <b>2013</b> , 8, e65790	103
1438	Highly variable microbiota development in the chicken gastrointestinal tract. <b>2013</b> , 8, e84290	155
1437	Monitoring of ribosomal RNA in the supernatant of activated sludge. <b>2013</b> , 69, III_231-III_239	
1436	A comprehensive census of microbial diversity in hot springs of Tengchong, Yunnan Province China using 16S rRNA gene pyrosequencing. <b>2013</b> , 8, e53350	140
1435	Stimulatory effect of xenobiotics on oxidative electron transport of chemolithotrophic nitrifying bacteria used as biosensing element. <b>2013</b> , 8, e53484	3
1434	Sputum microbiota in tuberculosis as revealed by 16S rRNA pyrosequencing. <b>2013</b> , 8, e54574	67
1433	Bacterial diversity in two Neonatal Intensive Care Units (NICUs). <b>2013</b> , 8, e54703	97
1432	Comparison of the distal gut microbiota from people and animals in Africa. <b>2013</b> , 8, e54783	52
1431	The poultry-associated microbiome: network analysis and farm-to-fork characterizations. <b>2013</b> , 8, e57190	85
1430	Analysis of metagenomic data containing high biodiversity levels. <b>2013</b> , 8, e58118	10
1429	Bacterial communities associated with the surfaces of fresh fruits and vegetables. <b>2013</b> , 8, e59310	259
1428	Pyrosequencing reveals high-temperature cellulolytic microbial consortia in Great Boiling Spring after in situ lignocellulose enrichment. <b>2013</b> , 8, e59927	33
1427	Assessing the consequences of denoising marker-based metagenomic data. <b>2013</b> , 8, e60458	49

1426	phyloseq: an R package for reproducible interactive analysis and graphics of microbiome census data. <b>2013</b> , 8, e61217	6869
1425	A cross-taxon analysis of insect-associated bacterial diversity. <b>2013</b> , 8, e61218	105
1424	Shedding light on the microbial community of the macropod foregut using 454-amplicon pyrosequencing. <b>2013</b> , 8, e61463	25
1423	Discovery of trypanosomatid parasites in globally distributed <i>Drosophila</i> species. <b>2013</b> , 8, e61937	16
1422	Association of the vaginal microbiota with human papillomavirus infection in a Korean twin cohort. <b>2013</b> , 8, e63514	163
1421	Home life: factors structuring the bacterial diversity found within and between homes. <b>2013</b> , 8, e64133	213
1420	Gut microbiota contributes to the growth of fast-growing transgenic common carp ( <i>Cyprinus carpio</i> L.). <b>2013</b> , 8, e64577	71
1419	Archaea and fungi of the human gut microbiome: correlations with diet and bacterial residents. <b>2013</b> , 8, e66019	447
1418	Factors Controlling Soil Microbial Biomass and Bacterial Diversity and Community Composition in a Cold Desert Ecosystem: Role of Geographic Scale. <b>2013</b> , 8, e66103	75
1417	Monitoring Seasonal Changes in Winery-Resident Microbiota. <b>2013</b> , 8, e66437	131
1416	Specialized Hydrocarbonoclastic Bacteria Prevailing in Seawater around a Port in the Strait of Malacca. <b>2013</b> , 8, e66594	18
1415	Phylogenetic analysis of a microbialite-forming microbial mat from a hypersaline lake of the Kiritimati atoll, Central Pacific. <b>2013</b> , 8, e66662	111
1414	The Ecology of Microbial Communities Associated with <i>Macrocystis pyrifera</i> . <b>2013</b> , 8, e67480	47
1413	Ectomycorrhizal-dominated boreal and tropical forests have distinct fungal communities, but analogous spatial patterns across soil horizons. <b>2013</b> , 8, e68278	53
1412	Season, irrigation, leaf age, and <i>Escherichia coli</i> inoculation influence the bacterial diversity in the lettuce phyllosphere. <b>2013</b> , 8, e68642	96
1411	Prospecting environmental mycobacteria: combined molecular approaches reveal unprecedented diversity. <b>2013</b> , 8, e68648	29
1410	Assessing the fecal microbiota: an optimized ion torrent 16S rRNA gene-based analysis protocol. <b>2013</b> , 8, e68739	205
1409	Light structures phototroph, bacterial and fungal communities at the soil surface. <b>2013</b> , 8, e69048	16



1408	Characterization of the upper respiratory tract microbiomes of patients with pandemic H1N1 influenza. <b>2013</b> , 8, e69559	50
1407	Long-term temporal analysis of the human fecal microbiota revealed a stable core of dominant bacterial species. <b>2013</b> , 8, e69621	115
1406	Exploring the sources of bacterial spoilers in beefsteaks by culture-independent high-throughput sequencing. <b>2013</b> , 8, e70222	141
1405	The effect of primer choice and short read sequences on the outcome of 16S rRNA gene based diversity studies. <b>2013</b> , 8, e71360	90
1404	Bacterial communities associated with culex mosquito larvae and two emergent aquatic plants of bioremediation importance. <b>2013</b> , 8, e72522	52
1403	Impact of ileocecal resection and concomitant antibiotics on the microbiome of the murine jejunum and colon. <b>2013</b> , 8, e73140	43
1402	Development of the preterm gut microbiome in twins at risk of necrotising enterocolitis and sepsis. <b>2013</b> , 8, e73465	101
1401	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
1400	The effect of dietary supplementation with spent cider yeast on the Swine distal gut microbiome. <b>2013</b> , 8, e75714	30
1399	Soil-borne bacterial structure and diversity does not reflect community activity in Pampa biome. <b>2013</b> , 8, e76465	39
1398	An in vitro model of the horse gut microbiome enables identification of lactate-utilizing bacteria that differentially respond to starch induction. <b>2013</b> , 8, e77599	54
1397	Distinct phyllosphere bacterial communities on Arabidopsis wax mutant leaves. <b>2013</b> , 8, e78613	59
1396	Changes in bacterial and fungal communities across compost recipes, preparation methods, and composting times. <b>2013</b> , 8, e79512	193
1395	Differential effects of antibiotic therapy on the structure and function of human gut microbiota. <b>2013</b> , 8, e80201	132
1394	Characterization of the vaginal microbiota among sexual risk behavior groups of women with bacterial vaginosis. <b>2013</b> , 8, e80254	20
1393	Post-weaning diet affects faecal microbial composition but not selected adipose gene expression in the cat ( <i>Felis catus</i> ). <b>2013</b> , 8, e80992	13
1392	The enterocyte-associated intestinal microbiota of breast-fed infants and adults responds differently to a TNF- $\alpha$ -mediated pro-inflammatory stimulus. <b>2013</b> , 8, e81762	16
1391	Adlie penguin population diet monitoring by analysis of food DNA in scats. <b>2013</b> , 8, e82227	84

1390	Hexavalent chromium reduction under fermentative conditions with lactate stimulated native microbial communities. <b>2013</b> , 8, e83909	23
1389	Archaea appear to dominate the microbiome of <i>Inflatella pellicula</i> deep sea sponges. <b>2013</b> , 8, e84438	35
1388	Effect of DNA extraction methods and sampling techniques on the apparent structure of cow and sheep rumen microbial communities. <b>2013</b> , 8, e74787	208
1387	Reduced incidence of <i>Prevotella</i> and other fermenters in intestinal microflora of autistic children. <b>2013</b> , 8, e68322	537
1386	Metagenomic evidence for sulfur lithotrophy by Epsilonproteobacteria as the major energy source for primary productivity in a sub-aerial arctic glacial deposit, Borup Fiord Pass. <b>2013</b> , 4, 63	26
1385	Dinitrogen fixation in aphotic oxygenated marine environments. <b>2013</b> , 4, 227	65
1384	Prerequisites for amplicon pyrosequencing of microbial methanol utilizers in the environment. <b>2013</b> , 4, 268	26
1383	Microbial diversity and methanogenic activity of Antrim Shale formation waters from recently fractured wells. <b>2013</b> , 4, 367	63
1382	Vertical transmission explains the specific <i>Burkholderia</i> pattern in <i>Sphagnum</i> mosses at multi-geographic scale. <b>2013</b> , 4, 394	34
1381	Effect of Different Feed Structures and Bedding on the Horizontal Spread of <i>Campylobacter jejuni</i> within Broiler Flocks. <b>2013</b> , 3, 741-760	7
1380	Introduction of <i>Aureobasidium pullulans</i> to the Phyllosphere of Organically Grown Strawberries with Focus on Its Establishment and Interactions with the Resident Microbiome. <b>2013</b> , 3, 704-731	19
1379	Cohabiting family members share microbiota with one another and with their dogs. <b>2013</b> , 2, e00458	616
1378	Microbial diversity and biochemical potential encoded by thermal spring metagenomes derived from the Kamchatka Peninsula. <b>2013</b> , 2013, 136714	56
1377	Ocean acidification shows negligible impacts on high-latitude bacterial community structure in coastal pelagic mesocosms. <b>2013</b> , 10, 555-566	40
1376	Investigation of Hydrogen Sulfide Production in a Polluted Estuary by Using a Vertical Column Simulator. <b>2013</b> , 46, 359-366	
1375	Aerosol <i>Mycobacterium tuberculosis</i> infection causes rapid loss of diversity in gut microbiota. <b>2014</b> , 9, e97048	85
1374	Changes in abundance of oral microbiota associated with oral cancer. <b>2014</b> , 9, e98741	197
1373	Free glycogen in vaginal fluids is associated with <i>Lactobacillus</i> colonization and low vaginal pH. <b>2014</b> , 9, e102467	113

1372	Strengths and limitations of 16S rRNA gene amplicon sequencing in revealing temporal microbial community dynamics. <b>2014</b> , 9, e93827	323
1371	Assessment of helminth biodiversity in wild rats using 18S rDNA based metagenomics. <b>2014</b> , 9, e110769	35
1370	Structure, composition and metagenomic profile of soil microbiomes associated to agricultural land use and tillage systems in Argentine Pampas. <b>2014</b> , 9, e99949	129
1369	Microbial communities of three sympatric Australian stingless bee species. <b>2014</b> , 9, e105718	31
1368	The skin microbiome in healthy and allergic dogs. <b>2014</b> , 9, e83197	125
1367	Recruiting human microbiome shotgun data to site-specific reference genomes. <b>2014</b> , 9, e84963	4
1366	Altered mucus glycosylation in core 1 O-glycan-deficient mice affects microbiota composition and intestinal architecture. <b>2014</b> , 9, e85254	89
1365	Potential role of the bovine rumen microbiome in modulating milk composition and feed efficiency. <b>2014</b> , 9, e85423	274
1364	Saliva from obese individuals suppresses the release of aroma compounds from wine. <b>2014</b> , 9, e85611	70
1363	In vivo Pyro-SIP assessing active gut microbiota of the cotton leafworm, <i>Spodoptera littoralis</i> . <b>2014</b> , 9, e85948	54
1362	Application of microarray and functional-based screening methods for the detection of antimicrobial resistance genes in the microbiomes of healthy humans. <b>2014</b> , 9, e86428	45
1361	The personal human oral microbiome obscures the effects of treatment on periodontal disease. <b>2014</b> , 9, e86708	66
1360	Polyphasic analysis of a middle ages coprolite microbiota, Belgium. <b>2014</b> , 9, e88376	34
1359	Optimal eukaryotic 18S and universal 16S/18S ribosomal RNA primers and their application in a study of symbiosis. <b>2014</b> , 9, e90053	64
1358	Seasonal variation in human gut microbiome composition. <b>2014</b> , 9, e90731	179
1357	Redefining the human oral mycobiome with improved practices in amplicon-based taxonomy: discovery of <i>Malassezia</i> as a prominent commensal. <b>2014</b> , 9, e90899	154
1356	Fecal microbial composition of ulcerative colitis and Crohn's disease patients in remission and subsequent exacerbation. <b>2014</b> , 9, e90981	76
1355	Airborne bacterial communities in residences: similarities and differences with fungi. <b>2014</b> , 9, e91283	99

1354	Relationship between the rumen microbiome and residual feed intake-efficiency of Brahman bulls stocked on bermudagrass pastures. <b>2014</b> , 9, e91864	68
1353	The gut of geographically disparate <i>Ciona intestinalis</i> harbors a core microbiota. <b>2014</b> , 9, e93386	78
1352	Toward understanding the dynamics of microbial communities in an estuarine system. <b>2014</b> , 9, e94449	19
1351	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
1350	The gut microbial community of Midas cichlid fish in repeatedly evolved limnetic-benthic species pairs. <b>2014</b> , 9, e95027	41
1349	Short-term effect of antibiotics on human gut microbiota. <b>2014</b> , 9, e95476	199
1348	Arbuscular mycorrhizal fungi associated with the olive crop across the Andalusian landscape: factors driving community differentiation. <b>2014</b> , 9, e96397	24
1347	Understanding cultivar-specificity and soil determinants of the cannabis microbiome. <b>2014</b> , 9, e99641	45
1346	Community shifts in the surface microbiomes of the coral <i>Porites astreoides</i> with unusual lesions. <b>2014</b> , 9, e100316	72
1345	Geosphere-biosphere interactions in bio-activity volcanic lakes: evidences from Hule and Rõ Cuarto (Costa Rica). <b>2014</b> , 9, e102456	13
1344	Nutrient addition dramatically accelerates microbial community succession. <b>2014</b> , 9, e102609	69
1343	Improved yield of high molecular weight DNA coincides with increased microbial diversity access from iron oxide cemented sub-surface clay environments. <b>2014</b> , 9, e102826	18
1342	Two different bacterial community types are linked with the low-methane emission trait in sheep. <b>2014</b> , 9, e103171	145
1341	Comparison of the rhizosphere bacterial communities of Zigongdongdou soybean and a high-methionine transgenic line of this cultivar. <b>2014</b> , 9, e103343	23
1340	The colonization dynamics of the gut microbiota in tilapia larvae. <b>2014</b> , 9, e103641	53
1339	Characterization of microbiota composition and presence of selected antibiotic resistance genes in carriage water of ornamental fish. <b>2014</b> , 9, e103865	28
1338	Differential responses of cecal microbiota to fishmeal, <i>Eimeria</i> and <i>Clostridium perfringens</i> in a necrotic enteritis challenge model in chickens. <b>2014</b> , 9, e104739	110
1337	Microbial community structure of relict niter-beds previously used for saltpeter production. <b>2014</b> , 9, e104752	4

1336	Diversity and community composition of methanogenic archaea in the rumen of Scottish upland sheep assessed by different methods. <b>2014, 9, e106491</b>	22
1335	<i>Helicobacter hepaticus</i> infection promotes hepatitis and preneoplastic foci in farnesoid X receptor (FXR) deficient mice. <b>2014, 9, e106764</b>	11
1334	Paleomicrobiology: revealing fecal microbiomes of ancient indigenous cultures. <b>2014, 9, e106833</b>	47
1333	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
1332	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
1331	Faecal microbiota of cats with insulin-treated diabetes mellitus. <b>2014, 9, e108729</b>	20
1330	Comparing bacterial community composition of healthy and dark spot-affected <i>Siderastrea siderea</i> in Florida and the Caribbean. <b>2014, 9, e108767</b>	18
1329	Biogeochemical typing of paddy field by a data-driven approach revealing sub-systems within a complex environment--a pipeline to filtrate, organize and frame massive dataset from multi-omics analyses. <b>2014, 9, e110723</b>	21
1328	Illumina amplicon sequencing of 16S rRNA tag reveals bacterial community development in the rhizosphere of apple nurseries at a replant disease site and a new planting site. <b>2014, 9, e111744</b>	70
1327	Relationships between bacterial community composition, functional trait composition and functioning are context dependent--but what is the context?. <b>2014, 9, e112409</b>	2
1326	Faecal microbiota of forage-fed horses in New Zealand and the population dynamics of microbial communities following dietary change. <b>2014, 9, e112846</b>	79
1325	Maternal obesity is associated with alterations in the gut microbiome in toddlers. <b>2014, 9, e113026</b>	112
1324	Early canine plaque biofilms: characterization of key bacterial interactions involved in initial colonization of enamel. <b>2014, 9, e113744</b>	43
1323	Bacteria and methanogens differ along the gastrointestinal tract of Chinese roe deer ( <i>Capreolus pygargus</i> ). <b>2014, 9, e114513</b>	37
1322	Diversity, distribution and hydrocarbon biodegradation capabilities of microbial communities in oil-contaminated cyanobacterial mats from a constructed wetland. <b>2014, 9, e114570</b>	41
1321	IM-TORNADO: a tool for comparison of 16S reads from paired-end libraries. <b>2014, 9, e114804</b>	76
1320	Succession and replacement of bacterial populations in the caecum of egg laying hens over their whole life. <b>2014, 9, e115142</b>	99
1319	The antipsychotic olanzapine interacts with the gut microbiome to cause weight gain in mouse. <b>2014, 9, e115225</b>	97

1318	Investigation of bacterial diversity in the feces of cattle fed different diets. <b>2014</b> , 92, 683-94	99
1317	Temporal dynamics in the ruminal microbiome of dairy cows during the transition period. <b>2014</b> , 92, 4014-22	64
1316	Pyrosequencing analysis of the microbial diversity of airag, khoormog and tarag, traditional fermented dairy products of mongolia. <b>2014</b> , 33, 53-64	38
1315	Biodegradation Potential of Organically Enriched Sediments under Sulfate- and Iron-Reducing Conditions as Revealed by the 16S rRNA Deep Sequencing. <b>2014</b> , 12, 357-366	18
1314	Living at the Limits: Evidence for Microbial Eukaryotes Thriving under Pressure in Deep Anoxic, Hypersaline Habitats. <b>2014</b> , 2014, 1-9	15
1313	An antimethanogenic nutritional intervention in early life of ruminants modifies ruminal colonization by Archaea. <b>2014</b> , 2014, 841463	49
1312	Effect of an oxygenating agent on oral bacteria in vitro and on dental plaque composition in healthy young adults. <b>2014</b> , 4, 95	10
1311	Zooplankton diversity across three Red Sea reefs using pyrosequencing. <b>2014</b> , 1,	31
1310	Potential benefits of the application of yeast starters in table olive processing. <b>2012</b> , 5, 34	93
1309	Fermentation couples Chloroflexi and sulfate-reducing bacteria to Cyanobacteria in hypersaline microbial mats. <b>2014</b> , 5, 61	43
1308	Assessment of the Deepwater Horizon oil spill impact on Gulf coast microbial communities. <b>2014</b> , 5, 130	128
1307	The impact of the pathogen <i>Rhizoctonia solani</i> and its beneficial counterpart <i>Bacillus amyloliquefaciens</i> on the indigenous lettuce microbiome. <b>2014</b> , 5, 175	96
1306	<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
1305	Structural and functional changes in the gut microbiota associated to <i>Clostridium difficile</i> infection. <b>2014</b> , 5, 335	65
1304	Development of aminoglycoside and $\beta$ -lactamase resistance among intestinal microbiota of swine treated with lincomycin, chlortetracycline, and amoxicillin. <b>2014</b> , 5, 580	22
1303	Two distinct microbial communities revealed in the sponge <i>Cinachyrella</i> . <b>2014</b> , 5, 581	27
1302	Microbiome associations of therapeutic enteral nutrition. <b>2014</b> , 6, 5298-311	9
1301	Evaluation of automated ribosomal intergenic spacer analysis for bacterial fingerprinting of rumen microbiome compared to pyrosequencing technology. <b>2014</b> , 3, 109-20	19

1300	High-Throughput Sequencing, a Versatile Weapon to Support Genome-Based Diagnosis in Infectious Diseases: Applications to Clinical Bacteriology. <b>2014</b> , 3, 258-79	19
1299	Bacterial pathogens associated with hidradenitis suppurativa, France. <b>2014</b> , 20, 1990-8	83
1298	Swarm: robust and fast clustering method for amplicon-based studies. <b>2014</b> , 2, e593	474
1297	Environmental arsenic exposure and microbiota in induced sputum. <b>2014</b> , 11, 2299-313	10
1296	Current status and prospects of intestinal microbiome studies. <b>2014</b> , 12, 178-83	13
1295	The microbiome revolution. <b>2014</b> , 124, 4162-5	171
1294	Meat Science and Muscle Biology Symposium: Escherichia coli O157:H7, diet, and fecal microbiome in beef cattle. <b>2014</b> , 92, 1345-55	12
1293	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. <b>2014</b> , 2, e545	395
1292	A new strain of Wolbachia in an alpine population of the viviparous Oreina cacaliae (Coleoptera: Chrysomelidae). <b>2014</b> , 43, 913-22	9
1291	Membership and behavior of ultra-low-diversity pathogen communities present in the gut of humans during prolonged critical illness. <b>2014</b> , 5, e01361-14	203
1290	Chemical-biogeographic survey of secondary metabolism in soil. <b>2014</b> , 111, 3757-62	98
1289	T lymphocytes control microbial composition by regulating the abundance of Vibrio in the zebrafish gut. <b>2014</b> , 5, 737-47	26
1288	Gut microbiome of the Hadza hunter-gatherers. <b>2014</b> , 5, 3654	780
1287	Microbial community composition and diversity via 16S rRNA gene amplicons: evaluating the Illumina platform. <b>2014</b> ,	2
1286	Microbial reduction of uranium(VI) in sediments of different lithologies collected from Sellafield. <b>2014</b> , 51, 55-64	32
1285	Windrow composting mitigated CH <sub>4</sub> emissions: characterization of methanogenic and methanotrophic communities in manure management. <b>2014</b> , 90, 575-86	21
1284	The loss of topography in the microbial communities of the upper respiratory tract in the elderly. <b>2014</b> , 11, 513-21	124
1283	Replication of obesity and associated signaling pathways through transfer of microbiota from obese-prone rats. <b>2014</b> , 63, 1624-36	122

1282	Glycan degradation (GlyDeR) analysis predicts mammalian gut microbiota abundance and host diet-specific adaptations. <b>2014</b> , 5,	27
1281	Diversity of Rickettsiales in the microbiome of the lone star tick, <i>Amblyomma americanum</i> . <b>2014</b> , 80, 354-9	62
1280	Probiotics and virulent human rotavirus modulate the transplanted human gut microbiota in gnotobiotic pigs. <b>2014</b> , 6, 39	44
1279	Metagenomic analyses of bacteria on human hairs: a qualitative assessment for applications in forensic science. <b>2014</b> , 5, 16	52
1278	Diet and exercise orthogonally alter the gut microbiome and reveal independent associations with anxiety and cognition. <b>2014</b> , 9, 36	184
1277	Respiratory tract clinical sample selection for microbiota analysis in patients with pulmonary tuberculosis. <b>2014</b> , 2, 29	40
1276	Effects of straw amendment and moisture on microbial communities in Chinese fluvo-aquic soil. <b>2014</b> , 14, 1829-1840	60
1275	16S rRNA gene pyrosequencing of reference and clinical samples and investigation of the temperature stability of microbiome profiles. <b>2014</b> , 2, 31	46
1274	Modulation of fecal Clostridiales bacteria and butyrate by probiotic intervention with <i>Lactobacillus paracasei</i> DG varies among healthy adults. <b>2014</b> , 144, 1787-96	127
1273	An expanded genomic representation of the phylum cyanobacteria. <b>2014</b> , 6, 1031-45	186
1272	HIV-induced alteration in gut microbiota: driving factors, consequences, and effects of antiretroviral therapy. <b>2014</b> , 5, 562-70	106
1271	The gut microbiota of Colombians differs from that of Americans, Europeans and Asians. <b>2014</b> , 14, 311	125
1270	Gut microbiota influences low fermentable substrate diet efficacy in children with irritable bowel syndrome. <b>2014</b> , 5, 165-75	94
1269	Metagenomic analysis of size-fractionated picoplankton in a marine oxygen minimum zone. <b>2014</b> , 8, 187-211	194
1268	Interactions between fungi and bacteria influence microbial community structure in the <i>Megachile rotundata</i> larval gut. <b>2014</b> , 281, 20132653	35
1267	Indoor-air microbiome in an urban subway network: diversity and dynamics. <b>2014</b> , 80, 6760-70	105
1266	A review of software for analyzing molecular sequences. <b>2014</b> , 7, 830	37
1265	LotuS: an efficient and user-friendly OTU processing pipeline. <b>2014</b> , 2, 30	186



1264	Complex host genetics influence the microbiome in inflammatory bowel disease. <b>2014</b> , 6, 107	253
1263	Effect of <i>Lactobacillus rhamnosus</i> CGMCC1.3724 supplementation on weight loss and maintenance in obese men and women. <b>2014</b> , 111, 1507-19	219
1262	Dietary supplementation with lactose or artificial sweetener enhances swine gut <i>Lactobacillus</i> population abundance. <b>2014</b> , 111 Suppl 1, S30-5	64
1261	Arbuscular mycorrhizal fungal succession in a long-lived perennial. <b>2014</b> , 92, 313-320	17
1260	The SIRT1 deacetylase protects mice against the symptoms of metabolic syndrome. <b>2014</b> , 28, 1306-16	63
1259	The effects of propidium monoazide treatment on the measured composition of polymicrobial biofilms after treatment with chlorhexidine. <b>2014</b> , 48, 291-8	13
1258	Impact of fire on active layer and permafrost microbial communities and metagenomes in an upland Alaskan boreal forest. <b>2014</b> , 8, 1904-19	106
1257	MixS-BE: a MixS extension defining a minimum information standard for sequence data from the built environment. <b>2014</b> , 8, 1-3	109
1256	Reprogramming of gut microbiome energy metabolism by the FUT2 Crohn's disease risk polymorphism. <b>2014</b> , 8, 2193-206	140
1255	The airway microbiome of intubated premature infants: characteristics and changes that predict the development of bronchopulmonary dysplasia. <b>2014</b> , 76, 294-301	84
1254	Diverse capacity for 2-methylhopanoid production correlates with a specific ecological niche. <b>2014</b> , 8, 675-684	61
1253	Microbial cargo: do bacteria on symbiotic propagules reinforce the microbiome of lichens?. <b>2014</b> , 16, 3743-52	54
1252	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
1251	Removal of pharmaceuticals and personal care products during water recycling: microbial community structure and effects of substrate concentration. <b>2014</b> , 80, 2440-50	32
1250	Beneficial effect of oral tigecycline treatment on <i>Clostridium difficile</i> infection in gnotobiotic piglets. <b>2014</b> , 58, 7560-4	11
1249	Primers: Functional Genes for Anaerobic Hydrocarbon Degrading Microbes. <b>2014</b> , 39-55	3
1248	Intestinal dysbiosis associated with systemic lupus erythematosus. <b>2014</b> , 5, e01548-14	309
1247	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

1246	Waste not, want not: why rarefying microbiome data is inadmissible. <b>2014</b> , 10, e1003531	1536
1245	Fermented dairy products modulate <i>Citrobacter rodentium</i> -induced colonic hyperplasia. <b>2014</b> , 210, 1029-41	22
1244	Evaluation of Hand Bacteria as a Human Biometric Identifier. <b>2014</b> ,	
1243	Noma affected children from Niger have distinct oral microbial communities based on high-throughput sequencing of 16S rRNA gene fragments. <b>2014</b> , 8, e3240	12
1242	Communities of microbial eukaryotes in the mammalian gut within the context of environmental eukaryotic diversity. <b>2014</b> , 5, 298	98
1241	Chemolithotrophy in the continental deep subsurface: Sanford Underground Research Facility (SURF), USA. <b>2014</b> , 5, 610	74
1240	Benthic protists and fungi of Mediterranean deep hypersaline anoxic basin redoxcline sediments. <b>2014</b> , 5, 605	33
1239	Oral mycobiome analysis of HIV-infected patients: identification of <i>Pichia</i> as an antagonist of opportunistic fungi. <b>2014</b> , 10, e1003996	207
1238	Diversity and transport of microorganisms in intertidal sands of the California coast. <b>2014</b> , 80, 3943-51	34
1237	Biogeography of anaerobic ammonia-oxidizing (anammox) bacteria. <b>2014</b> , 5, 399	126
1236	Characterizing the avian gut microbiota: membership, driving influences, and potential function. <b>2014</b> , 5, 223	220
1235	Meta-omic platforms to assist in the understanding of NAFLD gut microbiota alterations: tools and applications. <b>2014</b> , 15, 684-711	21
1234	Soil bacterial community structure remains stable over a 5-year chronosequence of insect-induced tree mortality. <b>2014</b> , 5, 681	24
1233	Scabies mites alter the skin microbiome and promote growth of opportunistic pathogens in a porcine model. <b>2014</b> , 8, e2897	47
1232	Applications of Next-Generation Sequencing Technologies to the Study of the Human Microbiome. <b>2014</b> , 75-106	
1231	Microbial eukaryote diversity in the marine oxygen minimum zone off northern Chile. <b>2014</b> , 5, 543	26
1230	Microbial succession in the gut: directional trends of taxonomic and functional change in a birth cohort of Spanish infants. <b>2014</b> , 10, e1004406	115
1229	ARTIST: high-resolution genome-wide assessment of fitness using transposon-insertion sequencing. <b>2014</b> , 10, e1004782	101

1228	Helminth colonization is associated with increased diversity of the gut microbiota. <b>2014</b> , 8, e2880	225
1227	Temporal dynamics of fibrolytic and methanogenic rumen microorganisms during in situ incubation of switchgrass determined by 16S rRNA gene profiling. <b>2014</b> , 5, 307	49
1226	Aerobic methanotrophic communities at the Red Sea brine-seawater interface. <b>2014</b> , 5, 487	24
1225	Illuminating microbial dark matter in meromictic Sakinaw Lake. <b>2014</b> , 80, 6807-18	79
1224	Ecological consistency of SSU rRNA-based operational taxonomic units at a global scale. <b>2014</b> , 10, e1003594	58
1223	Bacterial population succession and adaptation affected by insecticide application and soil spraying history. <b>2014</b> , 5, 457	70
1222	Site- and horizon-specific patterns of microbial community structure and enzyme activities in permafrost-affected soils of Greenland. <b>2014</b> , 5, 541	62
1221	<i>Bacteroides dorei</i> dominates gut microbiome prior to autoimmunity in Finnish children at high risk for type 1 diabetes. <b>2014</b> , 5, 678	159
1220	Metagenomic evidence for metabolism of trace atmospheric gases by high-elevation desert Actinobacteria. <b>2014</b> , 5, 698	47
1219	Pyrosequencing detects human and animal pathogenic taxa in the grapevine endosphere. <b>2014</b> , 5, 327	20
1218	Microbial succession and the functional potential during the fermentation of Chinese soy sauce brine. <b>2014</b> , 5, 556	52
1217	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
1216	Captivity results in disparate loss of gut microbial diversity in closely related hosts. <b>2014</b> , 2, cou009	88
1215	GPU-Meta-Storms: computing the structure similarities among massive amount of microbial community samples using GPU. <b>2014</b> , 30, 1031-3	15
1214	Comparative metagenomic analysis of human gut microbiome composition using two different bioinformatic pipelines. <b>2014</b> , 2014, 325340	44
1213	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
1212	Depth-dependent geochemical and microbiological gradients in Fe(III) deposits resulting from coal mine-derived acid mine drainage. <b>2014</b> , 5, 215	28
1211	Changes in the deep subsurface microbial biosphere resulting from a field-scale CO <sub>2</sub> geosequestration experiment. <b>2014</b> , 5, 209	34

1210	Differences between the rhizosphere microbiome of Beta vulgaris ssp. maritima-ancestor of all beet crops-and modern sugar beets. <b>2014</b> , 5, 415	73
1209	Demonstrating microbial co-occurrence pattern analyses within and between ecosystems. <b>2014</b> , 5, 358	175
1208	Effects of sample handling and cultivation bias on the specificity of bacterial communities in keratose marine sponges. <b>2014</b> , 5, 611	27
1207	Effects of bacterial inoculants on the indigenous microbiome and secondary metabolites of chamomile plants. <b>2014</b> , 5, 64	76
1206	Microbial dysbiosis is associated with human breast cancer. <b>2014</b> , 9, e83744	233
1205	A compositional look at the human gastrointestinal microbiome and immune activation parameters in HIV infected subjects. <b>2014</b> , 10, e1003829	259
1204	High temporal and spatial diversity in marine RNA viruses implies that they have an important role in mortality and structuring plankton communities. <b>2014</b> , 5, 703	29
1203	Late winter under ice pelagic microbial communities in the high Arctic Ocean and the impact of short-term exposure to elevated CO2 levels. <b>2014</b> , 5, 490	18
1202	Metagenome sequencing of the prokaryotic microbiota of the hypersaline and meromictic soap lake, washington. <b>2014</b> , 2,	2
1201	Effect of copper treatment on the composition and function of the bacterial community in the sponge Haliclona cymaeformis. <b>2014</b> , 5, e01980	24
1200	Exposure to a social stressor disrupts the community structure of the colonic mucosa-associated microbiota. <b>2014</b> , 14, 189	203
1199	Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition. <b>2014</b> , 15, R76	150
1198	Anal microbiota profiles in HIV-positive and HIV-negative MSM. <b>2014</b> , 28, 753-60	54
1197	DNA extraction protocols cause differences in 16S rRNA amplicon sequencing efficiency but not in community profile composition or structure. <b>2014</b> , 3, 910-21	64
1196	Protocols for Investigating the Microbiology of Drilling Fluids, Hydraulic Fracturing Fluids, and Formations in Unconventional Natural Gas Reservoirs. <b>2014</b> , 133-156	1
1195	Infectious Microecology. <b>2014</b> ,	4
1194	Prolonged use of a proton pump inhibitor reduces microbial diversity: implications for Clostridium difficile susceptibility. <b>2014</b> , 2, 42	100
1193	The adult nasopharyngeal microbiome as a determinant of pneumococcal acquisition. <b>2014</b> , 2, 44	48

1192	Fast dendrogram-based OTU clustering using sequence embedding. <b>2014,</b>	3
1191	Microbial diversity and community structure across environmental gradients in Bransfield Strait, Western Antarctic Peninsula. <b>2014, 5, 647</b>	39
1190	IL-22-producing CD4+ cells are depleted in actively inflamed colitis tissue. <b>2014, 7, 124-33</b>	99
1189	A global comparison of <i>Bactericera cockerelli</i> (Hemiptera: Triozidae) microbial communities. <b>2014, 43, 344-52</b>	13
1188	Skyport - Container-Based Execution Environment Management for Multi-cloud Scientific Workflows. <b>2014,</b>	52
1187	Characterization of bacteriophage communities and CRISPR profiles from dental plaque. <b>2014, 14, 175</b>	41
1186	Prasinovirus distribution in the Northwest Mediterranean Sea is affected by the environment and particularly by phosphate availability. <b>2014, 466-467, 146-57</b>	13
1185	Ecological succession and stochastic variation in the assembly of <i>Arabidopsis thaliana</i> phyllosphere communities. <b>2014, 5, e00682-13</b>	174
1184	Altered oral viral ecology in association with periodontal disease. <b>2014, 5, e01133-14</b>	108
1183	Evaluation of the nasal microbiota in slaughter-age pigs and the impact on nasal methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) carriage. <b>2014, 10, 69</b>	37
1182	Single clinical isolates from acute uncomplicated urinary tract infections are representative of dominant in situ populations. <b>2014, 5, e01064-13</b>	27
1181	Population genetic structure of traditional populations in the Peruvian Central Andes and implications for South American population history. <b>2014, 86, 147-65</b>	21
1180	Multiple omics uncovers host-gut microbial mutualism during prebiotic fructooligosaccharide supplementation. <b>2014, 21, 469-80</b>	62
1179	Microbiome composition by pyrosequencing in mesenteric lymph nodes of rats with CCl4-induced cirrhosis. <b>2014, 6, 263-71</b>	15
1178	Metagenomic sequencing of two salton sea microbiomes. <b>2014, 2,</b>	6
1177	Seasonal microbial community dynamics correlate with phytoplankton-derived polysaccharides in surface coastal waters. <b>2014, 8, 245-8</b>	75
1176	Microbial community composition and in silico predicted metabolic potential reflect biogeochemical gradients between distinct peatland types. <b>2014, 90, 633-46</b>	21
1175	Nitrogen deposition alters plant-fungal relationships: linking belowground dynamics to aboveground vegetation change. <b>2014, 23, 1364-78</b>	51

1174	Temporal changes and the effect of subtherapeutic concentrations of antibiotics in the gut microbiota of swine. <b>2014</b> , 90, 599-608	42
1173	Intestinal epithelial MyD88 is a sensor switching host metabolism towards obesity according to nutritional status. <b>2014</b> , 5, 5648	160
1172	Feature subset selection for inferring relative importance of taxonomy. <b>2014</b> ,	1
1171	Large-Scale Pairwise Sequence Alignments on a Large-Scale GPU Cluster. <b>2014</b> , 31, 51-61	0
1170	Evolution of asexuality via different mechanisms in grass thrips (thysanoptera: Aptinothrips). <b>2014</b> , 68, 1883-93	25
1169	A phylogenetic perspective on species diversity, $\beta$ diversity and biogeography for the microbial world. <b>2014</b> , 23, 5868-76	18
1168	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
1167	Hyperimmune bovine colostrum as a novel therapy to combat <i>Clostridium difficile</i> infection. <b>2015</b> , 211, 1334-41	24
1166	Relationships between phyllosphere bacterial communities and plant functional traits in a neotropical forest. <b>2014</b> , 111, 13715-20	302
1165	Bacterial communities of traditional salted and fermented seafoods from Jeju Island of Korea using 16S rRNA gene clone library analysis. <b>2014</b> , 79, M927-34	30
1164	Amplicon pyrosequencing reveals the soil microbial diversity associated with invasive Japanese barberry ( <i>Berberis thunbergii</i> DC.). <b>2014</b> , 23, 1318-32	26
1163	Microbial sequencing analyses suggest the presence of a fecal veneer on indoor climbing wall holds. <b>2014</b> , 69, 681-9	7
1162	Identifying the core microbial community in the gut of fungus-growing termites. <b>2014</b> , 23, 4631-44	108
1161	Shotgun microbial profiling of fossil remains. <b>2014</b> , 23, 1780-98	43
1160	Microbial community structure of wastewater treatment subjected to high mortality rate due to ozonation of return activated sludge. <b>2014</b> , 117, 587-96	6
1159	Intertidal epilithic bacteria diversity changes along a naturally occurring carbon dioxide and pH gradient. <b>2014</b> , 89, 670-8	28
1158	Identification accuracy and diversity reproducibility associated with internal transcribed spacer-based fungal taxonomic library preparation. <b>2014</b> , 16, 2764-76	14
1157	Feeding rates and prey selectivity of planktonic decapod larvae in the Western English Channel. <b>2014</b> , 161, 2479-2494	12

1156	Shifts in microbial community structure and function in light- and dark-grown biofilms driven by warming. <b>2014</b> , 16, 2550-67	29
1155	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
1154	Deodorization of pig slurry and characterization of bacterial diversity using 16S rDNA sequence analysis. <b>2014</b> , 52, 918-29	7
1153	The Sphagnum microbiome supports bog ecosystem functioning under extreme conditions. <b>2014</b> , 23, 4498-510	69
1152	An analysis of geothermal and carbonic springs in the western United States sustained by deep fluid inputs. <b>2014</b> , 12, 83-98	5
1151	Endospores of thermophilic bacteria as tracers of microbial dispersal by ocean currents. <b>2014</b> , 8, 1153-65	85
1150	Does urbanization shape bacterial community composition in urban park soils? A case study in 16 representative Chinese cities based on the pyrosequencing method. <b>2014</b> , 87, 182-92	59
1149	Bacterial community structure and soil properties of a subarctic tundra soil in Council, Alaska. <b>2014</b> , 89, 465-75	74
1148	Methanotrophs, methanogens and microbial community structure in livestock slurry surface crusts. <b>2014</b> , 117, 1066-78	13
1147	Host-specific microbial communities in three sympatric North Sea sponges. <b>2014</b> , 90, 390-403	21
1146	Sampling of intestinal microbiota and targeted amplification of bacterial 16S rRNA genes for microbial ecologic analysis. <b>2014</b> , 107, 7.41.1-7.41.11	47
1145	The giraffe ( <i>Giraffa camelopardalis</i> ) rumen microbiome. <b>2014</b> , 90, 237-46	23
1144	Characterization of growing bacterial populations in McMurdo Dry Valley soils through stable isotope probing with (18) O-water. <b>2014</b> , 89, 415-25	31
1143	Spatial distribution of microbial communities associated with dune landform in the Gurbantunggut Desert, China. <b>2014</b> , 52, 898-907	16
1142	Arctic root-associated fungal community composition reflects environmental filtering. <b>2014</b> , 23, 649-59	54
1141	Indoor airborne bacterial communities are influenced by ventilation, occupancy, and outdoor air source. <b>2014</b> , 24, 41-8	197
1140	Performance of a pilot scale microbial electrolysis cell fed on domestic wastewater at ambient temperatures for a 12 month period. <b>2014</b> , 173, 87-95	177
1139	Low host specificity of root-associated fungi at an Arctic site. <b>2014</b> , 23, 975-85	55

1138	Galacto-oligosaccharides attenuate renal injury with microbiota modification. <b>2014</b> , 2, e12029	35
1137	Anaerobic oxidation of methane by sulfate in hypersaline groundwater of the Dead Sea aquifer. <b>2014</b> , 12, 511-28	34
1136	The microbiome of New World vultures. <b>2014</b> , 5, 5498	177
1135	Individuals' diet diversity influences gut microbial diversity in two freshwater fish (threespine stickleback and Eurasian perch). <b>2014</b> , 17, 979-87	178
1134	The skin microbiome of caspase-14-deficient mice shows mild dysbiosis. <b>2014</b> , 23, 561-7	11
1133	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
1132	DNA Metabarcoding Meets Experimental Ecotoxicology: Advancing Knowledge on the Ecological Effects of Copper in Freshwater Ecosystems. <b>2014</b> , 51, 79-104	24
1131	Faster, Higher and Stronger? The Pros and Cons of Molecular Faunal Data for Assessing Ecosystem Condition. <b>2014</b> , 51, 1-40	24
1130	Encyclopedia of Metagenomics. <b>2014</b> , 1-5	1
1129	Encyclopedia of Metagenomics. <b>2014</b> , 1-7	2
1128	The potential role of lung microbiota in lung cancer attributed to household coal burning exposures. <b>2014</b> , 55, 643-51	116
1127	Diversity and genomic insights into the uncultured Chloroflexi from the human microbiota. <b>2014</b> , 16, 2635-43	38
1126	Comparative analysis of bacterial community-metagenomics in coastal Gulf of Mexico sediment microcosms following exposure to Macondo oil (MC252). <b>2014</b> , 106, 993-1009	13
1125	Similarity and differentiation between bacteria associated with skin of salamanders ( <i>Plethodon jordani</i> ) and free-living assemblages. <b>2014</b> , 88, 482-94	44
1124	First evidence of amoebae-mycobacteria association in drinking water network. <b>2014</b> , 48, 11872-82	85
1123	Oxygen suppresses light-driven anodic current generation by a mixed phototrophic culture. <b>2014</b> , 48, 14000-6	15
1122	Co-inoculating ruminal content neither provides active hydrolytic microbes nor improves methanization of $\text{H}_2\text{C}$ -cellulose in batch digesters. <b>2014</b> , 87, 616-29	23
1121	Culture-dependent and culture-independent analyses reveal no prokaryotic community shifts or recovery of <i>Serratia marcescens</i> in <i>Acropora palmata</i> with white pox disease. <b>2014</b> , 88, 457-67	26



1120	Dietary mangostin, a xanthone from mangosteen fruit, exacerbates experimental colitis and promotes dysbiosis in mice. <b>2014</b> , 58, 1226-38	32
1119	Unique and shared responses of the gut microbiota to prolonged fasting: a comparative study across five classes of vertebrate hosts. <b>2014</b> , 90, 883-94	134
1118	Anaerobic codigestion of sewage sludge and glycerol, focusing on process kinetics, microbial dynamics and sludge dewaterability. <b>2014</b> , 67, 355-66	76
1117	Herbivorous rodents ( <i>Neotoma</i> spp.) harbour abundant and active foregut microbiota. <b>2014</b> , 16, 2869-78	54
1116	Marek's disease virus influences the core gut microbiome of the chicken during the early and late phases of viral replication. <b>2014</b> , 90, 300-12	22
1115	Impact of inocula and operating conditions on the microbial community structure of two anammox reactors. <b>2014</b> , 35, 1811-22	37
1114	Distribution of PAHs and the PAH-degrading bacteria in the deep-sea sediments of the high-latitude Arctic Ocean. <b>2014</b> ,	5
1113	Exercise prevents weight gain and alters the gut microbiota in a mouse model of high fat diet-induced obesity. <b>2014</b> , 9, e92193	344
1112	Analysis of plant microbe interactions in the era of next generation sequencing technologies. <b>2014</b> , 5, 216	150
1111	Rhizosphere heterogeneity shapes abundance and activity of sulfur-oxidizing bacteria in vegetated salt marsh sediments. <b>2014</b> , 5, 309	41
1110	Soluble maize fibre affects short-term calcium absorption in adolescent boys and girls: a randomised controlled trial using dual stable isotopic tracers. <b>2014</b> , 112, 446-56	68
1109	High-throughput sequencing of 16S RNA genes of soil bacterial communities from a naturally occurring CO <sub>2</sub> gas vent. <b>2014</b> , 29, 176-184	36
1108	Microbiota of human breast tissue. <b>2014</b> , 80, 3007-14	248
1107	Acidobacteria appear to dominate the microbiome of two sympatric Caribbean Sponges and one Zoanthid. <b>2014</b> , 47, 67	16
1106	Comparison of environmental and isolate <i>Sulfobacillus</i> genomes reveals diverse carbon, sulfur, nitrogen, and hydrogen metabolisms. <b>2014</b> , 15, 1107	54
1105	Pyrosequencing of supra- and subgingival biofilms from inflamed peri-implant and periodontal sites. <b>2014</b> , 14, 157	33
1104	ITScan: a web-based analysis tool for Internal Transcribed Spacer (ITS) sequences. <b>2014</b> , 7, 857	8
1103	Bacterial community composition of chronic periodontitis and novel oral sampling sites for detecting disease indicators. <b>2014</b> , 2, 32	54

1102	Intestinal anastomotic injury alters spatially defined microbiome composition and function. <b>2014</b> , 2, 35	99
1101	Sânce: reference-based phylogenetic analysis for 18S rRNA studies. <b>2014</b> , 14, 235	8
1100	Bacterial associates of seed-parasitic wasps (Hymenoptera: Megastigmus). <b>2014</b> , 14, 224	15
1099	Alcohol and tobacco consumption affects bacterial richness in oral cavity mucosa biofilms. <b>2014</b> , 14, 250	42
1098	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
1097	Improved characterization of medically relevant fungi in the human respiratory tract using next-generation sequencing. <b>2014</b> , 15, 487	76
1096	Microbial shifts in the aging mouse gut. <b>2014</b> , 2, 50	224
1095	Randomized open-label pilot study of the influence of probiotics and the gut microbiome on toxic metal levels in Tanzanian pregnant women and school children. <b>2014</b> , 5, e01580-14	115
1094	The gastrointestinal tract of the white-throated Woodrat ( <i>Neotoma albigula</i> ) harbors distinct consortia of oxalate-degrading bacteria. <b>2014</b> , 80, 1595-601	53
1093	The Bio-Community Perl toolkit for microbial ecology. <b>2014</b> , 30, 1926-7	13
1092	Elucidation of bacteria found in car interiors and strategies to reduce the presence of potential pathogens. <b>2014</b> , 30, 337-46	17
1091	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
1090	Prebiotic oligosaccharides in premature infants. <b>2014</b> , 58, 352-60	27
1089	RNA-stable-isotope probing shows utilization of carbon from inulin by specific bacterial populations in the rat large bowel. <b>2014</b> , 80, 2240-7	33
1088	Impaired innate immune function associated with fecal supernatant from Crohn's disease patients: insights into potential pathogenic role of the microbiome. <b>2014</b> , 20, 1139-46	6
1087	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
1086	Microbially mediated reduction of FeIII and AsV in Cambodian sediments amended with <sup>13</sup> C-labelled hexadecane and kerogen. <b>2014</b> , 11, 538	10
1085	Multisubstrate isotope labeling and metagenomic analysis of active soil bacterial communities. <b>2014</b> , 5, e01157-14	89

1084	Conditionally rare taxa disproportionately contribute to temporal changes in microbial diversity. <b>2014</b> , 5, e01371-14	359
1083	Protein quality and the protein to carbohydrate ratio within a high fat diet influences energy balance and the gut microbiota in C57BL/6J mice. <b>2014</b> , 9, e88904	57
1082	Analysis, optimization and verification of Illumina-generated 16S rRNA gene amplicon surveys. <b>2014</b> , 9, e94249	237
1081	Human and environmental impacts on river sediment microbial communities. <b>2014</b> , 9, e97435	83
1080	Severity-related changes of bronchial microbiome in chronic obstructive pulmonary disease. <b>2014</b> , 52, 4217-23	127
1079	Restricted streptomycin use in apple orchards did not adversely alter the soil bacteria communities. <b>2013</b> , 4, 383	22
1078	The Variation of Microbial Communities in a Depth Profile of an Acidic, Nutrient-Poor Boreal Bog in Southwestern Finland. <b>2014</b> , 04, 832-859	30
1077	Sampling locality is more detectable than taxonomy or ecology in the gut microbiota of the brood-parasitic Brown-headed Cowbird ( <i>Molothrus ater</i> ). <b>2014</b> , 2, e321	78
1076	Evidence that the Tibetan fox is an obligate predator of the plateau pika: conservation implications. <b>2014</b> , 95, 1207-1221	18
1075	Soil bacterial community composition altered by increased nutrient availability in Arctic tundra soils. <b>2014</b> , 5, 516	107
1074	The effect of malnutrition on norovirus infection. <b>2014</b> , 5, e01032-13	40
1073	Ribosomal DNA sequence heterogeneity reflects intraspecies phylogenies and predicts genome structure in two contrasting yeast species. <b>2014</b> , 63, 543-54	19
1072	A possible link between food and mood: dietary impact on gut microbiota and behavior in BALB/c mice. <b>2014</b> , 9, e103398	103
1071	The structures of the colonic mucosa-associated and luminal microbial communities are distinct and differentially affected by a prolonged murine stressor. <b>2014</b> , 5, 748-60	66
1070	Early life establishment of site-specific microbial communities in the gut. <b>2014</b> , 5, 192-201	45
1069	Deterministic processes guide long-term synchronised population dynamics in replicate anaerobic digesters. <b>2014</b> , 8, 2015-28	224
1068	Diurnal expression of SAR11 proteorhodopsin and 16S rRNA genes in coastal North Atlantic waters. <b>2014</b> , 73, 185-194	8
1067	Planktonic Euryarchaeota are a significant source of archaeal tetraether lipids in the ocean. <b>2014</b> , 111, 9858-63	113

1066	Selective proliferation of intestinal <i>Barnesiella</i> under fucosyllactose supplementation in mice. <b>2014</b> , 111, 1602-10	55
1065	Impact of dietary fatty acids on metabolic activity and host intestinal microbiota composition in C57BL/6J mice. <b>2014</b> , 111, 1905-17	115
1064	. <b>2014</b> ,	6
1063	Fecal bacterial community changes associated with isoflavone metabolites in postmenopausal women after soy bar consumption. <b>2014</b> , 9, e108924	64
1062	Signatures of conical intersections in two-dimensional electronic spectra. <b>2014</b> , 47, 124019	26
1061	Consumption of acidic water alters the gut microbiome and decreases the risk of diabetes in NOD mice. <b>2014</b> , 62, 237-50	55
1060	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
1059	Application of Bioinformatics in Microbial Ecology. <b>2014</b> , 955-959, 276-280	
1058	The denitrification characteristics of <i>Pseudomonas stutzeri</i> SC221-M and its application to water quality control in grass carp aquaculture. <b>2014</b> , 9, e114886	22
1057	Characterization of the 18S rRNA gene for designing universal eukaryote specific primers. <b>2014</b> , 9, e87624	244
1056	Validation of IMP dehydrogenase inhibitors in a mouse model of cryptosporidiosis. <b>2014</b> , 58, 1603-14	44
1055	Metabolic alterations to the mucosal microbiota in inflammatory bowel disease. <b>2014</b> , 20, 723-31	55
1054	Analysis of run-to-run variation of bar-coded pyrosequencing for evaluating bacterial community shifts and individual taxa dynamics. <b>2014</b> , 9, e99414	10
1053	Microbes in the neonatal intensive care unit resemble those found in the gut of premature infants. <b>2014</b> , 2, 1	251
1052	Intestinal microbiota of preterm infants differ over time and between hospitals. <b>2014</b> , 2, 36	49
1051	Host lifestyle affects human microbiota on daily timescales. <b>2014</b> , 15, R89	548
1050	Predictors of neutrophilic airway inflammation in young smokers with asthma. <b>2014</b> , 51, 341-7	4
1049	Comment on "The hologenomic basis of speciation: gut bacteria cause hybrid lethality in the genus <i>Nasonia</i> ". <b>2014</b> , 345, 1011	16

1048	Indoor-biofilter growth and exposure to airborne chemicals drive similar changes in plant root bacterial communities. <b>2014</b> , 80, 4805-13	16
1047	The amphibian skin-associated microbiome across species, space and life history stages. <b>2014</b> , 23, 1238-50	220
1046	High-fat diet alters gut microbiota physiology in mice. <b>2014</b> , 8, 295-308	393
1045	Unearthing carrion beetles' microbiome: characterization of bacterial and fungal hindgut communities across the Silphidae. <b>2014</b> , 23, 1251-67	65
1044	Improving accuracy of DNA diet estimates using food tissue control materials and an evaluation of proxies for digestion bias. <b>2014</b> , 23, 3706-18	73
1043	Long term effect of gut microbiota transfer on diabetes development. <b>2014</b> , 53, 85-94	105
1042	Early empiric antibiotic use in preterm infants is associated with lower bacterial diversity and higher relative abundance of Enterobacter. <b>2014</b> , 165, 23-9	225
1041	Biodegradation of naphthenic acids in oils sands process waters in an immobilized soil/sediment bioreactor. <b>2014</b> , 109, 164-72	46
1040	Altered gut microbiota and activity in a murine model of autism spectrum disorders. <b>2014</b> , 37, 197-206	268
1039	Assessing variation in bacterial composition between the rhizospheres of two mangrove tree species. <b>2014</b> , 139, 40-45	25
1038	Fractionation of microbial populations in a PHA accumulating mixed culture and associated PHA content and composition. <b>2014</b> , 71, 53-8	7
1037	Bacterial Communities in Soil Under Moss and Lichen-Moss Crusts. <b>2014</b> , 31, 152-160	16
1036	Phylogenetic and structural response of heterotrophic bacteria to dissolved organic matter of different chemical composition in a continuous culture study. <b>2014</b> , 16, 1668-81	84
1035	Is metagenomics resolving identification of functions in microbial communities?. <b>2014</b> , 7, 1-4	28
1034	Host-specific adaptation governs the interaction of the marine diatom, Pseudo-nitzschia and their microbiota. <b>2014</b> , 8, 63-76	85
1033	Using high-throughput sequencing to assess the impacts of treated and untreated wastewater discharge on prokaryotic communities in an urban river. <b>2014</b> , 98, 1841-51	45
1032	Prolonged antibiotic use induces intestinal injury in mice that is repaired after removing antibiotic pressure: implications for empiric antibiotic therapy. <b>2014</b> , 10, 8-20	11
1031	Bronchial microbiome of severe COPD patients colonised by Pseudomonas aeruginosa. <b>2014</b> , 33, 1101-11	87

1030	ITEP: an integrated toolkit for exploration of microbial pan-genomes. <b>2014</b> , 15, 8	77
1029	Seasonal variations in bacterial communities and antibiotic-resistant strains associated with green bottle flies (Diptera: Calliphoridae). <b>2014</b> , 98, 4197-208	23
1028	16S rRNA gene pyrosequencing reveals shift in patient faecal microbiota during high-dose chemotherapy as conditioning regimen for bone marrow transplantation. <b>2014</b> , 67, 690-9	89
1027	Litter quality versus soil microbial community controls over decomposition: a quantitative analysis. <b>2014</b> , 174, 283-94	130
1026	Bacterial diversity in Greenlandic soils as affected by potato cropping and inorganic versus organic fertilization. <b>2014</b> , 37, 61-71	41
1025	Two amplicon sequencing strategies revealed different facets of the prokaryotic community associated with the anaerobic treatment of vinasses from ethanol distilleries. <b>2014</b> , 153, 388-92	10
1024	Patterns of rare and abundant marine microbial eukaryotes. <b>2014</b> , 24, 813-21	306
1023	Illumina sequencing of the V4 hypervariable region 16S rRNA gene reveals extensive changes in bacterial communities in the cecum following carbohydrate oral infusion and development of early-stage acute laminitis in the horse. <b>2014</b> , 168, 436-41	37
1022	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
1021	Fungal high-throughput taxonomic identification tool for use with next-generation sequencing (FHITINGS). <b>2014</b> , 54, 315-21	51
1020	Next-generation DNA sequencing reveals that low fungal diversity in house dust is associated with childhood asthma development. <b>2014</b> , 24, 236-47	115
1019	Microbiota and epigenetic regulation of inflammatory mediators in type 2 diabetes and obesity. <b>2014</b> , 5, 33-43	85
1018	Links between plant and fungal communities across a deforestation chronosequence in the Amazon rainforest. <b>2014</b> , 8, 1548-50	83
1017	A molecular-based approach for examining responses of eukaryotes in microcosms to contaminant-spiked estuarine sediments. <b>2014</b> , 33, 359-69	43
1016	Convergence of gut microbiomes in myrmecophagous mammals. <b>2014</b> , 23, 1301-17	179
1015	The bacteriological composition of biomass recovered by flushing an operational drinking water distribution system. <b>2014</b> , 54, 100-14	70
1014	Impacts of naturally elevated soil CO <sub>2</sub> concentrations on communities of soil archaea and bacteria. <b>2014</b> , 68, 348-356	39
1013	Combining real-time PCR and next-generation DNA sequencing to provide quantitative comparisons of fungal aerosol populations. <b>2014</b> , 84, 113-121	83

1012	Identification of key nitrous oxide production pathways in aerobic partial nitrifying granules. <b>2014</b> , 16, 3168-80	42
1011	Improved appreciation of the functioning and importance of biological soil crusts in Europe: the Soil Crust International Project (SCIN). <b>2014</b> , 23, 1639-1658	73
1010	Initial copper stress strengthens the resistance of soil microorganisms to a subsequent copper stress. <b>2014</b> , 67, 931-41	39
1009	Characterization of bacterial diversity associated with microbial mats, gypsum evaporites and carbonate microbialites in thalassic wetlands: Tebenquiche and La Brava, Salar de Atacama, Chile. <b>2014</b> , 18, 311-29	90
1008	Spatial and temporal distribution of archaeal diversity in meromictic, hypersaline Ocnei Lake (Transylvanian Basin, Romania). <b>2014</b> , 18, 399-413	26
1007	Divergent responses of soil fungi functional groups to short-term warming. <b>2014</b> , 68, 708-15	45
1006	The temporal scaling of bacterioplankton composition: high turnover and predictability during shrimp cultivation. <b>2014</b> , 67, 256-64	45
1005	VAMPS: a website for visualization and analysis of microbial population structures. <b>2014</b> , 15, 41	138
1004	Bacterial diversity within five unexplored freshwater lakes interconnected by surface channels in East Antarctic Dronning Maud Land (Schirmacher Oasis) using amplicon pyrosequencing. <b>2014</b> , 37, 359-366	6
1003	Analysis of the bovine rumen microbiome reveals a diversity of Sus-like polysaccharide utilization loci from the bacterial phylum Bacteroidetes. <b>2014</b> , 41, 601-6	23
1002	Multiple ITS haplotypes in the genome of the lichenized basidiomycete <i>Cora inversa</i> (Hygrophoraceae): fact or artifact?. <b>2014</b> , 78, 148-62	28
1001	Bacterial communities in trace metal contaminated lake sediments are dominated by endospore-forming bacteria. <b>2014</b> , 76, 33-46	23
1000	Mutualistic ants as an indirect defence against leaf pathogens. <b>2014</b> , 202, 640-650	28
999	Amplification primers of SSU rDNA for soil protists. <b>2014</b> , 69, 328-342	44
998	Salivary microbiota and metabolome associated with celiac disease. <b>2014</b> , 80, 3416-25	70
997	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
996	Diversity of the vaginal microbiome correlates with preterm birth. <b>2014</b> , 21, 32-40	183
995	Gene-targeted metagenomic analysis of glucan-branching enzyme gene profiles among human and animal fecal microbiota. <b>2014</b> , 8, 493-503	23

994	Resilience of the natural phyllosphere microbiota of the grapevine to chemical and biological pesticides. <b>2014</b> , 80, 3585-96	99
993	Rumen bacterial community evaluated by 454 pyrosequencing and terminal restriction fragment length polymorphism analyses in dairy sheep fed marine algae. <b>2014</b> , 97, 1661-9	55
992	Taxonomic identification of commensal bacteria associated with the mucosa and digesta throughout the gastrointestinal tracts of preweaned calves. <b>2014</b> , 80, 2021-8	132
991	Life with compass: diversity and biogeography of magnetotactic bacteria. <b>2014</b> , 16, 2646-58	84
990	Enhanced microbial diversity in the saliva microbiome induced by short-term probiotic intake revealed by 16S rRNA sequencing on the IonTorrent PGM platform. <b>2014</b> , 190, 30-9	26
989	FXR is a molecular target for the effects of vertical sleeve gastrectomy. <b>2014</b> , 509, 183-8	692
988	Fish gut microbiota analysis differentiates physiology and behavior of invasive Asian carp and indigenous American fish. <b>2014</b> , 8, 541-551	159
987	Bacterial community composition of divergent soil habitats in a polar desert. <b>2014</b> , 89, 490-4	32
986	Natural soil microbes alter flowering phenology and the intensity of selection on flowering time in a wild Arabidopsis relative. <b>2014</b> , 17, 717-26	184
985	The bacterial communities in plant phloem-sap-feeding insects. <b>2014</b> , 23, 1433-44	76
984	Kefir fermented milk and kefiran promote growth of Bifidobacterium bifidum PRL2010 and modulate its gene expression. <b>2014</b> , 178, 50-9	50
983	Meta'omic analytic techniques for studying the intestinal microbiome. <b>2014</b> , 146, 1437-1448.e1	116
982	The gut microbiome in health and disease. <b>2014</b> , 146, 1433-6	42
981	Kingdom-agnostic metagenomics and the importance of complete characterization of enteric microbial communities. <b>2014</b> , 146, 1459-69	124
980	Reactor performance and microbial ecology of a nitrification membrane bioreactor. <b>2014</b> , 462, 139-146	47
979	Altered fecal microbiota composition associated with food allergy in infants. <b>2014</b> , 80, 2546-54	217
978	Coupled cryoconite ecosystem structure-function relationships are revealed by comparing bacterial communities in alpine and Arctic glaciers. <b>2014</b> , 89, 222-37	70
977	Quantitative divergence of the bacterial root microbiota in Arabidopsis thaliana relatives. <b>2014</b> , 111, 585-92	330



976	Distribution and diversity of Verrucomicrobia methanotrophs in geothermal and acidic environments. <b>2014</b> , 16, 1867-78	95
975	Mosquitoes rely on their gut microbiota for development. <b>2014</b> , 23, 2727-39	263
974	Fungal pathogen accumulation at the expense of plant-beneficial fungi as a consequence of consecutive peanut monoculturing. <b>2014</b> , 72, 11-18	134
973	Longitudinal study of murine microbiota activity and interactions with the host during acute inflammation and recovery. <b>2014</b> , 8, 1101-14	121
972	Impact of experimental hookworm infection on the human gut microbiota. <b>2014</b> , 210, 1431-4	100
971	Fungal succession in an in-vessel composting system characterized using 454 pyrosequencing. <b>2014</b> , 88, 296-308	73
970	Microbial community dynamics and stability during an ammonia-induced shift to syntrophic acetate oxidation. <b>2014</b> , 80, 3375-83	100
969	Temporal dynamics of prokaryotic communities in the marine sponge <i>Sarcotragus spinosulus</i> . <b>2014</b> , 23, 3097-112	37
968	Diversity of diversity: conceptual and methodological differences in biodiversity estimates of eukaryotic microbes as compared to bacteria. <b>2014</b> , 22, 432-7	32
967	Shifts in microbial community in response to dissolved oxygen levels in activated sludge. <b>2014</b> , 165, 257-64	77
966	The placenta harbors a unique microbiome. <b>2014</b> , 6, 237ra65	1326
965	Bacterial phylogeny structures soil resistomes across habitats. <b>2014</b> , 509, 612-6	649
964	Stability and phylogenetic correlation in gut microbiota: lessons from ants and apes. <b>2014</b> , 23, 1268-83	168
963	Improved group-specific primers based on the full SILVA 16S rRNA gene reference database. <b>2014</b> , 16, 2389-407	28
962	Endemism and functional convergence across the North American soil mycobiome. <b>2014</b> , 111, 6341-6	351
961	Intestinal microbiota reduces genotoxic endpoints induced by high-energy protons. <b>2014</b> , 181, 45-53	24
960	River organic matter shapes microbial communities in the sediment of the Rhône prodelta. <b>2014</b> , 8, 2327-38	38
959	Improving ITS sequence data for identification of plant pathogenic fungi. <b>2014</b> , 67, 11-19	101

958	Altered profile of human gut microbiome is associated with cirrhosis and its complications. <b>2014</b> , 60, 940-7	587
957	Watershed-scale fungal community characterization along a pH gradient in a subsurface environment cocontaminated with uranium and nitrate. <b>2014</b> , 80, 1810-20	10
956	A glimpse of <i>Escherichia coli</i> O157:H7 survival in soils from eastern China. <b>2014</b> , 476-477, 49-56	21
955	Impact of a phytoplankton bloom on the diversity of the active bacterial community in the southern North Sea as revealed by metatranscriptomic approaches. <b>2014</b> , 87, 378-89	76
954	Characterizing changes in soil bacterial community structure in response to short-term warming. <b>2014</b> , 89, 281-92	75
953	Spatial and temporal variations of microbial community in a mixed plug-flow loop reactor fed with dairy manure. <b>2014</b> , 7, 332-46	41
952	Fungi ahoy! Diversity on marine wooden substrata in the high North. <b>2014</b> , 8, 46-58	64
951	Contrasting elevational diversity patterns between eukaryotic soil microbes and plants. <b>2014</b> , 95, 3190-3202	110
950	Host-specificity among abundant and rare taxa in the sponge microbiome. <b>2014</b> , 8, 1198-209	159
949	Partner choice and fidelity stabilize coevolution in a Cretaceous-age defensive symbiosis. <b>2014</b> , 111, 6359-64	71
948	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
947	The marriage of nutrigenomics with the microbiome: the case of infant-associated bifidobacteria and milk. <b>2014</b> , 99, 697S-703S	33
946	Effect of photosynthetic bacteria on water quality and microbiota in grass carp culture. <b>2014</b> , 30, 2523-31	31
945	Humboldt's spa: microbial diversity is controlled by temperature in geothermal environments. <b>2014</b> , 8, 1166-74	113
944	Diet rapidly and reproducibly alters the human gut microbiome. <b>2014</b> , 505, 559-63	5264
943	Single-cell analyses revealed transfer ranges of IncP-1, IncP-7, and IncP-9 plasmids in a soil bacterial community. <b>2014</b> , 80, 138-45	58
942	AIEC pathobiont instigates chronic colitis in susceptible hosts by altering microbiota composition. <b>2014</b> , 63, 1069-80	149
941	An assessment of microbial communities associated with surface mining-disturbed overburden. <b>2014</b> , 186, 1917-29	21

940	From genus to phylum: large-subunit and internal transcribed spacer rRNA operon regions show similar classification accuracies influenced by database composition. <b>2014</b> , 80, 829-40	70
939	Specificity and transcriptional activity of microbiota associated with low and high microbial abundance sponges from the Red Sea. <b>2014</b> , 23, 1348-63	92
938	Exploring links between pH and bacterial community composition in soils from the Craibstone Experimental Farm. <b>2014</b> , 87, 403-15	102
937	Sequence-based analysis of the bacterial and fungal compositions of multiple kombucha (tea fungus) samples. <b>2014</b> , 38, 171-8	190
936	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
935	Biogeography of the sediment bacterial community responds to a nitrogen pollution gradient in the East China Sea. <b>2014</b> , 80, 1919-25	62
934	Microbial community dynamics and effect of environmental microbial reservoirs on red-backed salamanders ( <i>Plethodon cinereus</i> ). <b>2014</b> , 8, 830-40	196
933	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
932	Conventional CD4+ T cells regulate IL-22-producing intestinal innate lymphoid cells. <b>2014</b> , 7, 1045-57	58
931	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
930	Characterisation of the soil bacterial community structure and composition of natural and constructed wetlands. <b>2014</b> , 473-474, 63-71	160
929	Microbial mechanisms coupling carbon and phosphorus cycles in phosphorus-limited northern Adriatic Sea. <b>2014</b> , 470-471, 1173-83	9
928	Distinct microbial communities associated with buried soils in the Siberian tundra. <b>2014</b> , 8, 841-53	111
927	Soil extracellular enzyme activities correspond with abiotic factors more than fungal community composition. <b>2014</b> , 117, 23-37	67
926	Phylogeny-based classification of microbial communities. <b>2014</b> , 30, 449-56	19
925	Whole-genome sequencing of the snub-nosed monkey provides insights into folivory and evolutionary history. <b>2014</b> , 46, 1303-10	122
924	Human genetics shape the gut microbiome. <b>2014</b> , 159, 789-99	1750
923	Phyllosphere microbiota composition and microbial community transplantation on lettuce plants grown indoors. <b>2014</b> , 5,	56

922	High-fat maternal diet during pregnancy persistently alters the offspring microbiome in a primate model. <b>2014</b> , 5, 3889	288
921	EBI metagenomics--a new resource for the analysis and archiving of metagenomic data. <b>2014</b> , 42, D600-6	104
920	Phenolic metabolites and substantial microbiome changes in pig feces by ingesting grape seed proanthocyanidins. <b>2014</b> , 5, 2298-308	84
919	Diet alters probiotic <i>Lactobacillus</i> persistence and function in the intestine. <b>2014</b> , 16, 2915-26	45
918	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
917	Evidence of natural <i>Wolbachia</i> infections in field populations of <i>Anopheles gambiae</i> . <b>2014</b> , 5, 3985	110
916	Evidence for greater production of colonic short-chain fatty acids in overweight than lean humans. <b>2014</b> , 38, 1525-31	144
915	Wild-caught rodents retain a majority of their natural gut microbiota upon entrance into captivity. <b>2014</b> , 6, 191-5	71
914	Fecal microbiota of cats with naturally occurring chronic diarrhea assessed using 16S rRNA gene 454-pyrosequencing before and after dietary treatment. <b>2014</b> , 28, 59-65	32
913	Outlining microbial community dynamics during temperature drop and subsequent recovery period in anaerobic co-digestion systems. <b>2014</b> , 192 Pt A, 179-86	48
912	Effects of substratum type on bacterial community structure in biofilms in relation to settlement of plantigrades of the mussel <i>Mytilus coruscus</i> . <b>2014</b> , 96, 41-49	32
911	Forestry impacts on the hidden fungal biodiversity associated with bryophytes. <b>2014</b> , 90, 313-25	16
910	Changes in free-living bacterial community diversity reflect the magnitude of environmental variability. <b>2014</b> , 87, 291-301	23
909	A new species of <i>Burkholderia</i> isolated from sugarcane roots promotes plant growth. <b>2014</b> , 7, 142-54	63
908	Exopolysaccharide-producing probiotic <i>Lactobacilli</i> reduce serum cholesterol and modify enteric microbiota in ApoE-deficient mice. <b>2014</b> , 144, 1956-62	60
907	GeoChip-based insights into the microbial functional gene repertoire of marine sponges (high microbial abundance, low microbial abundance) and seawater. <b>2014</b> , 90, 832-43	34
906	STAMP: statistical analysis of taxonomic and functional profiles. <b>2014</b> , 30, 3123-4	1960
905	Population structure of the clover rhizobia <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> upon transition from soil into the nodular niche. <b>2014</b> , 83, 422-429	4

904	The communities of tomato ( <i>Solanum lycopersicum</i> L.) leaf endophytic bacteria, analyzed by 16S-ribosomal RNA gene pyrosequencing. <b>2014</b> , 351, 187-94	90
903	Genome-wide association study of <i>Arabidopsis thaliana</i> leaf microbial community. <b>2014</b> , 5, 5320	198
902	Bacterial degradation of Aroclor 1242 in the mycorrhizosphere soils of zucchini ( <i>Cucurbita pepo</i> L.) inoculated with arbuscular mycorrhizal fungi. <b>2014</b> , 21, 12790-9	20
901	Urea uptake and carbon fixation by marine pelagic bacteria and archaea during the Arctic summer and winter seasons. <b>2014</b> , 80, 6013-22	38
900	Pezizomycotina dominates the fungal communities of South China Sea sponges <i>Theonella swinhoei</i> and <i>Xestospongia testudinaria</i> . <b>2014</b> , 90, 935-45	14
899	Characterization of the rat oral microbiome and the effects of dietary nitrate. <b>2014</b> , 77, 249-57	61
898	Technology and techniques for microbial ecology via DNA sequencing. <b>2014</b> , 11 Suppl 1, S16-20	6
897	Gut microbiome composition and function in experimental colitis during active disease and treatment-induced remission. <b>2014</b> , 8, 1403-17	275
896	Biofouling and microbial communities in membrane distillation and reverse osmosis. <b>2014</b> , 48, 13155-64	59
895	Internal porosity of mineral coating supports microbial activity in rapid sand filters for groundwater treatment. <b>2014</b> , 80, 7010-20	27
894	Correlation between intraluminal oxygen gradient and radial partitioning of intestinal microbiota. <b>2014</b> , 147, 1055-63.e8	464
893	Transkingdom control of microbiota diurnal oscillations promotes metabolic homeostasis. <b>2014</b> , 159, 514-29	691
892	Native microbiome impedes vertical transmission of <i>Wolbachia</i> in <i>Anopheles</i> mosquitoes. <b>2014</b> , 111, 12498-503	153
891	Soil microbial responses to increased moisture and organic resources along a salinity gradient in a polar desert. <b>2014</b> , 80, 3034-43	103
890	Microbial community composition and dynamics in high-temperature biogas reactors using industrial bioethanol waste as substrate. <b>2014</b> , 98, 9095-106	28
889	Methane dynamics regulated by microbial community response to permafrost thaw. <b>2014</b> , 514, 478-81	240
888	Exploring the functional soil-microbe interface and exoenzymes through soil metaexoproteomics. <b>2014</b> , 8, 2148-50	30
887	Microbial reduction of U(VI) under alkaline conditions: implications for radioactive waste geodisposal. <b>2014</b> , 48, 13549-56	31

886	Microbial biogeography of wine grapes is conditioned by cultivar, vintage, and climate. <b>2014</b> , 111, E139-48	557
885	Assessing the impact of water treatment on bacterial biofilms in drinking water distribution systems using high-throughput DNA sequencing. <b>2014</b> , 117, 185-92	29
884	Gill bacteria enable a novel digestive strategy in a wood-feeding mollusk. <b>2014</b> , 111, E5096-104	67
883	Gastric microbiota is altered in oesophagitis and Barrett's oesophagus and further modified by proton pump inhibitors. <b>2014</b> , 16, 2905-14	105
882	Structural changes in the gut microbiome of constipated patients. <b>2014</b> , 46, 679-86	175
881	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
880	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
879	Vertebrate decomposition is accelerated by soil microbes. <b>2014</b> , 80, 4920-9	62
878	Hand bacterial communities vary across two different human populations. <b>2014</b> , 160, 1144-1152	44
877	Effect of postextraction algal residue supplementation on the ruminal microbiome of steers consuming low-quality forage. <b>2014</b> , 92, 5063-75	18
876	Systematic evaluation of bias in microbial community profiles induced by whole genome amplification. <b>2014</b> , 16, 643-57	27
875	Dynamics of gut microbiota in autoimmune lupus. <b>2014</b> , 80, 7551-60	167
874	Bacteria from diverse habitats colonize and compete in the mouse gut. <b>2014</b> , 159, 253-66	226
873	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
872	Plant traits and taxonomy drive host associations in tropical phyllosphere fungal communities. <b>2014</b> , 92, 303-311	108
871	Methanotrophic bacteria in warm geothermal spring sediments identified using stable-isotope probing. <b>2014</b> , 90, 92-102	23
870	Clustering of fungal community internal transcribed spacer sequence data obscures taxonomic diversity. <b>2014</b> , 16, 2491-500	16
869	Temperature response of denitrification and anaerobic ammonium oxidation rates and microbial community structure in Arctic fjord sediments. <b>2014</b> , 16, 3331-44	68

868	Development of methane emission from lambs fed milk replacer and cream for a prolonged period. <b>2014</b> , 198, 38-48	6
867	Investigation of bacterial and fungal diversity in tarag using high-throughput sequencing. <b>2014</b> , 97, 6085-96	47
866	Longitudinal analysis of microbial interaction between humans and the indoor environment. <b>2014</b> , 345, 1048-52	543
865	Associations of the fecal microbiome with urinary estrogens and estrogen metabolites in postmenopausal women. <b>2014</b> , 99, 4632-40	141
864	Routes of Acquisition of the Gut Microbiota of the Honey Bee <i>Apis mellifera</i> . <b>2014</b> , 80, 7378-87	250
863	"Social" network of isomers based on bond count distance: algorithms. <b>2014</b> , 54, 57-68	4
862	Responsiveness of cardiometabolic-related microbiota to diet is influenced by host genetics. <b>2014</b> , 25, 583-99	48
861	An Illumina metabarcoding pipeline for fungi. <b>2014</b> , 4, 2642-53	89
860	Rapid fucosylation of intestinal epithelium sustains host-commensal symbiosis in sickness. <b>2014</b> , 514, 638-41	343
859	Effects of a nutrient additive on the density of functional bacteria and the microbial community structure of bioorganic fertilizer. <b>2014</b> , 172, 328-334	8
858	Nitrate shaped the selenate-reducing microbial community in a hydrogen-based biofilm reactor. <b>2014</b> , 48, 3395-402	86
857	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
856	The application of bacterial indicator phylotypes to predict shrimp health status. <b>2014</b> , 98, 8291-9	45
855	Geochemical and microbiological responses to oxidant introduction into reduced subsurface sediment from the Hanford 300 Area, Washington. <b>2014</b> , 48, 9197-204	8
854	Biogeographic patterns in below-ground diversity in New York City's Central Park are similar to those observed globally. <b>2014</b> , 281,	201
853	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
852	Microbial genome-enabled insights into plant-microorganism interactions. <b>2014</b> , 15, 797-813	135
851	Tongue images and tongue coating microbiome in patients with colorectal cancer. <b>2014</b> , 77, 1-6	28

850	High-throughput sequencing reveals neustonic and planktonic microbial eukaryote diversity in coastal waters. <b>2014</b> , 50, 960-5	21
849	Diversity and Abundance of Ammonia-Oxidizing Archaea and Bacteria in Diverse Chinese Paddy Soils. <b>2014</b> , 31, 12-22	19
848	Latitudinal distribution of ammonia-oxidizing bacteria and archaea in the agricultural soils of eastern China. <b>2014</b> , 80, 5593-602	36
847	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. <b>2014</b> , 8, 1464-75	262
846	Who's for dinner? High-throughput sequencing reveals bat dietary differentiation in a biodiversity hotspot where prey taxonomy is largely undescribed. <b>2014</b> , 23, 3605-17	48
845	Lactobacillus rhamnosus HN001 decreases the severity of necrotizing enterocolitis in neonatal mice and preterm piglets: evidence in mice for a role of TLR9. <b>2014</b> , 306, G1021-32	79
844	The composition and transmission of microbiome in hard tick, Ixodes persulcatus, during blood meal. <b>2014</b> , 5, 864-70	64
843	Altered FXR signalling is associated with bile acid dysmetabolism in short bowel syndrome-associated liver disease. <b>2014</b> , 61, 1115-25	56
842	From barcoding single individuals to metabarcoding biological communities: towards an integrative approach to the study of global biodiversity. <b>2014</b> , 29, 566-71	239
841	Microbial determinants of biochemical individuality and their impact on toxicology and pharmacology. <b>2014</b> , 20, 761-768	43
840	High-fat-diet-mediated dysbiosis promotes intestinal carcinogenesis independently of obesity. <b>2014</b> , 514, 508-12	284
839	Agricultural soil and drilosphere as reservoirs of new and unusual assimilators of 2,4-dichlorophenol carbon. <b>2014</b> , 16, 84-100	32
838	Effect of metformin on metabolic improvement and gut microbiota. <b>2014</b> , 80, 5935-43	247
837	Marked seasonality of aerobic anoxygenic phototrophic bacteria in the coastal NW Mediterranean Sea as revealed by cell abundance, pigment concentration and pyrosequencing of pufM gene. <b>2014</b> , 16, 2953-65	41
836	Temporal dynamics of the cecal gut microbiota of juvenile arctic ground squirrels: a strong litter effect across the first active season. <b>2014</b> , 80, 4260-8	13
835	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
834	Stratified microbial structure and activity in sulfide- and methane-producing anaerobic sewer biofilms. <b>2014</b> , 80, 7042-52	67
833	Evaluating bias of illumina-based bacterial 16S rRNA gene profiles. <b>2014</b> , 80, 5717-22	163



832	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
831	Endospore-enriched sequencing approach reveals unprecedented diversity of Firmicutes in sediments. <b>2014</b> , 6, 631-9	34
830	Sequentially aerated membrane biofilm reactors for autotrophic nitrogen removal: microbial community composition and dynamics. <b>2014</b> , 7, 32-43	36
829	Protocols for metagenomic DNA extraction and Illumina amplicon library preparation for faecal and swab samples. <b>2014</b> , 14, 1183-97	45
828	Back to the future: natural history and the way forward in modern fungal ecology. <b>2014</b> , 12, 4-9	50
827	Animal rennets as sources of dairy lactic acid bacteria. <b>2014</b> , 80, 2050-61	33
826	Sputum microbiota in moderate versus severe patients with COPD. <b>2014</b> , 43, 1787-90	39
825	Smoking decreases structural and functional resilience in the subgingival ecosystem. <b>2014</b> , 41, 1037-47	54
824	Discrimination of plant-parasitic nematodes from complex soil communities using ecometagenetics. <b>2014</b> , 104, 749-61	8
823	Shifts in the microbial community, nitrifiers and denitrifiers in the biofilm in a full-scale rotating biological contactor. <b>2014</b> , 48, 8044-52	65
822	Nonpareil: a redundancy-based approach to assess the level of coverage in metagenomic datasets. <b>2014</b> , 30, 629-35	126
821	Molecular analysis for screening human bacterial pathogens in municipal wastewater treatment and reuse. <b>2014</b> , 48, 11610-9	56
820	An investigation of the biodiversity of thermophilic and thermotolerant fungal species in composts using culture-based and molecular techniques. <b>2014</b> , 11, 132-144	48
819	Plant defence inducers rapidly influence the diversity of bacterial communities in a potting mix. <b>2014</b> , 84, 1-5	23
818	Effects of almond and pistachio consumption on gut microbiota composition in a randomised cross-over human feeding study. <b>2014</b> , 111, 2146-52	88
817	Agricultural Bioinformatics. <b>2014</b> ,	1
816	Coinfection. Virus-helminth coinfection reveals a microbiota-independent mechanism of immunomodulation. <b>2014</b> , 345, 578-82	195
815	Biochar impacts soil microbial community composition and nitrogen cycling in an acidic soil planted with rape. <b>2014</b> , 48, 9391-9	305

814	Evolutionary Biology: Genome Evolution, Speciation, Coevolution and Origin of Life. <b>2014</b> ,	4
813	The impact of postnatal antibiotics on the preterm intestinal microbiome. <b>2014</b> , 76, 150-8	45
812	Gut microbial metabolism drives transformation of MSH2-deficient colon epithelial cells. <b>2014</b> , 158, 288-299	283
811	Microbial community dynamics in a submerged fixed bed bioreactor during biological treatment of saline urban wastewater. <b>2014</b> , 71, 126-132	51
810	Conducting a microbiome study. <b>2014</b> , 158, 250-262	428
809	Using metabarcoding to ask if easily collected soil and leaf-litter samples can be used as a general biodiversity indicator. <b>2014</b> , 46, 379-389	53
808	SnapShot: the human microbiome. <b>2014</b> , 158, 690-690.e1	20
807	Causal relationship between microbial ecology dynamics and proteolysis during manufacture and ripening of protected designation of origin (PDO) cheese Canestrato Pugliese. <b>2014</b> , 80, 4085-94	42
806	Altering the intestinal microbiota during a critical developmental window has lasting metabolic consequences. <b>2014</b> , 158, 705-721	1126
805	A comprehensive insight into bacterial virulence in drinking water using 454 pyrosequencing and Illumina high-throughput sequencing. <b>2014</b> , 109, 15-21	50
804	Evidence of environmental and vertical transmission of Burkholderia symbionts in the oriental chinch bug, Cavalerius saccharivorus (Heteroptera: Blissidae). <b>2014</b> , 80, 5974-83	70
803	Correlation between viral production and carbon mineralization under nitrate-reducing conditions in aquifer sediment. <b>2014</b> , 8, 1691-703	25
802	Cheese rind communities provide tractable systems for in situ and in vitro studies of microbial diversity. <b>2014</b> , 158, 422-433	328
801	Computational integration of genomic traits into 16S rDNA microbiota sequencing studies. <b>2014</b> , 549, 186-91	15
800	Improved resolution of bacteria by high throughput sequence analysis of the rRNA internal transcribed spacer. <b>2014</b> , 105, 82-7	21
799	Methodological approaches for studying the microbial ecology of drinking water distribution systems. <b>2014</b> , 65, 134-56	148
798	Individual diet has sex-dependent effects on vertebrate gut microbiota. <b>2014</b> , 5, 4500	330
797	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

796	The role of bacteria in the pathogenesis and progression of idiopathic pulmonary fibrosis. <b>2014</b> , 190, 906-13	320
795	Bacterial diversity assessment in soil of an active Brazilian copper mine using high-throughput sequencing of 16S rDNA amplicons. <b>2014</b> , 106, 879-90	31
794	Handling temperature bursts reaching 464°C: different microbial strategies in the sisters peak hydrothermal chimney. <b>2014</b> , 80, 4585-98	17
793	Low temperature partial nitrification/anammox in a moving bed biofilm reactor treating low strength wastewater. <b>2014</b> , 48, 8784-92	257
792	Getting started with microbiome analysis: sample acquisition to bioinformatics. <b>2014</b> , 82, 18.8.1-29	79
791	Microbial genomic analysis reveals the essential role of inflammation in bacteria-induced colorectal cancer. <b>2014</b> , 5, 4724	222
790	Molecular methods for biofilms. <b>2014</b> , 87-137	
789	Evaluation of bifidobacterial community composition in the human gut by means of a targeted amplicon sequencing (ITS) protocol. <b>2014</b> , 90, 493-503	62
788	Synchronous dynamics and correlations between bacteria and phytoplankton in a subtropical drinking water reservoir. <b>2014</b> , 90, 126-38	47
787	A guide to statistical analysis in microbial ecology: a community-focused, living review of multivariate data analyses. <b>2014</b> , 90, 543-50	197
786	An effective intervention to reduce intravaginal practices among HIV-1 uninfected Kenyan women. <b>2014</b> , 30, 1046-54	15
785	Gastrointestinal microbiota of wild and inbred individuals of two house mouse subspecies assessed using high-throughput parallel pyrosequencing. <b>2014</b> , 23, 5048-60	47
784	The effect of captivity on the cutaneous bacterial community of the critically endangered Panamanian golden frog ( <i>Atelopus zeteki</i> ). <b>2014</b> , 176, 199-206	80
783	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
782	Bacterial community composition and diversity of five different permafrost-affected soils of Northeast Greenland. <b>2014</b> , 89, 426-41	51
781	'Rare biosphere' bacteria as key phenanthrene degraders in coastal seawaters. <b>2014</b> , 194, 246-253	50
780	MT-Toolbox: improved amplicon sequencing using molecule tags. <b>2014</b> , 15, 284	17
779	Exercise induction of gut microbiota modifications in obese, non-obese and hypertensive rats. <b>2014</b> , 15, 511	171

778	Conservation of streptococcal CRISPRs on human skin and saliva. <b>2014</b> , 14, 146	15
777	SYNbiotics Easing Renal failure by improving Gut microbiology (SYNERGY): a protocol of placebo-controlled randomised cross-over trial. <b>2014</b> , 15, 106	34
776	Metataxonomic profiling and prediction of functional behaviour of wheat straw degrading microbial consortia. <b>2014</b> , 7, 92	69
775	Comparative assessment of the bacterial communities associated with <i>Aedes aegypti</i> larvae and water from domestic water storage containers. <b>2014</b> , 7, 391	43
774	Co-occurrence of driver and passenger bacteria in human colorectal cancer. <b>2014</b> , 6, 26	49
773	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
772	Characterization of the nasopharyngeal microbiota in health and during rhinovirus challenge. <b>2014</b> , 2, 22	87
771	Characterization of the vaginal microbiota of healthy Canadian women through the menstrual cycle. <b>2014</b> , 2, 23	139
770	Effect of chemotherapy on the microbiota and metabolome of human milk, a case report. <b>2014</b> , 2, 24	67
769	The Earth Microbiome project: successes and aspirations. <b>2014</b> , 12, 69	501
768	Artificial sweeteners induce glucose intolerance by altering the gut microbiota. <b>2014</b> , 514, 181-6	1088
767	Impact of primer choice on characterization of orchid mycorrhizal communities using 454 pyrosequencing. <b>2014</b> , 14, 679-99	75
766	Human oral viruses are personal, persistent and gender-consistent. <b>2014</b> , 8, 1753-67	107
765	Pyrosequencing reveals transient cystic fibrosis lung microbiome changes with intravenous antibiotics. <b>2014</b> , 44, 922-30	61
764	Immunoglobulin A coating identifies colitogenic bacteria in inflammatory bowel disease. <b>2014</b> , 158, 1000-1010	715
763	Data analysis for 16S microbial profiling from different benchtop sequencing platforms. <b>2014</b> , 107, 30-7	168
762	Beyond genome sequencing: lineage tracking with barcodes to study the dynamics of evolution, infection, and cancer. <b>2014</b> , 104, 417-30	52
761	A hidden pitfall in the preparation of agar media undermines microorganism cultivability. <b>2014</b> , 80, 7659-66	133

760	Will different OTU delineation methods change interpretation of arbuscular mycorrhizal fungal community patterns?. <b>2014</b> , 202, 1101-1104	50
759	Effects of temperature and hydraulic retention time on acetotrophic pathways and performance in high-rate sludge digestion. <b>2014</b> , 48, 6468-76	79
758	Fermentable fibres condition colon microbiota and promote diabetogenesis in NOD mice. <b>2014</b> , 57, 2183-92	32
757	Primate vaginal microbiomes exhibit species specificity without universal <i>Lactobacillus</i> dominance. <b>2014</b> , 8, 2431-44	110
756	A20 controls intestinal homeostasis through cell-specific activities. <b>2014</b> , 5, 5103	78
755	Foxp3(+) T cells regulate immunoglobulin a selection and facilitate diversification of bacterial species responsible for immune homeostasis. <b>2014</b> , 41, 152-65	333
754	Minor changes in soil bacterial and fungal community composition occur in response to monsoon precipitation in a semiarid grassland. <b>2014</b> , 68, 370-8	28
753	Rhizospheric microbiomics integrated with plant transcriptomics provides insight into the Cd response mechanisms of the newly identified Cd accumulator <i>Dahlia pinnata</i> . 13,	0
752	Grassland Degradation Has Stronger Effects on Soil Fungal Community Than Bacterial Community across the Semi-Arid Region of Northern China. <b>2022</b> , 11, 3488	0
751	An environmental DNA metabarcoding approach versus a visual survey for reefs of Koh Pha-ngan in Thailand.	0
750	Effects of Water Temperature on the Growth, Antioxidant Capacity, and Gut Microbiota of <i>Percocypris pingi</i> Juveniles. <b>2022</b> , 7, 374	0
749	Unveiling the Wheat Microbiome under Varied Agricultural Field Conditions. <b>2022</b> , 10,	0
748	Effects of replacing fishmeal with cottonseed protein concentrate on growth performance, blood metabolites, and the intestinal health of juvenile rainbow trout ( <i>Oncorhynchus mykiss</i> ). 13,	0
747	Oral Bacteriome and Mycobiome across Stages of Oral Carcinogenesis. <b>2022</b> , 10,	1
746	Effects of microbiota-directed supplementary foods on gut microbiota in fecal colonized mice of healthy infants. <b>2022</b> , 99, 105346	0
745	Computational estimation of sediment symbiotic bacterial structures of seagrasses overgrowing downstream of onshore aquaculture. <b>2022</b> , 115130	0
744	Methane Production Linked to Organic Matter Molecule and Methanogenic Community in Estuarine Benthic Sediments. <b>2022</b> , 127,	0
743	Plant and fungal species interactions differ between aboveground and belowground habitats in mountain forests of eastern China.	1

- 742 Dietary baicalein improves growth performance, antioxidant activity, and intestinal flora of koi carp (*Cyprinus carpio*). **2022**, 27, 101421 1
- 741 Allelopathic Effects of *Amomum villosum* Lour. Volatiles from Different Organs on Selected Plant Species and Soil Microbiota. **2022**, 11, 3550 0
- 740 Commensal Microbiota Regulate Renal Gene Expression. 0
- 739 Climate-smart agricultural practices influence the fungal communities and soil properties under major agri-food systems. 13, 0
- 738 Dietary Fish Meal Level and a Package of Choline,  $\beta$ -Glucan, and Nucleotides Modulate Gut Function, Microbiota, and Health in Atlantic Salmon (*Salmo salar*, L.). **2023**, 2023, 1-29 0
- 737 Gut Microbiome Composition of the Fire Ant *Solenopsis invicta*: an Integrated Analysis of Host Genotype and Geographical Distribution. 0
- 736 Microcystin-LR exposure interfered maintenance of colonic microenvironmental homeostasis in rat. **2023**, 113611 0
- 735 Dietary supplemental coated essential oils and organic acids mixtures improves growth performance and gut health along with reduces *Salmonella* load of broiler chickens infected with *Salmonella Enteritidis*. 0
- 734 Soil microbial community shifts explain habitat heterogeneity in two *Haloxylon* species from a nutrient perspective. **2023**, 13, 0
- 733 The impact of iron and heme availability on the healthy human gut microbiome in vivo and in vitro. **2023**, 0
- 732 Effects of copper oxide nanoparticles on soil diazotrophic communities in maize rhizosphere. 0
- 731 Fecal and Tissue Microbiota Are Associated with Tumor T-Cell Infiltration and Mesenteric Lymph Node Involvement in Colorectal Cancer. **2023**, 15, 316 0
- 730 Hydropower dam alters the microbial structure of fish gut in different habitats in upstream and downstream rivers. 0
- 729 Effect of Post-Ruminal Urea Supply on Growth Performance of Grazing Nellore Young Bulls at Dry Season. **2023**, 13, 207 0
- 728 Linkages between the molecular composition of dissolved organic matter and soil microbial community in a boreal forest during freeze-thaw cycles. 13, 0
- 727 Bacterial community characteristics in the rhizosphere of *Suaeda glauca* versus bulk soil in coastal silt soil modified by sea-sand and their implications. 9, 0
- 726 The response of rumen pH, fermentation parameters and rumen bacteria to feeds of different concentrate to roughage ratios in buffalos. 1, 0
- 725 Gut microbiota signatures in tissues of the colorectal polyp and normal colorectal mucosa, and faeces. 12, 0

- 724 Rhizosphere Microbial Community Shows a Greater Response Than Soil Properties to Tea (*Camellia sinensis* L.) Cultivars. **2023**, 13, 221 ○
- 723 The effects of dietary supplementation with mushroom or selenium enriched mushroom powders on the growth performance and intestinal health of post-weaned pigs. **2023**, 14, ○
- 722 Microbiota-dependent proteolysis of gluten subverts diet-mediated protection against type 1 diabetes. **2023**, ○
- 721 Association of indoor dust microbiota with cognitive function and behavior in preschool-aged children. **2023**, 11, ○
- 720 Mechanism of Enhancing Pyrazines in Daqu via Inoculating *Bacillus licheniformis* with Strains Specificity. **2023**, 12, 304 ○
- 719 Metagenomic data reveals microbiome characteristics of culture-negative brain abscess samples. **2023**, 108893 ○
- 718 The characters of root-derived fungi from *Gentiana scabra* Bunge and the relations with their habitats. ○
- 717 In Vitro Fermentation of *Pleurotus eryngii* Mushrooms by Human Fecal Microbiota: Metataxonomic Analysis and Metabolomic Profiling of Fermentation Products. **2023**, 9, 128 ○
- 716 Modelling the Gut Fungal-Community in TIM-2 with a Microbiota from Healthy Individuals. **2023**, 9, 104 ○
- 715 The Effects of Atrazine, Diuron, Fluazifop-P-butyl, Haloxyfop-P-methyl, and Pendimethalin on Soil Microbial Activity and Diversity. **2023**, 3, 79-89 ○
- 714 6His-tatritin promotes antimicrobial defense via regulating immune ability and intestinal microbial community in grass carp (*Ctenopharyngodon idella*). **2023**, 108532 ○
- 713 Edible exosome-like nanoparticles from *Portulaca oleracea* L prevent DSS-induced colitis via the promotion of double-positive CD4 + CD8 + T cells. ○
- 712 Culturomics- and metagenomics-based insights into the microbial community and function of rhizosphere soils in Sinai desert farming systems. **2023**, 18, ○
- 711 Dynamics of Microbial Community and Potential Microbial Pollutants in Shopping Malls. ○
- 710 Insular holobionts: persistence and seasonal plasticity of the Balearic wall lizard (*Podarcis lilfordi*) gut microbiota. 11, e14511 ○
- 709 Role of biochar in anaerobic microbiome enrichment and methane production enhancement during olive mill wastewater biomethanization. 10, ○
- 708 Dietary nano-selenium alleviates heat stress-induced intestinal damage through affecting intestinal antioxidant capacity and microbiota in rainbow trout (*Oncorhynchus mykiss*). **2023**, 108537 ○
- 707 Intercropping enhances microbial community diversity and ecosystem functioning in maize fields. 13, ○

706	Effects of Zhishi Daozhi Decoction on the intestinal flora of nonalcoholic fatty liver disease mice induced by a high-fat diet. 12,	0
705	Roles of vaginal flora in human papillomavirus infection, virus persistence and clearance. 12,	1
704	Akkermansia muciniphila protects mice against an emerging tick-borne viral pathogen. 2023, 8, 91-106	1
703	Methanol extract of Inonotus obliquus improves type 2 diabetes mellitus through modifying intestinal flora. 13,	0
702	Microbial community and predictive functionalities associated with the marine sediment of Coastal Gujarat.	0
701	The alteration of intrauterine microbiota in chronic endometritis patients based on 16S rRNA sequencing analysis. 2023, 22,	0
700	Organo-mineral complexes in soil colloids from an eight-year field experiment: Implications for carbon storage in saline-alkaline paddy soil. 2023,	0
699	Construction of Model Animals to Explore Intestinal Microbiome for Detection of Breast Cancer.	0
698	Microbial community structure and biogenic amines content variations in chilled chicken during storage.	1
697	Microbiome Data Analysis and Interpretation: Correlation Inference and Dynamic Pattern Discovery. 2023, 119-144	0
696	Immunomagnetic Capture of Faecalibacterium prausnitzii Selectively Modifies the Fecal Microbiota and Its Immunomodulatory Profile.	1
695	Lorcaserin and phentermine exert anti-obesity effects with modulation of the gut microbiota. 13,	0
694	Biodegradation of chemicals tested in mixtures and individually: mixture effects on biodegradation kinetics and microbial composition.	0
693	Rice Straw Composting Improves the Microbial Diversity of Paddy Soils to Stimulate the Growth, Yield, and Grain Quality of Rice. 2023, 15, 932	1
692	An oral cancer vaccine using a Bifidobacterium vector enhances the efficacy of combination therapy with anti-PD-1 and anti-CTLA-4 antibodies in a mouse renal cell carcinoma model.	0
691	Continuous-cropping-tolerant soybean cultivars alleviate continuous cropping obstacles by improving structure and function of rhizosphere microorganisms. 13,	0
690	Changes in the Ixodes ricinus microbiome associated with artificial tick feeding. 13,	0
689	Impacts of co-contaminants and dilution on perchlorate biodegradation using various carbon sources.	0



- 688 Different patterns and drivers of fungal communities between phyllosphere and rhizosphere in alpine grasslands. ○
- 687 Exacerbation of allergic rhinitis by the commensal bacterium *Streptococcus salivarius*. ○
- 686 *Poria cocos* Polysaccharide Ameliorated Antibiotic-Associated Diarrhea in Mice via Regulating the Homeostasis of the Gut Microbiota and Intestinal Mucosal Barrier. **2023**, 24, 1423 ○
- 685 Fecal microbiota transplantation and short-chain fatty acids protected against cognitive dysfunction in a rat model of chronic cerebral hypoperfusion. 1
- 684 A global perspective on bacterial diversity in the terrestrial deep subsurface. **2023**, 169, ○
- 683 Dietary-Induced Bacterial Metabolites Reduce Inflammation and Inflammation-Associated Cancer via Vitamin D Pathway. **2023**, 24, 1864 ○
- 682 Stochastic processes dominate community assembly of ectomycorrhizal fungi associated with *Picea crassifolia* in the Helan Mountains, China. 13, ○
- 681 Deep mowing rather than fire restrains grassland *Miscanthus* growth via affecting soil nutrient loss and microbial community redistribution. 13, ○
- 680 Effects of Different-Sized Cages on the Production Performance, Serum Parameters, and Caecal Microbiota Composition of Laying Hens. **2023**, 13, 266 ○
- 679 Enrichment of keystone fungal taxa after flue gas desulphurization gypsum application drives reclamation of the saline-sodic soil. ○
- 678 Multi-Omics Data Analysis for Inflammation Disease Research: Correlation Analysis, Causal Analysis and Network Analysis. **2023**, 101-118 ○
- 677 Microbial Community Dynamics during a Harmful *Chrysochromulina leadbeateri* Bloom in Northern Norway. ○
- 676 Preventive effect of *Terminalia bellirica* (Gaertn.) Roxb. extract on mice infected with *Salmonella Typhimurium*. 12, ○
- 675 Surrogate fostering of mice prevents prenatal estradiol-induced insulin resistance via modulation of the microbiota-gut-brain axis. 13, ○
- 674 Metagenomic analysis of oral plaques and aortic valve tissues reveals oral bacteria associated with aortic stenosis. ○
- 673 Association of Fructo-oligosaccharides and Arginine Improves Severity of Mucositis and Modulate the Intestinal Microbiota. ○
- 672 Alterations of gut mycobiota profiles in intrahepatic cholangiocarcinoma. 13, ○
- 671 Protocooperative Effect of *Sphaerodes mycoparasitica* Biocontrol and Crop Genotypes on FHB Mycotoxin Reduction in Bread and Durum Wheat Grains Intended for Human and Animal Consumption. **2023**, 11, 159 ○

- 670 eDNA Biomonitoring of Macroinvertebrate Communities for the Bioassessment of a River's Ecological Status. **2023**, 15, 308 ○
- 669 Microbial community composition and function in an urban waterway with combined sewer overflows before and after implementation of a stormwater storage pipe. 11, e14684 ○
- 668 Bacteroides-derived isovaleric acid enhances mucosal immunity by facilitating intestinal IgA response in broilers. **2023**, 14, ○
- 667 The root enrichment of bacteria is consistent across different stress-resistant plant species. 11, e14683 ○
- 666 Effect of whole oilseeds in the diet on bacterial diversity in the solid fraction of the ruminal content of steers. **2023**, 55, ○
- 665 Protective Effect of Vegan Microbiota on Liver Steatosis Is Conveyed by Dietary Fiber: Implications for Fecal Microbiota Transfer Therapy. **2023**, 15, 454 ○
- 664 Effects of substrate improvement on winter nitrogen removal in riparian reed (*Phragmites australis*) wetlands: Rhizospheric crosstalk between plants and microbes. ○
- 663 3L, three-Lactobacilli on recovering of microbiome and immune-damage by cyclophosphamide chemotherapy – pilot experiment in rats ○
- 662 Assessment of Mound Soils Bacterial Community of the Red Imported Fire Ant, *Solenopsis invicta* across Guangdong Province of China. **2023**, 15, 1350 1
- 661 Co-invasive ectomycorrhizal fungi alter native soil fungal communities. ○
- 660 Functional insights into succession in a phyllospheric microbial community across a full stage of plant litter decomposition in wetlands. ○
- 659 Glucose addition improves the culture performance of Pacific white shrimp by regulating the assembly of Rhodobacteraceae taxa in gut bacterial community. **2023**, 739254 ○
- 658 Combined microbiome and metabolome analysis of gut microbiota and metabolite interactions in chronic spontaneous urticaria. 12, ○
- 657 High-throughput sequencing to detect the bacterial microbiome in *Ixodes granulatus* in China. ○
- 656 Effects of a probiotic suspension Symprove™ on a rat early-stage Parkinson's disease model. 14, ○
- 655 Plant Community Associates with Rare Rather than Abundant Fungal Taxa in Alpine Grassland Soils. ○
- 654 Long-term effects of soluble and insoluble ferric irons on anaerobic oxidation of methane in paddy soil. **2023**, 137901 ○
- 653 Effects of Citrus Pulp on the Composition and Diversity of Broiler Caecal Microbes. **2023**, 102454 ○

- 652 Comparing diversity patterns and processes of microbial community assembly in water column and sediment in Lake Wuchang, China. 11, e14592 ○
- 651 Characterization of the Fecal and Mucosa-Associated Microbiota in Dogs with Chronic Inflammatory Enteropathy. **2023**, 13, 326 1
- 650 Enrichment cultivation of VOC-degrading bacteria using diffusion bioreactor and development of bacterial-immobilized biochar for VOC bioremediation. **2023**, 121089 ○
- 649 Current Progress of Bioinformatics for Human Health. **2023**, 145-162 ○
- 648 TRIM27 maintains gut homeostasis by promoting intestinal stem cell self-renewal. ○
- 647 Spatiotemporal evolution and assembly processes of ammonia-oxidizing prokaryotic communities in 1000 years of coastal reclaimed soils. **2023**, ○
- 646 Hydrological connections in a glaciated Andean catchment under permafrost conditions (33°S). **2023**, 101311 ○
- 645 Seasonal Hypoxia Enhances Benthic Nitrogen Fixation and Shapes Specific Diazotrophic Community in the Eutrophic Marine Ranch. **2023**, 11, 138 ○
- 644 Impact of COVID-19 on the Microbiome and Inflammatory Status of Type 2 Diabetes Patients. **2023**, 11, 179 ○
- 643 Food web structure and microenvironment affect Chagas disease vector infection and abundance in a rural landscape. **2023**, 14, ○
- 642 3L, three-Lactobacilli on recovering of microbiome and immune-damage by cyclophosphamide chemotherapy — pilot experiment — ○
- 641 Association between microbial community composition and quality indicators of strong-flavor Daqu of different producing regions in China. **2023**, 21, 82-92 ○
- 640 The composition and function profile of the gut microbiota of patients with primary Sjögren's syndrome. ○
- 639 Grain, Gluten, and Dietary Fiber Intake Influence Gut Microbial Diversity: Data from the Food and Microbiome Longitudinal Investigation. **2023**, 3, 43-53 ○
- 638 The role of protein contents in promoting wastewater phosphorus and bioenergy recovery during anaerobic digestion. **2023**, 169, 106694 ○
- 637 Effects of the addition of starches with different amylose contents on kimchi microbiota and metabolites. **2023**, 175, 114475 ○
- 636 Quantifying relative contributions of biotic interactions to bacterial diversity and community assembly by using community characteristics of microbial eukaryotes. **2023**, 146, 109841 ○
- 635 Long-term afforestation enhances stochastic processes of bacterial community assembly in a temperate grassland. **2023**, 430, 116317 ○

- 634 Deep vertical rotary tillage mitigates salinization hazards and shifts microbial community structure in salt-affected anthropogenic-alluvial soil. **2023**, 227, 105627 ○
- 633 Elevated antimony concentration stimulates rare taxa of potential autotrophic bacteria in the Xikuangshan groundwater. **2023**, 864, 161105 ○
- 632 Biological conversion of methane to methanol at high H<sub>2</sub>S concentrations with an H<sub>2</sub>S-tolerant methanotrophic consortium. **2023**, 204, 475-484 ○
- 631 Soil pH determines arsenic-related functional gene and bacterial diversity in natural forests on the Taibai Mountain. **2023**, 220, 115181 1
- 630 Antibiotic and heavy metal resistance genes in sewage sludge survive during aerobic composting. **2023**, 866, 161386 ○
- 629 Interaction among biofilter microbiome, fecal metabolome and water quality and regulation of sewage discharge in the recirculating aquaculture system of *Apostichopus japonicus*. **2023**, 330, 117100 ○
- 628 Hazard reduction and persistence of risk of antibiotic resistance during thermophilic composting of animal waste. **2023**, 330, 117249 ○
- 627 Changes in bacterial diversity, co-occurrence pattern, and potential pathogens following digestate fertilization: Extending pathogen management to field for anaerobic digestion of livestock manure. **2023**, 158, 107-115 ○
- 626 Characterization of root microbial communities associated with *Astragalus membranaceus* and their correlation with soil environmental factors. **2023**, 25, 100656 ○
- 625 Exposure to cadmium induced gut antibiotic resistance genes (ARGs) and microbiota alternations of *Babylonia areolata*. **2023**, 865, 161243 ○
- 624 Methane concentration and bacterial communities dynamics during the anoxic desulfurization of landfill biogas under diverse nitrate sources and hydraulic residence times. **2023**, 11, 109285 ○
- 623 Soil microbiota impact on *Boletus edulis* mycelium in chestnut orchards of different ages. **2023**, 185, 104790 ○
- 622 Effects of solarisation combined with compost on soil pathogens and the microbial community in a spinach cropping system. **2023**, 346, 108359 ○
- 621 A special drop: Characterising yeast isolates associated with fermented beverages produced by Australia's indigenous peoples. **2023**, 112, 104216 ○
- 620 Fusion of blockchain and IoT in scientific publishing: Taxonomy, tools, and future directions. **2023**, 142, 248-275 ○
- 619 Interconnected versus unconnected microorganisms: Does it matter in anaerobic digestion functioning. **2023**, 331, 117307 ○
- 618 Elevated CO<sub>2</sub> and/or O<sub>3</sub> shift the functional processes and structural complexity of soil protists in a paddy soil. **2023**, 185, 104806 ○
- 617 Soil bacterial community structure and functions but not assembly processes are affected by the conversion from monospecific *Cunninghamia lanceolata* plantations to mixed plantations. **2023**, 185, 104775 ○

- 616 Continuous cropping of cut chrysanthemum reduces rhizospheric soil bacterial community diversity and co-occurrence network complexity. **2023**, 185, 104801 ○
- 615 Proper Biochar Increases Maize Fine Roots and Yield via Altering Rhizosphere Bacterial Communities under Plastic Film Mulching. **2023**, 13, 60 ○
- 614 Sludge composition and characteristics shaped microbial community and further determined process performance: A study on full-scale thermal hydrolysis-anaerobic digestion processes. **2022**, 41, 98-104 ○
- 613 In situ cultivation of deep-sea water with bicarbonate fueled a different microbial community. **2022**, 41, 98-104 ○
- 612 Photodynamic therapy treats acne by altering the composition of the skin microbiota. **2023**, 29, ○
- 611 Prospects of endophytic fungi as a natural resource for the sustainability of crop production in the modern era of changing climate. ○
- 610 Seasonal Changes Modulate the Rhizosphere of Desert Plant Species. **2023**, 13, 57 ○
- 609 Bacterial and Fungal Symbionts in Pollen Provisions of a Native Solitary Bee in Urban and Rural Environments. ○
- 608 Prophylactic Effect of Bovine Colostrum on Intestinal Microbiota and Behavior in Wild-Type and Zonulin Transgenic Mice. **2023**, 11, 91 1
- 607 Gut microbiota diversity in human strongyloidiasis differs little in two different regions in endemic areas of Thailand. **2022**, 17, e0279766 ○
- 606 Inhibitory effect of nitrogen deposition on soil denitrifying activity in a subtropical forest. ○
- 605 Huangtu decoction alleviates chronic diarrhea of spleen-yang deficiency in mice by altering host metabolome and intestinal microbiota composition. ○
- 604 New Insights into the Effect of Fipronil on the Soil Bacterial Community. **2023**, 11, 52 ○
- 603 Pyuria Is Associated with Dysbiosis of the Urinary Microbiota in Type 2 Diabetes Patients Receiving Sodium-glucose Cotransporter 2 Inhibitors. **2023**, 14, 34-41 1
- 602 CCL17 Promotes Colitis-Associated Tumorigenesis Dependent on the Microbiota. **2022**, 209, 2227-2238 ○
- 601 The ground beetle *Pseudoophonus rufipes* gut microbiome is influenced by the farm management system. **2022**, 12, ○
- 600 Microbial Population Dynamics in Lemnaceae (Duckweed)-Based Wastewater Treatment System. **2023**, 80, ○
- 599 Multi-omics gut microbiome signatures in obese women: role of diet and uncontrolled eating behavior. **2022**, 20, 1

- 598 Application of DNA Metabarcoding for Identifying the Diet of Asian Clam (*Corbicula fluminea*, Müller, 1774). **2023**, 15, 441 ○
- 597 What Is the Impact of Leaky Sewers on Groundwater Contamination in Urban Semi-Confined Aquifers? A Test Study Related to Fecal Matter and Personal Care Products (PCPs). **2023**, 10, 3 ○
- 596 Modulating the Gut Microbiota with Alginate Oligosaccharides In Vitro. **2023**, 3, 26-38 ○
- 595 Amendment of a thermophile-fermented compost to humus improves the growth of female larvae of the Hercules beetle *Dynastes hercules* (Coleoptera: scarabaeidae). **2023**, 134, ○
- 594 Beneficial metabolic transformations and prebiotic potential of hemp bran and its alcalase hydrolysate, after colonic fermentation in a gut model. **2023**, 13, ○
- 593 Endolichenic actinobacterial association in fruticose, foliose, and crustose lichens. **2023**, 177-191 ○
- 592 Implementation of a Pilot-Scale Biotrickling Filtration Process for Biogas Desulfurization under Anoxic Conditions Using Agricultural Digestate as Trickle Liquid. **2023**, 10, 160 ○
- 591 Analysis of serum antioxidant capacity and gut microbiota in calves at different growth stages in Tibet. 13, ○
- 590 multiMiAT: an optimal microbiome-based association test for multicategory phenotypes. ○
- 589 Linking processes to community functions—insights into litter decomposition combining fungal metatranscriptomics and environmental NMR profiling. **2023**, 22, ○
- 588 Effect of Methionine Hydroxy Analog on Hu Sheep Digestibility, Rumen Fermentation, and Rumen Microbial Community In Vitro. **2023**, 13, 169 ○
- 587 EasyAmplicon: An easy-to-use, open-source, reproducible, and community-based pipeline for amplicon data analysis in microbiome research. ○
- 586 Cold sediment microbial community shifts in response to crude oil water-accommodated fraction with or without dispersant: a microcosm study. ○
- 585 The community profiles of symbiotic bacteria at the different life stages of coral *Dipsastraea favus*. 10, ○
- 584 Cell-Specific, Disease-Associated and Variant-Linked Alterations In Expression Of ERAP1, ERAP2 and LNPEP Aminopeptidases. **2023**, ○
- 583 Gut Microbiome Associated With Graves Disease and Graves Orbitopathy: The INDIGO Multicenter European Study. 1
- 582 Suppression of Banana Fusarium Wilt Disease with Soil Microbial Mechanisms via Pineapple Rotation and Residue Amendment. **2023**, 13, 377 ○
- 581 Development of the gut microbiota during early life in premature and term infants. **2023**, 15, ○

- 580 Response of the Soil Fungal Community and Its Function during the Conversion of Forestland to Tea Plantations: A Case Study in Southeast China. **2023**, 14, 209 ○
- 579 *Bacteroides uniformis* and its preferred substrate,  $\beta$ -cyclodextrin, enhance endurance exercise performance in mice and human males. **2023**, 9, ○
- 578 Cannabidiol and Cannabigerol Exert Antimicrobial Activity without Compromising Skin Microbiota. **2023**, 24, 2389 1
- 577 Plant selection and ecological microhabitat drive domestications of shrub-associated microbiomes in a revegetated shrub ecosystem. ○
- 576 Dynamic Changes in the Gut Microbiota and Metabolites during the Growth of Hainan Wenchang Chickens. **2023**, 13, 348 ○
- 575 Combined analysis of gut microbiome and serum metabolomics reveals novel biomarkers in patients with early-stage non-small cell lung cancer. 13, ○
- 574 Strengthening and microbial regulation mechanism of *Bacillus* on purification device for grass carp culture wastewater. 11, ○
- 573 Sex-specific competition differently regulates the response of the rhizosphere fungal community of *Hippophae rhamnoides* dioecious plant, under Mn stress. 14, ○
- 572 Residual Effects of Transgenic Cotton on the Intestinal Microbiota of *Dysdercus concinnus*. **2023**, 11, 261 ○
- 571 MBPD: A multiple bacterial pathogen detection pipeline for One Health practices. 1
- 570 Phosphorus Solubilization by Biological Acidification of Pig Slurry Using Agri-Food Waste: Efficiency and Underpinning Chemical and Microbiological Parameters. ○
- 569 Effect of Light Heterogeneity Caused by Photovoltaic Panels on the Plant-Soil-Microbial System in Solar Park. **2023**, 12, 367 ○
- 568 Recurrent phases of strict protein limitation inhibit tumor growth and restore lifespan in a *Drosophila* intestinal cancer model. ○
- 567 Fish Biomonitoring and Ecological Assessment in the Dianchi Lake Basin Based on Environmental DNA. **2023**, 15, 399 ○
- 566 Dietary Sodium Butyrate Improves Intestinal Health of Triploid *Oncorhynchus mykiss* Fed a Low Fish Meal Diet. **2023**, 12, 145 ○
- 565 Biogeography and potential ecological functions of prokaryotes in the hydrothermal and non-hydrothermal field sediments of the Indian Ocean Ridges. 9, ○
- 564 The effects of native lactic acid bacteria on the microbiome, fermentation profile, and nutritive value of Napier grass silage prepared with different legume ratios. 13, ○
- 563 Multi-Omic Profiling, Structural Characterization, and Potent Inhibitor Screening of Evasion-Related Proteins of a Parasitic Nematode, *Haemonchus contortus*, Surviving Vaccine Treatment. **2023**, 11, 411 ○

- 562 The Effect of Long-Term Agricultural Use on the Bacterial Microbiota of Chernozems of the Forest-Steppe Zone. **2023**, 15, 191 0
- 561 Replacing soybean meal with high-oil pumpkin seed cake in the diet of lactating Holstein dairy cows modulated rumen bacteria and milk fatty acid profile. **2023**, 2
- 560 Gastrointestinal microbiome: Evaluation of testing technologies. **2023**, 147-161 0
- 559 Fungal-Bacterial Interactions in the Human Gut of Healthy Individuals. **2023**, 9, 139 0
- 558 Failure To Launch—Development of a Reproductive Organ Linked to Symbiotic Bacteria. 0
- 557 A High Dose of Dietary Berberine Improves Gut Wall Morphology, Despite an Expansion of Enterobacteriaceae and a Reduction in Beneficial Microbiota in Broiler Chickens. 0
- 556 Sugarcane Wax Metabolites and Their Toxicity to Silkworms. **2023**, 13, 286 0
- 555 Ecophysiological and Genomic Characterization of the Freshwater Complete Ammonia Oxidizer *Nitrospira* sp. Strain BO4. 0
- 554 Effect of feed restriction and refeeding on body condition, digestive functionality and intestinal microbiota in rainbow trout (*Oncorhynchus mykiss*). 0
- 553 Association of gut microbiota and SCFAs with finishing weight of Diannan small ear pigs. 14, 1
- 552 *Moringa oleifera* leaf ethanolic extract benefits cashmere goat semen quality via improving rumen microbiota and metabolome. 10, 1
- 551 Root Exudates of Ginger Induced by *Ralstonia solanacearum* Infection Could Inhibit Bacterial Wilt. **2023**, 71, 1957-1969 0
- 550 Rhizosphere fungal community assembly varied across functional guilds in a temperate forest. **2023**, 12, 0
- 549 Impact of meltwater flow intensity on the spatiotemporal heterogeneity of microbial mats in the McMurdo Dry Valleys, Antarctica. **2023**, 3, 0
- 548 Prospective Placebo-Controlled Assessment of Spore-Based Probiotic Supplementation on Sebum Production, Skin Barrier Function, and Acne. **2023**, 12, 895 0
- 547 Gnotobiotic zebrafish microbiota display inter-individual variability affecting host physiology. 0
- 546 Effects of *Cinnamomum camphora* coppice planting on soil fertility, microbial community structure and enzyme activity in subtropical China. 14, 0
- 545 Distinct responses of abundant and rare foraminifera to environmental variables in the Antarctic region revealed by DNA metabarcoding. 10, 0



- 544 Phylogenetic diversity of stochasticity-dominated predatory myxobacterial community drives multi-nutrient cycling in typical farmland soils. **2023**, 871, 161680 ○
- 543 A synthetic community of siderophore-producing bacteria increases soil selenium bioavailability and plant uptake through regulation of the soil microbiome. **2023**, 871, 162076 ○
- 542 Impact of *Bacillus subtilis* on manure solids, odor, and microbiome. **2023**, 333, 117390 ○
- 541 Relationship between the microbial community and nutrient elution during the formation of hypoxic water mass in Nakaumi. **2022**, 83, 15-25 ○
- 540 Soil bacterial diversity in the Zaamar mining area, Mongolia. **2022**, 38, 134-153 ○
- 539 Associations between environmental characteristics, high-resolution indoor microbiome, metabolome and allergic and non-allergic rhinitis symptoms for junior high school students. ○
- 538 Analysis of Kefir Grains from Different Regions of the Planet Using High-Throughput Sequencing. **2022**, 77, 286-291 ○
- 537 Metagenome based analysis of groundwater from arsenic contaminated sites of West Bengal revealed community diversity and their metabolic potential. **2023**, 58, 91-106 ○
- 536 Genomics of microbial communities in African lakes. **2023**, 73-95 ○
- 535 Evaluating the Optimal Oil Concentrations in the Startup Performance of a Membrane Bioreactor Treating Oily Noodle-soup Wastewater. **2023**, 72, 357-367 ○
- 534 Genome-centric view of the microbiome in a new deep-sea glass sponge species *Bathydorus* sp.. 14, ○
- 533 Gallbladder microbiota in healthy dogs and dogs with mucocele formation. **2023**, 18, e0281432 ○
- 532 Interaction between Microbes and Host in Sow Vaginas in Early Pregnancy. ○
- 531 Red mark syndrome: Is the aquaculture water microbiome a keystone for understanding the disease aetiology?. 14, ○
- 530 Rapid remodeling of the soil lipidome in response to a drying-rewetting event. **2023**, 11, ○
- 529 Nitrogen cycling activities during decreased stratification in the coastal oxygen minimum zone off Namibia. 14, ○
- 528 Changes in the oral and nasal microbiota in pediatric obstructive sleep apnea. **2023**, 15, ○
- 527 Best practice for wildlife gut microbiome research: A comprehensive review of methodology for 16S rRNA gene investigations. 14, ○

- 526 Plantation rhizosphere soil microbes promote soil-plant phosphorus feedback on the Tibetan Plateau. ○
- 525 Identification and spatio-temporal tracking of ubiquitous phage families in the human microbiome. 1, ○
- 524 Planting American ginseng (*Panax quinquefolius* L.) caused soil acidification and bacterial and fungal communities changes. ○
- 523 Total parenteral nutrition impairs glucose metabolism by modifying the gut microbiome. **2023**, 5, 331-348 ○
- 522 Logging has legacy effects on the structure of soil fungal communities several decades after cessation in Western Cascade forest stands. 6, ○
- 521 Identification reproducible microbiota biomarkers for the diagnosis of cirrhosis and hepatocellular carcinoma. **2023**, 13, ○
- 520 Plant species shape the bacterial communities on the phyllosphere in a hyper-arid desert. **2023**, 269, 127314 ○
- 519 Intraperitoneal injection of  $\beta$ -glucan during the suckling period improved the intestinal health of newly weaned rabbits by enhancing immune responses. **2023**, 105214 ○
- 518 More Robust Co-Occurrence Patterns and Stronger Dispersal Limitations of Bacterial Communities in Wet than Dry Seasons of Riparian Wetlands. ○
- 517 Prolonged darkness attenuates imidacloprid toxicity through the brain-gut-microbiome axis in zebrafish, *Danio rerio*. **2023**, 163481 ○
- 516 Fecal microbiota transplantation from *Suncus murinus*, an obesity-resistant animal, to C57BL/6NCrSlc mice, and the antibiotic effects in the approach. 14, ○
- 515 Evaluating response mechanisms of soil microbiomes and metabolomes to Bt toxin additions. **2023**, 448, 130904 ○
- 514 Effects of Plant-Growth-Promoting Rhizobacteria on Soil Bacterial Community, Soil Physicochemical Properties, and Soil Enzyme Activities in the Rhizosphere of Alfalfa under Field Conditions. **2023**, 15, 537 ○
- 513 From invasion to fish fodder: Inclusion of the brown algae *Rugulopteryx okamurae* in aquafeeds for European sea bass *Dicentrarchus labrax* (L., 1758). **2023**, 568, 739318 1
- 512 Environment microorganism and mature daqu powder shaped microbial community formation in mechanically strong-flavor daqu. **2023**, 52, 102467 ○
- 511 Composition and function of the skin microbiota were altered of red leg syndrome in cultured bullfrog (*Rana catesbeiana*). **2023**, 29, 101487 ○
- 510 Microbiome Metabolome Integration Platform (MMIP): a web-based platform for microbiome and metabolome data integration and feature identification. ○
- 509 Amylopectin Partially Substituted by Cellulose in the Hindgut Was Beneficial to Short-Chain Fatty Acid Production and Probiotic Colonization. ○

- 508 Gut Microbiota-Derived Trimethylamine N-Oxide Contributes to Abdominal Aortic Aneurysm Through Inflammatory and Apoptotic Mechanisms. **2023**, 147, 1079-1096 ○
- 507 Maternal Rumen Bacteriota Shapes the Offspring Rumen Bacteriota, Affecting the Development of Young Ruminants. **2023**, 11, ○
- 506 Insights into the Gut Microbiota of the Freshwater Crab *Sinopotamon planum* across Three Seasons and Its Associations with the Surrounding Aquatic Microbiota. **2023**, 15, 519 ○
- 505 The Effects of Drug Addiction and Detoxification on the Human Oral Microbiota. **2023**, 11, ○
- 504 Mycorrhizae Enhance Soybean Plant Growth and Aluminum Stress Tolerance by Shaping the Microbiome Assembly in an Acidic Soil. **2023**, 11, ○
- 503 Effects of melittin on production performance, antioxidant function, immune function, heat shock protein, intestinal morphology, and cecal microbiota in heat-stressed quails. **2023**, 102713 ○
- 502 Acute temperature stresses trigger liver transcriptome and microbial community remodeling in largemouth bass (*Micropterus salmoides*). **2023**, 739573 ○
- 501 Effect of Enrofloxacin on the Microbiome, Metabolome, and Abundance of Antibiotic Resistance Genes in the Chicken Cecum. **2023**, 11, ○
- 500 Evaluation of a Red Grape Marc Extract as a Natural Nitrification Inhibitor and its Effect on Soil Bacterial Community. ○
- 499 Long-term field application of manure induces deep selection of antibiotic resistomes in leaf endophytes of Chinese cabbage. **2023**, 163334 ○
- 498 Discrepancies in rhizobacterial assembly caused by glyphosate application and herbicide-tolerant soybean Co-expressing GAT and EPSPS. **2023**, 450, 131053 ○
- 497 Hydrogen inhalation ameliorates hepatic inflammation and modulates gut microbiota in rats with high-fat diet-induced non-alcoholic fatty liver disease. **2023**, 947, 175698 ○
- 496 The function and community structure of arbuscular mycorrhizal fungi in ecological floating beds used for remediation of Pb contaminated wastewater. **2023**, 872, 162233 ○
- 495 Investigating the survival and activity of a bacteriophage in the complex colon environment with the use of a dynamic model of the colon (TIM-2). **2023**, 178, 106061 ○
- 494 *Ligularia virgaurea* improved nutrient digestion, ruminal fermentation, and bacterial composition in Tibetan sheep grazing on the Qinghai-Tibetan plateau in winter. **2023**, 299, 115628 ○
- 493 Response of granular anammox process under mainstream conditions to continuous and transient organic loads. **2023**, 464, 142681 ○
- 492 Fecal microbiota transplantation affects the recovery of AD-skin lesions and enhances gut microbiota homeostasis. **2023**, 118, 110005 ○
- 491 Elevated CO<sub>2</sub> alleviated the dissemination of antibiotic resistance genes in sulfadiazine-contaminated soil: A free-air CO<sub>2</sub> enrichment study. **2023**, 450, 131079 ○

- 490 Deciphering community assembly and succession in sequencing batch moving bed biofilm reactor: Differentiation between attached and suspended communities. **2023**, 873, 162448 ○
- 489 Improvement of cadmium immobilization in contaminated paddy soil by using ureolytic bacteria and rice straw. **2023**, 874, 162594 ○
- 488 Gut microbial and metabolic characterization of Atlantic salmon (*Salmon salar*) challenged with *Aeromonas salmonicida*. **2023**, 570, 739420 ○
- 487 Evaluation of fish meal replacement by *Clostridium autoethanogenum* protein in diets for juvenile red swamp crayfish (*Procambarus clarkii*). **2023**, 570, 739379 ○
- 486 Effects of salinity on growth, physiology, biochemistry and gut microbiota of juvenile grass carp (*Ctenopharyngodon idella*). **2023**, 258, 106482 ○
- 485 Trade-off between microbial ecophysiological features regulated by soil fertility governs plant residue decomposition. **2023**, 229, 105679 1
- 484 Stress-buster *Enterobacter* sp. alleviates salinity stress in *Cajanus cajan* together with impacting its rhizospheric microbiome. **2023**, 156, 202-212 ○
- 483 Ablation of CD226 on CD4+ T cells modulates asthma progress associated with altered IL-10 response and gut microbiota. **2023**, 118, 110051 ○
- 482 A joint role of iron oxide and temperature for methane production and methanogenic community in paddy soils. **2023**, 433, 116462 ○
- 481 Metabarcoding analysis of meiobenthic biodiversity along the Gulf of Mexico continental shelf. **2023**, 285, 108303 ○
- 480 Climate and edaphic factors drive soil nematode diversity and community composition in urban ecosystems. **2023**, 180, 109010 ○
- 479 Bacterial diversity and its correlation with sensory quality of two types of zha-chili from Shennongjia region, China. **2023**, 168, 112789 ○
- 478 Natural restoration enhances soil multitrophic network complexity and ecosystem functions in the Loess Plateau. **2023**, 226, 107059 ○
- 477 A comparative study on effects of dietary three strains of lactic acid bacteria on the growth performance, immune responses, disease resistance and intestinal microbiota of Pacific white shrimp, *Penaeus vannamei*. **2023**, 136, 108707 ○
- 476 How arsenic contamination influences downslope wetland plant and microbial community structure and function. **2023**, 876, 162839 ○
- 475 The effects of flow field on the succession of the microbial community on artificial reefs. **2023**, 191, 114920 ○
- 474 The characteristics and metabolic potentials of the soil bacterial community of two typical military demolition ranges in China. **2023**, 874, 162562 ○
- 473 Microbial assessment of water, sanitation, and hygiene (WaSH) in temporary and permanent settlements two years after Nepal 2015 earthquake. **2023**, 877, 162867 ○

- 472 Spatial and temporal changes in the assembly mechanism and co-occurrence network of the chromophytic phytoplankton communities in coastal ecosystems under anthropogenic influences. **2023**, 877, 162831 ○
- 471 Stable oxic-anoxic transitional interface is beneficial to retard soil carbon loss in drained peatland. **2023**, 181, 109024 ○
- 470 Understanding the ecological effects of the fungicide difenoconazole on soil and *Enchytraeus crypticus* gut microbiome. **2023**, 326, 121518 ○
- 469 Water mass age and dissolved organic matter properties drive the diversity of pelagic prokaryotes in the Western Mediterranean Sea. **2023**, 196, 104022 ○
- 468 Evaluation of the effects of dietary mycotoxin-degrading adsorbent on juvenile turbot (*Scophthalmus maximus* L.) fed aflatoxin B1-contaminated diets. **2023**, 30, 101539 ○
- 467 Structure, stability, and potential function of groundwater microbial community responses to permafrost degradation on varying permafrost of the Qinghai-Tibet Plateau. **2023**, 875, 162693 ○
- 466 Poly- $\gamma$ -glutamic acid-producing *Bacillus velezensis* fermentation can improve the feed properties of soybean meal. **2023**, 53, 102503 ○
- 465 Effects of microbial succession on the dynamics of flavor metabolites and physicochemical properties during soy sauce koji making. **2023**, 53, 102636 ○
- 464 Temporal loss of fungal taxa driven by drift contributes to community stability during soybean development. **2023**, 186, 104819 ○
- 463 RNA outperforms DNA-based metabarcoding in assessing the diversity and response of microeukaryotes to environmental variables in the Arctic Ocean. **2023**, 876, 162608 ○
- 462 An in vitro model of the chicken gastrointestinal tract with special emphasis to the cecal microbiota. **2023**, 102, 102654 ○
- 461 Intercropped *Amygdalus persica* and *Pteris vittata* applied with additives presents a safe utilization and remediation mode for arsenic-contaminated orchard soil. **2023**, 879, 163034 ○
- 460 Changes in soil bacterial communities and functional groups beneath coarse woody debris across a subalpine forest successional series. **2023**, 43, e02436 ○
- 459 Long-term chemical fertilization results in a loss of temporal dynamics of diazotrophic communities in the wheat rhizosphere. **2023**, 875, 162663 ○
- 458 Response of soil microbial Communities, inorganic and organic soil carbon pools in arid saline soils to alternative land use practices. **2023**, 150, 110227 ○
- 457 Agricultural practice negatively affects soil bacterial diversity and nitrogen functional genes comparing to adjacent native forest soils. **2023**, 186, 104856 ○
- 456 Depth-dependent effects of tree species identity on soil microbial community characteristics and multifunctionality. **2023**, 878, 162972 ○
- 455 Unravelling diversity, drivers, and indicators of soil microbiome of *Trillium govianum*, an endangered plant species of the Himalaya. **2023**, 227, 115819 ○

- 454 Regenerated woody plants influence soil microbial communities in a subtropical forest. **2023**, 188, 104890 ○
- 453 Effects of long-term warming on soil prokaryotic communities in shrub and alpine meadows on the eastern edge of the Qinghai-Tibetan Plateau. **2023**, 188, 104871 ○
- 452 Identification and synergetic mechanism of TCE, H<sub>2</sub> and O<sub>2</sub> metabolic microorganisms in the joint H<sub>2</sub>/O<sub>2</sub> system. **2023**, 879, 163026 ○
- 451 Response of murine gut microbiota to a prebiotic based on oligosaccharides derived via hydrolysis of fungal  $\beta$ (1-3)-d-glucan: Preclinical trial study on mice. **2023**, 417, 135928 ○
- 450 Dietary yeast cell wall enhanced intestinal health of broiler chickens by modulating intestinal integrity, immune responses, and microbiota. **2023**, 102, 102660 ○
- 449 Soil nutrients and the responses of microbial community structure to pine bark and vinegar residues in blueberry cultivation. **2023**, 189, 104907 ○
- 448 Soil carbon-fixing bacterial communities respond to plant community change in coastal salt marsh wetlands. **2023**, 189, 104918 ○
- 447 Decreased CH<sub>4</sub> emissions associated with methanogenic and methanotrophic communities and their interactions following Fe(III) fertiliser application in rice paddies. **2023**, 431, 116375 ○
- 446 Grapefruit Root and Rhizosphere Responses to Varying Planting Densities, Fertilizer Concentrations and Application Methods. **2023**, 12, 1659 ○
- 445 Revealing the relative importance among plant species, slope positions, and soil types on rhizosphere microbial communities in northern tropical karst and non-karst seasonal rainforests of China. 14, ○
- 444 Plant-soil-microbial interactions mediate vegetation succession in retreating glacial forefields. **2023**, 873, 162393 ○
- 443 Effect of dietary *Pediococcus pentosaceus* MR001 on intestinal bacterial diversity and white spot syndrome virus protection in Pacific white shrimp. **2023**, 30, 101570 ○
- 442 Nitrogen application influences the effect of bacteria on the belowground allocation of photosynthesized carbon under elevated CO<sub>2</sub>. **2023**, 180, 109021 ○
- 441 Plant invasion mediates the regulation of topsoil organic carbon sequestration by the fungal community in coastal wetlands. **2023**, 227, 107118 ○
- 440 *Bacillus amyloliquefaciens* FG14 as a potential biocontrol strain against rusty root rot of *Panax ginseng*, and its impact on the rhizosphere microbial community. **2023**, 182, 105221 ○
- 439 Efficient nitrogen removal of a novel *Pseudomonas chengduensis* strain BF6 mainly through assimilation in the recirculating aquaculture systems. **2023**, 379, 129036 1
- 438 Effect of hydraulic retention time on performances of gravity-driven membrane (GDM) reactor for seawater pretreatment. **2023**, 53, 103599 ○
- 437 Biofilm colonization of stone materials from an Australian outdoor sculpture: Importance of geometry and exposure. **2023**, 339, 117948 ○

- 436 Responses of bacterial community and N-cycling functions stability to different wetting-drying alternation frequencies in a riparian zone. **2023**, 228, 115778 ○
- 435 Turfgrass-dependent mycotrophic change enhances soil deterioration in dry, cold and high-alkali environments. **2023**, 134, ○
- 434 Soil bacteria respond intensely to resource limitations regulated by edaphic properties during secondary succession on a semiarid abandoned farmland. **2023**, 223, 106944 ○
- 433 Revisiting Mt Fuji's groundwater origins with helium, vanadium and environmental DNA tracers. **2023**, 1, 60-73 ○
- 432 (Meta)genomics -assisted screening of novel antibacterial lactic acid bacteria strains from traditional fermented milk from Western China and their bioprotective effects on cheese. **2023**, 175, 114507 ○
- 431 Different types of land use influence soil physiochemical properties, the abundance of nitrifying bacteria, and microbial interactions in tropical urban soil. **2023**, 869, 161722 ○
- 430 A novel insight into energy conservation and efficiency enhancement in wastewater treatment process: Low-frequency mechanical vibration induced. **2023**, 52, 103492 ○
- 429 The Relationship between Core Rhizosphere Taxa and Peanut Nodulation Capacity under Different Cover Crop Amendments. **2023**, 13, 311 ○
- 428 Effective removal of trace 1,4-dioxane by biological treatments augmented with propanotrophic single culture versus synthetic consortium. **2023**, 9, 100246 ○
- 427 Reducing nitrogen loss during kitchen waste composting using a bioaugmented mechanical process with low pH and enhanced ammonia assimilation. **2023**, 372, 128664 ○
- 426 Dietary Application of the Microalga *Lobosphaera incisa* P127 Reduces Severity of Intestinal Inflammation, Modulates Gut-Associated Gene Expression, and Microbiome in the Zebrafish Model of IBD. **2023**, 67, 2200253 ○
- 425 No evidence that modification of soil microbiota by woody invader facilitates subsequent invasion by herbaceous species. 1
- 424 Mining metatranscriptomes reveals a vast world of viroid-like circular RNAs. **2023**, 186, 646-661.e4 ○
- 423 Disturbance and restoration of soil microbial communities after in-situ thermal desorption in a chlorinated hydrocarbon contaminated site. **2023**, 448, 130870 ○
- 422 Oregano extract fed to pre-weaned dairy calves. Part 1: Effects on intake, digestibility, body weight, and rumen and intestinal bacteria microbiota. **2023**, 269, 105165 ○
- 421 Enhanced MFC sensor performances and extracellular electron transport efficiency mediated by biochar and underlying biochemical mechanisms. **2023**, 332, 117282 ○
- 420 Microbial food webs share similar biogeographic patterns and driving mechanisms with depths in oligotrophic tropical western Pacific Ocean. 14, ○
- 419 Pyrethroids exposure alters the community and function of the internal microbiota in *Aedes albopictus*. **2023**, 252, 114579 ○



- 418 Effects of Continuous Straw Returning on Soil Functional Microorganisms and Microbial Communities. **2023**, 61, 49-62 ○
- 417 Immunomodulatory effects of complex probiotics on the immuno-suppressed mice induced by cyclophosphamide. 14, ○
- 416 Retention of post-harvest residues enhances soil fungal biodiversity in Eucalyptus plantations. **2023**, 532, 120806 ○
- 415 LC / MS analysis of mushrooms provided new insights into dietary management of diabetes mellitus in rats. 1
- 414 Comparison of network connectivity and environmental driving factors of root-associated fungal communities of desert ephemeral plants in two habitat soils. **2023**, 332, 117375 ○
- 413 Studying Fungal-Bacterial Relationships in the Human Gut Using an In Vitro Model (TIM-2). **2023**, 9, 174 ○
- 412 Non-Surgical Periodontal Treatment Impact on Subgingival Microbiome and Intra-Oral Halitosis. **2023**, 24, 2518 ○
- 411 Mitochondrial ND4 Gene as a Marker Trait for Studying Structure and Dynamics of Aphid (Hemiptera, Aphididae) Populations. **2022**, 102, 820-828 ○
- 410 The Molecular Effect of Wearing Silver-Threaded Clothing on the Human Skin. **2023**, 8, ○
- 409 Microbial species from multiple maternal body sites shape the developing giant panda ( *Ailuropoda melanoleuca* ) cub gut microbiome. ○
- 408 Dredged sediments contain potentially beneficial microorganisms for agriculture and little harmful cyanobacteria. **2023**, 2, 45-57 ○
- 407 Immune priming prior to pathogen exposure sheds light on the relationship between host, microbiome and pathogen in disease. **2023**, 10, 1
- 406 Fungal diversities and community assembly processes show different biogeographical patterns in forest and grassland soil ecosystems. 14, ○
- 405 Human microbiome transfer in the built environment differs based on occupants, objects, and buildings. ○
- 404 Oral microbiome in older adults with mild cognitive impairment. **2023**, 15, ○
- 403 Differential responses of canonical nitrifiers and comammox *Nitrospira* to long-term fertilization in an Alfisol of Northeast China. 14, ○
- 402 Dominated "Inheritance" of Endophytes in Grapevines from Stock Plants via In Vitro-Cultured Plantlets: The Dawn of Plant Endophytic Modifications. **2023**, 9, 180 ○
- 401 Nitrogen and Phosphorus Discriminate the Assembly Processes of Prokaryotic and Eukaryotic Algae in an Agricultural Drainage Receiving Lake. **2023**, 15, 2584 ○



- 400 Specific suppression of vascular wilt disease of onion is linked with fungal soil community structure. **2023**, 25, 100671 ○
- 399 Cyprinid herpesvirus 2 infection changes microbiota and metabolites in the gibel carp (*Carassius auratus gibelio*) midgut. **2023**, 12, ○
- 398 The ecology of bacterial communities in groundwater of industrial areas: Diversity, composition, network, and assembly. **2023**, 322, 121207 ○
- 397 Antibiotic resistome in groundwater and its association with mountain springs and river. **2023**, 252, 114603 ○
- 396 Influence of root cortical aerenchyma on the rhizosphere microbiome of field-grown maize. ○
- 395 Analysis of microbial diversity in the feces of *Arborophila rufipectus*. **2023**, 13, ○
- 394 Weanling gut microbiota composition of a mouse model selectively bred for high voluntary wheel-running behavior. **2023**, 226, ○
- 393 Microbial Taxonomical and Functional Diversities Increased with Wetland Productivity at Initial Stages of Vegetation Restoration on Denuded Tidal Flats. **2023**, 46, 829-843 ○
- 392 Microplastics in household fecal sewage treatment facilities of rural China. **2023**, 448, 130925 ○
- 391 Vitamin D alleviates non-alcoholic fatty liver disease via restoring gut microbiota and metabolism. **2023**, 14, ○
- 390 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. ○
- 389 Short-term effects of Chlorhexidine mouthwash and Listerine on oral microbiome in hospitalized patients. **2023**, 13, ○
- 388 The Epibiotic Microbiota of Wild Caribbean Sea Urchin Spines Is Species Specific. **2023**, 11, 391 ○
- 387 Rewilding in Miniature: Suburban Meadows Can Improve Soil Microbial Biodiversity and Soil Health. ○
- 386 Increased Nitrogen Loading Facilitates Nitrous Oxide Production through Fungal and Chemodenitrification in Estuarine and Coastal Sediments. **2023**, 57, 2660-2671 ○
- 385 Contrasting responses of bacterial community to 4,4'-dibromodiphenyl ether (BDE-15) contamination in soil microcosms at different temperatures. **2023**, 319, 138056 ○
- 384 The impact of Ag nanoparticles on methane emission in two typical paddy soils. **2023**, 323, 121215 ○
- 383 Gut microbiome variations in *Rhinopithecus roxellanae* caused by changes in the environment. **2023**, 24, 1

- 382 Postbiotic gel relieves clinical symptoms of bacterial vaginitis by regulating the vaginal microbiota. 13, ○
- 381 Legacy effects post removal of a range-expanding shrub influence soil fungal communities and create negative plant-soil feedbacks for conspecific seedlings. ○
- 380 Microbial community stratification in scale-up Anaerobic Fluidized Bed Reactor applied for 4-Nonylphenol degradation. **2023**, 21, 101359 ○
- 379 Microorganisms carrying nosZ I and nosZ II share similar ecological niches in a subtropical coastal wetland. **2023**, 870, 162008 ○
- 378 Chondroitin sulfate alleviates osteoporosis caused by calcium deficiency by regulating lipid metabolism. **2023**, 20, ○
- 377 Assembly and Network Stability of Planktonic Microorganisms under the Influence of Salinity Gradient: an Arctic Case Study from the Lena River Estuary to the Laptev Sea. **2023**, 11, ○
- 376 Dysbiosis of the larval gut microbiota of Spodoptera frugiperda strains feeding on different host plants. **2023**, 89, 197-211 ○
- 375 Effect of Abscisic Acid on Growth, Fatty Acid Profile, and Pigment Composition of the Chlorophyte *Chlorella* (*Chromochloris*) *zofingiensis* and Its Co-Culture Microbiome. **2023**, 13, 452 ○
- 374 Additive fungal interactions drive biocontrol of Fusarium wilt disease. **2023**, 238, 1198-1214 ○
- 373 Comparative Analyses of Soil Bacterial Colonies of Two Types of Chinese Ginger after a Major Flood Disaster. **2023**, 11, ○
- 372 Supergroup F Wolbachia with extremely reduced genome: transition to obligate insect symbionts. **2023**, 11, ○
- 371 Microplastic ingestion perturbs the microbiome of *Aedes albopictus* and *Aedes aegypti*. ○
- 370 The effects of a *Bacillus licheniformis* and phytase mixture added to broiler diets on growth performance, nutrient digestibility, and cecal microecosystem. **2023**, ○
- 369 A Tale of Two Seasons: Distinct Seasonal Viral Communities in a Thermokarst Lake. **2023**, 11, 428 ○
- 368 Seasonal Shifts in Bacterial Community Structures in the Lateral Root of Sugar Beet Grown in an Andosol Field in Japan. **2023**, 38, n/a ○
- 367 Microbial community structural response to variations in physicochemical features of different aquifers. 14, ○
- 366 Analysis of Dynamics and Diversity of Microbial Community during Production of Germinated Brown Rice. **2023**, 12, 755 ○
- 365 498. Preliminary investigation into the association of members of the rumen biome with production traits in Afrikaner cattle. **2022**, ○

- 364 Consequences of arthropod community structure for an at-risk insectivorous bird. **2023**, 18, e0281081 ○
- 363 Microbial community succession patterns and drivers of Luxiang-flavor Jiupei during long fermentation. 14, ○
- 362 The mechanism of promoting rhizosphere nutrient turnover for arbuscular mycorrhizal fungi attributes to recruited functional bacterial assembly. ○
- 361 Prévention du colmatage des puits lors du stockage dans lâquiffie dâbaux de drainage turbides riches en carbone organique dissous et en nutriments. ○
- 360 Environmental DNA sequencing reveals the regional difference in diversity and community assembly mechanisms of eukaryotic plankton in coastal waters. 14, ○
- 359 On the Oral Microbiome of Oral Potentially Malignant and Malignant Disorders: Dysbiosis, Loss of Diversity, and Pathogens Enrichment. **2023**, 24, 3466 ○
- 358 The Intestinal Microbiota Involves in the Deterioration of Live Sea Cucumber During Storage. **2023**, 32, 129-141 ○
- 357 Plant communities regulated by water-level gradient in Caohai aquaticâterrestrial ecotones affect bacterial and fungal structures and co-occurrence networks. **2023**, 25, 100674 ○
- 356 Turnover of the extracellular polymeric matrix of granules performing biological phosphate removal. **2023**, 107, 1997-2009 1
- 355 Core microbiome and bacterial diversity of the Italian Mediterranean river buffalo milk. **2023**, 107, 1875-1886 ○
- 354 Regulatory effect of moderate Jiang-flavour baijiu (Chinese liquor) dosage on organ function and gut microbiota in mice. **2023**, 135, 298-305 ○
- 353 Effects of dietary supplementation with prebiotics and *Pediococcus acidilactici* on gut health, transcriptome, microbiota, and metabolome in Atlantic salmon (*Salmo salar* L.) after seawater transfer. **2023**, 5, ○
- 352 Inter-basin water diversion homogenizes microbial communities mainly through stochastic assembly processes. **2023**, 223, 115473 ○
- 351 Bacterial composition along the digestive tract of the Horned Screamer (*Anhima cornuta*), a tropical herbivorous bird. 11, e14805 ○
- 350 Gut microbiota of white-headed black langurs (*Trachypithecus leucocephalus*) in responses to habitat fragmentation. 14, ○
- 349 Correlations between Gut Microbial Composition, Pathophysiological and Surgical Aspects in Endometriosis: A Review of the Literature. **2023**, 59, 347 ○
- 348 Microbiome Composition and Microbial Community Structure in Mosquito Vectors *Aedes aegypti* and *Aedes albopictus* in Northeastern Thailand, a Dengue-Endemic Area. **2023**, 14, 184 ○
- 347 Dark Fermentation of *Arundo donax*: Characterization of the Anaerobic Microbial Consortium. **2023**, 16, 1813 ○

- 346 Complementary effects of above- and belowground biodiversity on ecosystem functions across global grasslands. ○
- 345 Intestinal barrier dysfunction in murine sickle cell disease is associated with small intestine neutrophilic inflammation, oxidative stress, and dysbiosis. ○
- 344 A bacteriocyte symbiont determines whitefly sex ratio by regulating mitochondrial function. **2023**, 42, 112102 ○
- 343 Maternal T<sub>H</sub>17 cells shape offspring pulmonary type 2 immunity in a microbiota-dependent manner. **2023**, 42, 112074 ○
- 342 Orientation-driven photosynthesized carbon belowground mediates intercropped peanut microbiota changes for pathogen resistance. ○
- 341 Impact of diet and host genetics on the murine intestinal mycobiome. **2023**, 14, ○
- 340 Root-Associated Antagonistic Pseudomonas spp. Contribute to Soil Suppressiveness against Banana Fusarium Wilt Disease of Banana. **2023**, 11, ○
- 339 The relationship between shifts in the rhizosphere microbial community and root rot disease in a continuous cropping American ginseng system. 14, ○
- 338 Microbial Diversity Analysis in Spaceflight AIT Center. **2017**, 37, 185 ○
- 337 A comparison of bioinformatics pipelines for compositional analysis of the human gut microbiome. ○
- 336 Electric-Inductive Microbial Interactions in a Thermophilic Anaerobic Digester Revealed by High-Throughput Sequencing of Micron-Scale Single Floccs. **2023**, 57, 4367-4378 ○
- 335 Gut Microbiota in Patients with Postoperative Atrial Fibrillation Undergoing Off-Pump Coronary Bypass Graft Surgery. **2023**, 12, 1493 ○
- 334 Bio-organic fertilizers improve Dendrocalamus farinosus growth by remodeling the soil microbiome and metabolome. 14, ○
- 333 Intestinal Microbiota Differences in Litopenaeus vannamei Shrimp between Greenhouse and Aquaponic Rearing. **2023**, 13, 525 ○
- 332 A pilot study exploring the association of bronchial bacterial microbiota and recurrent wheezing in infants with atopy. 13, ○
- 331 Bacterial Community Composition and Isolation of Actinobacteria from the Soil of Flaming Mountain in Xinjiang, China. **2023**, 11, 489 ○
- 330 High-Throughput Sequencing of Oral Microbiota in Candida Carriage Sjögren's Syndrome Patients: A Pilot Cross-Sectional Study. **2023**, 12, 1559 ○
- 329 Rhizobacterial compositions and their relationships with soil properties and medicinal bioactive ingredients in Cinnamomum migao. 14, ○

- 328 Disentangling the Ecological Processes and Driving Forces Shaping the Seasonal Pattern of Halobacteriovorax Communities in a Subtropical Estuary. ○
- 327 Disrupted diurnal oscillations of the gut microbiota in patients with alcohol dependence. 13, ○
- 326 Effects of *Saccharina japonica* and spent mushroom compost mixed compost on composting quality and dynamic change of microbial diversity at different C/N ratios. ○
- 325 A Bacillaceae consortium positively impacts arbuscular mycorrhizal fungus colonisation, plant phosphate nutrition, and tuber yield in *Solanum tuberosum* cv. Jazzy. **2023**, 89, 235-250 ○
- 324 Interleukin-23 receptor signaling impairs the stability and function of colonic regulatory T cells. **2023**, 42, 112128 ○
- 323 Inulin prebiotic reinforces host cancer immunosurveillance via  $\gamma\delta$  T cell activation. 14, ○
- 322 Selection of rhizosphere communities of diverse rotation crops reveals unique core microbiome associated with reduced banana *Fusarium* wilt disease. ○
- 321 Structural diversity of bacterial communities in two divergent sunflower rhizosphere soils. **2023**, 73, ○
- 320 Structural characteristics and diversity of the rhizosphere bacterial communities of wild *Fritillaria przewalskii* Maxim. in the northeastern Tibetan Plateau. 14, ○
- 319 Effects of field inoculation of potato tubers with the arbuscular mycorrhizal fungus *Rhizophagus irregularis* DAOM 197198 are cultivar dependent. **2023**, 89, 213-226 ○
- 318 Fine cassava fibre utilization as a dietary fibre source for dogs: Effects on kibble characteristics, diet digestibility and palatability, faecal metabolites and microbiota. ○
- 317 Cooperation of arbuscular mycorrhizal fungi and bacteria to facilitate the host plant growth dependent on soil pH. 14, ○
- 316 Impacts of Different Reforestation Methods on Fungal Community and Nutrient Content in an Ex-Tea Plantation. **2023**, 14, 432 ○
- 315 Roe Deer Produce Less Methane and Harbor Distinct Gut Microbiota. **2023**, 9, 186 ○
- 314 Negative consequences of reduced protein diets supplemented with synthetic amino acids for performance, intestinal barrier function, and caecal microbiota composition of broiler chickens. **2023**, 13, 216-228 ○
- 313 Targeting the gut-lung axis by synbiotic feeding to infants in a randomized controlled trial. **2023**, 21, ○
- 312 Characteristics of Microbiota in Different Segments of the Digestive Tract of *Lycodon rufozonatus*. **2023**, 13, 731 ○
- 311 Randomized controlled trial demonstrates response to a probiotic intervention for metabolic syndrome that may correspond to diet. **2023**, 15, ○

- 310 Dynamics of Functional Genes and Bacterial Community during Bioremediation of Diesel-Contaminated Soil Amended with Compost. **2023**, ○
- 309 The Pathogen *Aeromonas salmonicida achromogenes* Induces Fast Immune and Microbiota Modifications in Rainbow Trout. **2023**, 11, 539 ○
- 308 Impacts of dietary supplementation of bamboo vinegar and charcoal powder on growth performance, intestinal morphology, and gut microflora of large-scale loach *Paramisgurnus dabryanus*. ○
- 307 Predicting Foodborne Pathogens and Probiotics Taxa within Poultry-Related Microbiomes Using a Machine Learning Approach. ○
- 306 NMR Metabolomics and DNA Sequencing of *Escherichia coli* and *Staphylococcus aureus* Cultures Treated with Hydrolyzable Tannins. **2023**, 13, 320 ○
- 305 Diet composition and interspecific niche of Taohongling Sika deer (*Cervus nippon kopschi*) and its sympatric Reeves' muntjac (*Muntiacus reevesi*) and Chinese hare (*Lepus sinensis*) in winter (Animalia, Mammalia). 1149, 17-36 ○
- 304 Influence of Parturition on Rumen Bacteria and SCFAs in Holstein Cows Based on 16S rRNA Sequencing and Targeted Metabolomics. **2023**, 13, 782 ○
- 303 A trade-off between space exploration and mobilization of organic phosphorus through associated microbiomes enables niche differentiation of arbuscular mycorrhizal fungi on the same root. ○
- 302 Microbiome diversity, composition and assembly in a California citrus orchard. 14, ○
- 301 Oral Exposure to Polystyrene Microplastics of Mice on a Normal or High-Fat Diet and Intestinal and Metabolic Outcomes. **2023**, 131, ○
- 300 Effect of composted pig manure, biochar, and their combination on antibiotic resistome dissipation in swine wastewater-treated soil. **2023**, 323, 121323 ○
- 299 Phagotrophic Protists Modulate Copper Resistance of the Bacterial Community in Soil. **2023**, 57, 3590-3601 ○
- 298 Effect of fabric mulch ground covers on lemon trees rhizosphere microbiome in Florida flatwood soils. 3, ○
- 297 Host Species and Environment Shape the Gut Microbiota of Cohabiting Marine Bivalves. ○
- 296 Do antimicrobial peptide levels alter performance of insect-based aquaculture feeds â a study using genetic models of insect immune activation. 1-16 ○
- 295 Carbon metabolism and biogeography of candidate phylum âCandidatus *Bipolaricaulota*â in geothermal environments of Biga Peninsula, Turkey. 14, ○
- 294 Association Studies on Gut and Lung Microbiomes in Patients with Lung Adenocarcinoma. **2023**, 11, 546 ○
- 293 Individual and Combined Effects of a Direct-Fed Microbial and Calcium Butyrate on Growth Performance, Intestinal Histology and Gut Microbiota of Broiler Chickens. **2023**, 2, 63-81 ○

- 292 Short- and long-term effects of continuous compost amendment on soil microbiome community. ○
- 291 Impact of environmental factors on diversity of fungi in sediments from the Shenzhen River Estuary. **2023**, 205, ○
- 290 Efficacy of acupuncture in patients with mild Alzheimer's disease and its impact on gut microbiota: Study protocol for a randomized sham-controlled trial. 10, ○
- 289 Trade-offs between fertilizer-N availability and Cd pollution potential under crop straw incorporation by  $^{15}\text{N}$  stable isotopes in rice. **2023**, 30, 51075-51088 ○
- 288 Orally administered *Lactiplantibacillus plantarum* OLL2712 decreased intestinal permeability, especially in the ileum: Ingested lactic acid bacteria alleviated obesity-induced inflammation by collaborating with gut microbiota. 14, ○
- 287 Effect of tillage state of paddy soils with heavy metal pollution on the *nosZ* gene of  $\text{N}_2\text{O}$  reductase. **2024**, 137, 469-477 ○
- 286 Metabolic and inflammatory linkage of the chicken cecal microbiome to growth performance. 14, ○
- 285 Validation of 16S rRNA Gene Sequencing of the Periocular Microbiome and Lack of Alteration by Topical Eyedrops. **2023**, 12, 32 ○
- 284 Enzyme adaptation to habitat thermal legacy shapes the thermal plasticity of marine microbiomes. **2023**, 14, ○
- 283 The Associations between Multiple Essential Metal(loid)s and Gut Microbiota in Chinese Community-Dwelling Older Adults. **2023**, 15, 1137 ○
- 282 The Taxonomic Structure of the Prokaryotic Biome of the Rhizosphere *Triticum Aestivum* L. Depending on the Variety and Application of Associative Bacteria. **2023**, 1878-1887 ○
- 281 Composition and Patterns of Taxa Assemblages in the Western Channel Assessed by 18S Sequencing, Microscopy and Flow Cytometry. **2023**, 11, 480 ○
- 280 Microbiota of Urine, Glans and Prostate Biopsies in Patients with Prostate Cancer Reveals a Dysbiosis in the Genitourinary System. **2023**, 15, 1423 ○
- 279 Microbially mediated molecular transformations of dissolved organic matter in bioelectrochemical systems treating beer brewery wastewater. **2023**, 461, 142111 ○
- 278 Reprogramming of the gut microbiota following feralization in *Sus scrofa*. **2023**, 5, ○
- 277 Effects of altitude on the gut microbiome and metabolomics of Sanhe heifers. 14, ○
- 276 Effect of two starters (Jiu Yao) on Chinese rice wine microbial community and flavour. **2023**, 58, 2391-2399 ○
- 275 High immigration rates critical for establishing emigration-driven diversity in microbial communities. ○

- 274 Distinct Bacterial Communities in S<sup>5</sup> Jorge Cheese with Protected Designation of Origin (PDO). **2023**, 12, 990 ○
- 273 Evaluation of the lignocellulose degradation potential of Mediterranean forests soil microbial communities through diversity and targeted functional metagenomics. 14, ○
- 272 In silico approaches for the quest of the novel enzymes. **2023**, 65-78 ○
- 271 Modern Rivularia Freshwater Stromatolites as Models for Formation of Laminated Stromatolitic Crusts. **2023**, 40, 382-398 ○
- 270 Gut-Microbiota Dysbiosis in Stroke-Prone Spontaneously Hypertensive Rats with Diet-Induced Steatohepatitis. **2023**, 24, 4603 ○
- 269 Hierarchical Effects of Lactic Fermentation and Grain Germination on the Microbial and Metabolomic Profile of Rye Doughs. **2023**, 12, 998 ○
- 268 The Colorectal Cancer Gut Environment Regulates Activity of the Microbiome and Promotes the Multidrug Resistant Phenotype of ESKAPE and Other Pathogens. **2023**, 8, 1
- 267 Comparison of carbon sources in a partial denitrification/anammox MBBR using glycerol, acetate, and methanol. **2023**, 9, 1041-1052 ○
- 266 Longitudinal Analysis of the Intestinal Microbiota among a Cohort of Children in Rural and Urban Areas of Pakistan. **2023**, 15, 1213 ○
- 265 Influence of Probiotic Feed Supplement on Nosema spp. Infection Level and the Gut Microbiota of Adult Honeybees (*Apis mellifera* L.). **2023**, 11, 610 ○
- 264 Comparison of Fecal Microbiota Communities between Primiparous and Multiparous Cows during Non-Pregnancy and Pregnancy. **2023**, 13, 869 ○
- 263 Disturbed rhythmicity of intestinal hydrogen peroxide alters gut microbial oscillations in BMAL1-deficient monkeys. **2023**, 42, 112183 ○
- 262 The Gut Microbiome of an Indigenous Agropastoralist Population in a Remote Area of Colombia with High Rates of Gastrointestinal Infections and Dysbiosis. **2023**, 11, 625 ○
- 261 Responses of the gastrointestinal microbiota to the protein metabolism of pond-cultured Japanese flounder (*Paralichthys olivaceus*). 10, ○
- 260 Shifts in soil nitrogen availability and associated microbial drivers during stand development of Mongolian pine plantations. ○
- 259 Microbial community profiling and culturing reveal functional groups of bacteria associated with Thai commercial stingless worker bees (*Tetragonula pagdeni*). **2023**, 18, e0280075 ○
- 258 Habitat severity characteristics structure soil communities at regional and local spatial scales along the Antarctica Peninsula. 1-17 ○
- 257 Multifeature analysis of age-related microbiome structures reveals defense mechanisms of *Populus tomentosa* trees. **2023**, 238, 1636-1650 ○



- 256 An integrated transcriptome and microbial community analysis reveals potential mechanisms for increased immune responses when replacing silybum marianum meal with soybean meal in growing lambs. 14, ○
- 255 Changes in upper airways microbiota in ventilator-associated pneumonia. **2023**, 11, ○
- 254 16S rDNA-based diversity analysis of bacterial communities associated with soft corals of the Red Sea, Al Rayyis, White Head, KSA. **2023**, 17, ○
- 253 Bacterial PncA improves diet-induced NAFLD in mice by enabling the transition from nicotinamide to nicotinic acid. **2023**, 6, ○
- 252 Irinotecan-gut microbiota interactions and the capability of probiotics to mitigate Irinotecan-associated toxicity. **2023**, 23, ○
- 251 Efficacy of cetylpridium chloride mouthwash compared to povidone iodine on oral flora for perioperative patient care: A randomized controlled feasibility study. **2023**, ○
- 250 Three decades of organic manure and chemical fertilizers co-application enhanced rice productivity through increasing the diversity and key network module of soil bacterial community. **2023**, 23, 2175-2188 ○
- 249 Polybacterial shift in benthic river biofilms attributed to organic pollution – prospect of a new biosentinel?. **2023**, 54, 348-359 ○
- 248 Soil Bacterial Community Response to Fire Varies with Slope Aspect at Zhenshan Mountain, East China. ○
- 247 Application of prophage sequence analysis to investigate a disease outbreak involving Salmonella Adjame, a rare serovar and implications for the population structure. 14, ○
- 246 Use of modified ichip for the cultivation of thermo-tolerant microorganisms from the hot spring. **2023**, 23, ○
- 245 Experimental community coalescence sheds light on microbial interactions in soil and restores impaired functions. **2023**, 11, ○
- 244 Cold Exposure-induced Alterations in the Brain Peptidome and Gut Microbiome Are Linked to Energy Homeostasis in Mice. **2023**, 22, 100525 ○
- 243 Encouraging news for in situ conservation: Translocation of salamander larvae has limited impacts on their skin microbiota. ○
- 242 Host selection has stronger impact on leaf microbiome assembly compared to land-management practices. ○
- 241 Influence of Pesticides and Mineral Fertilizers on the Bacterial Community of Arable Soils under Pea and Chickpea Crops. **2023**, 13, 750 ○
- 240 Organic Farming Favors phoD-Harboring Rhizospheric Bacterial Community and Alkaline Phosphatase Activity in Tropical Agroecosystem. **2023**, 12, 1068 ○
- 239 Novel Clustering Methods Identified Three Caries Status-Related Clusters Based on Oral Microbiome in Thai Mother-Child Dyads. **2023**, 14, 641 ○

- 238 Feeding *Spodoptera exigua* (Lepidoptera: Noctuidae) larvae with bacteria increase larval juvenile hormone levels inhibiting cannibalism under certain conditions. ○
- 237 Fungicidal Activity of Caproate Produced by *Clostridium* sp. strain E801, a Bacterium Isolated from Cocopeat Medium Subjected to Anaerobic Soil Disinfestation. **2023**, 13, 747 ○
- 236 Distinct response of total and active fungal communities and functions to seasonal changes in a semi-enclosed bay with mariculture ( Dongshan Bay , Southern China ). ○
- 235 Clinical and Microbial Changes in Orthodontic Patients Using Clear Aligners Vs. Fixed Appliances. **2019**, 47, 783-791 ○
- 234 Network Analysis Indicates Microbial Assemblage Differences in Life Stages of *Cladophora*. **2023**, 89, ○
- 233 Biophysical contexture of coastal biofilm-sediments varies heterogeneously and seasonally at the centimeter scale across the bed-water interface. 10, ○
- 232 Comparative microbiome analysis reveals the variation in microbial communities between 葡萄 and its bud mutant variety. ○
- 231 Developing and reusing bioinformatics data analysis pipelines using scientific workflow systems. **2023**, 21, 2075-2085 ○
- 230 Effects of rice blast biocontrol strain *Pseudomonas alcaliphila* Ej2 on the endophytic microbiome and proteome of rice under salt stress. 14, ○
- 229 Comparative analysis of two nonlethal methods for the study of the gut bacterial communities in wild lizards. ○
- 228 Bacterial Diversity and Community Characteristics of the Sinus and Dental Regions in Adults with Odontogenic Sinusitis. ○
- 227 JAMS - A framework for the taxonomic and functional exploration of microbiological genomic data. ○
- 226 Citrus Flavonoids Supplementation as an Alternative to Replace Zinc Oxide in Weanling Pigs Diets Minimizing the Use of Antibiotics. **2023**, 13, 967 ○
- 225 Earthworm-Driven Changes in Soil Chemico-Physical Properties, Soil Bacterial Microbiota, Tree/Tea Litter Decomposition, and Plant Growth in a Mesocosm Experiment with Two Plant Species. **2023**, 12, 1216 ○
- 224 Application of Computational Data Modeling to a Large-Scale Population Cohort Assists the Discovery of Inositol as a Strain-Specific Substrate for *Faecalibacterium prausnitzii*. **2023**, 15, 1311 ○
- 223 Alterations in the gut microbiome and metabolome profiles of septic mice treated with Shen FuHuang formula. 14, ○
- 222 Bovine Colostrum Supplementation Modulates the Intestinal Microbial Community in Rabbits. **2023**, 13, 976 ○
- 221 Phosphorus mining activities alter endophytic bacterial communities and metabolic functions of surrounding vegetables and crops. ○

220	Correlation of Soil Physiochemical Properties, Microorganism Numbers, and Bacterial Communities Following Unburned and Burned Sugarcane Harvest. <b>2023</b> , 2023, 1-9	0
219	Inoculation strategies affect the physicochemical properties and flavor of Zhenjiang aromatic vinegar. 14,	0
218	Microbiome and function alterations in the gastric mucosa of asymptomatic patients with <i>Helicobacter pylori</i> infection.	0
217	External and internal microbiomes of Antarctic nematodes are distinct, but more similar to each other than the surrounding environment. <b>2023</b> , 55,	0
216	Differences in Soil Microbial Communities between Healthy and Diseased <i>Lycium barbarum</i> cv. Ningqi-5 Plants with Root Rot. <b>2023</b> , 11, 694	0
215	Comammox <i>Nitrospira</i> clade A recovers faster than clade B after cyanobacteria outbreak in the Three Gorges tributary, China. <b>2023</b> , 23, 2273-2283	0
214	Bestimmung der Endophyten im Blutungssaft der Rebe mittels Next Generation Sequencing. <b>2022</b> , 73, 123-133	0
213	Response of microbial community of surface and deep chlorophyll maximum to nutrients and light in South China Sea. 10,	0
212	Metabolome and Microbiome Changes Associated with a Diet-Induced Reduction in Hepatic Fat among Adolescent Boys. <b>2023</b> , 13, 401	0
211	Soil protist functional composition shifts with atmospheric nitrogen deposition in subtropical forests.	0
210	Alteration of the Respiratory Microbiome in Hospitalized Patients with Asthma and COPD Overlap during and after an Exacerbation. <b>2023</b> , 12, 2118	1
209	Changing Rhizosphere Microbial Community and Metabolites with Developmental Stages of <i>Coleus barbatus</i> . <b>2023</b> , 11, 705	0
208	Impact of high altitude on composition and functional profiling of oral microbiome in Indian male population. <b>2023</b> , 13,	0
207	Deterministic processes dominate microbial community assembly in artificially bred <i>Schizothorax wangchiachii</i> juveniles after being released into wild.	0
206	A parasitic nematode induces dysbiosis in susceptible but not resistant gastropod hosts. <b>2023</b> , 12,	0
205	Algal amendment enhances biogenic methane production from coals of different thermal maturity. 14,	0
204	Microbiota and functional analyses of nitrogen-fixing bacteria in root-knot nematode parasitism of plants. <b>2023</b> , 11,	0
203	Quantitative 16S rRNA Gene Amplicon Sequencing for Comprehensive Pathogenic Bacterial Tracking in a Municipal Wastewater Treatment Plant. <b>2023</b> , 3, 923-933	0

- 202 Comammox Nitrospira and Ammonia-Oxidizing Archaea Are Dominant Ammonia Oxidizers in Sediments of an Acid Mine Lake Containing High Ammonium Concentrations. **2023**, 89, ○
- 201 Bacterial diversity and co-occurrence patterns differ across a world-wide spatial distribution of habitats in glacier ecosystems. ○
- 200 Chrysophyllum albidum Deterioration Entails Decline in Pseudomonas and Increase in Acetobacter Abundance. ○
- 199 Responses of bacterial communities along vertical soil profile to the chromium-contamination stress. **2023**, 179, 105584 ○
- 198 Environmental factors and host genotype control foliar epiphytic microbial community of wild soybeans across China. 14, ○
- 197 Bacterial community assembly and antibiotic resistance genes in soils exposed to antibiotics at environmentally relevant concentrations. ○
- 196 From river to ocean: Connectivity and heterogeneity of aquatic ecosystems depicted by planktonic microeukaryotes. **2023**, 148, 110136 ○
- 195 New insights into the impact of microbiome on horizontal and vertical transmission of a tick-borne pathogen. **2023**, 11, ○
- 194 Ubiquitous, B12-dependent virioplankton utilizing ribonucleotide triphosphate reductase demonstrate interseasonal dynamics and associate with a diverse range of bacterial hosts in the pelagic ocean. ○
- 193 Fermented Total Mixed Ration Alters Rumen Fermentation Parameters and Microbiota in Dairy Cows. **2023**, 13, 1062 ○
- 192 A phytobiotic extract, in an aqueous or in a cyclodextrin encapsulated form, added in diet affects meat oxidation, cellular responses and intestinal morphometry and microbiota of broilers. 4, ○
- 191 Global research on the crosstalk between intestinal microbiome and colorectal cancer: A visualization analysis. 13, ○
- 190 The gut microbiota diversity of five Orthoptera (Insecta, Polyneoptera) insects determined by DNA metabarcoding. 11, ○
- 189 Temporal dynamics of geothermal microbial communities in Aotearoa-New Zealand. 14, ○
- 188 Gut microbial community in proboscis monkeys: implications for effects of geographical and social factors. ○
- 187 EpiCRISPR targeted methylation of Arx gene initiates transient switch of mouse pancreatic alpha to insulin-producing cells. 14, ○
- 186 Microbial network and composition changes according to tobacco varieties and interferes differently in black shank disease defense. **2023**, 134, ○
- 185 Fermented cottonseed and rapeseed meals outperform soybean meal in improving performance, rumen fermentation, and bacterial composition in Hu sheep. 14, ○

- 184 Bioinformatic and Statistical Analysis of Microbiome Data. **2023**, 183-229 ○
- 183 Combined Effects of Temperature and Dietary Lipid Level on Body Composition, Growth, and Freshness Profile in European Seabass, *Dicentrarchus labrax*. **2023**, 13, 1068 ○
- 182 Changes of intestinal microbiota in the giant salamander (*Andrias davidianus*) during growth based on high-throughput sequencing. 14, ○
- 181 Exploring the effects of short-course antibiotics on children's gut flora by using 16S rRNA gene sequencing: a case-control study. ○
- 180 Camellia oil (*Camellia oleifera* Abel.) alleviates gastric injury induced by ethanol associated with modulation of gut microbiota in mice. **2023**, 8, 61-71 ○
- 179 Repeated divergence of amphibians and reptiles across an elevational gradient in northern Madagascar. **2023**, 13, ○
- 178 Hepatotoxicity of polymeric proanthocyanidins is caused by translocation of bacterial lipopolysaccharides through impaired gut epithelium. **2023**, 379, 35-47 ○
- 177 Efficacy of faecal microbiota transplantation in patients with progressive supranuclear palsy-Richardson's syndrome: a phase 2, single centre, randomised clinical trial. **2023**, 58, 101888 ○
- 176 Deciphering the mechanism of fungal pathogen-induced disease-suppressive soil. ○
- 175 Fungal Community Composition and Function Associated with Loose Smokeless Tobacco Products. **2023**, 80, ○
- 174 Endorhizosphere of indigenous succulent halophytes: a valuable resource of plant growth promoting bacteria. **2023**, 18, ○
- 173 Characterization of dysbiosis of the conjunctival microbiome and nasal microbiome associated with allergic rhinoconjunctivitis and allergic rhinitis. 14, ○
- 172 Snow Microorganisms Colonise Arctic Soils Following Snow Melt. ○
- 171 Interspecific plant interaction via root exudates structures the disease suppressiveness of rhizosphere microbiomes. **2023**, ○
- 170 Arabinoxylan-based substrate preferences and predicted metabolic properties of *Bifidobacterium longum* subspecies as a basis to design differential media. **2023**, 167, 112711 ○
- 169 Comparison of the effects of compound probiotics and antibiotics on yellow-feather broilers based on growth performance, small intestine morphology and digestive enzymes activity, gut microbiota and fecal emissions. ○
- 168 Effects of Hanwoo (Korean cattle) manure as organic fertilizer on plant growth, feed quality, and soil bacterial community. 14, ○
- 167 Amino Acids Drive the Deterministic Assembly Process of Fungal Community and Affect the Flavor Metabolites in Bajjiu Fermentation. **2023**, 11, ○

- 166 Histological, microecological and transcriptomic physiological responses underlying hypoxia and reoxygenation adaptation in yellowtail kingfish (*Seriola lalandi*). 10, ○
- 165 Impavido attenuates inflammation, reduces atherosclerosis, and alters gut microbiota in hyperlipidemic mice. **2023**, 26, 106453 ○
- 164 Buchnera breaks the specialization of the cotton-specialized aphid (*Aphis gossypii*) by providing nutrition through zucchini. 10, ○
- 163 Significant antimicrobial-producing vegetation uniquely shapes the stormwater biofilter microbiome with implications for enhanced faecal pathogen inactivation. **2023**, 2, e0000094 ○
- 162 A mechanism by which gut microbiota elevates permeability and inflammation in obese/diabetic mice and human gut. *gutjnl-2022-327365* ○
- 161 16S-rRNA-Based Metagenomic Profiling of the Bacterial Communities in Traditional Bulgarian Sourdoughs. **2023**, 11, 803 ○
- 160 Metabarcoding analysis of the bacterial and fungal communities during the maturation of preparation 500, used in biodynamic agriculture, suggests a rational link between horn and manure. ○
- 159 Revisiting Microbial Diversity in Hypersaline Microbial Mats from Guerrero Negro for a Better Understanding of Methanogenic Archaeal Communities. **2023**, 11, 812 ○
- 158 Composition of Particulate Matter and Bacterial Community in Gut Contents and Surrounding Sediments of Three Sipunculan Species (*Siphonostoma australe*, *Phascolosoma arcuatum*, and *Sipunculus nudus*). **2023**, 24, 6001 ○
- 157 Spatial Distribution of airborne bacterial communities in caged poultry houses. ○
- 156 Time-restricted feeding effect on overweight and obese patients with chronic kidney disease stages 3-4: A prospective non-randomized control pilot study. 14, ○
- 155 Heavy Metal Pollution Impacts Soil Bacterial Community Structure and Antimicrobial Resistance at the Birmingham 35th Avenue Superfund Site. **2023**, 11, ○
- 154 Upper respiratory tract mycobiome alterations in different kinds of pulmonary disease. 14, ○
- 153 FICZ activating AHR protects against intestinal injury in mice with DSS-induced colitis by regulating intestinal flora and metabolism. ○
- 152 Phod-harboring bacterial communities mediated slow and fast phosphorus transformation in alkaline soil of a *Robinia pseudoacacia* afforestation chronosequence. ○
- 151 Impacts of 10 years of elevated CO<sub>2</sub> and warming on soil fungal diversity and network complexity in a Chinese paddy field. ○
- 150 Diversity of bacterial community in the rhizosphere and bulk soil of *Artemisia annua* grown in highlands of Uganda. **2023**, 18, e0269662 ○
- 149 Melatonin Alleviates Chronic Intermittent Hypoxia-induced Microbiota Dysbiosis and Attenuates Intestinal Barrier Dysfunction via STAT3/Th17 signalling pathway. ○

- 148 The cascading effects of submerged macrophyte collapse on geese at Poyang Lake, China. ○
- 147 Construction of hybrid constructed wetlands for phosphorus chemical industry tailwater treatment in the middle Yangtze river basin: Responses of plant growth and root-associated microbial communities. **2023**, 100144 ○
- 146 Dysbiosis of gut microbiota due to diet, alcohol intake, body mass index, and gastrointestinal diseases in India. **2023**, 107, 2547-2560 ○
- 145 <i>Fusobacterium nucleatum</i> Induces Gut Dysbiosis and Inflammation and Promotes Colonic Inflammation. **2023**, 21, 60-70 ○
- 144 Effect of different additions of low-density polyethylene and microplastics polyadipate/butylene terephthalate on soil bacterial community structure. **2023**, 30, 55649-55661 ○
- 143 The single and combined effects of sulfamethazine and cadmium on soil nitrification and ammonia-oxidizing microorganisms. **2023**, 30, 56108-56120 ○
- 142 Microbial diversity and metabolic function in duodenum, jejunum and ileum of emu (*Dromaius novaehollandiae*). **2023**, 13, ○
- 141 Effects of *Thymbra capitata* essential oil on in vitro fermentation end-products and ruminal bacterial communities. **2023**, 13, ○
- 140 Effects of Microbial Communities on Elevational Gradient Adaptation Strategies of *Pinus yunnanensis* Franch. and *Pinus densata* Mast. in a Mixed Zone. **2023**, 14, 685 ○
- 139 Effects of dissolved oxygen on intestinal bacterial community and immunity of Atlantic salmon *Salmo salar*. **2023**, 41, 364-375 ○
- 138 Lethal and sublethal effects on stingless bee (*Partamona helleri*) larvae caused by chronic exposure to three agrochemicals. ○
- 137 Glycoursodeoxycholic acid regulates bile acids level and alters gut microbiota and glycolipid metabolism to attenuate diabetes. **2023**, 15, ○
- 136 Effects of different concentrations of biochar amendments and Pb toxicity on rhizosphere soil characteristics and bacterial community of red clover (*Trifolium pretense* L.). 14, ○
- 135 Physiological, metabolic and microbial responses to obesogenic cafeteria diet in rats: The impact of strain and sex. **2023**, 117, 109338 ○
- 134 Management of dog sperm parameters and gut microbiota composition with *Lactobacillus rhamnosus* supplementation. ○
- 133 Testing the stress gradient hypothesis in soil bacterial communities associated with vegetation belts in the Andean Atacama Desert. **2023**, 18, ○
- 132 Gut Microbiota Accelerate the Insecticidal Activity of Plastid-Expressed *Bacillus thuringiensis* Cry3Bb to a Leaf Beetle, *Plagioderma versicolora*. **2023**, 11, ○
- 131 Monitoring the changes in physicochemical, sensory properties and microbiota of village-type homemade yoghurts along three consecutive back-slopping procedures. **2023**, 143, 105663 ○

- 130 *Klebsiella quasipneumoniae* in intestine damages bile acid metabolism in hematopoietic stem cell transplantation patients with bloodstream infection. **2023**, 21, ○
- 129 Genome-resolved analyses of oligotrophic groundwater microbial communities along phenol pollution in a continuous-flow biodegradation model system. 14, ○
- 128 Environmental DNA metabarcoding from flowers reveals arthropod pollinators, plant pests, parasites, and potential predator-prey interactions while revealing more arthropod diversity than camera traps. ○
- 127 Behavioral phenotype, intestinal microbiome, and brain neuronal activity of male serotonin transporter knockout mice. **2023**, 16, ○
- 126 Analysis of the Microbial Diversity and Population Dynamics during the Pulque Fermentation Process. **2023**, 9, 342 ○
- 125 The Gut Microbiota of Broilers Reared with and without Antibiotic Treatment. **2023**, 11, 876 ○
- 124 Biochar improves soil organic carbon stability by shaping the microbial community structures at different soil depths four years after an incorporation in a farmland soil. **2023**, 5, 100214 ○
- 123 Mycobiome Study Reveals Different Pathogens of Vulvovaginal Candidiasis Shape Characteristic Vaginal Bacteriome. ○
- 122 Regulation of bacterial behavior to mitigate membrane fouling in gravity-driven membrane system: The beneficial effects of gravity-driven up-flow slow biofilter. **2023**, 53, 103669 ○
- 121 The inhibition of high ammonia to in vitro rumen fermentation is pH dependent. 10, ○
- 120 Trophic interrelationships of bacteria are important for shaping soil protist communities. ○
- 119 Effect of *Limosilactobacillus reuteri* ZJF036 on Growth Performance and Gut Microbiota in Juvenile Beagle Dogs. **2023**, 80, ○
- 118 Dynamics of oral microbiome acquisition in healthy infants: A pilot study. 4, ○
- 117 Niche differentiation of comammox *Nitrospira* and canonical nitrifiers in riparian wetland ecosystems around Taihu Lake. ○
- 116 Oral microbiome changes associated with the menstrual cycle in healthy young adult females. 13, ○
- 115 Vaginal Infections during Pregnancy Increase Breast Milk Microbiome Alpha Diversity and Alter Taxonomic Composition. **2023**, 28, 1-9 ○
- 114 Microbial diversity and community composition of fecal microbiota in dual-purpose and egg type ducks. 14, ○
- 113 Aerosol partitioning potential of bacteria presenting antimicrobial resistance from different stages of a small decentralized septic treatment system. 1-15 ○



- 112 Plant Rhizospheres Harbour Specific Fungal Groups and Form a Stable Co-Occurrence Pattern in the Saline-Alkali Soil. **2023**, 13, 1036 ○
- 111 A Randomized Controlled Trial of Probiotics Targeting Gut Dysbiosis in Huntington's Disease. **2023**, 1-13 ○
- 110 Metagenomic assessment of nitrate-contaminated mine wastewaters and optimization of complete denitrification by indigenous enriched bacteria. 11, ○
- 109 Diversity and assembly of root-associated microbiomes of rubber trees. 14, ○
- 108 Oral metagenomes from Native American Ancestors reveal distinct microbial lineages in the pre-contact era. ○
- 107 Vaginal Microbiome Dysbiosis is Associated with the Different Cervical Disease Status. ○
- 106 Rhizosphere Effect and Bacterial Community Structure in the Horizons of Podzolic Soil under Norway Spruce (*Picea abies* L.). **2023**, 56, 29-37 ○
- 105 Influence of Gut Microbiota on Metabolism of Bisphenol A, a Major Component of Polycarbonate Plastics. **2023**, 11, 340 ○
- 104 Gut Microbiota in Children with Hand Foot and Mouth Disease on 16S rRNA Gene Sequencing. **2023**, 80, ○
- 103 The impact of culture systems on the gut microbiota and gut metabolome of bighead carp (*Hypophthalmichthys nobilis*). **2023**, 5, ○
- 102 Plant Genotype Shapes the Soil Nematode Community in the Rhizosphere of Tomatoes with Different Resistance to *Meloidogyne incognita*. **2023**, 12, 1528 ○
- 101 Association between gut microbial diversity and technique failure in peritoneal dialysis patients. **2023**, 45, ○
- 100 Belowground microbiota analysis indicates that *Fusarium* spp. exacerbate grapevine trunk disease. **2023**, 18, ○
- 99 Microbial mat compositions and localization patterns explain the virulence of black band disease in corals. **2023**, 9, ○
- 98 *Spodoptera frugiperda* (Lepidoptera: Noctuidae) Life Table Comparisons and Gut Microbiome Analysis Reared on Corn Varieties. **2023**, 14, 358 ○
- 97 Response of the *Pardosa astrigera* bacterial community to Cry1B protein. **2023**, 256, 114855 ○
- 96 Microbial gradual shifts during the process of species replacement in Taihang Mountain. 14, ○
- 95 Alterations of Epidermal Lipid Profiles and Skin Microbiome in Children With Atopic Dermatitis. **2023**, 15, 186 ○

- 94 Supplementation with alpha-glycerol monolaurate during late gestation and lactation enhances sow performance, ameliorates milk composition, and improves growth of suckling piglets. **2023**, 14, ○
- 93 Potential of *Medicago sativa* and *Perilla frutescens* for overcoming the soil sickness caused by ginseng cultivation. 14, ○
- 92 Evolving approaches to profiling the microbiome in skin disease. 14, ○
- 91 Agroecosystem edge effects on vegetation, soil properties, and the soil microbial community in the Canadian prairie. **2023**, 18, e0283832 ○
- 90 Wildlife gut microbiomes of sympatric generalist species respond differently to anthropogenic landscape disturbances. **2023**, 5, ○
- 89 Freshwater transfer affected intestinal microbiota with correlation to cytokine gene expression in Asian sea bass. 14, ○
- 88 Effects of Mexican *Ganoderma lucidum* extracts on liver, kidney, and the gut microbiota of Wistar rats: A repeated dose oral toxicity study. **2023**, 18, e0283605 ○
- 87 THAPBI PICT - a fast, cautious, and accurate metabarcoding analysis pipeline. ○
- 86 Characteristics and intrasubject variation in the respiratory microbiome in interstitial lung disease. **2023**, 102, e33402 ○
- 85 Feeding citrus flavonoid extracts decreases bacterial endotoxin and systemic inflammation and improves immunometabolic status by modulating hindgut microbiome and metabolome in lactating dairy cows. **2023**, ○
- 84 Bacterial diversity and function shift of strawberry root in different cultivation substrates. **2023**, 100696 ○
- 83 Aquafeed fermentation improves dietary nutritional quality and benefits feeding behavior, meat flavor, and intestinal microbiota of Chinese mitten crab (*Eriocheir sinensis*). **2023**, ○
- 82 Decreasing lactate input for cost-effective sulfidogenic metal removal in sulfate-rich effluents: Mechanistic insights from (bio)chemical kinetics to microbiome response. **2023**, 330, 138662 ○
- 81 Plant pathogen resistance is mediated by recruitment of specific rhizosphere fungi. ○
- 80 Banxia Xiexin decoction alleviates AS co-depression disease by regulating the gut microbiome-lipid metabolic axis. **2023**, 116468 ○
- 79 Antibiotic treatment using amoxicillin-clavulanic acid impairs gut mycobiota development through modification of the bacterial ecosystem. **2023**, 11, ○
- 78 Response of Soil Microbial Communities to Elevation Gradient in Central Subtropical *Pinus taiwanensis* and *Pinus massoniana* Forests. **2023**, 14, 772 ○
- 77 Chemical Characterization and Metagenomic Identification of Endophytic Microbiome from South African Sunflower (*Helianthus annuus*) Seeds. **2023**, 11, 988 ○

- 76 MiSurv: an Integrative Web Cloud Platform for User-Friendly Microbiome Data Analysis with Survival Responses. ○
- 75 Review on the Epidemiology, Milk Composition Changes, and Antimicrobial Susceptibility of Causative Agents of Bubaline Mastitis in Asia. **2023**, 46, ○
- 74 Effects of whole-grain cereals on fecal microbiota and short-chain fatty acids in dogs - A comparison of rye, oats and wheat. ○
- 73 PhyloMed: a phylogeny-based test of mediation effect in microbiome. **2023**, 24, ○
- 72 Integrated Microbiome and Metabolomic Analysis Reveal Responses of Rhizosphere Bacterial Communities and Root exudate Composition to Drought and Genotype in Rice (*Oryza sativa* L.). **2023**, 16, ○
- 71 The Impact of Storage Temperature on the Development of Microbial Communities on the Surface of Blueberry Fruit. **2023**, 12, 1611 ○
- 70 Comprehensive Microbiome and Metabolome Analyses Reveal the Medicinal Components of *Paeonia lactiflora*. **2023**, 12, 1612 ○
- 69 Enhanced phytoremediation of petroleum-contaminated soil by biochar and urea. **2023**, 453, 131404 ○
- 68 First Study on profiling of gut microbiome in wild and captive Sumatran orangutans (*Pongo abelii*). **2023**, 717-727 ○
- 67 *Fusobacterium nucleatum* aggravates rheumatoid arthritis through FadA-containing outer membrane vesicles. **2023**, ○
- 66 Gut microbiota response to sucralose or rebaudioside A in rats under two dietary conditions. ○
- 65 Constellation of the endophytic mycobiome in spring and winter wheat cultivars grown under various conditions. **2023**, 13, ○
- 64 A lncRNA from an inflammatory bowel disease risk locus maintains intestinal host-commensal homeostasis. ○
- 63 Graphene oxide exposure alters gut microbial community composition and metabolism in an in vitro human model. **2023**, 100463 ○
- 62 A comparison between Greengenes, SILVA, RDP, and NCBI reference databases in four published microbiota datasets. ○
- 61 The Potential Roles of Free and Attached Microbial Community in Decreasing Cadmium Level from Cadmium-Contaminated Soils by Mixotrophic Acidophiles of Different Scale-Up Cultivation Stages. **2023**, 13, 546 ○
- 60 Early Oral Administration of Ginseng Stem-Leaf Saponins Enhances the Peyer's Patch-Dependent Maternal IgA Antibody Response to a PEDV Inactivated Vaccine in Mice, with Gut Microbiota Involvement. **2023**, 11, 830 ○
- 59 Contrasting influences of two dominant plants, *Dasiphora fruticosa* and *Ligularia virguarea*, on aboveground and belowground communities in an alpine meadow. 14, ○

- 58 Correlation between microbial diversity and flavor metabolism in Huangshui: A by-product of solid-state fermentation Baijiu. **2023**, 181, 114767 ○
- 57 Palmitoleic Acid on Top of HFD Ameliorates Insulin Resistance Independent of Diacylglycerols and Alters Gut Microbiota in C57BL/6J Mice. **2023**, 1-24 ○
- 56 Yield and Rhizosphere Soil Environment of Greenhouse Zucchini in Response to Different Planting and Breeding Waste Composts. **2023**, 11, 1026 ○
- 55 Short-term soil amendment by sewage sludge anaerobic digestate in a tomato monoculture suppresses *Fusarium vascular wilt* disease by changing the taxonomic characteristics of soil microbiota. **2023**, 189, 104915 ○
- 54 Exploring the fungal communities and their correlation with the physicochemical properties of Zaopocu, a distinctive fermented food on Hainan island. ○
- 53 Biochar significantly reduced nutrient-induced positive priming in a subtropical forest soil. ○
- 52 Diversity of endosymbionts in camellia spiny whitefly, *Aleurocanthus camelliae* (Hemiptera: Aleyrodidae), estimated by 16S rRNA analysis and their biological implications. 14, ○
- 51 Biodegradation of Persistent Organic Pollutant (POP) hexachlorocyclohexane in a hybrid reactor system. **2023**, 109948 ○
- 50 Influence of Maternal Breast Milk and Vaginal Microbiome on Neonatal Gut Microbiome: a Longitudinal Study during the First Year. ○
- 49 Co-Selection of Bacterial Metal and Antibiotic Resistance in Soil Laboratory Microcosms. **2023**, 12, 772 ○
- 48 Occurrence, Risk, and Treatment of Ciprofloxacin and Clarithromycin in Drainage. **2023**, 142968 ○
- 47 Intensified livestock farming increases antibiotic resistance genotypes and phenotypes in animal feces. **2023**, 4, ○
- 46 Indoleacrylic acid produced by *Parabacteroides distasonis* alleviates type 2 diabetes via activation of AhR to repair intestinal barrier. **2023**, 21, ○
- 45 Skin microbiome bacteria enriched following long sun exposure can reduce oxidative damage: a 5-month preliminary study of ten lifeguards. **2023**, 104059 ○
- 44 Hydrogen peroxide treatment mitigates antibiotic resistance gene and mobile genetic element propagation in mariculture sediment. **2023**, 121652 ○
- 43 Phosphorus amendment alters soil arbuscular mycorrhizal fungal functional guild compositions in a subtropical forest. ○
- 42 Unraveling the Dysbiosis of Vaginal Microbiome to Understand Cervical Cancer Disease Etiology—An Explainable AI Approach. **2023**, 14, 936 ○
- 41 Integrating Multi-Omics Data to Construct Reliable Interconnected Models of Signaling, Gene Regulatory, and Metabolic Pathways. **2023**, 139-151 ○

- 40 Evaluating the Reproducibility of Amplicon Sequencing Data Derived from Deep-Sea Cold Seep Sediment-Associated Microbiota. ○
- 39 Anti-diarrheal drug loperamide induces dysbiosis in zebrafish microbiota via bacterial inhibition. ○
- 38 The effect of wheat genotype on the microbiome is more evident in roots and varies through time. **2023**, 3, ○
- 37 Microbial functional genes within soil aggregates drive organic carbon mineralization under contrasting tillage practices. ○
- 36 Fungal community remediate quartz tailings soil under plant combined with urban sludge treatments. 14, ○
- 35 Surfaces of gymnastic equipment as reservoirs of microbial pathogens with potential for transmission of bacterial infection and antimicrobial resistance. 14, ○
- 34 Osmium-grafted Magnetic Nanobeads Improve Microbial Current Generation via Culture-free and Quick Enrichment of Electrogenic Bacteria. **2023**, 142936 ○
- 33 Closed aerobic biodegradation kinetics test with activated sludge and low concentration chemical mixtures. **2023**, 138752 ○
- 32 Decline in Morel Production upon Continuous Cropping Is Related to Changes in Soil Mycobiome. **2023**, 9, 492 ○
- 31 Dual use of solar power plants as biocrust nurseries for large-scale arid soil restoration. ○
- 30 Hybridization alters the gut microbial and metabolic profile concurrent with modifying intestinal functions in Tunchang pigs. 14, ○
- 29 Pruning Wound Protection Products Induce Alterations in the Wood Mycobiome Profile of Grapevines. **2023**, 9, 488 ○
- 28 Human microbiome transfer in the built environment differs based on occupants, objects, and buildings. **2023**, 13, ○
- 27 Disruption of peritrophic matrix chitin metabolism and gut immune by chlorantraniliprole results in pathogenic bacterial infection in *Bombyx mori*. **2023**, 105430 ○
- 26 Feeding with resistant maltodextrin suppresses excessive calorie intake in a high-fat diet, mediated by changes in mouse gut microbiota composition, appetite-related gut hormone secretion, and neuropeptide transcriptional levels. 2, ○
- 25 Sustained anaerobic degradation of 4-chloro-2-methylphenoxyacetic acid by acclimated sludge in a continuous-flow reactor. **2023**, 138749 ○
- 24 Impact of prophylactic and "rescue pack" antibiotics on the airway microbiome in chronic lung disease. **2023**, 10, e001335 ○
- 23 Diet replacement with whole insect larvae affects intestinal morphology and microbial ecosystem of broiler chickens. ○

- 22 Parents with periodontitis drive the early acquisition of dysbiotic microbiomes in their offspring. ○
- 21 Specific gut microbiome signature predicts hepatitis B virus-related hepatocellular carcinoma patients with microvascular invasion. ○
- 20 The gut microbiome of solitary bees is mainly affected by pathogen assemblage and partially by land use. **2023**, 18, ○
- 19 Differential response of denitrifying and diazotrophic soil populations to short and long-term exposure of glyphosate and atrazine. ○
- 18 DeepMicroGen: a generative adversarial network-based method for longitudinal microbiome data imputation. **2023**, 39, ○
- 17 MKMR: a multi-kernel machine regression model to predict health outcomes using human microbiome data. **2023**, 24, ○
- 16 Application of *Clostridium butyricum*, *Rummeliibacillus suwonensis*, and *Issatchenkia orientalis* for Nongxiangxing baijiu fermentation: Improves the microbial communities and flavor of upper fermented grain. **2023**, 169, 112885 ○
- 15 The spatio-temporal diversity and succession of microbial community and its environment driving factors during stacking fermentation of Maotai-flavor baijiu. **2023**, 169, 112892 ○
- 14 COMPOSITION OF BACTERIAL COMMUNITIES IN OIL-CONTAMINATED BOTTOM SEDIMENTS OF THE KAMENKA RIVER. **2023**, 78, 17-24 ○
- 13 Prokaryotic Responses to Estuarine Coalescence Contribute to Planktonic Community Assembly in a Mediterranean Nutrient-Rich Estuary. **2023**, 11, 933 ○
- 12 Revealing the correlation between the bacterial communities and physicochemical properties of ZaoPoCu, a traditional fermented food from Hainan Island. **2023**, 21, 344-356 ○
- 11 Software Tools for Microbiome Data Analysis. **2023**, 612-621 ○
- 10 Host selection has a stronger impact on leaf microbiome assembly compared to land-management practices. ○
- 9 Intestinal microbiota analyses of five economic fishery resources in the South China Sea. **2023**, 46, 101085 ○
- 8 *Mycena* species can be opportunist-generalist plant root invaders. ○
- 7 A reduced but stable core microbiome found in seeds of hyperaccumulators. **2023**, 887, 164131 ○
- 6 Postnatal 14D is the Key Window for Mice Intestinal Development- An Insight from Age-Dependent Antibiotic-Mediated Gut Microbial Dysbiosis Study. ○
- 5 Gut microbiome modified by bariatric surgery improves insulin sensitivity and correlates with increased brown fat activity and energy expenditure. **2023**, 4, 101051 ○

- 4 Differences of bacterial community co-occurrence network and assembly processes between sediment and water in lakes on the Qinghai-Tibet Plateau. **2023**, 35, 959-971
- 3 Composition of Soil Bacterial and Nematode Communities within Soil Aggregates in a Kiwifruit Orchard under Cover Crop Treatment. **2023**, 13, 1377
- 2 Exploring Molecular Interactions between Human Milk Hormone Insulin and Bifidobacteria.
- 1 Precipitation Drives Soil Protist Diversity and Community Structure in Dry Grasslands.