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An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea

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2246	Terrestrial runoff controls the bacterial community composition of biofilms along a water quality gradient in the Great Barrier Reef. <b>2012</b> , 78, 7786-91		21
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2240	The effect of training set on the classification of honey bee gut microbiota using the Naïve Bayesian Classifier. <b>2012</b> , 12, 221		40
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2187	An arbuscular mycorrhizal fungus significantly modifies the soil bacterial community and nitrogen cycling during litter decomposition. <b>2013</b> , 15, 1870-81		196
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2092	Rhizosphere heterogeneity shapes abundance and activity of sulfur-oxidizing bacteria in vegetated salt marsh sediments. <b>2014</b> , 5, 309	41
2091	Bacterial community composition of chronic periodontitis and novel oral sampling sites for detecting disease indicators. <b>2014</b> , 2, 32	54
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2083	A possible link between food and mood: dietary impact on gut microbiota and behavior in BALB/c mice. <b>2014</b> , 9, e103398		103
2082	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
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2078	Resistance and resilience of the forest soil microbiome to logging-associated compaction. <i>ISME Journal</i> , <b>2014</b> , 8, 226-44	11.9	194
2077	The amphibian skin-associated microbiome across species, space and life history stages. <b>2014</b> , 23, 1238-50		220
2076	Analysis of bacterial diversity in sponges collected from Chuuk and Kosrae Islands in Micronesia. <b>2014</b> , 52, 20-6		3
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2072	Convergence of gut microbiomes in myrmecophagous mammals. <b>2014</b> , 23, 1301-17		179
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2067	Why are some microbes more ubiquitous than others? Predicting the habitat breadth of soil bacteria. <b>2014</b> , 17, 794-802	147
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2065	Mosquitoes rely on their gut microbiota for development. <b>2014</b> , 23, 2727-39	263
2064	Obtaining genomes from uncultivated environmental microorganisms using FACS-based single-cell genomics. <b>2014</b> , 9, 1038-48	177
2063	POGO-DB--a database of pairwise-comparisons of genomes and conserved orthologous genes. <b>2014</b> , 42, D625-32	19
2062	Further steps in TANGO: improved taxonomic assignment in metagenomics. <b>2014</b> , 30, 17-23	17
2061	Towards a taxonomic coherence between average nucleotide identity and 16S rRNA gene sequence similarity for species demarcation of prokaryotes. <b>2014</b> , 64, 346-351	1657
2060	<i>Thermoflexus hugenholtzii</i> gen. nov., sp. nov., a thermophilic, microaerophilic, filamentous bacterium representing a novel class in the Chloroflexi, <i>Thermoflexia</i> classis nov., and description of <i>Thermoflexaceae</i> fam. nov. and <i>Thermoflexales</i> ord. nov. <b>2014</b> , 64, 2119-2127	36
2059	AIEC pathobiont instigates chronic colitis in susceptible hosts by altering microbiota composition. <b>2014</b> , 63, 1069-80	149
2058	Microbial community dynamics and effect of environmental microbial reservoirs on red-backed salamanders ( <i>Plethodon cinereus</i> ). <i>ISME Journal</i> , <b>2014</b> , 8, 830-40	11.9 196
2057	The SILVA and "All-species Living Tree Project (LTP)" taxonomic frameworks. <b>2014</b> , 42, D643-8	1369
2056	Impact of single-cell genomics and metagenomics on the emerging view of extremophile "microbial dark matter". <b>2014</b> , 18, 865-75	96
2055	Characterization of the bacterioplankton community and its antibiotic resistance genes in the Baltic Sea. <b>2014</b> , 61, 23-32	10
2054	Heme in the marine environment: from cells to the iron cycle. <b>2014</b> , 6, 1107-20	34
2053	Biofouling and microbial communities in membrane distillation and reverse osmosis. <b>2014</b> , 48, 13155-64	59

2052	Gill bacteria enable a novel digestive strategy in a wood-feeding mollusk. <b>2014</b> , 111, E5096-104		67
2051	Effect of postextraction algal residue supplementation on the ruminal microbiome of steers consuming low-quality forage. <b>2014</b> , 92, 5063-75		18
2050	Dynamics of gut microbiota in autoimmune lupus. <b>2014</b> , 80, 7551-60		167
2049	Bacteria from diverse habitats colonize and compete in the mouse gut. <b>2014</b> , 159, 253-66		226
2048	Routes of Acquisition of the Gut Microbiota of the Honey Bee <i>Apis mellifera</i> . <b>2014</b> , 80, 7378-87		250
2047	Effect of pine bark on the biotransformation of trinitrotoluene and on the bacterial community structure in a batch experiment. <b>2014</b> , 35, 2456-65		1
2046	Biogeographic patterns in below-ground diversity in New York City's Central Park are similar to those observed globally. <b>2014</b> , 281,		201
2045	Research on neonatal microbiomes: what neonatologists need to know. <b>2014</b> , 105, 14-24		11
2044	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. <i>ISME Journal</i> , <b>2014</b> , 8, 1464-75	11.9	262
2043	Discovery of a novel methanogen prevalent in thawing permafrost. <b>2014</b> , 5, 3212		131
2042	Down under the tunic: bacterial biodiversity hotspots and widespread ammonia-oxidizing archaea in coral reef ascidians. <i>ISME Journal</i> , <b>2014</b> , 8, 575-588	11.9	56
2041	Animal rennets as sources of dairy lactic acid bacteria. <b>2014</b> , 80, 2050-61		33
2040	Diet-induced alterations in gut microflora contribute to lethal pulmonary damage in TLR2/TLR4-deficient mice. <b>2014</b> , 8, 137-49		35
2039	Coinfection. Virus-helminth coinfection reveals a microbiota-independent mechanism of immunomodulation. <b>2014</b> , 345, 578-82		195
2038	Conducting a microbiome study. <b>2014</b> , 158, 250-262		428
2037	<i>Lactivibrio alcoholicus</i> gen. nov., sp. nov., an anaerobic, mesophilic, lactate-, alcohol-, carbohydrate- and amino-acid-degrading bacterium in the phylum Synergistetes. <b>2014</b> , 64, 2137-2145		24
2036	Altering the intestinal microbiota during a critical developmental window has lasting metabolic consequences. <b>2014</b> , 158, 705-721		1126
2035	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

2034	Low temperature partial nitrification/anammox in a moving bed biofilm reactor treating low strength wastewater. <b>2014</b> , 48, 8784-92	257
2033	Getting started with microbiome analysis: sample acquisition to bioinformatics. <b>2014</b> , 82, 18.8.1-29	79
2032	Deciphering microbial landscapes of fish eggs to mitigate emerging diseases. <i>ISME Journal</i> , <b>2014</b> , 8, 2002-14	44
2031	Metataxonomic profiling and prediction of functional behaviour of wheat straw degrading microbial consortia. <b>2014</b> , 7, 92	69
2030	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
2029	The Earth Microbiome project: successes and aspirations. <b>2014</b> , 12, 69	501
2028	A hidden pitfall in the preparation of agar media undermines microorganism cultivability. <b>2014</b> , 80, 7659-66	133
2027	A20 controls intestinal homeostasis through cell-specific activities. <b>2014</b> , 5, 5103	78
2026	International Space Station environmental microbiome - microbial inventories of ISS filter debris. <b>2014</b> , 98, 6453-66	73
2025	Native soil fungi associated with compostable plastics in three contrasting agricultural settings. <b>2014</b> , 98, 6467-85	28
2024	CopyRighter: a rapid tool for improving the accuracy of microbial community profiles through lineage-specific gene copy number correction. <b>2014</b> , 2, 11	158
2023	An improved dual-indexing approach for multiplexed 16S rRNA gene sequencing on the Illumina MiSeq platform. <b>2014</b> , 2, 6	930
2022	Spatial biodiversity of bacteria along the largest Arctic river determined by next-generation sequencing. <b>2014</b> , 89, 442-50	32
2021	Airway microbiome dynamics in exacerbations of chronic obstructive pulmonary disease. <b>2014</b> , 52, 2813-23	206
2020	Processing faecal samples: a step forward for standards in microbial community analysis. <b>2014</b> , 14, 112	99
2019	Indigenous bacteria and fungi drive traditional kimoto sake fermentations. <b>2014</b> , 80, 5522-9	59
2018	Response of different nitrospira species to anoxic periods depends on operational do. <b>2014</b> , 48, 2934-41	107
2017	Genomic heterogeneity and ecological speciation within one subspecies of <i>Bacillus subtilis</i> . <b>2014</b> , 80, 4842-53	35

2016	The pattern of change in the abundances of specific bacterioplankton groups is consistent across different nutrient-enriched habitats in Crete. <b>2014</b> , 80, 3784-92	35
2015	Persistent gut microbiota immaturity in malnourished Bangladeshi children. <b>2014</b> , 510, 417-21	703
2014	Comparison of the vaginal microbial communities in women with recurrent genital HSV receiving acyclovir intravaginal rings. <b>2014</b> , 102, 87-94	17
2013	Interplay of host microbiota, genetic perturbations, and inflammation promotes local development of intestinal neoplasms in mice. <b>2014</b> , 211, 457-72	57
2012	Simulated geologic carbon storage leak reduces bacterial richness and alters bacterial community composition in surface soil. <b>2014</b> , 76, 286-296	11
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2008	Bacterial symbiont sharing in <i>Megalomyrmex</i> social parasites and their fungus-growing ant hosts. <b>2015</b> , 24, 3151-69	23
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1999	Rumen microbial community composition varies with diet and host, but a core microbiome is found across a wide geographical range. <b>2015</b> , 5, 14567	659

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1995	Increased diversity of egg-associated bacteria on brown trout ( <i>Salmo trutta</i> ) at elevated temperatures. <b>2015</b> , 5, 17084	18
1994	Archaeal and bacterial communities across a chronosequence of drained lake basins in Arctic Alaska. <b>2015</b> , 5, 18165	13
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1992	Microbiomes of the dust particles collected from the International Space Station and Spacecraft Assembly Facilities. <b>2015</b> , 3, 50	113
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1990	METAXA2: improved identification and taxonomic classification of small and large subunit rRNA in metagenomic data. <b>2015</b> , 15, 1403-14	252
1989	Freshwater ice as habitat: partitioning of phytoplankton and bacteria between ice and water in central European reservoirs. <b>2015</b> , 7, 887-98	8
1988	PanFP: pangenome-based functional profiles for microbial communities. <b>2015</b> , 8, 479	28
1987	Stability of operational taxonomic units: an important but neglected property for analyzing microbial diversity. <b>2015</b> , 3, 20	88
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1983	Impact of dietary deviation on disease progression and gut microbiome composition in lupus-prone SNF1 mice. <b>2015</b> , 181, 323-37	87
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1981	Resistivity and induced polarization monitoring of biogas combined with microbial ecology at a brownfield site. <b>2015</b> , 3, SAB43-SAB56	2



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1973	The Intestinal Microbiota in Acute Anorexia Nervosa and During Renourishment: Relationship to Depression, Anxiety, and Eating Disorder Psychopathology. <b>2015</b> , 77, 969-81	166
1972	Composition, Diversity and Abundance of Gut Microbiome in Prediabetes and Type 2 Diabetes. <b>2015</b> , 2, 1-7	99
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1970	Characterization of the Bacterial Community Naturally Present on Commercially Grown Basil Leaves: Evaluation of Sample Preparation Prior to Culture-Independent Techniques. <b>2015</b> , 12, 10171-97	12
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1967	Methane and microbial dynamics in the Gulf of Mexico water column. <b>2015</b> , 2,	12
1966	Increased seawater temperature increases the abundance and alters the structure of natural <i>Vibrio</i> populations associated with the coral <i>Pocillopora damicornis</i> . <b>2015</b> , 6, 432	77
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1960	An abundance of Epsilonproteobacteria revealed in the gut microbiome of the laboratory cultured sea urchin, <i>Lytechinus variegatus</i> . <b>2015</b> , 6, 1047	36
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1957	Solute Concentrations Influence Microbial Methanogenesis in Coal-bearing Strata of the Cherokee Basin, USA. <b>2015</b> , 6, 1287	25
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1954	Microbial community analysis of anaerobic reactors treating soft drink wastewater. <b>2015</b> , 10, e0119131	20
1953	Microbial iron mats at the Mid-Atlantic Ridge and evidence that Zetaproteobacteria may be restricted to iron-oxidizing marine systems. <b>2015</b> , 10, e0119284	48
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1951	The source of the river as a nursery for microbial diversity. <b>2015</b> , 10, e0120608	30
1950	Impact of the CFTR-potentiator ivacaftor on airway microbiota in cystic fibrosis patients carrying a G551D mutation. <b>2015</b> , 10, e0124124	49
1949	Exercise is More Effective at Altering Gut Microbial Composition and Producing Stable Changes in Lean Mass in Juvenile versus Adult Male F344 Rats. <b>2015</b> , 10, e0125889	106
1948	The effect of sampling and storage on the fecal microbiota composition in healthy and diseased subjects. <b>2015</b> , 10, e0126685	110
1947	Pyrosequencing characterization of the microbiota from Atlantic intertidal marine sponges reveals high microbial diversity and the lack of co-occurrence patterns. <b>2015</b> , 10, e0127455	25
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1945	Deconstructing the polymerase chain reaction: understanding and correcting bias associated with primer degeneracies and primer-template mismatches. <b>2015</b> , 10, e0128122	117

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1942	A Pyrosequencing Investigation of Differences in the Feline Subgingival Microbiota in Health, Gingivitis and Mild Periodontitis. <b>2015</b> , 10, e0136986	29
1941	Impact of Water Chemistry, Pipe Material and Stagnation on the Building Plumbing Microbiome. <b>2015</b> , 10, e0141087	82
1940	Lactobacillus casei Shirota Supplementation Does Not Restore Gut Microbiota Composition and Gut Barrier in Metabolic Syndrome: A Randomized Pilot Study. <b>2015</b> , 10, e0141399	33
1939	Plant Invasions Associated with Change in Root-Zone Microbial Community Structure and Diversity. <b>2015</b> , 10, e0141424	51
1938	The Influence of Age and Gender on Skin-Associated Microbial Communities in Urban and Rural Human Populations. <b>2015</b> , 10, e0141842	119
1937	Mapping microbial ecosystems and spoilage-gene flow in breweries highlights patterns of contamination and resistance. <b>2015</b> , 4,	47
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1935	Effect of different heterotrophic plate count methods on the estimation of the composition of the culturable microbial community. <b>2015</b> , 3, e862	19
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1929	High-Resolution Analyses of Overlap in the Microbiota Between Mothers and Their Children. <b>2015</b> , 71, 283-90	21
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1927	Deriving accurate microbiota profiles from human samples with low bacterial content through post-sequencing processing of Illumina MiSeq data. <b>2015</b> , 3, 19	126

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1919	Characterization of microbial community structure during continuous anaerobic digestion of straw and cow manure. <b>2015</b> , 8, 815-27		139
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1917	Cyanobacterial community composition in Arctic soil crusts at different stages of development. <b>2015</b> , 91,		48
1916	<i>Euphorbia</i> plant latex is inhabited by diverse microbial communities. <b>2015</b> , 102, 1966-77		6
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1914	Captured metagenomics: large-scale targeting of genes based on 'sequence capture' reveals functional diversity in soils. <b>2015</b> , 22, 451-60		19
1913	Parallel Hierarchical Clustering in Linearithmic Time for Large-Scale Sequence Analysis. <b>2015</b> ,		6
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1909	Early gradual feeding with bovine colostrum improves gut function and NEC resistance relative to infant formula in preterm pigs. <b>2015</b> , 309, G310-23		59

1908	Gut microbiome composition is associated with temperament during early childhood. <b>2015</b> , 45, 118-27	101
1907	Gut microbiota. Antimicrobial peptide resistance mediates resilience of prominent gut commensals during inflammation. <b>2015</b> , 347, 170-5	240
1906	Genetic distance for a general non-stationary markov substitution process. <b>2015</b> , 64, 281-93	12
1905	Biogeography and biophysicochemical traits link N <sub>2</sub> O emissions, N <sub>2</sub> O emission potential and microbial communities across New Zealand pasture soils. <b>2015</b> , 82, 87-98	27
1904	Bacteria and yeast microbiota in milk kefir grains from different Italian regions. <b>2015</b> , 49, 123-33	159
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1902	Vertically transmitted faecal IgA levels determine extra-chromosomal phenotypic variation. <b>2015</b> , 521, 90-93	169
1901	Directed shift of vaginal microbiota induced by vaginal application of sucrose gel in rhesus macaques. <b>2015</b> , 33, 32-6	11
1900	The nexus of syntrophy-associated microbiota in anaerobic digestion revealed by long-term enrichment and community survey. <b>2015</b> , 17, 1707-20	111
1899	Prepartum and postpartum rumen fluid microbiomes: characterization and correlation with production traits in dairy cows. <b>2015</b> , 81, 1327-37	109
1898	Disease-specific alterations in the enteric virome in inflammatory bowel disease. <b>2015</b> , 160, 447-60	696
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1896	Whole-grain wheat consumption reduces inflammation in a randomized controlled trial on overweight and obese subjects with unhealthy dietary and lifestyle behaviors: role of polyphenols bound to cereal dietary fiber. <b>2015</b> , 101, 251-61	198
1895	Investigating the long-term effect of subchronic phencyclidine-treatment on novel object recognition and the association between the gut microbiota and behavior in the animal model of schizophrenia. <b>2015</b> , 141, 32-9	43
1894	Assembly of root-associated bacteria communities: interactions between abiotic and biotic factors. <b>2015</b> , 7, 102-10	14
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1890	Dietary emulsifiers impact the mouse gut microbiota promoting colitis and metabolic syndrome. <b>2015</b> , 519, 92-6	1016
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1888	Transmission of atherosclerosis susceptibility with gut microbial transplantation. <b>2015</b> , 290, 5647-60	294
1887	Minimum entropy decomposition: unsupervised oligotyping for sensitive partitioning of high-throughput marker gene sequences. <i>ISME Journal</i> , <b>2015</b> , 9, 968-79	11.9 355
1886	A new era in palaeomicrobiology: prospects for ancient dental calculus as a long-term record of the human oral microbiome. <b>2015</b> , 370, 20130376	136
1885	Application of 16S rRNA metagenomics to analyze bacterial communities at a respiratory care centre in Taiwan. <b>2015</b> , 99, 2871-81	12
1884	Long-term nickel exposure altered the bacterial community composition but not diversity in two contrasting agricultural soils. <b>2015</b> , 22, 10496-505	19
1883	Mapping axillary microbiota responsible for body odours using a culture-independent approach. <b>2015</b> , 3, 3	56
1882	Persistent shifts in Caribbean coral microbiota are linked to the 2010 warm thermal anomaly. <b>2015</b> , 7, 471-9	22
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1878	Characterization of para-Nitrophenol-Degrading Bacterial Communities in River Water by Using Functional Markers and Stable Isotope Probing. <b>2015</b> , 81, 6890-900	24
1877	High organic loading treatment for industrial molasses wastewater and microbial community shifts corresponding to system development. <b>2015</b> , 196, 225-34	41
1876	Comparing the inhibitory thresholds of dairy manure co-digesters after prolonged acclimation periods: Part 2--correlations between microbiomes and environment. <b>2015</b> , 87, 458-66	29
1875	Finding and identifying the viral needle in the metagenomic haystack: trends and challenges. <b>2014</b> , 5, 739	12
1874	Databases for Microbiologists. <b>2015</b> , 197, 2458-67	21
1873	High-throughput assessment of bacterial ecology in hog, cow and ovine casings used in sausages production. <b>2015</b> , 212, 49-59	18

1872	Characterization of the rumen microbial community composition of buffalo breeds consuming diets typical of dairy production systems in Southern China. <b>2015</b> , 207, 75-84	16
1871	Changes in intestinal barrier function and gut microbiota in high-fat diet-fed rats are dynamic and region dependent. <b>2015</b> , 308, G840-51	182
1870	Biotransformation of pink water TNT on the surface of a low-cost adsorbent pine bark. <b>2015</b> , 26, 375-86	9
1869	Proton Pump Inhibitors Alter Specific Taxa in the Human Gastrointestinal Microbiome: A Crossover Trial. <b>2015</b> , 149, 883-5.e9	192
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1867	Capturing prokaryotic dark matter genomes. <b>2015</b> , 166, 814-30	11
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1865	A multiple endpoint analysis of the effects of chronic exposure to sediment contaminated with Deepwater Horizon oil on juvenile Southern flounder and their associated microbiomes. <b>2015</b> , 165, 197-209	57
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1859	Sequencing and beyond: integrating molecular 'omics' for microbial community profiling. <b>2015</b> , 13, 360-72	394
1858	The infant nasopharyngeal microbiome impacts severity of lower respiratory infection and risk of asthma development. <b>2015</b> , 17, 704-15	512
1857	Contrasting taxonomic stratification of microbial communities in two hypersaline meromictic lakes. <i>ISME Journal</i> , <b>2015</b> , 9, 2642-56	11.9 55
1856	Mesophilic versus thermophilic anaerobic digestion of cattle manure: methane productivity and microbial ecology. <b>2015</b> , 8, 787-800	107
1855	The microbiome of uncontacted Amerindians. <b>2015</b> , 1,	517

1854	Continental-scale distributions of dust-associated bacteria and fungi. <b>2015</b> , 112, 5756-61	259
1853	Mitigation of colitis with NovaSil clay therapy. <b>2015</b> , 60, 382-92	4
1852	Dynamics of extracellular DNA decomposition and bacterial community composition in soil. <b>2015</b> , 86, 42-49	46
1851	A molecular survey of Australian and North American termite genera indicates that vertical inheritance is the primary force shaping termite gut microbiomes. <b>2015</b> , 3, 5	71
1850	Dynamic changes in short- and long-term bacterial composition following fecal microbiota transplantation for recurrent <i>Clostridium difficile</i> infection. <b>2015</b> , 3, 10	175
1849	Effects of diurnal variation of gut microbes and high-fat feeding on host circadian clock function and metabolism. <b>2015</b> , 17, 681-9	440
1848	Kinship, inbreeding and fine-scale spatial structure influence gut microbiota in a hindgut-fermenting tortoise. <b>2015</b> , 24, 2521-36	59
1847	High throughput sequencing reveals distinct microbial populations within the mucosal and luminal niches in healthy individuals. <b>2015</b> , 6, 173-81	99
1846	Influence of anode surface chemistry on microbial fuel cell operation. <b>2015</b> , 106, 141-9	69
1845	16S classifier: a tool for fast and accurate taxonomic classification of 16S rRNA hypervariable regions in metagenomic datasets. <b>2015</b> , 10, e0116106	53
1844	Monitoring of the microbiota of fermented sausages by culture independent rRNA-based approaches. <b>2015</b> , 212, 67-75	77
1843	Phylogenetic and functional alterations in bacterial community compositions in broiler ceca as a result of mannan oligosaccharide supplementation. <b>2015</b> , 81, 3460-70	59
1842	Impact of metagenomic DNA extraction procedures on the identifiable endophytic bacterial diversity in <i>Sorghum bicolor</i> (L. Moench). <b>2015</b> , 112, 104-17	49
1841	Processing Environment and Ingredients Are Both Sources of <i>Leuconostoc gelidum</i> , Which Emerges as a Major Spoiler in Ready-To-Eat Meals. <b>2015</b> , 81, 3529-41	29
1840	The genetic potential of N <sub>2</sub> emission via denitrification and ANAMMOX from the soils and sediments of a created riverine treatment wetland complex. <b>2015</b> , 80, 181-190	32
1839	Host Response to the Lung Microbiome in Chronic Obstructive Pulmonary Disease. <b>2015</b> , 192, 438-45	154
1838	Biosurfactant production from marine hydrocarbon-degrading consortia and pure bacterial strains using crude oil as carbon source. <b>2015</b> , 6, 274	95
1837	Methanogenic archaea in marcellus shale: a possible mechanism for enhanced gas recovery in unconventional shale resources. <b>2015</b> , 49, 7048-55	12



1836	Oligofructose protects against arsenic-induced liver injury in a model of environment/obesity interaction. <b>2015</b> , 284, 304-14	18
1835	Associations between host gene expression, the mucosal microbiome, and clinical outcome in the pelvic pouch of patients with inflammatory bowel disease. <b>2015</b> , 16, 67	119
1834	Two decades of warming increases diversity of a potentially lignolytic bacterial community. <b>2015</b> , 6, 480	50
1833	Differences in organic matter and bacterioplankton between sections of the largest Arctic river: Mosaic or continuum?. <b>2015</b> , 60, 1314-1331	30
1832	Effect of preservation method on spider monkey ( <i>Ateles geoffroyi</i> ) fecal microbiota over 8 weeks. <b>2015</b> , 113, 16-26	84
1831	Chemometrics comes to court: evidence evaluation of chemBio threat agent attacks. <b>2015</b> , 29, 267-276	9
1830	Declining diversity of egg-associated bacteria during development of naturally spawned whitefish embryos ( <i>Coregonus</i> spp.). <b>2015</b> , 77, 481-497	13
1829	Molecular cartography of the human skin surface in 3D. <b>2015</b> , 112, E2120-9	237
1828	Long-term monitoring reveals stable and remarkably similar microbial communities in parallel full-scale biogas reactors digesting energy crops. <b>2015</b> , 91,	62
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1826	Complementary seminovaginal microbiome in couples. <b>2015</b> , 166, 440-447	96
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1823	The gut microbiota of nonalcoholic fatty liver disease: current methods and their interpretation. <b>2015</b> , 9, 406-15	28
1822	Vineyard soil bacterial diversity and composition revealed by 16S rRNA genes: Differentiation by geographic features. <b>2015</b> , 91, 232-247	82
1821	Cilantro microbiome before and after nonselective pre-enrichment for <i>Salmonella</i> using 16S rRNA and metagenomic sequencing. <b>2015</b> , 15, 160	38
1820	Statistical Tools for Data Analysis. <b>2015</b> , 41-57	
1819	Seasonal patterns of bacterial communities in the coastal brackish sediments of the Gulf of Finland, Baltic Sea. <b>2015</b> , 165, 86-96	14

1818	Commensal Bifidobacterium promotes antitumor immunity and facilitates anti-PD-L1 efficacy. <b>2015</b> , 350, 1084-9	1852
1817	Methanobacterium enables high rate electricity-driven autotrophic sulfate reduction. <b>2015</b> , 5, 89368-89374	31
1816	Impact of urine and the application of the nitrification inhibitor DCD on microbial communities in dairy-grazed pasture soils. <b>2015</b> , 88, 344-353	22
1815	Dietary analysis on the shallow-water hydrothermal vent crab <i>Xenograpsus testudinatus</i> using Illumina sequencing. <b>2015</b> , 162, 1787-1798	14
1814	Quo vadis? Microbial profiling revealed strong effects of cleanroom maintenance and routes of contamination in indoor environments. <b>2015</b> , 5, 9156	31
1813	Towards the unification of sequence-based classification and sequence-based identification of host-associated microorganisms. <b>2015</b> , 205, 27-31	17
1812	Genetic and environmental control of host-gut microbiota interactions. <b>2015</b> , 25, 1558-69	199
1811	The prebiotics 3'Sialyllactose and 6'Sialyllactose diminish stressor-induced anxiety-like behavior and colonic microbiota alterations: Evidence for effects on the gut-brain axis. <b>2015</b> , 50, 166-177	173
1810	Silencing a key gene of the common symbiosis pathway in <i>Nicotiana attenuata</i> specifically impairs arbuscular mycorrhizal infection without influencing the root-associated microbiome or plant growth. <b>2015</b> , 38, 2398-416	17
1809	The airway microbiome in patients with severe asthma: Associations with disease features and severity. <b>2015</b> , 136, 874-84	260
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1805	Consistent responses of soil microbial communities to elevated nutrient inputs in grasslands across the globe. <b>2015</b> , 112, 10967-72	649
1804	Variation in the Microbiota of Ixodes Ticks with Regard to Geography, Species, and Sex. <b>2015</b> , 81, 6200-9	110
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1802	Collection media and delayed freezing effects on microbial composition of human stool. <b>2015</b> , 3, 33	87
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1798	Coexistence of Lactic Acid Bacteria and Potential Spoilage Microbiota in a Dairy Processing Environment. <b>2015</b> , 81, 7893-904	100
1797	Ecological significance of Synergistetes in the biological treatment of tuna cooking wastewater by an anaerobic sequencing batch reactor. <b>2015</b> , 22, 18230-8	27
1796	Pyrosequencing reveals bacterial diversity in Korean traditional wheat-based nuruk. <b>2015</b> , 53, 812-9	7
1795	The effects of entombment on water chemistry and bacterial assemblages in closed cryoconite holes on Antarctic glaciers. <b>2015</b> , 91,	22
1794	The short-chain fatty acid receptor, FFA2, contributes to gestational glucose homeostasis. <b>2015</b> , 309, E840-51	42
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1791	Prevalence of antibiotic resistance genes and bacterial pathogens in long-term manured greenhouse soils as revealed by metagenomic survey. <b>2015</b> , 49, 1095-104	198
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1788	Spatial structuring of bacterial communities within individual Ginkgo biloba trees. <b>2015</b> , 17, 2352-61	67
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1781	Assessing the global phylum level diversity within the bacterial domain: A review. <b>2015</b> , 6, 269-82		41
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1777	Hemolymph microbiome of Pacific oysters in response to temperature, temperature stress and infection. <i>ISME Journal</i> , <b>2015</b> , 9, 670-82	11.9	171
1776	Bacterial diversity in typical Italian salami at different ripening stages as revealed by high-throughput sequencing of 16S rRNA amplicons. <b>2015</b> , 46, 342-356		157
1775	Bacterial assembly and temporal dynamics in activated sludge of a full-scale municipal wastewater treatment plant. <i>ISME Journal</i> , <b>2015</b> , 9, 683-95	11.9	260
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1766	Microbial dynamics in a High Arctic glacier forefield: a combined field, laboratory, and modelling approach. <b>2016</b> , 13, 5677-5696		27
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1746	Mississippi River Plume Enriches Microbial Diversity in the Northern Gulf of Mexico. <b>2016</b> , 7, 1048	25
1745	Methane Inhibition Alters the Microbial Community, Hydrogen Flow, and Fermentation Response in the Rumen of Cattle. <b>2016</b> , 7, 1122	58
1744	Dramatic Increases of Soil Microbial Functional Gene Diversity at the Treeline Ecotone of Changbai Mountain. <b>2016</b> , 7, 1184	23
1743	Rumen Bacterial Community Composition in Holstein and Jersey Cows Is Different under Same Dietary Condition and Is Not Affected by Sampling Method. <b>2016</b> , 7, 1206	86
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1741	Phylogeography, Salinity Adaptations and Metabolic Potential of the Candidate Division KB1 Bacteria Based on a Partial Single Cell Genome. <b>2016</b> , 7, 1266	19
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1737	Coupling Bacterioplankton Populations and Environment to Community Function in Coastal Temperate Waters. <b>2016</b> , 7, 1533	11
1736	Response of Core Microbial Consortia to Chronic Hydrocarbon Contaminations in Coastal Sediment Habitats. <b>2016</b> , 7, 1637	44
1735	Seasonal Succession of Free-Living Bacterial Communities in Coastal Waters of the Western Antarctic Peninsula. <b>2016</b> , 7, 1731	31
1734	Deconstructing the Bat Skin Microbiome: Influences of the Host and the Environment. <b>2016</b> , 7, 1753	50
1733	Waste Conversion into -Caprylate and -Caproate: Resource Recovery from Wine Lees Using Anaerobic Reactor Microbiomes and In-line Extraction. <b>2016</b> , 7, 1892	74
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1730	Dietary Gluten-Induced Gut Dysbiosis Is Accompanied by Selective Upregulation of microRNAs with Intestinal Tight Junction and Bacteria-Binding Motifs in Rhesus Macaque Model of Celiac Disease. <b>2016</b> , 8,	37
1729	Bacterial Communities Associated with Atherosclerotic Plaques from Russian Individuals with Atherosclerosis. <b>2016</b> , 11, e0164836	34

1728	Ingestion of Milk Containing Very Low Concentration of Antimicrobials: Longitudinal Effect on Fecal Microbiota Composition in Preweaned Calves. <b>2016</b> , 11, e0147525	32
1727	Chronic Psychological Stress Disrupted the Composition of the Murine Colonic Microbiota and Accelerated a Murine Model of Inflammatory Bowel Disease. <b>2016</b> , 11, e0150559	19
1726	Helicobacter pylori Eradication Causes Perturbation of the Human Gut Microbiome in Young Adults. <b>2016</b> , 11, e0151893	82
1725	Body Site Is a More Determinant Factor than Human Population Diversity in the Healthy Skin Microbiome. <b>2016</b> , 11, e0151990	84
1724	Longitudinal Analysis of the Intestinal Microbiota in Persistently Stunted Young Children in South India. <b>2016</b> , 11, e0155405	53
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1722	Detection of Invertebrate Suppressive Soils, and Identification of a Possible Biological Control Agent for Nematodes Using High Resolution Rhizosphere Microbial Community Analysis. <b>2016</b> , 7, 1946	20
1721	Development of the Chick Microbiome: How Early Exposure Influences Future Microbial Diversity. <b>2016</b> , 3, 2	149
1720	Novel Strategies for Applied Metagenomics. <b>2016</b> , 22, 709-18	13
1719	Direct and indirect effects of native range expansion on soil microbial community structure and function. <b>2016</b> , 104, 1271-1283	40
1718	Microbial ecology of the salmon necrobiome: evidence salmon carrion decomposition influences aquatic and terrestrial insect microbiomes. <b>2016</b> , 18, 1511-22	43
1717	Bacterial microbiomes from vertically transmitted fungal inocula of the leaf-cutting ant <i>Atta texana</i> . <b>2016</b> , 8, 630-640	31
1716	Genomic characterization of the uncultured Bacteroidales family S24-7 inhabiting the guts of homeothermic animals. <b>2016</b> , 4, 36	322
1715	Spatial scale drives patterns in soil bacterial diversity. <b>2016</b> , 18, 2039-51	131
1714	The gut microbiome of the sea urchin, <i>Lytechinus variegatus</i> , from its natural habitat demonstrates selective attributes of microbial taxa and predictive metabolic profiles. <b>2016</b> , 92,	52
1713	Impact of soil heat on reassembly of bacterial communities in the rhizosphere microbiome and plant disease suppression. <b>2016</b> , 19, 375-82	94
1712	Biologically Induced Hydrogen Production Drives High Rate/High Efficiency Microbial Electrosynthesis of Acetate from Carbon Dioxide. <b>2016</b> , 3, 581-591	94
1711	Carbon content and climate variability drive global soil bacterial diversity patterns. <b>2016</b> , 86, 373-390	97

1710	Characterizing the bacterial communities in retail stores in the United States. <b>2016</b> , 26, 857-868	22
1709	On the use of high-throughput sequencing for the study of cyanobacterial diversity in Antarctic aquatic mats. <b>2016</b> , 52, 356-68	20
1708	Microbial Fe(III) oxide reduction potential in Chocolate Pots hot spring, Yellowstone National Park. <b>2016</b> , 14, 255-75	26
1707	Effects of Specimen Collection Methodologies and Storage Conditions on the Short-Term Stability of Oral Microbiome Taxonomy. <b>2016</b> , 82, 5519-29	22
1706	Geological connectivity drives microbial community structure and connectivity in polar, terrestrial ecosystems. <b>2016</b> , 18, 1834-49	30
1705	Bacterial indicator taxa in soils under different long-term agricultural management. <b>2016</b> , 120, 921-33	33
1704	Characterization of pollen and bacterial community composition in brood provisions of a small carpenter bee. <b>2016</b> , 25, 2302-11	62
1703	Temporal Development of Gut Microbiota in Triclocarban Exposed Pregnant and Neonatal Rats. <b>2016</b> , 6, 33430	18
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1701	Comparison of faecal microbiota in Blastocystis-positive and Blastocystis-negative irritable bowel syndrome patients. <b>2016</b> , 4, 47	54
1700	From an imbalance to a new imbalance: Italian-style gluten-free diet alters the salivary microbiota and metabolome of African celiac children. <b>2015</b> , 5, 18571	22
1699	Disturbance Regimes Predictably Alter Diversity in an Ecologically Complex Bacterial System. <b>2016</b> , 7,	26
1698	Enrichment dynamics of <i>Listeria monocytogenes</i> and the associated microbiome from naturally contaminated ice cream linked to a listeriosis outbreak. <b>2016</b> , 16, 275	83
1697	Aspect has a greater impact on alpine soil bacterial community structure than elevation. <b>2017</b> , 93,	8
1696	The human milk oligosaccharide 2'-fucosyllactose attenuates the severity of experimental necrotising enterocolitis by enhancing mesenteric perfusion in the neonatal intestine. <b>2016</b> , 116, 1175-1187	106
1695	Amphibian gut microbiota shifts differentially in community structure but converges on habitat-specific predicted functions. <b>2016</b> , 7, 13699	79
1694	Domestic shower hose biofilms contain fungal species capable of causing opportunistic infection. <b>2016</b> , 14, 727-737	14
1693	Microbial diversity in pitted sweet cherries ( <i>Prunus avium</i> L.) as affected by High-Hydrostatic Pressure treatment. <b>2016</b> , 89, 790-796	13



1692	The developing hypopharyngeal microbiota in early life. <b>2016</b> , 4, 70	34
1691	Lessons learned from the microbial ecology resulting from different inoculation strategies for biogas production from waste products of the bioethanol/sugar industry. <b>2016</b> , 9, 144	15
1690	Metabolic Model-Based Integration of Microbiome Taxonomic and Metabolomic Profiles Elucidates Mechanistic Links between Ecological and Metabolic Variation. <b>2016</b> , 1,	108
1689	Towards the development of multifunctional molecular indicators combining soil biogeochemical and microbiological variables to predict the ecological integrity of silvicultural practices. <b>2016</b> , 9, 316-29	3
1688	Age-related changes in gut microbiota composition from newborn to centenarian: a cross-sectional study. <b>2016</b> , 16, 90	598
1687	Low temperature treatment of domestic wastewater by purple phototrophic bacteria: Performance, activity, and community. <b>2016</b> , 100, 537-545	64
1686	Insights into the metabolism of the high temperature microbial community of Tramway Ridge, Mount Erebus, Antarctica. <b>2016</b> , 28, 241-249	3
1685	Immunization with a heat-killed preparation of the environmental bacterium <i>Mycobacterium vaccae</i> promotes stress resilience in mice. <b>2016</b> , 113, E3130-9	137
1684	Prevalent high-risk HPV infection and vaginal microbiota in Nigerian women. <b>2016</b> , 144, 123-37	79
1683	Domestic wastewater treatment with purple phototrophic bacteria using a novel continuous photo anaerobic membrane bioreactor. <b>2016</b> , 100, 486-495	125
1682	Composition and function of the pediatric colonic mucosal microbiome in untreated patients with ulcerative colitis. <b>2016</b> , 7, 384-96	65
1681	Bacterial and eukaryal diversity in soils forming from acid mine drainage precipitates under reclaimed vegetation and biological crusts. <b>2016</b> , 105, 57-66	25
1680	Analysis of Gut Microbiome Reveals Significant Differences between Men with Chronic Prostatitis/Chronic Pelvic Pain Syndrome and Controls. <b>2016</b> , 196, 435-41	39
1679	Uncultured bacterial diversity in a seawater recirculating aquaculture system revealed by 16S rRNA gene amplicon sequencing. <b>2016</b> , 54, 296-304	28
1678	Impact of Dietary Lipids on Colonic Function and Microbiota: An Experimental Approach Involving Orlistat-Induced Fat Malabsorption in Human Volunteers. <b>2016</b> , 7, e161	43
1677	Gut microbiota analysis reveals a marked shift to bifidobacteria by a starter infant formula containing a synbiotic of bovine milk-derived oligosaccharides and <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> CNCM I-3446. <b>2016</b> , 18, 2185-95	54
1676	Long-term salinity tolerance is accompanied by major restructuring of the coral bacterial microbiome. <b>2016</b> , 25, 1308-23	80
1675	Temporal variability of soil microbial communities after application of dicyandiamide-treated swine slurry and mineral fertilizers. <b>2016</b> , 97, 71-82	31

1674	Microbiota of an Italian Grana-Like Cheese during Manufacture and Ripening, Unraveled by 16S rRNA-Based Approaches. <b>2016</b> , 82, 3988-3995		64
1673	Tissue Microbiome Profiling Identifies an Enrichment of Specific Enteric Bacteria in <i>Opisthorchis viverrini</i> Associated Cholangiocarcinoma. <b>2016</b> , 8, 195-202		61
1672	Incorporating microbiota data into epidemiologic models: examples from vaginal microbiota research. <b>2016</b> , 26, 360-5		15
1671	CARD9 impacts colitis by altering gut microbiota metabolism of tryptophan into aryl hydrocarbon receptor ligands. <b>2016</b> , 22, 598-605		628
1670	Shifts in microbial community structure during in situ surfactant-enhanced bioremediation of polycyclic aromatic hydrocarbon-contaminated soil. <b>2016</b> , 23, 14451-61		59
1669	Impact of Hypocaloric Hyperproteic Diet on Gut Microbiota in Overweight or Obese Patients with Nonalcoholic Fatty Liver Disease: A Pilot Study. <b>2016</b> , 61, 2721-31		41
1668	Natural decay process affects the abundance and community structure of Bacteria and Archaea in <i>Picea abies</i> logs. <b>2016</b> , 92,		37
1667	Towards a functional hypothesis relating anti-islet cell autoimmunity to the dietary impact on microbial communities and butyrate production. <b>2016</b> , 4, 17		67
1666	Phylogeny-aware identification and correction of taxonomically mislabeled sequences. <b>2016</b> , 44, 5022-33		67
1665	Evaluating community-environment relationships along fine to broad taxonomic resolutions reveals evolutionary forces underlying community assembly. <i>ISME Journal</i> , <b>2016</b> , 10, 2867-2878	11.9	21
1664	Changes in the community structure of free-living heterotrophic bacteria in the open tropical Pacific Ocean in response to microalgal lysate-derived dissolved organic matter. <b>2016</b> , 92,		12
1663	Microbiome changes through ontogeny of a tick pathogen vector. <b>2016</b> , 25, 4963-77		86
1662	Disease Progression and Resolution in Rodent Models of <i>Clostridium difficile</i> Infection and Impact of Antitoxin Antibodies and Vancomycin. <b>2016</b> , 60, 6471-6482		24
1661	The Core Gut Microbiome of the American Cockroach, <i>Periplaneta americana</i> , Is Stable and Resilient to Dietary Shifts. <b>2016</b> , 82, 6603-6610		65
1660	Characterization of an anaerobic marine microbial community exposed to combined fluxes of perchlorate and salinity. <b>2016</b> , 100, 9719-9732		18
1659	Dynamics of <i>Heterocapsa</i> sp. and the associated attached and free-living bacteria under the influence of dispersed and undispersed crude oil. <b>2016</b> , 63, 419-425		16
1658	Antimicrobial Chemicals Are Associated with Elevated Antibiotic Resistance Genes in the Indoor Dust Microbiome. <b>2016</b> , 50, 9807-15		93
1657	Microbiome Changes during Tuberculosis and Antituberculous Therapy. <b>2016</b> , 29, 915-26		49

1656	Bacterial microbiota associated with flower pollen is influenced by pollination type, and shows a high degree of diversity and species-specificity. <b>2016</b> , 18, 5161-5174	77
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1654	Organic farming induces changes in soil microbiota that affect agro-ecosystem functions. <b>2016</b> , 103, 327-336	80
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1652	Response of germ-free mice to colonization with <i>O. formigenes</i> and altered Schaedler flora. <b>2016</b> , 82, 6952-6960	15
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1649	Effects of field conditions on fecal microbiota. <b>2016</b> , 130, 180-188	24
1648	16S rRNA gene profiling of planktonic and biofilm microbial populations in the Gulf of Guinea using Illumina NGS. <b>2016</b> , 122, 105-112	28
1647	Influence of commercial (Fluka) naphthenic acids on acid volatile sulfide (AVS) production and divalent metal precipitation. <b>2016</b> , 134P1, 86-94	4
1646	Hydrocarbon and Lipid Microbiology Protocols. <b>2016</b> ,	
1645	JAR3D Webserver: Scoring and aligning RNA loop sequences to known 3D motifs. <b>2016</b> , 44, W320-7	12
1644	Rapid change of fecal microbiome and disappearance of <i>Clostridium difficile</i> in a colonized infant after transition from breast milk to cow milk. <b>2016</b> , 4, 53	44
1643	Microbial ecology involved in the ripening of naturally fermented llama meat sausages. A focus on lactobacilli diversity. <b>2016</b> , 236, 17-25	35
1642	Gene Sequence Analyses of the Healthy Oral Microbiome in Humans and Companion Animals. <b>2016</b> , 33, 97-107	11
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1640	Effects of host genetics and environment on egg-associated microbiotas in brown trout ( <i>Salmo trutta</i> ). <b>2016</b> , 25, 4930-45	22
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1638	Effects of environmental conditions on aerobic degradation of a commercial naphthenic acid. <b>2016</b> , 161, 491-500	6
1637	Bacterial community composition in relation to bedrock type and macrobiota in soils from the Sñ Rondane Mountains, East Antarctica. <b>2016</b> , 92,	35
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1635	The Core and Seasonal Microbiota of Raw Bovine Milk in Tanker Trucks and the Impact of Transfer to a Milk Processing Facility. <b>2016</b> , 7,	77
1634	Fermentation of African kale ( <i>Brassica carinata</i> ) using <i>L. plantarum</i> BFE 5092 and <i>L. fermentum</i> BFE 6620 starter strains. <b>2016</b> , 238, 103-112	18
1633	<i>Solanum lycopersicum</i> (tomato) hosts robust phyllosphere and rhizosphere bacterial communities when grown in soil amended with various organic and synthetic fertilizers. <b>2016</b> , 573, 555-563	34
1632	Extreme Dysbiosis of the Microbiome in Critical Illness. <b>2016</b> , 1,	190
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1621	Contrasting elevational diversity patterns for soil bacteria between two ecosystems divided by the treeline. <b>2016</b> , 59, 1177-1186	12

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1615	Neonatal gut microbiota associates with childhood multisensitized atopy and T cell differentiation. <b>2016</b> , 22, 1187-1191	548
1614	Longitudinal Survey of Microbiota in Hospitalized Preterm Very-Low-Birth-Weight Infants. <b>2016</b> , 62, 292-303	48
1613	A Microbial Link to Weathering of Postglacial Rocks and Sediments, Mount Viso Area, Western Alps, Demonstrated through Analysis of a Soil/Paleosol Bio/Chronosequence. <b>2016</b> , 124, 149-169	6
1612	Antibiotics, birth mode, and diet shape microbiome maturation during early life. <b>2016</b> , 8, 343ra82	680
1611	Midtrimester Cervicovaginal Microbiota: Identification of Microbial Variations Associated with Puerperal Infection at Term. <b>2016</b> , 33, 1165-75	7
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1609	Antibiotic-mediated gut microbiome perturbation accelerates development of type 1 diabetes in mice. <b>2016</b> , 1, 16140	209
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1606	A perspective on 16S rRNA operational taxonomic unit clustering using sequence similarity. <b>2016</b> , 2, 16004	126
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1586	Metatranscriptomics reveals temperature-driven functional changes in microbiome impacting cheese maturation rate. <b>2016</b> , 6, 21871	111
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1567	Taxonmer: an interactive metagenomics analysis portal for universal pathogen detection and host mRNA expression profiling. <b>2016</b> , 17, 111	113

1566	The pediatric intestinal mucosal microbiome remains altered after clinical resolution of inflammatory and ischemic disease. <b>2016</b> , 160, 350-8	6
1565	Ecological differentiation in planktonic and sediment-associated chemotrophic microbial populations in Yellowstone hot springs. <b>2016</b> , 92,	19
1564	Culture-independent bacterial community profiling of carbon dioxide treated raw milk. <b>2016</b> , 233, 81-89	13
1563	Lotic bacterioplankton and phytoplankton community changes under dissolved organic-carbon amendment: evidence for competition for nutrients. <b>2016</b> , 67, 1362	4
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1560	Decontamination of 16S rRNA gene amplicon sequence datasets based on bacterial load assessment by qPCR. <b>2016</b> , 16, 73	43
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1556	Colonization potential to reconstitute a microbe community in patients detected early after fecal microbe transplant for recurrent <i>C. difficile</i> . <b>2016</b> , 16, 5	16
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1554	Infection with a Shoot-Specific Fungal Endophyte ( <i>Epichloa</i> ) Alters Tall Fescue Soil Microbial Communities. <b>2016</b> , 72, 197-206	48
1553	Large differences in potential denitrification and sediment microbial communities across the Laurentian great lakes. <b>2016</b> , 128, 353-368	27
1552	Characterization of the first cultured representative of Verrucomicrobia subdivision 5 indicates the proposal of a novel phylum. <i>ISME Journal</i> , <b>2016</b> , 10, 2801-2816	11.9 98
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1550	Predominance of <i>Lactobacillus</i> spp. Among Patients Who Do Not Acquire Multidrug-Resistant Organisms. <b>2016</b> , 63, 937-943	17
1549	Sex differences and hormonal effects on gut microbiota composition in mice. <b>2016</b> , 7, 313-322	329



1548	Examining the diversity of microbes in a deep-sea coral community impacted by the Deepwater Horizon oil spill. <b>2016</b> , 129, 157-166	18
1547	Ice cover extent drives phytoplankton and bacterial community structure in a large north-temperate lake: implications for a warming climate. <b>2016</b> , 18, 1704-19	45
1546	Endometrial microbiome at the time of embryo transfer: next-generation sequencing of the 16S ribosomal subunit. <b>2016</b> , 33, 129-36	127
1545	Vaginal Microbiota in Pregnancy: Evaluation Based on Vaginal Flora, Birth Outcome, and Race. <b>2016</b> , 33, 401-8	24
1544	Impact of Nisin-Activated Packaging on Microbiota of Beef Burgers during Storage. <b>2016</b> , 82, 549-59	35
1543	Effects of biochar and compost amendments on soil physico-chemical properties and the total community within a temperate agricultural soil. <b>2016</b> , 98, 243-253	137
1542	Microbial community dynamics in thermophilic undefined milk starter cultures. <b>2016</b> , 217, 59-67	18
1541	Perfluoroalkyl Acids Inhibit Reductive Dechlorination of Trichloroethene by Repressing Dehalococcoides. <b>2016</b> , 50, 240-8	32
1540	Influence of rice straw amendment on mercury methylation and nitrification in paddy soils. <b>2016</b> , 209, 53-9	36
1539	Effects of organic/inorganic compound fertilizer with reduced chemical fertilizer application on crop yields, soil biological activity and bacterial community structure in a rice/wheat cropping system. <b>2016</b> , 99, 1-12	173
1538	Conversion of L-lactate into n-caproate by a continuously fed reactor microbiome. <b>2016</b> , 93, 163-171	128
1537	Genome-Based Microbial Taxonomy Coming of Age. <b>2016</b> , 8,	50
1536	A polyphenol-rich fraction obtained from table grapes decreases adiposity, insulin resistance and markers of inflammation and impacts gut microbiota in high-fat-fed mice. <b>2016</b> , 31, 150-65	72
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1534	The microbiota-derived metabolite indole decreases mucosal inflammation and injury in a murine model of NSAID enteropathy. <b>2016</b> , 7, 246-61	67
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1531	16S metagenomics reveals changes in the soil bacterial community driven by soil organic C, N-fertilizer and tillage-crop residue management. <b>2016</b> , 159, 1-8	56

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1529	Direct and Indirect Horizontal Transmission of the Antifungal Probiotic Bacterium <i>Janthinobacterium lividum</i> on Green Frog ( <i>Lithobates clamitans</i> ) Tadpoles. <b>2016</b> , 82, 2457-2466	30
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1527	Lambda Interferon Restructures the Nasal Microbiome and Increases Susceptibility to <i>Staphylococcus aureus</i> Superinfection. <b>2016</b> , 7, e01939-15	70
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1525	Gastric <i>Helicobacter pylori</i> Infection Affects Local and Distant Microbial Populations and Host Responses. <b>2016</b> , 14, 1395-1407	88
1524	Relationships among house, rind and core microbiotas during manufacture of traditional Italian cheeses at the same dairy plant. <b>2016</b> , 54, 115-126	60
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1522	Increased water contamination and grow-out Pekin duck mortality when raised with water troughs compared to pin-metered water lines using a United States management system. <b>2016</b> , 95, 736-48	7
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1520	Inhibition of bacterial growth in sweet cheese whey by carbon dioxide as determined by culture-independent community profiling. <b>2016</b> , 217, 20-8	8
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1518	Chasing the elusive Euryarchaeota class WSA2: genomes reveal a uniquely fastidious methyl-reducing methanogen. <i>ISME Journal</i> , <b>2016</b> , 10, 2478-87	11.9 146
1517	Cervical Microbiota Associated with Higher Grade Cervical Intraepithelial Neoplasia in Women Infected with High-Risk Human Papillomaviruses. <b>2016</b> , 9, 357-66	66
1516	Biofilms in shower hoses [choice of pipe material influences bacterial growth and communities. <b>2016</b> , 2, 670-682	44
1515	SIV Infection-Mediated Changes in Gastrointestinal Bacterial Microbiome and Virome Are Associated with Immunodeficiency and Prevented by Vaccination. <b>2016</b> , 19, 323-35	61
1514	Impact of the [GAR+] Prion on Fermentation and Bacterial Community Composition with <i>Saccharomyces cerevisiae</i> UCD932. <b>2016</b> , 67, 296-307	11
1513	Characterization of microbiota in Plaisentif cheese by high-throughput sequencing. <b>2016</b> , 69, 490-496	55

1512	The Urinary Microbiome Differs Significantly Between Patients With Chronic Prostatitis/Chronic Pelvic Pain Syndrome and Controls as Well as Between Patients With Different Clinical Phenotypes. <b>2016</b> , 92, 26-32	64
1511	Bacterial communities potentially involved in iron-cycling in Baltic Sea and North Sea sediments revealed by pyrosequencing. <b>2016</b> , 92, fiw054	29
1510	Modern water/rock reactions in Oman hyperalkaline peridotite aquifers and implications for microbial habitability. <b>2016</b> , 179, 217-241	77
1509	Comparative Genomics of Candidate Phylum TM6 Suggests That Parasitism Is Widespread and Ancestral in This Lineage. <b>2016</b> , 33, 915-27	50
1508	Identification of Unknown Carboxydovore Bacteria Dominant in Deciduous Forest Soil via Succession of Bacterial Communities, coxL Genotypes, and Carbon Monoxide Oxidation Activity in Soil Microcosms. <b>2016</b> , 82, 1324-1333	13
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1506	Skin bacterial diversity of Panamanian frogs is associated with host susceptibility and presence of <i>Batrachochytrium dendrobatidis</i> . <i>ISME Journal</i> , <b>2016</b> , 10, 1682-95	11.9 98
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1504	Agricultural applications of insect ecological genomics. <b>2016</b> , 13, 61-69	17
1503	Bacterial community dynamics in surface flow constructed wetlands for the treatment of swine waste. <b>2016</b> , 544, 68-76	33
1502	High concentrations of bioavailable heavy metals impact freshwater sediment microbial communities. <b>2016</b> , 66, 1003-1012	32
1501	Impact of forest management practices on soil bacterial diversity and consequences for soil processes. <b>2016</b> , 94, 200-210	37
1500	Coral microbial community dynamics in response to anthropogenic impacts near a major city in the central Red Sea. <b>2016</b> , 105, 629-40	133
1499	Microbial and Functional Diversity within the Phyllosphere of <i>Espeletia</i> Species in an Andean High-Mountain Ecosystem. <b>2016</b> , 82, 1807-1817	37
1498	A Meta-analysis of Bacterial Diversity in the Feces of Cattle. <b>2016</b> , 72, 145-151	26
1497	Glyphosate effects on soil rhizosphere-associated bacterial communities. <b>2016</b> , 543, 155-160	117
1496	Fungal Dysbiosis in Mucosa-associated Microbiota of Crohn's Disease Patients. <b>2016</b> , 10, 296-305	156
1495	Organoheterotrophic Bacterial Abundance Associates with Zinc Removal in Lignocellulose-Based Sulfate-Reducing Systems. <b>2016</b> , 50, 378-87	20

1494	From Rare to Dominant: a Fine-Tuned Soil Bacterial Bloom during Petroleum Hydrocarbon Bioremediation. <b>2016</b> , 82, 888-96		83
1493	Intraspecific Variation in Microbial Symbiont Communities of the Sun Sponge, <i>Hymeniacidon heliophila</i> , from Intertidal and Subtidal Habitats. <b>2016</b> , 82, 650-8		39
1492	Bacterial diversity indicates dietary overlap among bats of different feeding habits. <b>2016</b> , 182, 99-108		26
1491	An 'omics' approach towards the characterisation of laboratory scale anaerobic digesters treating municipal sewage sludge. <b>2016</b> , 88, 346-357		46
1490	Herbicide-mediated promotion of <i>Lotus tenuis</i> (Waldst. & Kit. ex Wild.) did not influence soil bacterial communities, in soils of the Flooding Pampa, Argentina. <b>2016</b> , 98, 83-91		4
1489	Microbiota studies in the bile duct strongly suggest a role for <i>Helicobacter pylori</i> in extrahepatic cholangiocarcinoma. <b>2016</b> , 22, 178.e11-178.e22		36
1488	The microbiota of high-moisture mozzarella cheese produced with different acidification methods. <b>2016</b> , 216, 9-17		40
1487	16Stimator: statistical estimation of ribosomal gene copy numbers from draft genome assemblies. <i>ISME Journal</i> , <b>2016</b> , 10, 1020-4	11.9	20
1486	Table grape consumption reduces adiposity and markers of hepatic lipogenesis and alters gut microbiota in butter fat-fed mice. <b>2016</b> , 27, 123-35		64
1485	Changes in microbial diversity of brined green asparagus upon treatment with high hydrostatic pressure. <b>2016</b> , 216, 1-8		17
1484	Metabolic and microbial community dynamics during the anaerobic digestion of maize silage in a two-phase process. <b>2016</b> , 100, 479-91		57
1483	Phylogeny and physiology of candidate phylum 'Atribacteria' (OP9/JS1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , <b>2016</b> , 10, 273-86	11.9	118
1482	Over-represented pairwise 16S rRNA gene sequence distance levels among prokaryotes. <b>2016</b> , 66, 489-493		
1481	Carcass mass has little influence on the structure of gravesoil microbial communities. <b>2016</b> , 130, 253-63		34
1480	Influence of housing characteristics on bacterial and fungal communities in homes of asthmatic children. <b>2016</b> , 26, 179-92		110
1479	Provision of Amniotic Fluid During Parenteral Nutrition Increases Weight Gain With Limited Effects on Gut Structure, Function, Immunity, and Microbiology in Newborn Preterm Pigs. <b>2016</b> , 40, 552-66		19
1478	Soil pH effects on the interactions between dissolved zinc, non-nano- and nano-ZnO with soil bacterial communities. <b>2016</b> , 23, 4120-8		63
1477	Fungal and bacterial growth in floor dust at elevated relative humidity levels. <b>2017</b> , 27, 354-363		66

1476	Machine learning for metagenomics: methods and tools. <b>2017</b> , 1,	19
1475	Conservative tracer bromide inhibits pesticide mineralisation in soil. <b>2017</b> , 222, 404-411	6
1474	Identity of biocrust species and microbial communities drive the response of soil multifunctionality to simulated global change. <b>2017</b> , 107, 208-217	48
1473	Microbial community structures in high rate algae ponds for bioconversion of agricultural wastes from livestock industry for feed production. <b>2017</b> , 580, 1185-1196	42
1472	Greater Species Richness of Bacterial Skin Symbionts Better Suppresses the Amphibian Fungal Pathogen <i>Batrachochytrium Dendrobatidis</i> . <b>2017</b> , 74, 217-226	42
1471	Bovine milk oligosaccharides decrease gut permeability and improve inflammation and microbial dysbiosis in diet-induced obese mice. <b>2017</b> , 100, 2471-2481	50
1470	Ginkgo fruit extract as an additive to modify rumen microbiota and fermentation and to mitigate methane production. <b>2017</b> , 100, 1923-1934	25
1469	Polymetallic nodules, sediments, and deep waters in the equatorial North Pacific exhibit highly diverse and distinct bacterial, archaeal, and microeukaryotic communities. <b>2017</b> , 6, e00428	49
1468	Symbiotic bacterial communities in ants are modified by invasion pathway bottlenecks and alter host behavior. <b>2017</b> , 98, 861-874	12
1467	Association of HPV infection and clearance with cervicovaginal immunology and the vaginal microbiota. <b>2017</b> , 10, 1310-1319	78
1466	<i>Helicobacter pylori</i> infection is associated with an altered gastric microbiota in children. <b>2017</b> , 10, 1169-1177	59
1465	Effects of Exogenous Yeast and Bacteria on the Microbial Population Dynamics and Outcomes of Olive Fermentations. <b>2017</b> , 2,	7
1464	Frozen: Thawing and Its Effect on the Postmortem Microbiome in Two Pediatric Cases. <b>2017</b> , 62, 1399-1405	19
1463	The gut microbiome in human neurological disease: A review. <b>2017</b> , 81, 369-382	283
1462	Comparison of bacterial 16S rRNA variable regions for microbiome surveys of ticks. <b>2017</b> , 8, 453-461	34
1461	Simultaneous chemical oxygen demand removal, methane production and heavy metal precipitation in the biological treatment of landfill leachate using acid mine drainage as sulfate resource. <b>2017</b> , 124, 71-75	29
1460	The interaction between the proliferating macroalga <i>Asparagopsis taxiformis</i> and the coral <i>Astroides calycularis</i> induces changes in microbiome and metabolomic fingerprints. <b>2017</b> , 7, 42625	21
1459	Prebiotic milk oligosaccharides prevent development of obese phenotype, impairment of gut permeability, and microbial dysbiosis in high fat-fed mice. <b>2017</b> , 312, G474-G487	49

- 1458 Alterations to the Gut Microbiome Impair Bone Strength and Tissue Material Properties. **2017**, 32, 1343-1353 74
- 1457 Transplantation of fecal microbiota from patients with irritable bowel syndrome alters gut function and behavior in recipient mice. **2017**, 9, 246
- 1456 Supplementation with lipid sources alters the ruminal fermentation and duodenal flow of fatty acids in grazing Nellore steers. **2017**, 227, 142-153 15
- 1455 Metabolic in Vivo Labeling Highlights Differences of Metabolically Active Microbes from the Mucosal Gastrointestinal Microbiome between High-Fat and Normal Chow Diet. **2017**, 16, 1593-1604 21
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- 1453 The bovine colostrum microbiome and its association with clinical mastitis. **2017**, 100, 3031-3042 46
- 1452 Characterizing the endometrial microbiome by analyzing the ultra-low bacteria from embryo transfer catheter tips in IVF cycles: Next generation sequencing (NGS) analysis of the 16S ribosomal gene. **2017**, 3, 15-21 37
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- 1449 Biodegradation of Phenanthrene in Polycyclic Aromatic Hydrocarbon-Contaminated Wastewater Revealed by Coupling Cultivation-Dependent and -Independent Approaches. **2017**, 51, 3391-3401 61
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- 1446 Substituting whole grains for refined grains in a 6-wk randomized trial favorably affects energy-balance metrics in healthy men and postmenopausal women. **2017**, 105, 589-599 52
- 1445 Substituting whole grains for refined grains in a 6-wk randomized trial has a modest effect on gut microbiota and immune and inflammatory markers of healthy adults. **2017**, 105, 635-650 132
- 1444 Uranium mobility and accumulation along the Rio Paguete, Jackpile Mine in Laguna Pueblo, NM. **2017**, 19, 605-621 24
- 1443 Effect of predatory bacteria on the gut bacterial microbiota in rats. **2017**, 7, 43483 32
- 1442 Association of oral microbiome with type 2 diabetes risk. **2017**, 52, 636-643 85
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1440	Divergent Relationships between Fecal Microbiota and Metabolome following Distinct Antibiotic-Induced Disruptions. <b>2017</b> , 2,	18
1439	The microbiome of bulk tank milk: Characterization and associations with somatic cell count and bacterial count. <b>2017</b> , 100, 2536-2552	30
1438	Dynamics of the microbiota found in the vaginas of dairy cows during the transition period: Associations with uterine diseases and reproductive outcome. <b>2017</b> , 100, 3043-3058	41
1437	Dynamics of the human gut microbiome in inflammatory bowel disease. <b>2017</b> , 2, 17004	533
1436	Experimental fossilization of mat-forming cyanobacteria in coarse-grained siliciclastic sediments. <b>2017</b> , 15, 484-498	19
1435	Parkinson's disease and Parkinson's disease medications have distinct signatures of the gut microbiome. <b>2017</b> , 32, 739-749	405
1434	Convergence and contrast in the community structure of Bacteria, Fungi and Archaea along a tropical elevation-climate gradient. <b>2017</b> , 93,	53
1433	Characterization of bacterial communities of donkey milk by high-throughput sequencing. <b>2017</b> , 251, 67-72	33
1432	Potentially Active Iron, Sulfur, and Sulfate Reducing Bacteria in Skagerrak and Bothnian Bay Sediments. <b>2017</b> , 34, 840-850	17
1431	Analysis of the Duodenal Microbiome in Autistic Individuals: Association With Carbohydrate Digestion. <b>2017</b> , 64, e110-e116	47
1430	Smokeless tobacco products harbor diverse bacterial microbiota that differ across products and brands. <b>2017</b> , 101, 5391-5403	22
1429	Microbial communities and diazotrophic activity differ in the root-zone of Alamo and Dacotah switchgrass feedstocks. <b>2017</b> , 9, 1057-1070	20
1428	Effects of titanium dioxide nanoparticles on soil microbial communities and wheat biomass. <b>2017</b> , 111, 85-93	47
1427	Relationships between gut microbiota, plasma metabolites, and metabolic syndrome traits in the METSIM cohort. <b>2017</b> , 18, 70	167
1426	Size, Composition, and Source Profiles of Inhalable Bioaerosols from Colorado Dairies. <b>2017</b> , 51, 6430-6440	23
1425	Compositional Changes in the Gut Mucus Microbiota Precede the Onset of Colitis-Induced Inflammation. <b>2017</b> , 23, 912-922	33
1424	Following Rapoport's Rule: the geographic range and genome size of bacterial taxa decline at warmer latitudes. <b>2017</b> , 19, 3152-3162	20
1423	IL-22BP dictates characteristics of Peyer's patch follicle-associated epithelium for antigen uptake. <b>2017</b> , 214, 1607-1618	37



1422	Stable mucus-associated bacterial communities in bleached and healthy corals of <i>Porites lobata</i> from the Arabian Seas. <b>2017</b> , 7, 45362	43
1421	Soil aggregation and associated microbial communities modify the impact of agricultural management on carbon content. <b>2017</b> , 19, 3070-3086	99
1420	Perinatal Bacterial Exposure Contributes to IL-13 Aeroallergen Response. <b>2017</b> , 57, 419-427	9
1419	Competition drives the response of soil microbial diversity to increased grazing by vertebrate herbivores. <b>2017</b> , 98, 1922-1931	58
1418	Effects of heavy metals on soil microbial community structure and diversity in the rice ( <i>Oryza sativa</i> L. subsp. Japonica, Food Crops Institute of Jiangsu Academy of Agricultural Sciences) rhizosphere. <b>2017</b> , 63, 75-83	31
1417	Organic Carbon Amendments for Enhanced Biological Attenuation of Trace Organic Contaminants in Biochar-Amended Stormwater Biofilters. <b>2017</b> , 51, 9184-9193	33
1416	Application of Struvite Alters the Antibiotic Resistome in Soil, Rhizosphere, and Phyllosphere. <b>2017</b> , 51, 8149-8157	123
1415	Airway Microbial Diversity is Inversely Associated with Mite-Sensitized Rhinitis and Asthma in Early Childhood. <b>2017</b> , 7, 1820	41
1414	Impact of drinking water treatment and distribution on the microbiome continuum: an ecological disturbance's perspective. <b>2017</b> , 19, 3163-3174	29
1413	Characterizing bacterial communities in paper production-troublemakers revealed. <b>2017</b> , 6, e00487	10
1412	Comparison of biofilm ecology supporting growth of individual <i>Naegleria</i> species in a drinking water distribution system. <b>2017</b> , 93,	13
1411	Microbial network, phylogenetic diversity and community membership in the active layer across a permafrost thaw gradient. <b>2017</b> , 19, 3201-3218	52
1410	Variations in the structure of airborne bacterial communities in Tsogt-Ovoo of Gobi desert area during dust events. <b>2017</b> , 10, 249-260	35
1409	Changes in microbial ecology after fecal microbiota transplantation for recurrent <i>C. difficile</i> infection affected by underlying inflammatory bowel disease. <b>2017</b> , 5, 55	74
1408	Microbiota modulation counteracts Alzheimer's disease progression influencing neuronal proteolysis and gut hormones plasma levels. <b>2017</b> , 7, 2426	196
1407	Consequences of tropical forest conversion to oil palm on soil bacterial community and network structure. <b>2017</b> , 112, 258-268	38
1406	Yearlong semi-continuous operation of thermophilic two-stage anaerobic digesters amended with biochar for enhanced biomethane production. <b>2017</b> , 167, 863-874	70
1405	Bioaerosol sampling and detection methods based on molecular approaches: No pain no gain. <b>2017</b> , 599-600, 2095-2104	33



1404	Centralized Drinking Water Treatment Operations Shape Bacterial and Fungal Community Structure. <b>2017</b> , 51, 7648-7657	24
1403	Significant Impacts of Increasing Aridity on the Arid Soil Microbiome. <b>2017</b> , 2,	80
1402	Soy compared with milk protein in a Western diet changes fecal microbiota and decreases hepatic steatosis in obese OLETF rats. <b>2017</b> , 46, 125-136	22
1401	Characterization of the Gastric Microbiota in a Pediatric Population According to Helicobacter pylori Status. <b>2017</b> , 36, 173-178	52
1400	Faecal microbiota study reveals specific dysbiosis in spondyloarthritis. <b>2017</b> , 76, 1614-1622	173
1399	SILVA, RDP, Greengenes, NCBI and OTT - how do these taxonomies compare?. <b>2017</b> , 18, 114	201
1398	High-throughput amplicon sequencing and stream benthic bacteria: identifying the best taxonomic level for multiple-stressor research. <b>2017</b> , 7, 44657	26
1397	Effect of miglitol on the suppression of nonalcoholic steatohepatitis development and improvement of the gut environment in a rodent model. <b>2017</b> , 52, 1180-1191	17
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1395	Whey protein effects on energy balance link the intestinal mechanisms of energy absorption with adiposity and hypothalamic neuropeptide gene expression. <b>2017</b> , 313, E1-E11	17
1394	Bronchial microbiome, PA biofilm-forming capacity and exacerbation in severe COPD patients colonized by P. aeruginosa. <b>2017</b> , 12, 379-392	17
1393	Restoring ecological properties of acidic soils contaminated with elemental sulfur. <b>2017</b> , 587-588, 449-456	7
1392	Weaning age influences the severity of gastrointestinal microbiome shifts in dairy calves. <b>2017</b> , 7, 198	58
1391	Rectal microbiota among HIV-uninfected, untreated HIV, and treated HIV-infected in Nigeria. <b>2017</b> , 31, 857-862	29
1390	Upgrading syngas fermentation effluent using in a continuous fermentation. <b>2017</b> , 10, 83	70
1389	Bacterial carbon use plasticity, phylogenetic diversity and the priming of soil organic matter. <i>ISME Journal</i> , <b>2017</b> , 11, 1890-1899	11.9 54
1388	Changes in intestinal microbiota composition and metabolism coincide with increased intestinal permeability in young adults under prolonged physiological stress. <b>2017</b> , 312, G559-G571	154
1387	Microbial community composition of deep-sea corals from the Red Sea provides insight into functional adaption to a unique environment. <b>2017</b> , 7, 44714	27

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1385	Community structure of the gut microbiota in sympatric species of wild <i>Drosophila</i> . <b>2017</b> , 20, 629-639		64
1384	Impact of water heater temperature setting and water use frequency on the building plumbing microbiome. <i>ISME Journal</i> , <b>2017</b> , 11, 1318-1330	11.9	50
1383	Invasive Plants Rapidly Reshape Soil Properties in a Grassland Ecosystem. <b>2017</b> , 2,		53
1382	Sensitivity to oxazolone induced dermatitis is transferable with gut microbiota in mice. <b>2017</b> , 7, 44385		36
1381	Intestinal dysbiosis in preterm infants preceding necrotizing enterocolitis: a systematic review and meta-analysis. <b>2017</b> , 5, 31		273
1380	Indigenous microbial capability in solid manure residues to start-up solid-phase anaerobic digesters. <b>2017</b> , 64, 79-87		4
1379	Global Distribution Patterns and Pangenomic Diversity of the Candidate Phylum "Latescibacteria" (WS3). <b>2017</b> , 83,		54
1378	The role of inoculum and reactor configuration for microbial community composition and dynamics in mainstream partial nitrification anammox reactors. <b>2017</b> , 6, e00456		24
1377	Effect of bioaugmentation by cellulolytic bacteria enriched from sheep rumen on methane production from wheat straw. <b>2017</b> , 46, 122-130		48
1376	Oral Biology. <b>2017</b> ,		1
1375	Analysis of 16S rRNA Gene Amplicon Sequences Using the QIIME Software Package. <b>2017</b> , 1537, 153-163		38
1374	Intestinal adaptation in proximal and distal segments: Two epithelial responses diverge after intestinal separation. <b>2017</b> , 161, 1016-1027		3
1373	Helminth burden and ecological factors associated with alterations in wild host gastrointestinal microbiota. <i>ISME Journal</i> , <b>2017</b> , 11, 663-675	11.9	20
1372	Community structure of partial nitrification-anammox biofilms at decreasing substrate concentrations and low temperature. <b>2017</b> , 10, 761-772		35
1371	Pilot-scale testing of a passive water treatment system for Kumtor gold mine demonstrates beneficial microbes mediate treatment of ammonia produced from cyanide destruction. <b>2017</b> , 100, 231-236		
1370	Duodenal endoluminal barrier sleeve alters gut microbiota of ZDF rats. <b>2017</b> , 41, 381-389		13
1369	A metatranscriptomic survey of the invasive yellow crazy ant, <i>Anoplolepis gracilipes</i> , identifies several potential viral and bacterial pathogens and mutualists. <b>2017</b> , 64, 197-207		17

1368	Seasonal induced changes in spinach rhizosphere microbial community structure with varying salinity and drought. <b>2017</b> , 579, 1485-1495	26
1367	Depth-dependent influence of different land-use systems on bacterial biogeography. <b>2017</b> , 93,	27
1366	Bacterial community collapse: a meta-analysis of the sinonasal microbiota in chronic rhinosinusitis. <b>2017</b> , 19, 381-392	104
1365	Relic DNA is abundant in soil and obscures estimates of soil microbial diversity. <b>2016</b> , 2, 16242	391
1364	Agricultural soil denitrifiers possess extensive nitrite reductase gene diversity. <b>2017</b> , 19, 1189-1208	38
1363	Long-Term Nickel Contamination Increases the Occurrence of Antibiotic Resistance Genes in Agricultural Soils. <b>2017</b> , 51, 790-800	159
1362	Effects of initial moisture content of Korean traditional wheat-based fermentation starter nuruk on microbial abundance and diversity. <b>2017</b> , 101, 2093-2106	11
1361	A Single Community Dominates Structure and Function of a Mixture of Multiple Methanogenic Communities. <b>2017</b> , 27, 3390-3395.e4	44
1360	Contaminants of emerging concern affect growth and development on artificial diets and a key host plant. <b>2017</b> , 114, E9923-E9931	17
1359	<i>Lactobacillus fermentum</i> FTDC 8312 combats hypercholesterolemia via alteration of gut microbiota. <b>2017</b> , 262, 75-83	33
1358	Agricultural land use determines functional genetic diversity of soil microbial communities. <b>2017</b> , 115, 423-432	27
1357	Strong impact of anthropogenic contamination on the co-occurrence patterns of a riverine microbial community. <b>2017</b> , 19, 4993-5009	110
1356	Assessment of variation in microbial community amplicon sequencing by the Microbiome Quality Control (MBQC) project consortium. <b>2017</b> , 35, 1077-1086	240
1355	A communal catalogue reveals Earth's multiscale microbial diversity. <b>2017</b> , 551, 457-463	1076
1354	Processing and Analyzing Human Microbiome Data. <b>2017</b> , 1666, 649-677	2
1353	Bioinformatics for Microbiome Research: Concepts, Strategies, and Advances. <b>2017</b> , 111-123	2
1352	Effects of contaminants of emerging concern on <i>Megaselia scalaris</i> (Lowe, Diptera: Phoridae) and its microbial community. <b>2017</b> , 7, 8165	15
1351	Natural polyreactive IgA antibodies coat the intestinal microbiota. <b>2017</b> , 358,	207

1350	Comparative soil microbial communities and activities in adjacent Sanqi ginseng monoculture and maize-Sanqi ginseng systems. <b>2017</b> , 120, 89-96	28
1349	Organic amendment type and application frequency affect crop yields, soil fertility and microbiome composition. <b>2017</b> , 120, 254-264	71
1348	Bio-electrochemical reactors using AMI-7001S and CMI-7000S membranes as separators for silver recovery and power generation. <b>2017</b> , 244, 1006-1014	19
1347	Does the maternal vaginal microbiota play a role in seeding the microbiota of neonatal gut and nose?. <b>2017</b> , 8, 763-778	34
1346	Metagenomic Cosmid Libraries Suitable for Functional Screening in Proteobacteria. <b>2017</b> , 1-11	1
1345	Development of a microbial test suite and data integration method for assessing microbial health of contaminated soil. <b>2017</b> , 143, 66-77	8
1344	Microbial taxonomy in the era of OMICS: application of DNA sequences, computational tools and techniques. <b>2017</b> , 110, 1357-1371	32
1343	Rhizosphere effect is stronger than PAH concentration on shaping spatial bacterial assemblages along centimetre-scale depth gradients. <b>2017</b> , 63, 881-893	7
1342	Bioinformatics for NGS-based metagenomics and the application to biogas research. <b>2017</b> , 261, 10-23	41
1341	Butyrate Supplementation at High Concentrations Alters Enteric Bacterial Communities and Reduces Intestinal Inflammation in Mice Infected with. <b>2017</b> , 2,	52
1340	Intestinal microbiota is altered in patients with colon cancer and modified by probiotic intervention. <b>2017</b> , 4, e000145	180
1339	Evolutionary conservation of a core root microbiome across plant phyla along a tropical soil chronosequence. <b>2017</b> , 8, 215	143
1338	Sources of Variation in the Gut Microbial Community of <i>Lycaeides melissa</i> Caterpillars. <b>2017</b> , 7, 11335	18
1337	Is microbial terroir related to geographic distance between vineyards?. <b>2017</b> , 9, 742-749	40
1336	Hiding in Plain Sight: Mining Bacterial Species Records for Phenotypic Trait Information. <b>2017</b> , 2,	43
1335	Culture independent assessment of human milk microbial community in lactational mastitis. <b>2017</b> , 7, 7804	79
1334	Introduced ascidians harbor highly diverse and host-specific symbiotic microbial assemblages. <b>2017</b> , 7, 11033	21
1333	Microbial communities in placentas from term normal pregnancy exhibit spatially variable profiles. <b>2017</b> , 7, 11200	90

1332	Evaluation of Sedum as driver for plant microbial fuel cells in a semi-arid green roof ecosystem. <b>2017</b> , 108, 203-210	27
1331	Unravelling diversity and metabolic potential of microbial consortia at each stage of leather sewage treatment. <b>2017</b> , 7, 41727-41737	8
1330	Microbial community characterization during anaerobic digestion of Scenedesmus spp. under mesophilic and thermophilic conditions. <b>2017</b> , 27, 121-130	36
1329	Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. <b>2017</b> , 2, 1533-1542	764
1328	The impact of immigration on microbial community composition in full-scale anaerobic digesters. <b>2017</b> , 7, 9343	83
1327	Low Lactobacilli abundance and polymicrobial diversity in the lower reproductive tract of female rhesus monkeys do not compromise their reproductive success. <b>2017</b> , 79, e22691	1
1326	Guanylate Cyclase C Activation Shapes the Intestinal Microbiota in Patients with Familial Diarrhea and Increased Susceptibility for Crohn's Disease. <b>2017</b> , 23, 1752-1761	7
1325	Potential role of intratumor bacteria in mediating tumor resistance to the chemotherapeutic drug gemcitabine. <b>2017</b> , 357, 1156-1160	577
1324	Protected sampling is preferable in bronchoscopic studies of the airway microbiome. <b>2017</b> , 3,	21
1323	Gut microbiota dysbiosis associated with glucose metabolism disorders and the metabolic syndrome in older adults. <b>2017</b> , 8, 545-556	134
1322	Consumption of Two Healthy Dietary Patterns Restored Microbiota Dysbiosis in Obese Patients with Metabolic Dysfunction. <b>2017</b> , 61, 1700300	66
1321	The Brazilian Microbiome. <b>2017</b> ,	0
1320	Comparative RNA function analysis reveals high functional similarity between distantly related bacterial 16 S rRNAs. <b>2017</b> , 7, 9993	21
1319	The saliva microbiome profiles are minimally affected by collection method or DNA extraction protocols. <b>2017</b> , 7, 8523	62
1318	Antibiotic-induced perturbations in microbial diversity during post-natal development alters amyloid pathology in an aged APP/PS1 murine model of Alzheimer's disease. <b>2017</b> , 7, 10411	133
1317	Stability in metabolic phenotypes and inferred metagenome profiles before the onset of colitis-induced inflammation. <b>2017</b> , 7, 8836	9
1316	A cross-sectional comparative study of gut bacterial community of Indian and Finnish children. <b>2017</b> , 7, 10555	26
1315	Milk microbiome and bacterial load following dry cow therapy without antibiotics in dairy cows with healthy mammary gland. <b>2017</b> , 7, 8067	38

1314	Effect of dairy matrices on the survival of <i>Streptococcus thermophilus</i> , <i>Brevibacterium aurantiacum</i> and <i>Hafnia alvei</i> during digestion. <b>2017</b> , 100, 477-488	5
1313	Microbiome Alterations Are Correlated with Occurrence of Postharvest Stem-End Rot in Mango Fruit. <b>2017</b> , 1, 117-127	38
1312	An Chicken Gut Model Demonstrates Transfer of a Multidrug Resistance Plasmid from to Commensal. <b>2017</b> , 8,	40
1311	Distinct bacterial community and diversity shifts after phytoplankton-derived dissolved organic matter addition in a coastal environment. <b>2017</b> , 495, 119-128	17
1310	Response of soil microbial community composition and function to a bottomland forest restoration intensity gradient. <b>2017</b> , 119, 317-326	41
1309	Specific Signatures of the Gut Microbiota and Increased Levels of Butyrate in Children Treated with Fermented Cow's Milk Containing Heat-Killed <i>Lactobacillus paracasei</i> CBA L74. <b>2017</b> , 83,	55
1308	Redox and temperature-sensitive changes in microbial communities and soil chemistry dictate greenhouse gas loss from thawed permafrost. <b>2017</b> , 134, 183-200	13
1307	Isolation and characterization of aerobic anoxygenic phototrophs from exposed soils from the Sør Rondane Mountains, East Antarctica. <b>2017</b> , 40, 357-369	37
1306	Relationships between gastrointestinal microbiota and blood group antigens. <b>2017</b> , 49, 473-483	23
1305	Metabolic gene-targeted monitoring of non-starter lactic acid bacteria during cheese ripening. <b>2017</b> , 257, 276-284	20
1304	The Variable Influence of Dispersant on Degradation of Oil Hydrocarbons in Subarctic Deep-Sea Sediments at Low Temperatures (0-5 °C). <b>2017</b> , 7, 2253	30
1303	Multi-omics Analysis of Periodontal Pocket Microbial Communities Pre- and Posttreatment. <b>2017</b> , 2,	35
1302	Effects of different biofilm carriers on biogas production during anaerobic digestion of corn straw. <b>2017</b> , 244, 445-451	46
1301	Do manure-borne or indigenous soil microorganisms influence the spread of antibiotic resistance genes in manured soil?. <b>2017</b> , 114, 229-237	102
1300	Revealing the insoluble metasecretome of lignocellulose-degrading microbial communities. <b>2017</b> , 7, 2356	23
1299	Hypersaline sapropels act as hotspots for microbial dark matter. <b>2017</b> , 7, 6150	7
1298	Large-scale differences in microbial biodiversity discovery between 16S amplicon and shotgun sequencing. <b>2017</b> , 7, 6589	110
1297	Richer gut microbiota with distinct metabolic profile in HIV infected Elite Controllers. <b>2017</b> , 7, 6269	56

1296	Symbiont dynamics and strain diversity in the defensive mutualism between <i>Lagria</i> beetles and <i>Burkholderia</i> . <b>2017</b> , 19, 3674-3688	24
1295	An underappreciated hotspot of antibiotic resistance: The groundwater near the municipal solid waste landfill. <b>2017</b> , 609, 966-973	82
1294	Predator trait evolution alters prey community composition. <b>2017</b> , 8, e01803	
1293	Bacterial community composition in Adlie ( <i>Pygoscelis adeliae</i> ) and Chinstrap ( <i>Pygoscelis antarctica</i> ) Penguin stomach contents from Signy Island, South Orkney Islands. <b>2017</b> , 40, 2517-2530	9
1292	The Skin Microbiome of Cohabiting Couples. <b>2017</b> , 2,	63
1291	MiDAS 2.0: an ecosystem-specific taxonomy and online database for the organisms of wastewater treatment systems expanded for anaerobic digester groups. <b>2017</b> , 2017,	82
1290	Daily thanatomicrobiome changes in soil as an approach of postmortem interval estimation: An ecological perspective. <b>2017</b> , 278, 388-395	27
1289	Predicting Microbial Fuel Cell Biofilm Communities and Bioreactor Performance using Artificial Neural Networks. <b>2017</b> , 51, 10881-10892	37
1288	Fecal concentrations of bacterially derived vitamin K forms are associated with gut microbiota composition but not plasma or fecal cytokine concentrations in healthy adults. <b>2017</b> , 106, 1052-1061	43
1287	Photosynthetic carbon uptake induces autoflocculation of the marine microalga <i>Nannochloropsis oculata</i> . <b>2017</b> , 26, 302-311	29
1286	Incorporation of bean plant residue in soil with different agricultural practices and its effect on the soil bacteria. <b>2017</b> , 119, 417-427	23
1285	Electrochemically active microorganisms from an acid mine drainage-affected site promote cathode oxidation in microbial fuel cells. <b>2017</b> , 118, 139-146	16
1284	A wellness study of 108 individuals using personal, dense, dynamic data clouds. <b>2017</b> , 35, 747-756	235
1283	Age, sex, and TNF associated differences in the gut microbiota of mice and their impact on acute TNBS colitis. <b>2017</b> , 103, 311-319	44
1282	Archaeal and Bacterial Community Structure in an Anaerobic Digestion Reactor (Lagoon Type) Used for Biogas Production at a Pig Farm. <b>2017</b> , 27, 306-317	25
1281	Legume crop rotation suppressed nitrifying microbial community in a sugarcane cropping soil. <b>2017</b> , 7, 16707	22
1280	Cecal microbiome divergence of broiler chickens by sex and body weight. <b>2017</b> , 55, 939-945	37
1279	High-resolution bacterial 16S rRNA gene profile meta-analysis and biofilm status reveal common colorectal cancer consortia. <b>2017</b> , 3, 34	145

1278	Microbial Diversity of Genital Ulcers of HSV-2 Seropositive Women. <b>2017</b> , 7, 15475	5
1277	Alteration of the intestinal microbiome characterizes preclinical inflammatory arthritis in mice and its modulation attenuates established arthritis. <b>2017</b> , 7, 15613	59
1276	Modeling and Optimization: Theory and Applications. <b>2017</b> ,	
1275	Previous crop and rotation history effects on maize seedling health and associated rhizosphere microbiome. <b>2017</b> , 7, 15709	45
1274	Brown rice and retrograded brown rice alleviate inflammatory response in dextran sulfate sodium (DSS)-induced colitis mice. <b>2017</b> , 8, 4630-4643	23
1273	Distinct microbial communities in the active and permafrost layers on the Tibetan Plateau. <b>2017</b> , 26, 6608-6620	61
1272	Gut microbiota profile in systemic sclerosis patients with and without clinical evidence of gastrointestinal involvement. <b>2017</b> , 7, 14874	42
1271	Inflammation-induced IgA+ cells dismantle anti-liver cancer immunity. <b>2017</b> , 551, 340-345	224
1270	Investigation of microbial communities in water dispensers. <b>2017</b> , 60, 667-672	2
1269	Understanding the variation of microbial community in heavy metals contaminated soil using high throughput sequencing. <b>2017</b> , 144, 300-306	122
1268	Intestinal virome changes precede autoimmunity in type I diabetes-susceptible children. <b>2017</b> , 114, E6166-E6175	151
1267	Influence of glacial melt and Atlantic water on bacterioplankton community of Kongsfjorden, an Arctic fjord. <b>2017</b> , 82, 143-151	9
1266	Large perturbations in CO flux and subsequent chemosynthesis are induced in agricultural soil by the addition of elemental sulfur. <b>2017</b> , 7, 4732	3
1265	Effect of cytomegalovirus and Epstein-Barr virus replication on intestinal mucosal gene expression and microbiome composition of HIV-infected and uninfected individuals. <b>2017</b> , 31, 2059-2067	16
1264	Disparity in the nasopharyngeal microbiota between healthy cattle on feed, at entry processing and with respiratory disease. <b>2017</b> , 208, 30-37	37
1263	Microbial survival strategies in ancient permafrost: insights from metagenomics. <i>ISME Journal</i> , <b>2017</b> , 11, 2305-2318	11.9 96
1262	Seasonal and spatial variations of prokaryoplankton communities in a salinity-influenced watershed, China. <b>2017</b> , 93,	9
1261	Culture-dependent and culture-independent assessment of spoilage community growth on VP lamb meat from packaging to past end of shelf-life. <b>2017</b> , 68, 71-80	23



1260	Fecal microbial characterization of hospitalized patients with suspected infectious diarrhea shows significant dysbiosis. <b>2017</b> , 7, 1088	24
1259	Inter-personal diversity and temporal dynamics of dental, tongue, and salivary microbiota in the healthy oral cavity. <b>2017</b> , 3, 2	103
1258	Characterisation and comparison of bacterial communities on reverse osmosis membranes of a full-scale desalination plant by bacterial 16S rRNA gene metabarcoding. <b>2017</b> , 3, 13	36
1257	Social Influences on Prevotella and the Gut Microbiome of Young Monkeys. <b>2017</b> , 79, 888-897	34
1256	Dynamics of the oral microbiota as a tool to estimate time since death. <b>2017</b> , 32, 511-516	23
1255	Relationship between nasopharyngeal and bronchoalveolar microbial communities in clinically healthy feedlot cattle. <b>2017</b> , 17, 138	29
1254	Bacteria as Emerging Indicators of Soil Condition. <b>2017</b> , 83,	120
1253	Trade-offs between microbiome diversity and productivity in a stratified microbial mat. <i>ISME Journal</i> , <b>2017</b> , 11, 405-414	11.9 21
1252	Cultivated Sub-Populations of Soil Microbiomes Retain Early Flowering Plant Trait. <b>2017</b> , 73, 394-403	35
1251	Identifying the microbial taxa that consistently respond to soil warming across time and space. <b>2017</b> , 23, 2117-2129	89
1250	Cultivation Versus Molecular Analysis of Banana ( <i>Musa</i> sp.) Shoot-Tip Tissue Reveals Enormous Diversity of Normally Uncultivable Endophytic Bacteria. <b>2017</b> , 73, 885-899	19
1249	Microbial Nursery Production of High-Quality Biological Soil Crust Biomass for Restoration of Degraded Dryland Soils. <b>2017</b> , 83,	38
1248	Dynamic change of surface microbiota with different environmental cleaning methods between two wards in a hospital. <b>2017</b> , 101, 771-781	11
1247	High-calorific biogas production from anaerobic digestion of food waste using a two-phase pressurized biofilm (TPPB) system. <b>2017</b> , 224, 56-62	56
1246	Amplicon-based taxonomic characterization of bacteria in urban and peri-urban roof-harvested rainwater stored in tanks. <b>2017</b> , 576, 326-334	29
1245	Microbial Factors Associated with Postoperative Crohn's Disease Recurrence. <b>2017</b> , 11, 191-203	52
1244	Study of microbial community plasticity for anaerobic digestion of vegetable waste in Anaerobic Baffled Reactor. <b>2017</b> , 101, 59-66	74
1243	Flowers and Wild Megachilid Bees Share Microbes. <b>2017</b> , 73, 188-200	84

1242	The Bacterial Community Structure and Dynamics of Carbon and Nitrogen when Maize ( <i>Zea mays</i> L.) and Its Neutral Detergent Fibre Were Added to Soil from Zimbabwe with Contrasting Management Practices. <b>2017</b> , 73, 135-152		21
1241	D-tryptophan from probiotic bacteria influences the gut microbiome and allergic airway disease. <b>2017</b> , 139, 1525-1535		76
1240	Shifting Cyanobacterial Diversity in Response to Agricultural Soils Associated with Dust Emission. <b>2017</b> , 28, 878-886		8
1239	Analysis of bacterial composition in marine sponges reveals the influence of host phylogeny and environment. <b>2017</b> , 93,		22
1238	The lung mycobiome in the next-generation sequencing era. <b>2017</b> , 8, 334-341		37
1237	The antibiotic resistome of swine manure is significantly altered by association with the <i>Musca domestica</i> larvae gut microbiome. <i>ISME Journal</i> , <b>2017</b> , 11, 100-111	11.9	72
1236	Molecular biosignatures reveal common benthic microbial sources of organic matter in ooids and grapestones from Pigeon Cay, The Bahamas. <b>2017</b> , 15, 112-130		42
1235	Bringing microbial diversity into focus: high-resolution analysis of iron mats from the Lōhi Seamount. <b>2017</b> , 19, 301-316		17
1234	Dual-specificity phosphatase 6 deficiency regulates gut microbiome and transcriptome response against diet-induced obesity in mice. <b>2016</b> , 2, 16220		33
1233	Influence of early life exposure, host genetics and diet on the mouse gut microbiome and metabolome. <b>2016</b> , 2, 16221		63
1232	Shared and host-specific microbiome diversity and functioning of grapevine and accompanying weed plants. <b>2017</b> , 19, 1407-1424		60
1231	Plant domestication and the assembly of bacterial and fungal communities associated with strains of the common sunflower, <i>Helianthus annuus</i> . <b>2017</b> , 214, 412-423		116
1230	Trophic state and geographic gradients influence planktonic cyanobacterial diversity and distribution in New Zealand lakes. <b>2017</b> , 93,		19
1229	Interleukin-15 promotes intestinal dysbiosis with butyrate deficiency associated with increased susceptibility to colitis. <i>ISME Journal</i> , <b>2017</b> , 11, 15-30	11.9	36
1228	The commensal microbiota exacerbate infectious colitis in stressor-exposed mice. <b>2017</b> , 60, 44-50		23
1227	Assessing effects of the entomopathogenic fungus <i>Metarhizium brunneum</i> on soil microbial communities in <i>Agriotes</i> spp. biological pest control. <b>2017</b> , 93,		18
1226	Alterations in oral bacterial communities are associated with risk factors for oral and oropharyngeal cancer. <b>2017</b> , 7, 17686		63
1225	A switch of chlorinated substrate causes emergence of a previously undetected native <i>Dehalobacter</i> population in an established <i>Dehalococcoides</i> -dominated chloroethene-dechlorinating enrichment culture. <b>2017</b> , 93,		7

1224	RNAcentral: a comprehensive database of non-coding RNA sequences. <b>2017</b> , 45, D128-D134	119
1223	Variations in airborne bacterial communities at high altitudes over the Noto Peninsula (Japan) in response to Asian dust events. <b>2017</b> , 17, 11877-11897	40
1222	Tracking Human Gut Microbiome Changes Resulting from a Colonoscopy. <b>2017</b> , 56, 442-447	3
1221	High Organic Loading Treatment of Synthetic Soy-sauce Production Wastewater Using a Combined System Consisting of a Psychrophilic (20 &ordm;C) UASB Reactor and a DHS Reactor at Ambient Temperature. <b>2017</b> , 40, 67-75	1
1220	Microbial Community Structure and Enumeration of Bacillus species in Activated Sludge. <b>2017</b> , 15, 233-240	13
1219	Moderate Exercise Has Limited but Distinguishable Effects on the Mouse Microbiome. <b>2017</b> , 2,	46
1218	Preparing for the crewed Mars journey: microbiota dynamics in the confined Mars500 habitat during simulated Mars flight and landing. <b>2017</b> , 5, 129	35
1217	Impact of hypoxia on gene expression patterns by the human pathogen, , and bacterial community composition in a North Carolina estuary. <b>2017</b> , 1, 37-50	2
1216	Influence of short-term dietary starch inclusion on the equine cecal microbiome. <b>2017</b> , 95, 5077-5090	18
1215	Diversity and mineral substrate preference in endolithic microbial communities from marine intertidal outcrops (Isla de Mona, Puerto Rico). <b>2017</b> , 14, 311-324	19
1214	A Combined LC-MS Metabolomics- and 16S rRNA Sequencing Platform to Assess Interactions between Herbal Medicinal Products and Human Gut Bacteria : a Pilot Study on Willow Bark Extract. <b>2017</b> , 8, 893	18
1213	You Are What You Eat: A Genomic Analysis of the Gut Microbiome of Captive and Wild Paralarvae and Their Zooplankton Prey. <b>2017</b> , 8, 362	18
1212	and in the Vaginal Microbiota and Persistent High-Risk Human Papillomavirus Infection. <b>2017</b> , 5, 140	30
1211	Gut microbiome as a biomarker of cardiometabolic disorders. <b>2017</b> , 24, 416-422	25
1210	Molecular and Microscopic Insights into the Formation of Soil Organic Matter in a Red Pine Rhizosphere. <b>2017</b> , 1, 4	9
1209	Macrophage dysfunction initiates colitis during weaning of infant mice lacking the interleukin-10 receptor. <b>2017</b> , 6,	16
1208	Characterizing and Functionally Defining the Gut Microbiota: Methodology and Implications. <b>2017</b> , 15-25	3
1207	Microbiological Contamination at Workplaces in a Combined Heat and Power (CHP) Station Processing Plant Biomass. <b>2017</b> , 14,	9

1206	Laboratory-Cultured Strains of the Sea Anemone <i>Exaiptasia</i> Reveal Distinct Bacterial Communities. <b>2017</b> , 4,	14
1205	Distinct Bacterial Microbiomes Associate with the Deep-Sea Coral <i>Eguchipsammia fistula</i> from the Red Sea and from Aquaria Settings. <b>2017</b> , 4,	16
1204	Characterization of Gut Microbiome Dynamics in Developing Pekin Ducks and Impact of Management System. <b>2016</b> , 7, 2125	34
1203	Nutritional Models of Experimentally-Induced Subacute Ruminal Acidosis (SARA) Differ in Their Impact on Rumen and Hindgut Bacterial Communities in Dairy Cows. <b>2016</b> , 7, 2128	44
1202	A New Approach to Modify Plant Microbiomes and Traits by Introducing Beneficial Bacteria at Flowering into Progeny Seeds. <b>2017</b> , 8, 11	191
1201	Geological and Geochemical Controls on Subsurface Microbial Life in the Samail Ophiolite, Oman. <b>2017</b> , 8, 56	61
1200	Genomic Analysis of , the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum. <b>2017</b> , 8, 195	30
1199	A Few Oligotypes Dominate in the Meat and Dairy Processing Environment. <b>2017</b> , 8, 264	47
1198	The Effect of Increased Loads of Dissolved Organic Matter on Estuarine Microbial Community Composition and Function. <b>2017</b> , 8, 351	48
1197	Inbred Mouse Populations Exhibit Intergenerational Changes in Intestinal Microbiota Composition and Function Following Introduction to a Facility. <b>2017</b> , 8, 608	15
1196	From Vineyard Soil to Wine Fermentation: Microbiome Approximations to Explain the " Concept. <b>2017</b> , 8, 821	78
1195	Dietary High Zinc Oxide Modulates the Microbiome of Ileum and Colon in Weaned Piglets. <b>2017</b> , 8, 825	41
1194	The Gut Microbiota of Healthy Chilean Subjects Reveals a High Abundance of the Phylum Verrucomicrobia. <b>2017</b> , 8, 1221	125
1193	Cyanobacterial Diversity in Microbial Mats from the Hypersaline Lagoon System of Araruama, Brazil: An In-depth Polyphasic Study. <b>2017</b> , 8, 1233	24
1192	Effects of Physiochemical Factors on Prokaryotic Biodiversity in Malaysian Circumneutral Hot Springs. <b>2017</b> , 8, 1252	34
1191	Spatial and Temporal Microbial Patterns in a Tropical Macrotidal Estuary Subject to Urbanization. <b>2017</b> , 8, 1313	17
1190	Microbial Communities and Their Predicted Metabolic Functions in Growth Laminae of a Unique Large Conical Mat from Lake Untersee, East Antarctica. <b>2017</b> , 8, 1347	32
1189	Bacteria Associated to Plants Naturally Selected in a Historical PCB Polluted Soil Show Potential to Sustain Natural Attenuation. <b>2017</b> , 8, 1385	18

1188	Mesozooplankton Graze on Cyanobacteria in the Amazon River Plume and Western Tropical North Atlantic. <b>2017</b> , 8, 1436	18
1187	Fast and Simple Analysis of MiSeq Amplicon Sequencing Data with MetaAmp. <b>2017</b> , 8, 1461	47
1186	Cyanobacterial Allelochemicals But Not Cyanobacterial Cells Markedly Reduce Microbial Community Diversity. <b>2017</b> , 8, 1495	22
1185	Decreased Taxon-Specific IgA Response in Relation to the Changes of Gut Microbiota Composition in the Elderly. <b>2017</b> , 8, 1757	12
1184	Phloroglucinol Degradation in the Rumen Promotes the Capture of Excess Hydrogen Generated from Methanogenesis Inhibition. <b>2017</b> , 8, 1871	22
1183	Isotopic Labeling of Symbiotic Bacteria Involved in Cellulose Degradation and Nitrogen Recycling within the Gut of the Forest Cockchafer (). <b>2017</b> , 8, 1970	15
1182	Seasonal Shifts in Bacterial Community Responses to Phytoplankton-Derived Dissolved Organic Matter in the Western Antarctic Peninsula. <b>2017</b> , 8, 2117	22
1181	Progressive Colonization of Bacteria and Degradation of Rice Straw in the Rumen by Illumina Sequencing. <b>2017</b> , 8, 2165	17
1180	Low-Molecular-Weight Chitosan Supplementation Increases the Population of in the Cecal Contents of Weanling Pigs. <b>2017</b> , 8, 2182	19
1179	Low Microbial Diversity and Abnormal Microbial Succession Is Associated with Necrotizing Enterocolitis in Preterm Infants. <b>2017</b> , 8, 2243	44
1178	Antibiotic-Induced Alterations in Gut Microbiota Are Associated with Changes in Glucose Metabolism in Healthy Mice. <b>2017</b> , 8, 2306	66
1177	Parallelized, Aerobic, Single Carbon-Source Enrichments from Different Natural Environments Contain Divergent Microbial Communities. <b>2017</b> , 8, 2321	14
1176	Seasonal Changes in a Maize-Based Polyculture of Central Mexico Reshape the Co-occurrence Networks of Soil Bacterial Communities. <b>2017</b> , 8, 2478	14
1175	Temporal Variation of the Skin Bacterial Community and Infection in the Terrestrial Cryptic Frog. <b>2017</b> , 8, 2535	19
1174	Age Drives Distortion of Brain Metabolic, Vascular and Cognitive Functions, and the Gut Microbiome. <b>2017</b> , 9, 298	62
1173	Dietary Prebiotics and Bioactive Milk Fractions Improve NREM Sleep, Enhance REM Sleep Rebound and Attenuate the Stress-Induced Decrease in Diurnal Temperature and Gut Microbial Alpha Diversity. <b>2016</b> , 10, 240	44
1172	Emerging Statistical Methodologies in the Field of Microbiome Studies. <b>2017</b> , 37-52	
1171	A phylogenetic transform enhances analysis of compositional microbiota data. <b>2017</b> , 6,	144

1170	Apigenin Impacts the Growth of the Gut Microbiota and Alters the Gene Expression of Enterococcus. <b>2017</b> , 22,	14
1169	Primary and heterotrophic productivity relate to multikingdom diversity in a hypersaline mat. <b>2017</b> , 93,	6
1168	The US National Mall Microbiome: A Census of Rhizosphere Bacteria Inhabiting Landscape Turf. <b>2017</b> , 57, S-341	4
1167	Comparison of bacterial communities from lava cave microbial mats to overlying surface soils from Lava Beds National Monument, USA. <b>2017</b> , 12, e0169339	34
1166	Urinary catheter-associated microbiota change in accordance with treatment and infection status. <b>2017</b> , 12, e0177633	24
1165	The feline skin microbiota: The bacteria inhabiting the skin of healthy and allergic cats. <b>2017</b> , 12, e0178555	27
1164	Natural and artificial feeding management before weaning promote different rumen microbial colonization but not differences in gene expression levels at the rumen epithelium of newborn goats. <b>2017</b> , 12, e0182235	28
1163	Microbial characterization of bee pollen from the Vesuvius area collected by using three different traps. <b>2017</b> , 12, e0183208	21
1162	Lactobacillus paracasei feeding improves immune control of influenza infection in mice. <b>2017</b> , 12, e0184976	51
1161	Taxonomic differences of gut microbiomes drive cellulolytic enzymatic potential within hind-gut fermenting mammals. <b>2017</b> , 12, e0189404	17
1160	Cross-modulation of pathogen-specific pathways enhances malnutrition during enteric co-infection with Giardia lamblia and enteroaggregative Escherichia coli. <b>2017</b> , 13, e1006471	49
1159	Two dynamic regimes in the human gut microbiome. <b>2017</b> , 13, e1005364	56
1158	Taxon abundance, diversity, co-occurrence and network analysis of the ruminal microbiota in response to dietary changes in dairy cows. <b>2017</b> , 12, e0180260	46
1157	The Gut-Brain Axis in Healthy Females: Lack of Significant Association between Microbial Composition and Diversity with Psychiatric Measures. <b>2017</b> , 12, e0170208	31
1156	Advanced glycation end products dietary restriction effects on bacterial gut microbiota in peritoneal dialysis patients; a randomized open label controlled trial. <b>2017</b> , 12, e0184789	71
1155	Fructose diet alleviates acetaminophen-induced hepatotoxicity in mice. <b>2017</b> , 12, e0182977	7
1154	Comparison of rumen bacterial communities in dairy herds of different production. <b>2017</b> , 17, 190	31
1153	Gene and transcript abundances of bacterial type III secretion systems from the rumen microbiome are correlated with methane yield in sheep. <b>2017</b> , 10, 367	6

1152	Longitudinal profiling reveals a persistent intestinal dysbiosis triggered by conventional anti-tuberculosis therapy. <b>2017</b> , 5, 71	76
1151	Normal milk microbiome is reestablished following experimental infection with <i>Escherichia coli</i> independent of intramammary antibiotic treatment with a third-generation cephalosporin in bovines. <b>2017</b> , 5, 74	34
1150	Feed-additive probiotics accelerate yet antibiotics delay intestinal microbiota maturation in broiler chicken. <b>2017</b> , 5, 91	104
1149	Space-type radiation induces multimodal responses in the mouse gut microbiome and metabolome. <b>2017</b> , 5, 105	43
1148	Microbial biodiversity assessment of the European Space Agency's ExoMars 2016 mission. <b>2017</b> , 5, 143	18
1147	The Inuit gut microbiome is dynamic over time and shaped by traditional foods. <b>2017</b> , 5, 151	32
1146	Identifying predictive features of <i>Clostridium difficile</i> infection recurrence before, during, and after primary antibiotic treatment. <b>2017</b> , 5, 148	20
1145	Impact of prematurity and nutrition on the developing gut microbiome and preterm infant growth. <b>2017</b> , 5, 158	72
1144	Increasing corn distillers solubles alters the liquid fraction of the ruminal microbiome. <b>2017</b> , 95, 3540-3551	0
1143	Variations in airborne bacterial communities at high altitudes over the Noto Peninsula (Japan) in response to Asian dust events. <b>2017</b> ,	4
1142	Bacterial Structure of Agricultural Soils with High and Low Yields. <b>2017</b> , 08,	2
1141	Full Issue PDF. <b>2017</b> , 1, 115-170	
1140	Differences among Soil-Inhabiting Microbial Communities in <i>Poa annua</i> Turf throughout the Growing Season. <b>2017</b> , 57, S-262	11
1139	Rubber plantation ageing controls soil biodiversity after land conversion from cassava. <b>2018</b> , 257, 92-102	21
1138	Cyanobacteria inhabiting biological soil crusts of a polar desert: Sør Rondane Mountains, Antarctica. <b>2018</b> , 41, 363-373	18
1137	Modulation of microbial consortia enriched from different polluted environments during petroleum biodegradation. <b>2018</b> , 29, 187-209	23
1136	Drought consistently alters the composition of soil fungal and bacterial communities in grasslands from two continents. <b>2018</b> , 24, 2818-2827	114
1135	Bacterial metataxonomic profile and putative functional behavior associated with C and N cycle processes remain altered for decades after forest harvest. <b>2018</b> , 119, 184-193	24

1134	Bacterial community changes in an industrial algae production system. <b>2018</b> , 31, 147-156		36
1133	Acute and repeated exposure to social stress reduces gut microbiota diversity in Syrian hamsters. <b>2018</b> , 345, 39-48		38
1132	Rotenone induces gastrointestinal pathology and microbiota alterations in a rat model of Parkinson's disease. <b>2018</b> , 65, 174-185		49
1131	Depth matters: effects of precipitation regime on soil microbial activity upon rewetting of a plant-soil system. <i>ISME Journal</i> , <b>2018</b> , 12, 1061-1071	11.9	53
1130	Grape seed proanthocyanidins influence gut microbiota and enteroendocrine secretions in female rats. <b>2018</b> , 9, 1672-1682		47
1129	Dog introduction alters the home dust microbiota. <b>2018</b> , 28, 539-547		30
1128	16S rRNA metagenomic analysis of the symbiotic community structures of bacteria in foregut, midgut, and hindgut of the wood-feeding termite <i>Bulbitermes</i> sp.. <b>2018</b> , 76, 187-197		11
1127	Predicting the structure of soil communities from plant community taxonomy, phylogeny, and traits. <i>ISME Journal</i> , <b>2018</b> , 12, 1794-1805	11.9	109
1126	Effects of nutrient loading on sediment bacterial and pathogen communities within seagrass meadows. <b>2018</b> , 7, e00600		16
1125	Updating the 97% identity threshold for 16S ribosomal RNA OTUs. <b>2018</b> , 34, 2371-2375		260
1124	Bacterial Diversity and Phylogenetic Analysis of Type II Polyketide Synthase Gene from Manao-Pee Cave, Thailand. <b>2018</b> , 35, 518-527		8
1123	Biodegradation of Poly(3-hydroxybutyrate- co-3-hydroxyhexanoate) Plastic under Anaerobic Sludge and Aerobic Seawater Conditions: Gas Evolution and Microbial Diversity. <b>2018</b> , 52, 5700-5709		45
1122	Bacterial-derived exopolysaccharides enhance antifungal drug tolerance in a cross-kingdom oral biofilm. <i>ISME Journal</i> , <b>2018</b> , 12, 1427-1442	11.9	73
1121	Different endophyte communities colonize buds of sprouts compared with mature trees of mountain birch recovered from moth herbivory. <b>2018</b> , 38, 1437-1444		2
1120	Impacts of Glutaraldehyde on Microbial Community Structure and Degradation Potential in Streams Impacted by Hydraulic Fracturing. <b>2018</b> , 52, 5989-5999		20
1119	Microbiota-accessible carbohydrates suppress <i>Clostridium difficile</i> infection in a murine model. <b>2018</b> , 3, 662-669		105
1118	The influence of diet and environment on the gut microbial community of field crickets. <b>2018</b> , 8, 4704-4720		29
1117	Microbiome analysis and bacterial isolation from Lejñ Lake soil in Atacama Desert. <b>2018</b> , 22, 665-673		19



1116	Potential for manganese biofouling in water transmission lines using model reactors. <b>2018</b> , 4, 761-772	4
1115	Lack of Microbial Diversity in an Extreme Mars Analog Setting: Poñ Volcano, Costa Rica. <b>2018</b> , 18, 923-933	12
1114	Redundancy in Anaerobic Digestion Microbiomes during Disturbances by the Antibiotic Monensin. <b>2018</b> , 84,	12
1113	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <b>2018</b> , 3,	181
1112	The effect of resistant starch (RS) on the bovine rumen microflora and isolation of RS-degrading bacteria. <b>2018</b> , 102, 4927-4936	11
1111	Revealing the microbiota of marketed edible insects through PCR-DGGE, metagenomic sequencing and real-time PCR. <b>2018</b> , 276, 54-62	26
1110	A methanotrophic archaeon couples anaerobic oxidation of methane to Fe(III) reduction. <i>ISME Journal</i> , <b>2018</b> , 12, 1929-1939	11.9 141
1109	The interplay between oral microbiome, lifestyle factors and genetic polymorphisms in the risk of oral squamous cell carcinoma. <b>2018</b> , 39, 778-787	54
1108	Microbial diversity and biomarker analysis of modern freshwater microbialites from Laguna Bacalar, Mexico. <b>2018</b> , 16, 319-337	8
1107	River Flow Impacts Bacterial and Archaeal Community Structure in Surface Sediments in the Northern Gulf of Mexico. <b>2018</b> , 76, 941-953	1
1106	Guided Protocol for Fecal Microbial Characterization by 16S rRNA-Amplicon Sequencing. <b>2018</b> ,	6
1105	Nematode-associated microbial taxa do not correlate with host phylogeny, geographic region or feeding morphology in marine sediment habitats. <b>2018</b> , 27, 1930-1951	24
1104	Rumen bacterial community structure impacts feed efficiency in beef cattle. <b>2018</b> , 96, 1045-1058	33
1103	High diversity and variability in the bacterial microbiota of the coffee berry borer (Coleoptera: Curculionidae), with emphasis on Wolbachia. <b>2018</b> , 125, 528-543	8
1102	Antibiotic-mediated bacteriome depletion in Apc mice is associated with reduction in mucus-producing goblet cells and increased colorectal cancer progression. <b>2018</b> , 7, 2003-2012	28
1101	Soil Bacterial Diversity Is Associated with Human Population Density in Urban Greenspaces. <b>2018</b> , 52, 5115-5124	21
1100	Responses in the rumen microbiome of Bos taurus and indicus steers fed a low-quality rice straw diet and supplemented protein. <b>2018</b> , 96, 1032-1044	12
1099	Long-term Western diet fed apolipoprotein E-deficient rats exhibit only modest early atherosclerotic characteristics. <b>2018</b> , 8, 5416	14

1098	Feeding-Related Gut Microbial Composition Associates With Peripheral T-Cell Activation and Mucosal Gene Expression in African Infants. <b>2018</b> , 67, 1237-1246	16
1097	A Consistent and Predictable Commercial Broiler Chicken Bacterial Microbiota in Antibiotic-Free Production Displays Strong Correlations with Performance. <b>2018</b> , 84,	72
1096	Endophytic bacterial microbiome associated with leaves of genetically modified (AtAREB1) and conventional (BR 16) soybean plants. <b>2018</b> , 34, 56	5
1095	Obese Mice Losing Weight Due to trans-10,cis-12 Conjugated Linoleic Acid Supplementation or Food Restriction Harbor Distinct Gut Microbiota. <b>2018</b> , 148, 562-572	30
1094	Oral insulin does not alter gut microbiota composition of NOD mice. <b>2018</b> , 34, e3010	4
1093	A large-scale survey of the postmortem human microbiome, and its potential to provide insight into the living health condition. <b>2018</b> , 8, 5724	57
1092	Microbiome profiling of commercial pigs from farrow to finish. <b>2018</b> , 96, 1778-1794	48
1091	Fecal Microbiota Composition Drives Immune Activation in HIV-infected Individuals. <b>2018</b> , 30, 192-202	53
1090	Structure and co-occurrence patterns in microbial communities under acute environmental stress reveal ecological factors fostering resilience. <b>2018</b> , 8, 5875	75
1089	Transient influence of blood meal and natural environment on blacklegged tick bacterial communities. <b>2018</b> , 9, 563-572	21
1088	Longitudinal Effects of Supplemental Forage on the Honey Bee ( <i>Apis mellifera</i> ) Microbiota and Inter- and Intra-Colony Variability. <b>2018</b> , 76, 814-824	29
1087	Optimal extraction methods for the simultaneous analysis of DNA from diverse organisms and sample types. <b>2018</b> , 18, 557-569	35
1086	Microbiome assembly of avian eggshells and their potential as transgenerational carriers of maternal microbiota. <i>ISME Journal</i> , <b>2018</b> , 12, 1375-1388	11.9 24
1085	Bacterial density rather than diversity correlates with hatching success across different avian species. <b>2018</b> , 94,	15
1084	Taxonomic patterns in the nitrogen assimilation of soil prokaryotes. <b>2018</b> , 20, 1112-1119	22
1083	<i>Abditibacterium utsteinense</i> sp. nov., the first cultivated member of candidate phylum FBP, isolated from ice-free Antarctic soil samples. <b>2018</b> , 41, 279-290	26
1082	Methanogens Are Major Contributors to Nitrogen Fixation in Soils of the Florida Everglades. <b>2018</b> , 84,	37
1081	Predator identity more than predator richness structures aquatic microbial assemblages in <i>Sarracenia purpurea</i> leaves. <b>2018</b> , 99, 652-660	10

1080	Gut Microbial Diversity in Women With Polycystic Ovary Syndrome Correlates With Hyperandrogenism. <b>2018</b> , 103, 1502-1511	113
1079	Antibiotics Disturb the Microbiome and Increase the Incidence of Resistance Genes in the Gut of a Common Soil Collembolan. <b>2018</b> , 52, 3081-3090	93
1078	Autochthonous Bioaugmentation-Modified Bacterial Diversity of Phenanthrene Degraders in PAH-Contaminated Wastewater as Revealed by DNA-Stable Isotope Probing. <b>2018</b> , 52, 2934-2944	47
1077	Bacteria and fungi in day-old turkeys vary among companies, collection periods, and breeder flocks. <b>2018</b> , 97, 1400-1411	7
1076	MicrobiomeDB: a systems biology platform for integrating, mining and analyzing microbiome experiments. <b>2018</b> , 46, D684-D691	26
1075	Stachyose Improves Inflammation through Modulating Gut Microbiota of High-Fat Diet/Streptozotocin-Induced Type 2 Diabetes in Rats. <b>2018</b> , 62, e1700954	52
1074	Bolus Weekly Vitamin D3 Supplementation Impacts Gut and Airway Microbiota in Adults With Cystic Fibrosis: A Double-Blind, Randomized, Placebo-Controlled Clinical Trial. <b>2018</b> , 103, 564-574	51
1073	Regulation of Th17 cells by P. UF1 against systemic <i>Listeria monocytogenes</i> infection. <b>2018</b> , 9, 279-287	7
1072	Effects of bentonite Bgp35b-p on the gut microbiota of mice fed a high-fat diet. <b>2018</b> , 98, 4369-4373	8
1071	Temporal changes of the bacterial community colonizing wheat straw in the cow rumen. <b>2018</b> , 50, 1-8	12
1070	<i>Lactobacillus kunkeei</i> strains decreased the infection by honey bee pathogens <i>Paenibacillus</i> larvae and <i>Nosema ceranae</i> . <b>2018</b> , 9, 279-290	50
1069	Co-occurring Mangroves and Salt Marshes Differ in Microbial Community Composition. <b>2018</b> , 38, 497-508	23
1068	Biofilm community structure and the associated drag penalties of a groomed fouling release ship hull coating. <b>2018</b> , 34, 162-172	22
1067	Soil microbial beta-diversity is linked with compositional variation in aboveground plant biomass in a semi-arid grassland. <b>2018</b> , 423, 465-480	17
1066	The Combined Effect of Temperature and Host Clonal Line on the Microbiota of a Planktonic Crustacean. <b>2018</b> , 76, 506-517	18
1065	Associations between <i>Escherichia coli</i> O157 shedding and the faecal microbiota of dairy cows. <b>2018</b> , 124, 881-898	9
1064	Higher phylogenetic diversity prevents loss of functional diversity caused by successive drying and rewetting cycles. <b>2018</b> , 111, 1033-1045	2
1063	Microbial community shifts trigger loss of orthophosphate in wetland soils subjected to experimental warming. <b>2018</b> , 424, 351-365	6

1062	Dysbiosis of the fecal microbiota in feedlot cattle with hemorrhagic diarrhea. <b>2018</b> , 115, 123-130	26
1061	Field study reveals core plant microbiota and relative importance of their drivers. <b>2018</b> , 20, 124-140	126
1060	Symposium review: Mining metagenomic and metatranscriptomic data for clues about microbial metabolic functions in ruminants. <b>2018</b> , 101, 5605-5618	15
1059	Interactions Between Diet and the Intestinal Microbiota Alter Intestinal Permeability and Colitis Severity in Mice. <b>2018</b> , 154, 1037-1046.e2	167
1058	Comparative analyses of microbial structures and gene copy numbers in the anaerobic digestion of various types of sewage sludge. <b>2018</b> , 253, 315-322	19
1057	Characterization of a microbial community developing during refrigerated storage of vacuum packed Yao meat, a Chinese traditional food. <b>2018</b> , 90, 562-569	16
1056	Maturation of the gut microbiome and risk of asthma in childhood. <b>2018</b> , 9, 141	216
1055	Assessment of bacterial communities and activities of thermotolerant enzymes produced by bacteria indigenous to oil-bearing sandstone cores for potential application in Enhanced Oil Recovery. <b>2018</b> , 163, 295-302	13
1054	Melonet-DB, a Grand RNA-Seq Gene Expression Atlas in Melon ( <i>Cucumis melo</i> L.). <b>2018</b> , 59, e4	22
1053	The commensal microbiome is associated with anti-PD-1 efficacy in metastatic melanoma patients. <b>2018</b> , 359, 104-108	1227
1052	Greatest soil microbial diversity found in micro-habitats. <b>2018</b> , 118, 217-226	132
1051	Differences in Clinical Course, Genetics, and the Microbiome Between Familial and Sporadic Inflammatory Bowel Diseases. <b>2018</b> , 12, 525-531	16
1050	A role for the endometrial microbiome in dysfunctional menstrual bleeding. <b>2018</b> , 111, 933-943	33
1049	The Effect of Vitamin D on Intestinal Inflammation and Faecal Microbiota in Patients with Ulcerative Colitis. <b>2018</b> , 12, 963-972	52
1048	Identification of Key Bacteria Involved in the Induction of Incident Bacterial Vaginosis: A Prospective Study. <b>2018</b> , 218, 966-978	45
1047	Grapevine rootstocks shape underground bacterial microbiome and networking but not potential functionality. <b>2018</b> , 6, 3	108
1046	Correcting for 16S rRNA gene copy numbers in microbiome surveys remains an unsolved problem. <b>2018</b> , 6, 41	153
1045	Interleukin-22-deficiency and microbiota contribute to the exacerbation of <i>Toxoplasma gondii</i> -induced intestinal inflammation. <b>2018</b> , 11, 1181-1190	17

1044	Dominance of bacteria throughout coral bleaching and mortality suggests structural inflexibility of the microbiome. <b>2018</b> , 8, 2240-2252	61
1043	Pumpkin polysaccharide modifies the gut microbiota during alleviation of type 2 diabetes in rats. <b>2018</b> , 115, 711-717	64
1042	A town on fire! Integrating 16S rRNA gene amplicon analyses into an undergraduate microbiology lecture class. <b>2018</b> , 365,	3
1041	Microcystin-LR Degradation Following Copper-Based Algacide Exposures. <b>2018</b> , 229, 1	6
1040	Ketogenic diet enhances neurovascular function with altered gut microbiome in young healthy mice. <b>2018</b> , 8, 6670	115
1039	Kenaf addition has mixed effects on process performance of sequencing batch reactors treating municipal wastewater. <b>2018</b> , 4, 711-720	1
1038	Gut microbiota recovery and immune response in ampicillin-treated mice. <b>2018</b> , 118, 357-364	9
1037	Allometry and Ecology of the Bilaterian Gut Microbiome. <b>2018</b> , 9,	20
1036	Frontline Science: Microbiota reconstitution restores intestinal integrity after cisplatin therapy. <b>2018</b> , 103, 799-805	34
1035	Isolation and Identification of the Follicular Microbiome: Implications for Acne Research. <b>2018</b> , 138, 2033-2040	36
1034	Effects of indigenous soil cyanobacteria on seed germination and seedling growth of arid species used in restoration. <b>2018</b> , 429, 91-100	32
1033	Oral Antibiotic Treatment of Mice Exacerbates the Disease Severity of Multiple Flavivirus Infections. <b>2018</b> , 22, 3440-3453.e6	65
1032	Use of an improved high-throughput absolute abundance quantification method to characterize soil bacterial community and dynamics. <b>2018</b> , 633, 360-371	25
1031	Changes in Larval Mosquito Microbiota Reveal Non-target Effects of Insecticide Treatments in Hurricane-Created Habitats. <b>2018</b> , 76, 719-728	7
1030	Differential immune responses and microbiota profiles in children with autism spectrum disorders and co-morbid gastrointestinal symptoms. <b>2018</b> , 70, 354-368	102
1029	Bacterial communities in mining soils and surrounding areas under regeneration process in a former ore mine. <b>2018</b> , 49, 489-502	23
1028	GraftM: a tool for scalable, phylogenetically informed classification of genes within metagenomes. <b>2018</b> , 46, e59	74
1027	Analysis of paper foxing by newly available omics techniques. <b>2018</b> , 132, 157-165	14

1026	Impact of parenteral antimicrobial administration on the structure and diversity of the fecal microbiota of growing pigs. <b>2018</b> , 118, 220-229	14
1025	Gut Microbiota Offers Universal Biomarkers across Ethnicity in Inflammatory Bowel Disease Diagnosis and Infliximab Response Prediction. <b>2018</b> , 3,	115
1024	Spatial scale affects the relative role of stochasticity versus determinism in soil bacterial communities in wheat fields across the North China Plain. <b>2018</b> , 6, 27	152
1023	Community structure and distribution of benthic cyanobacteria in Antarctic lacustrine microbial mats. <b>2018</b> , 94,	9
1022	LysMD3 is a type II membrane protein without an role in the response to a range of pathogens. <b>2018</b> , 293, 6022-6038	5
1021	Oyster microbial communities and implications for chalky deposit formation. <b>2018</b> , 816, 121-135	7
1020	Influence of fecal collection conditions and 16S rRNA gene sequencing at two centers on human gut microbiota analysis. <b>2018</b> , 8, 4386	26
1019	Physiological Regulation of Drug Metabolism and Transport: Pregnancy, Microbiome, Inflammation, Infection, and Fasting. <b>2018</b> , 46, 503-513	22
1018	Subgingival microbiota in individuals with severe chronic periodontitis. <b>2018</b> , 51, 226-234	48
1017	Inflammatory phenotypes in patients with severe asthma are associated with distinct airway microbiology. <b>2018</b> , 141, 94-103.e15	159
1016	Assessment of bacterial community composition, methanotrophic and nitrogen-cycling bacteria in three soils with different biochar application rates. <b>2018</b> , 18, 148-158	52
1015	Solid-State Co-digestion of NaOH-Pretreated Corn Straw and Chicken Manure Under Mesophilic Condition. <b>2018</b> , 9, 1027-1035	15
1014	Diet Versus Phylogeny: a Comparison of Gut Microbiota in Captive Colobine Monkey Species. <b>2018</b> , 75, 515-527	63
1013	Lung Microbiota Is Related to Smoking Status and to Development of Acute Respiratory Distress Syndrome in Critically Ill Trauma Patients. <b>2018</b> , 197, 621-631	65
1012	Antibiotic exposure and interpersonal variance mask the effect of ivacaftor on respiratory microbiota composition. <b>2018</b> , 17, 50-56	26
1011	Bifidobacterium longum BB536 alleviated upper respiratory illnesses and modulated gut microbiota profiles in Malaysian pre-school children. <b>2018</b> , 9, 61-70	27
1010	A comparison of bioinformatic approaches for 16S rRNA gene profiling of food bacterial microbiota. <b>2018</b> , 265, 9-17	21
1009	Lower airway microbiota and mycobiota in children with severe asthma. <b>2018</b> , 141, 808-811.e7	26

1008	Gut Microbiota Perturbations in Reactive Arthritis and Postinfectious Spondyloarthritis. <b>2018</b> , 70, 242-254	57
1007	Supplementation of pancreatic digestive enzymes alters the composition of intestinal microbiota in mice. <b>2018</b> , 495, 273-279	26
1006	Excess labile carbon promotes the expression of virulence factors in coral reef bacterioplankton. <i>ISME Journal</i> , <b>2018</b> , 12, 59-76	11.9 34
1005	Unbiased Taxonomic Annotation of Metagenomic Samples. <b>2018</b> , 25, 348-360	8
1004	Dietary copper-fructose interactions alter gut microbial activity in male rats. <b>2018</b> , 314, G119-G130	25
1003	The plant circadian clock influences rhizosphere community structure and function. <i>ISME Journal</i> , <b>2018</b> , 12, 400-410	11.9 47
1002	-dominated vaginal microbiota is associated with increased susceptibility to infection in Dutch women: a case-control study. <b>2018</b> , 94, 117-123	58
1001	Maternal obesity is associated with gut microbial metabolic potential in offspring during infancy. <b>2018</b> , 74, 159-169	24
1000	Mucosa-associated microbiota dysbiosis in colitis associated cancer. <b>2018</b> , 9, 131-142	83
999	Antibiotic-induced microbiota perturbation causes gut endocannabinoidome changes, hippocampal neuroglial reorganization and depression in mice. <b>2018</b> , 67, 230-245	138
998	Soil Microbiomes Associated with Verticillium Wilt-Suppressive Broccoli and Chitin Amendments are Enriched with Potential Biocontrol Agents. <b>2018</b> , 108, 31-43	45
997	High-fat, high-fructose, high-cholesterol feeding causes severe NASH and cecal microbiota dysbiosis in juvenile Ossabaw swine. <b>2018</b> , 314, E78-E92	44
996	DNA Methylation and Transcription Patterns in Intestinal Epithelial Cells From Pediatric Patients With Inflammatory Bowel Diseases Differentiate Disease Subtypes and Associate With Outcome. <b>2018</b> , 154, 585-598	126
995	Alterations in ruminal bacterial populations at induction and recovery from diet-induced milk fat depression in dairy cows. <b>2018</b> , 101, 295-309	29
994	Metagenomics-guided analysis of microbial chemolithoautotrophic phosphite oxidation yields evidence of a seventh natural CO fixation pathway. <b>2018</b> , 115, E92-E101	61
993	Microbial communities in natural rubber coagula during maturation: impacts on technological properties of dry natural rubber. <b>2018</b> , 124, 444-456	6
992	Homogenization of lake cyanobacterial communities over a century of climate change and eutrophication. <b>2018</b> , 2, 317-324	82
991	Temperature-Phased Conversion of Acid Whey Waste Into Medium-Chain Carboxylic Acids via Lactic Acid: No External e-Donor. <b>2018</b> , 2, 280-295	84

990	Biological crusts of serpentine and non-serpentine soils from the Barberton Greenstone Belt of South Africa. <b>2018</b> , 33, 629-640	9
989	Temporal characterization and statistical analysis of flowback and produced waters and their potential for reuse. <b>2018</b> , 619-620, 654-664	50
988	Production of biogenic manganese oxides coupled with methane oxidation in a bioreactor for removing metals from wastewater. <b>2018</b> , 130, 224-233	32
987	Hyperthermophilic Composting Accelerates the Removal of Antibiotic Resistance Genes and Mobile Genetic Elements in Sewage Sludge. <b>2018</b> , 52, 266-276	185
986	Spatially distinct, temporally stable microbial populations mediate biogeochemical cycling at and below the seafloor in hydrothermal vent fluids. <b>2018</b> , 20, 769-784	36
985	Gut Microbiota in Human Systemic Lupus Erythematosus and a Mouse Model of Lupus. <b>2018</b> , 84,	125
984	Diversity and dynamics of lactic acid bacteria in Atole agrio, a traditional maize-based fermented beverage from South-Eastern Mexico, analysed by high throughput sequencing and culturing. <b>2018</b> , 111, 385-399	25
983	Have you tried spermine? A rapid and cost-effective method to eliminate dextran sodium sulfate inhibition of PCR and RT-PCR. <b>2018</b> , 144, 1-7	47
982	Impact of <i>Lactobacillus curvatus</i> 54M16 on microbiota composition and growth of <i>Listeria monocytogenes</i> in fermented sausages. <b>2018</b> , 72, 1-15	29
981	Exposure of soil collembolans to microplastics perturbs their gut microbiota and alters their isotopic composition. <b>2018</b> , 116, 302-310	260
980	Droplet distribution and airborne bacteria in an experimental shower unit. <b>2018</b> , 130, 47-57	14
979	Analysis of Bacterial and Fungal Nucleic Acid in Canine Sterile Granulomatous and Pyogranulomatous Dermatitis and Panniculitis. <b>2018</b> , 55, 124-132	5
978	Detecting macroecological patterns in bacterial communities across independent studies of global soils. <b>2018</b> , 3, 189-196	86
977	Enrichment of lignocellulose-degrading microbial communities from natural and engineered methanogenic environments. <b>2018</b> , 102, 1035-1043	15
976	Variation in range size and dispersal capabilities of microbial taxa. <b>2018</b> , 99, 322-334	34
975	<i>Wolbachia</i> infection alters the relative abundance of resident bacteria in adult <i>Aedes aegypti</i> mosquitoes, but not larvae. <b>2018</b> , 27, 297-309	38
974	Specificities of the intestinal microbiota in patients with inflammatory bowel disease and <i>Clostridium difficile</i> infection. <b>2018</b> , 9, 55-60	49
973	The influence of in vitro pectin fermentation on the human fecal microbiome. <b>2018</b> , 8, 98	41



972	Effects of Attached and Suspended Biomass on the Dynamics of the Microbial Community and Wastewater Characteristics in Sewers. <b>2018</b> , 16, 233-244	5
971	Predominance of methanogens over methanotrophs in rewetted fens characterized by high methane emissions. <b>2018</b> , 15, 6519-6536	24
970	Comparing Two Common DNA Extraction Kits for the Characterization of Symbiotic Microbial Communities from Ascidian Tissue. <b>2018</b> , 33, 435-439	5
969	Long-range transported bioaerosols captured in snow cover on Mount Tateyama, Japan: Impacts of Asian-dust events on airborne bacterial dynamics relating to ice-nucleation activities. <b>2018</b> ,	
968	The all-intracellular order Legionellales is unexpectedly diverse, globally distributed and lowly abundant. <b>2018</b> , 94,	7
967	Quantitative Genetics of the Maize Leaf Microbiome. <b>2018</b> , 2, 208-224	65
966	Spatial and Seasonal Variability of Reef Bacterial Communities in the Upper Gulf of Thailand. <b>2018</b> , 5,	13
965	Characterization of the Microbiota in Air- or Vacuum-Packed Crisp Grass Carp ( <i>Ctenopharyngodon idella</i> C. et V.) Fillets by 16S rRNA PCR-Denaturing Gradient Gel Electrophoresis and High-Throughput Sequencing. <b>2018</b> , 81, 1022-1029	4
964	Using Core Genome Alignments To Assign Bacterial Species. <b>2018</b> , 3,	37
963	Host species, pathogens and disease associated with divergent nasal microbial communities in tortoises. <b>2018</b> , 5, 181068	3
962	Similar Levels of Antimicrobial Resistance in U.S. Food Service Ground Beef Products with and without a "Raised without Antibiotics" Claim. <b>2018</b> , 81, 2007-2018	21
961	Next-generation sequencing analysis reveals high bacterial diversity in wild venomous and non-venomous snakes from India. <b>2018</b> , 24, 41	6
960	Culture-independent Profiling of the Fecal Microbiome to Identify Microbial Species Associated with a Diarrheal Outbreak in Immunocompromised Mice. <b>2018</b> , 68, 261-268	2
959	Desert plant bacteria reveal host influence and beneficial plant growth properties. <b>2018</b> , 13, e0208223	46
958	Impact of anaerobic co-digestion between sewage sludge and carbon-rich organic waste on microbial community resilience. <b>2018</b> , 4, 1956-1965	12
957	Loss of deep roots limits biogenic agents of soil development that are only partially restored by decades of forest regeneration. <b>2018</b> , 6,	21
956	Intergenerational effects of macroalgae on a reef coral: major declines in larval survival but subtle changes in microbiomes. <b>2018</b> , 589, 97-114	14
955	The fallopian tube microbiome: implications for reproductive health. <b>2018</b> , 9, 21541-21551	23

954	Microbiome shifts with onset and progression of Sea Star Wasting Disease revealed through time course sampling. <b>2018</b> , 8, 16476	17
953	An exploration of Prevotella-rich microbiomes in HIV and men who have sex with men. <b>2018</b> , 6, 198	64
952	Taxa: An R package implementing data standards and methods for taxonomic data. <b>2018</b> , 7, 272	7
951	Coral metabolite gradients affect microbial community structures and act as a disease cue. <b>2018</b> , 1, 184	15
950	Land Use Influences Antibiotic Resistance in the Microbiome of Soil Collembolans Orchesellides sinensis. <b>2018</b> , 52, 14088-14098	30
949	Stochastic and Deterministic Effects of a Moisture Gradient on Soil Microbial Communities in the McMurdo Dry Valleys of Antarctica. <b>2018</b> , 9, 2619	17
948	Coral-associated bacteria demonstrate phyllosymbiosis and cophylogeny. <b>2018</b> , 9, 4921	118
947	The Microbial Metabolite Butyrate Stimulates Bone Formation via T Regulatory Cell-Mediated Regulation of WNT10B Expression. <b>2018</b> , 49, 1116-1131.e7	144
946	Evaluating the Information Content of Shallow Shotgun Metagenomics. <b>2018</b> , 3,	175
945	Bacterial Community Composition of Throughfall and Stemflow. <b>2018</b> , 1,	7
944	Commensal bacteria contribute to insulin resistance in aging by activating innate B1a cells. <b>2018</b> , 10,	70
943	Identifying and Predicting Novelty in Microbiome Studies. <b>2018</b> , 9,	21
942	Targeting the gut microbiome to treat the osteoarthritis of obesity. <b>2018</b> , 3,	104
941	Lysozyme-rich milk mitigates effects of malnutrition in a pig model of malnutrition and infection. <b>2018</b> , 120, 1131-1148	5
940	The Microbial Diversity of Caves. <b>2018</b> , 69-90	9
939	Stability and resilience of the intestinal microbiota in children in daycare - a 12 month cohort study. <b>2018</b> , 18, 223	10
938	Phosphorus-mineralizing Communities Reflect Nutrient-Rich Characteristics in Japanese Arable Andisols. <b>2018</b> , 33, 282-289	11
937	Both the intratumoral immune and microbial microenvironment are linked to recurrence in human colon cancer: results from a prospective, multicenter nodal ultrastaging trial. <b>2018</b> , 9, 23564-23576	1

936	A 12-wk whole-grain wheat intervention protects against hepatic fat: the Graandioos study, a randomized trial in overweight subjects. <b>2018</b> , 108, 1264-1274	30
935	The Dietary Intervention of Transgenic Low-Gliadin Wheat Bread in Patients with Non-Celiac Gluten Sensitivity (NCGS) Showed No Differences with Gluten Free Diet (GFD) but Provides Better Gut Microbiota Profile. <b>2018</b> , 10,	19
934	New Insights into Human Nostril Microbiome from the Expanded Human Oral Microbiome Database (eHOMD): a Resource for the Microbiome of the Human Aerodigestive Tract. <b>2018</b> , 3,	184
933	Summer shifts of bacterial communities associated with the invasive brown seaweed <i>Sargassum muticum</i> are location and tissue dependent. <b>2018</b> , 13, e0206734	31
932	Possible association of Firmicutes in the gut microbiota of patients with major depressive disorder. <b>2018</b> , 14, 3329-3337	93
931	Host-targeted niclosamide inhibits <i>C. difficile</i> virulence and prevents disease in mice without disrupting the gut microbiota. <b>2018</b> , 9, 5233	26
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212	Gut microbiota on admission as predictive biomarker for acute necrotizing pancreatitis. 13,	0
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208	The gastrointestinal and microbiome impact of a resistant starch blend from potato, banana, and apple fibers: A randomized clinical trial using smart caps. 9,	1
207	Integrative analysis of the mouse fecal microbiome and metabolome reveal dynamic phenotypes in the development of colorectal cancer. 13,	0
206	Comparison of 16S rRNA Gene Primers on Studying Microbial Community Composition in Bottom Water and Sediment of Artificial Reefs in Laoshan Bay, China. <b>2022</b> , 21, 1313-1322	0
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204	Bacteria communities and water quality parameters in riverine water and sediments near wastewater discharges. <b>2022</b> , 9,	0
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201	Western diet-induced shifts in the maternal microbiome are associated with altered microRNA expression in baboon placenta and fetal liver. 3,	0
200	Differences in Intestinal Microbial Composition between Red Claw Crayfish ( <i>Cherax quadricarinatus</i> ) and Red Swamp Crayfish ( <i>Procambarus clarkii</i> ) Cultured in Pond. <b>2022</b> , 7, 241	0
199	Ruminal Bacterial Community Successions in Response to Monensin Supplementation in Goats. <b>2022</b> , 12, 2291	0

198	Modulatory effect of <i>Gracilaria gracilis</i> on European seabass gut microbiota community and its functionality. <b>2022</b> , 12,	0
197	Alignment-free microbiome-based classification of fresh produce safety and quality.	0
196	Altered microbial biogeography in an innate model of colitis. <b>2022</b> , 14,	0
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194	Improved assessments of bulk milk microbiota composition via sample preparation and DNA extraction methods. <b>2022</b> , 17, e0267992	0
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191	Vaginal microbial shifts are unaffected by oral pre-exposure prophylaxis in South African women. <b>2022</b> , 12,	0
190	Longitudinal disease-associated gut microbiome differences in infants with food protein-induced allergic proctocolitis. <b>2022</b> , 10,	0
189	Feeding up to 91% concentrate to Holstein and Jersey dairy cows: Effects on enteric methane emission, rumen fermentation and bacterial community, digestibility, production, and feeding behavior. <b>2022</b> ,	1
188	Improvement of growth, yield and diversity of bacterial community of rice by the application of probiotic <i>Paraburkholderia</i> and <i>Delftia</i> .	0
187	Suppression of Methicillin-Resistant <i>Staphylococcus aureus</i> and Reduction of Other Bacteria by Black Soldier Fly Larvae Reared on Potato Substrate.	0
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182	Integrating current analyses of the breast cancer microbiome.	0
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161	Alignment-free Comparison of Metagenomics Sequences via Approximate String Matching.	0
160	Detection and Monitoring of Corrosive Oilfield Microorganisms via Novel Biomarker Technologies. <b>2022</b> ,	0
159	The co-occurrence network patterns and keystone species of microbial communities in cattle manure-corn straw composting.	0
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157	Artificial intelligence-based personalized diet: A pilot clinical study for irritable bowel syndrome. <b>2022</b> , 14,	1
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149	Hypothalamic integrity is necessary for sustained weight loss after bariatric surgery: A prospective, cross-sectional study. <b>2023</b> , 138, 155341	0
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147	Gut microbiota impairment following graphene oxide exposure is associated to physiological alterations in <i>Xenopus laevis</i> tadpoles. <b>2023</b> , 857, 159515	0
146	Precision Nutrition from the View of the Gut Microbiome. <b>2022</b> , 67-96	0
145	Responses of various carbon to nitrogen ratios to microbial communities, kinetics, and nitrogen metabolic pathways in aerobic granular sludge reactor. <b>2023</b> , 367, 128225	1

144	Unravelling Diabetes-related Pathways Using 16S rRNA Microbiome Data from Human Gut and Nasal Cavity. <b>2022</b> ,	0
143	Genetic variations and microbiome of the poultry red mite <i>Dermanyssus gallinae</i> . 13,	0
142	Effect of two-week red beetroot juice consumption on modulation of gut microbiota in healthy human volunteers in a pilot study. <b>2022</b> , 134989	1
141	Spatial self-segregation of pioneer cyanobacterial species drives microbiome organization in biocrusts. <b>2022</b> , 2,	0
140	Meta-analysis of 16S rRNA microbial data identified alterations of the gut microbiota in COVID-19 patients during the acute and recovery phases. <b>2022</b> , 22,	2
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138	Early Biofilm Accumulation in Freshwater Environments on Different Types of Plastic. <b>2022</b> , 83-105	0
137	Dysbiosis and reduced small intestinal function are required to induce intestinal insufficiency in mice.	0
136	Exploring the alterations and function of skin microbiome mediated by ionizing radiation injury. 12,	0
135	Distribution and phylogeny of mercury methylation, demethylation, and reduction genes in the Seto Inland Sea of Japan. <b>2023</b> , 186, 114381	0
134	Emergence of hydrocarbon-degrading bacteria in crude oil-contaminated soil in a hyperarid ecosystem: Effect of phosphate addition and augmentation with nitrogen-fixing cyanobacteria on oil bioremediation. <b>2023</b> , 178, 105556	0
133	Polyphenol-Rich Liupao Tea Extract Prevents High-Fat Diet-Induced MAFLD by Modulating the Gut Microbiota. <b>2022</b> , 14, 4930	1
132	Standardized multi-omics of Earth's microbiomes reveals microbial and metabolite diversity. <b>2022</b> , 7, 2128-2150	0
131	Heterogeneous selection dominated the temporal variation of the planktonic prokaryotic community during different seasons in the coastal waters of Bohai Bay. <b>2022</b> , 12,	0
130	Challenges of Comparing Marine Microbiome Community Composition Data Provided by Different Commercial Laboratories and Classification Databases. <b>2022</b> , 14, 3855	0
129	Effect of temperature variations in anaerobic fluidized membrane bioreactor: membrane fouling and microbial community dynamics assessment.	0
128	Morphine mediated neutrophil infiltration in intestinal tissue play essential role in histological damage and microbial dysbiosis. <b>2022</b> , 14,	1
127	Diet standardization reduces intra-individual microbiome variation. <b>2022</b> , 14,	0

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- 125 More than *Mycobacterium tuberculosis*: site-of-disease microbial communities, and their functional and clinical profiles in tuberculous lymphadenitis. *thoraxjnl-2022-219103* ○
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- 119 Effects of *Lactobacillus plantarum* and *Pediococcus acidilactici* co-fermented feed on growth performance and gut microbiota of nursery pigs. 9, 1
- 118 Elevated inflammatory fecal immune factors in men who have sex with men with HIV associate with microbiome composition and gut barrier function. 13, 1
- 117 Gut microbiome composition is similar between pregnant women with excess body fat with healthy and less healthy dietary intake patterns. 1
- 116 Phagotrophic protist-mediated control of *Polymyxa graminis* in the wheat rhizosphere. ○
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108	Antimicrobial Activity of Tannic Acid In Vitro and Its Protective Effect on Mice against <i>Clostridioides difficile</i> .	0
107	Gut microbiota-mediated nucleotide synthesis attenuates the response to neoadjuvant chemoradiotherapy in rectal cancer. <b>2022</b> ,	0
106	The gut microbiota and depressive symptoms across ethnic groups. <b>2022</b> , 13,	1
105	Gut microbiota profiling varied during colorectal cancer development in mouse. <b>2022</b> , 23,	0
104	Taxonomic Profiling of Microbes in Glyphosate-Treated Sediment Microcosms.	0
103	Multi-amplicon microbiome data analysis pipelines for mixed orientation sequences using QIIME2: Assessing reference database, variable region and pre-processing bias in classification of mock bacterial community samples. <b>2023</b> , 18, e0280293	0
102	Naso-oropharyngeal microbiome from breast cancer patients diagnosed with COVID-19. 13,	0
101	Microbiota-dependent proteolysis of gluten subverts diet-mediated protection against type 1 diabetes. <b>2023</b> ,	0
100	Longitudinal, Multi-Platform Metagenomics Yields a High-Quality Genomic Catalog and Guides an In Vitro Model for Cheese Communities.	0
99	Oropharyngeal, proximal colonic, and vaginal microbiomes of healthy Korean native black pig gilts. <b>2023</b> , 23,	0
98	<i>Akkermansia muciniphila</i> counteracts the deleterious effects of dietary emulsifiers on microbiota and host metabolism. <i>gutjnl-2021-326835</i>	0
97	Severe, short-term sleep restriction reduces gut microbiota community richness but does not alter intestinal permeability in healthy young men. <b>2023</b> , 13,	0
96	Fermented table olives from Cyprus: Microbiota profile of three varieties from different regions through metabarcoding sequencing. 13,	0
95	Machine learning and network analysis of the gut microbiome from patients with schizophrenia and non-psychiatric subject controls reveal behavioral risk factors and bacterial interactions. <b>2023</b> , 251, 49-58	0
94	Microbial communities on eelgrass ( <i>Zostera marina</i> ) thriving in Tokyo Bay and the possible source of leaf-attached microbes. 13,	0
93	Microbial community composition and function in an urban waterway with combined sewer overflows before and after implementation of a stormwater storage pipe. 11, e14684	0
92	Diversity and structure of bacterial and archaeal communities associated with the vulnerable sponge <i>Halichondria cebimarensis</i> .	0
91	Epiphytic Microbiome of Alvarinho Wine Grapes From Different Geographic Regions in Portugal. <b>2023</b> , 12, 146	0

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- 89 Association between microbial community composition and quality indicators of strong-flavor Daqu of different producing regions in China. **2023**, 21, 82-92 ○
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