

Profiling of complex microbial populations by denaturing gradient temperature
analysis of polymerase chain reaction-amplified genes

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Citation Report

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2010	Scratching the surface of the rare biosphere with ribosomal sequence tag primers. <i>FEMS Microbiology Letters</i> , 2008, 283, 146-153.	0.7	11
2011	Linkage of microbial ecology to phenotype: correlation of rumen microbial ecology to cattle's feed efficiency. <i>FEMS Microbiology Letters</i> , 2008, 288, 85-91.	0.7	251
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2013	Does Liebig's law of the minimum scale up from species to communities?. <i>Oikos</i> , 2008, 117, 1741-1751.	1.2	169
2014	A strain of <i>Lactobacillus plantarum</i> affects segmented filamentous bacteria in the intestine of immunosuppressed mice. <i>FEMS Microbiology Ecology</i> , 2008, 63, 65-72.	1.3	35
2015	Development and application of a PCR-denaturing gradient gel electrophoresis tool to study the diversity of Nitrobacter-like nxrA sequences in soil. <i>FEMS Microbiology Ecology</i> , 2008, 63, 261-271.	1.3	80
2016	Covariation between zooplankton community composition and cyanobacterial community dynamics in Lake Blaarmeersen (Belgium). <i>FEMS Microbiology Ecology</i> , 2008, 63, 222-237.	1.3	17
2017	Planktonic bacteria and fungi are selectively eliminated by exposure to marine macroalgae in close proximity. <i>FEMS Microbiology Ecology</i> , 2008, 63, 283-291.	1.3	57
2018	Spatiotemporal heterogeneity of plankton communities in Lake Donghu, China, as revealed by PCR-denaturing gradient gel electrophoresis and its relation to biotic and abiotic factors. <i>FEMS Microbiology Ecology</i> , 2008, 63, 328-337.	1.3	41
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2026	Evaluation of terminal-restriction fragment length polymorphism analysis in contrasting marine environments. <i>FEMS Microbiology Ecology</i> , 2008, 65, 169-178.	1.3	66
2027	Acclimation of subsurface microbial communities to mercury. <i>FEMS Microbiology Ecology</i> , 2008, 65, 145-155.	1.3	16
2028	Molecular analysis of bacterial community succession during prolonged compost curing. <i>FEMS Microbiology Ecology</i> , 2008, 65, 133-144.	1.3	132
2029	Prokaryotic diversity in Tuz Lake, a hypersaline environment in Inland Turkey. <i>FEMS Microbiology Ecology</i> , 2008, 65, 474-483.	1.3	90
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2031	Changes in abundance of <i>Lactobacillus</i> spp. and <i>Streptococcus suis</i> in the stomach, jejunum and ileum of piglets after weaning. <i>FEMS Microbiology Ecology</i> , 2008, 66, 546-555.	1.3	104
2032	Monitoring bacterial and archaeal community shifts in a mesophilic anaerobic batch reactor treating a high-strength organic wastewater. <i>FEMS Microbiology Ecology</i> , 2008, 65, 544-554.	1.3	90
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2034	Spatial heterogeneity in sediment-associated bacterial and eukaryotic communities in a landfill leachate-contaminated aquifer. <i>FEMS Microbiology Ecology</i> , 2008, 65, 534-543.	1.3	32
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2036	Evaluation of PCR primers for universal <i>nifH</i> gene targeting and for assessment of transcribed <i>nifH</i> pools in roots of <i>Oryza longistaminata</i> with and without low nitrogen input. <i>FEMS Microbiology Ecology</i> , 2008, 65, 220-228.	1.3	33
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2883	Novel green sulfur bacteria phylotypes detected in saline environments: ecophysiological characters versus phylogenetic taxonomy. <i>Antonie Van Leeuwenhoek</i> , 2010, 97, 419-431.	0.7	3
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2988	Municipal landfill leachate nitrification in RBC biofilm – Process efficiency and molecular analysis of microbial structure. <i>Bioresource Technology</i> , 2010, 101, 3400-3405.	4.8	47
2989	Evaluation of performance and community dynamics of microorganisms during treatment of distillery spent wash in a three stage bioreactor. <i>Bioresource Technology</i> , 2010, 101, 4296-4305.	4.8	38
2990	Structure of the bacterial community in a biofilter during dimethyl sulfide (DMS) removal processes. <i>Bioresource Technology</i> , 2010, 101, 7165-7168.	4.8	23
2991	Landfill leachate pollutant removal performance of a novel biofilter packed with mixture medium. <i>Bioresource Technology</i> , 2010, 101, 7754-7760.	4.8	37
2992	Qualitative and quantitative assessment of microbial community in batch anaerobic digestion of secondary sludge. <i>Bioresource Technology</i> , 2010, 101, 9461-9470.	4.8	144
2993	Batch kinetics of ferrous iron oxidation by <i>Leptospirillum ferriphilum</i> at moderate to high total iron concentration. <i>Biochemical Engineering Journal</i> , 2010, 50, 54-62.	1.8	25
2994	Electrochemical activity and bacterial diversity of natural marine biofilm in laboratory closed-systems. <i>Bioelectrochemistry</i> , 2010, 78, 30-38.	2.4	38
2995	Towards implementation of a benthic microbial fuel cell in lake Furnas (Azores): Phylogenetic affiliation and electrochemical activity of sediment bacteria. <i>Bioelectrochemistry</i> , 2010, 78, 67-71.	2.4	47
2996	Identification of fungi associated with municipal compost using DNA-based techniques. <i>Bioresource Technology</i> , 2010, 101, 1021-1027.	4.8	87
2997	Microbial fuel cells operating on mixed fatty acids. <i>Bioresource Technology</i> , 2010, 101, 1233-1238.	4.8	188
2998	Rate determination and distribution of anammox activity in activated sludge treating swine wastewater. <i>Bioresource Technology</i> , 2010, 101, 2685-2690.	4.8	42

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2999	Utilising bacterial communities associated with digested piggery effluent as a primary food source for the batch culture of <i>Moina australiensis</i> . <i>Bioresource Technology</i> , 2010, 101, 3371-3378.	4.8	17
3000	Assessment of toxicity of tetrahydrofuran on the microbial community in activated sludge. <i>Bioresource Technology</i> , 2010, 101, 5213-5221.	4.8	52
3001	Field scale molecular analysis for the monitoring of bacterial community structures during on-site diesel bioremediation. <i>Bioresource Technology</i> , 2010, 101, 5235-5241.	4.8	11
3002	Microbial community dynamics associated with biomass granulation in low-temperature (15°C) anaerobic wastewater treatment bioreactors. <i>Bioresource Technology</i> , 2010, 101, 6336-6344.	4.8	37
3003	The effect of organic loading on bacterial community composition of membrane biofilms in a submerged polyvinyl chloride membrane bioreactor. <i>Bioresource Technology</i> , 2010, 101, 6601-6609.	4.8	67
3004	Microbial communities involved in the bioremediation of an aged recalcitrant hydrocarbon polluted soil by using organic amendments. <i>Bioresource Technology</i> , 2010, 101, 6916-6923.	4.8	89
3005	Characterization and biotechnological potential of petroleum-degrading bacteria isolated from oil-contaminated soils. <i>Bioresource Technology</i> , 2010, 101, 8452-8456.	4.8	114
3006	Stable aerobic granules for continuous-flow reactors: Precipitating calcium and iron salts in granular interiors. <i>Bioresource Technology</i> , 2010, 101, 8051-8057.	4.8	102
3007	Treatment of a BTo-X-contaminated gas stream with a biotrickling filter inoculated with microbes bound to a wheat bran/red wood powder/diatomaceous earth carrier. <i>Bioresource Technology</i> , 2010, 101, 8067-8073.	4.8	41
3008	Characterization and spatial distribution of bacterial communities within passively aerated cattle manure composting piles. <i>Bioresource Technology</i> , 2010, 101, 9631-9637.	4.8	65
3009	Chemical and microbial changes during autothermal thermophilic aerobic digestion (ATAD) of sewage sludge. <i>Bioresource Technology</i> , 2010, 101, 9438-9444.	4.8	74
3010	Ecological assessment of groundwater ecosystems – Vision or illusion?. <i>Ecological Engineering</i> , 2010, 36, 1174-1190.	1.6	87
3011	Formation, physical characteristics and microbial community structure of aerobic granules in a pilot-scale sequencing batch reactor for real wastewater treatment. <i>Enzyme and Microbial Technology</i> , 2010, 46, 520-525.	1.6	178
3012	Potential to produce biohydrogen from various wastewaters. <i>Energy for Sustainable Development</i> , 2010, 14, 143-148.	2.0	103
3013	Comparison of DNA extraction kits for PCR-DGGE analysis of human intestinal microbial communities from fecal specimens. <i>Nutrition Journal</i> , 2010, 9, 23.	1.5	113
3014	Microbial characterisation and stability of a farmhouse natural fermented milk from Spain. <i>International Journal of Dairy Technology</i> , 2010, 63, 423-430.	1.3	6
3015	The bacteriology of chronic venous leg ulcer examined by culture-independent molecular methods. <i>Wound Repair and Regeneration</i> , 2010, 18, 38-49.	1.5	124
3016	<i>Tuber melanosporum</i> , when dominant, affects fungal dynamics in truffle grounds. <i>New Phytologist</i> , 2010, 185, 237-247.	3.5	77

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3017	Labile soil carbon inputs mediate the soil microbial community composition and plant residue decomposition rates. <i>New Phytologist</i> , 2010, 188, 1055-1064.	3.5	352
3018	Assessment of sample handling practices on microbial activity in sputum samples from patients with cystic fibrosis. <i>Letters in Applied Microbiology</i> , 2010, 51, 272-277.	1.0	22
3019	Determination of microbial diversity in meju, fermented cooked soya beans, using nested PCR-denaturing gradient gel electrophoresis. <i>Letters in Applied Microbiology</i> , 2010, 51, 388-394.	1.0	46
3020	Evaluation of the potential of trap plants to detect arbuscular mycorrhizal fungi using polymerase chain reaction-denaturing gradient gel electrophoresis analysis. <i>Soil Science and Plant Nutrition</i> , 2010, 56, 205-211.	0.8	10
3021	Microbial populations in various paddy soils respond differently to denitrification-inducing conditions, albeit background bacterial populations are similar. <i>Soil Science and Plant Nutrition</i> , 2010, 56, 220-224.	0.8	14
3022	Compost amendment enhances the biological properties of Andosols and improves phosphorus utilization from added rock phosphate. <i>Soil Science and Plant Nutrition</i> , 2010, 56, 607-616.	0.8	15
3023	Vertical changes in bacterial and archaeal communities with soil depth in Japanese paddy fields. <i>Soil Science and Plant Nutrition</i> , 2010, 56, 705-715.	0.8	42
3024	Molecular approaches to study the insect gut symbiotic microbiota at the "omics" age. <i>Insect Science</i> , 2010, 17, 199-219.	1.5	69
3025	Molecular analysis of intestinal microbiota of rainbow trout (<i>Oncorhynchus mykiss</i>). <i>FEMS Microbiology Ecology</i> , 2010, 71, 148-156.	1.3	87
3026	Both <i>Cycloclasticus</i> spp. and <i>Pseudomonas</i> spp. as PAH-degrading bacteria in the Seine estuary (France). <i>FEMS Microbiology Ecology</i> , 2010, 71, 137-147.	1.3	60
3027	Shifts in desulfonating bacterial communities along a soil chronosequence in the forefield of a receding glacier. <i>FEMS Microbiology Ecology</i> , 2010, 71, 208-217.	1.3	27
3028	Antibiotic effects of three strains of chrysophytes (<i>Ochromonas</i> , <i>Poterioochromonas</i>) on freshwater bacterial isolates. <i>FEMS Microbiology Ecology</i> , 2010, 71, 281-290.	1.3	42
3029	Dynamic changes in microbial community structure and function in phenol-degrading microcosms inoculated with cells from a contaminated aquifer. <i>FEMS Microbiology Ecology</i> , 2010, 71, 247-259.	1.3	17
3030	Changes in fecal microbiota of healthy dogs administered amoxicillin. <i>FEMS Microbiology Ecology</i> , 2010, 71, 313-326.	1.3	61
3031	Microbial communities in streambed sediments recovering from desiccation. <i>FEMS Microbiology Ecology</i> , 2010, 71, 374-386.	1.3	67
3032	Enrichment and cultivation of pelagic bacteria from a humic lake using phenol and humic matter additions. <i>FEMS Microbiology Ecology</i> , 2010, 72, 58-73.	1.3	100
3033	Prokaryotic functional diversity in different biogeochemical depth zones in tidal sediments of the Severn Estuary, UK, revealed by stable-isotope probing. <i>FEMS Microbiology Ecology</i> , 2010, 72, 179-197.	1.3	87
3034	Denitrification gene pools, transcription and kinetics of NO , N_2O and N_2 production as affected by soil pH. <i>FEMS Microbiology Ecology</i> , 2010, 72, 407-417.	1.3	401

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3035	Distribution, ecology and molecular identification of <i>Thioploca</i> from Danish brackish water sediments. <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	1.3	19
3036	Abundance, diversity, and activity of microbial assemblages associated with coral reef fish guts and feces. <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	1.3	113
3037	Seasonal succession and UV sensitivity of marine bacterioplankton at an Antarctic coastal site. <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	1.3	14
3038	Potential alteration of $\delta^{13}C$ paleothermometer due to selective degradation of alkenones by marine bacteria isolated from the haptophyte <i>Emiliania huxleyi</i> . <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	1.3	25
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3040	Chemosynthetic bacteria found in bivalve species from mud volcanoes of the Gulf of Cadiz. <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	1.3	29
3041	Comparative analysis of bacterioplankton assemblages from <i>Karenia brevis</i> bloom and nonbloom water on the west Florida shelf (Gulf of Mexico, USA) using 16S rRNA gene clone libraries. <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	1.3	51
3042	Effects of autochthonous microbial community on the die-off of fecal indicators in tropical beach sand. <i>FEMS Microbiology Ecology</i> , 2010, 74, 214-225.	1.3	57
3043	Structural shifts of gut microbiota as surrogate endpoints for monitoring host health changes induced by carcinogen exposure. <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	1.3	44
3044	Annual variation of <i>Microcystis</i> genotypes and their potential toxicity in water and sediment from a eutrophic reservoir. <i>FEMS Microbiology Ecology</i> , 2010, 74, 93-102.	1.3	55
3045	Archaea rather than bacteria control nitrification in two agricultural acidic soils. <i>FEMS Microbiology Ecology</i> , 2010, 74, 566-574.	1.3	346
3046	Human faecal microbiota display variable patterns of glycerol metabolism. <i>FEMS Microbiology Ecology</i> , 2010, 74, 601-611.	1.3	150
3047	Intracellular <i>Oceanospirillales</i> bacteria inhabit gills of <i>Acesta</i> bivalves. <i>FEMS Microbiology Ecology</i> , 2010, 74, 523-533.	1.3	70
3048	Functional assembly of bacterial communities with activity for the biodegradation of an organophosphorus pesticide in the rape phyllosphere. <i>FEMS Microbiology Letters</i> , 2010, 306, 135-143.	0.7	32
3049	Nested PCR for the detection of <i>Candidatus arthromitus</i> in fish. <i>FEMS Microbiology Letters</i> , 2010, 308, 35-39.	0.7	7
3050	GC-clamp primer batches yield 16S rRNA gene amplicon pools with variable GC clamps, affecting denaturing gradient gel electrophoresis profiles. <i>FEMS Microbiology Letters</i> , 2010, 312, 55-62.	0.7	20
3051	Influence of indigenous eukaryotic microbial communities on the reduction of <i>Escherichia coli</i> O157:H7 in compost slurry. <i>FEMS Microbiology Letters</i> , 2010, 313, 148-154.	0.7	11
3052	Prebiotics in aquaculture: a review. <i>Aquaculture Nutrition</i> , 2010, 16, 117-136.	1.1	532

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3054	Microbiota of yellow grouper (<i>Epinephelus awoora</i> Temminck & Schlegel, 1842) fed two different diets. <i>Aquaculture Research</i> , 2010, 41, 1778-1790.	0.9	21
3055	Analysis of bacterial diversity in the intestine of grass carp (<i>Ctenopharyngodon idellus</i>) based on 16S rDNA gene sequences. <i>Aquaculture Research</i> , 2010, 42, 47-56.	0.9	104
3056	Molecular analysis of the intestinal bacterial flora in cage-cultured adult small abalone, <i>Haliotis diversicolor</i> . <i>Aquaculture Research</i> , 2010, 41, e760-e769.	0.9	57
3057	Denaturing gradient gel electrophoresis analysis with different primers of subgingival bacterial communities under mechanical debridement. <i>Microbiology and Immunology</i> , 2010, 54, 702-706.	0.7	5
3058	Negative priming effect on mineralization in a soil free of vegetation for 80 years. <i>European Journal of Soil Science</i> , 2010, 61, 384-391.	1.8	70
3059	<i>atz</i> gene expressions during atrazine degradation in the soil drilosphere. <i>Molecular Ecology</i> , 2010, 19, 749-759.	2.0	24
3060	Diversity and temporal stability of bacterial communities in a model passerine bird, the zebra finch. <i>Molecular Ecology</i> , 2010, 19, 5531-5544.	2.0	48
3061	Metalworking fluids biodiversity characterization. <i>Journal of Applied Microbiology</i> , 2010, 108, 437-449.	1.4	54
3062	PCR-DGGE-based methodologies to assess diversity and dynamics of <i>Aeromonas</i> communities. <i>Journal of Applied Microbiology</i> , 2010, 108, 611-623.	1.4	3
3063	Identification and antimicrobial susceptibility of porcine bacteria that inhibit the growth of <i>Brachyspira hyodysenteriae</i> in vitro. <i>Journal of Applied Microbiology</i> , 2010, 108, 1271-1280.	1.4	16
3064	Assessment of survival of <i>Listeria monocytogenes</i> , <i>Salmonella</i> <i>Infantis</i> and <i>Enterococcus faecalis</i> artificially inoculated into experimental waste or compost. <i>Journal of Applied Microbiology</i> , 2010, 108, 1797-1809.	1.4	15
3065	Interactions between gut microbiota, host genetics and diet relevant to development of metabolic syndromes in mice. <i>ISME Journal</i> , 2010, 4, 232-241.	4.4	845
3066	Evolutionary divergence and biogeography of sympatric niche-differentiated bacterial populations. <i>ISME Journal</i> , 2010, 4, 488-497.	4.4	61
3067	Investigation of archaeal and bacterial diversity in fermented seafood using barcoded pyrosequencing. <i>ISME Journal</i> , 2010, 4, 1-16.	4.4	256
3068	Bacteriochlorophyll and community structure of aerobic anoxygenic phototrophic bacteria in a particle-rich estuary. <i>ISME Journal</i> , 2010, 4, 945-954.	4.4	66
3069	Novel observations of <i>Thiobacterium</i> , a sulfur-storing Gammaproteobacterium producing gelatinous mats. <i>ISME Journal</i> , 2010, 4, 1031-1043.	4.4	12
3070	Dissimilatory reduction of nitrate in seawater by a <i>Methylophaga</i> strain containing two highly divergent <i>narG</i> sequences. <i>ISME Journal</i> , 2010, 4, 1302-1313.	4.4	43

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3072	Relevance of a crenarchaeotal subcluster related to <i>Candidatus</i> Nitrosopumilus maritimus to ammonia oxidation in the suboxic zone of the central Baltic Sea. <i>ISME Journal</i> , 2010, 4, 1496-1508.	4.4	110
3073	Molecular analysis of high-affinity methane-oxidizing enrichment cultures isolated from a forest biocenosis and agrocenoses. <i>Microbiology</i> , 2010, 79, 106-114.	0.5	22
3074	Multiple copies of 16S rRNA gene affect the restriction patterns and DGGE profile revealed by analysis of genome database. <i>Microbiology</i> , 2010, 79, 655-662.	0.5	14
3075	Phylogenetic composition of enrichment cultures of thermophilic prokaryotes reducing poorly crystalline Fe(III) oxide with and without direct contact between the cells and mineral. <i>Microbiology</i> , 2010, 79, 663-671.	0.5	2
3076	Diversity of the Predominant Spoilage Bacteria in Water-Boiled Salted Duck during Storage. <i>Journal of Food Science</i> , 2010, 75, M317-21.	1.5	17
3077	Temperature and Bacterial Profile of Post Chill Poultry Carcasses Stored in Processing Combo Held at Room Temperature. <i>Journal of Food Science</i> , 2010, 75, M515-20.	1.5	13
3078	Reduction of rare soil microbes modifies plant-herbivore interactions. <i>Ecology Letters</i> , 2010, 13, 292-301.	3.0	176
3079	Dynamics of marine bacterial and phytoplankton populations using multiplex liquid bead array technology. <i>Environmental Microbiology</i> , 2010, 12, 975-989.	1.8	28
3080	Karst pools in subsurface environments: collectors of microbial diversity or temporary residence between habitat types. <i>Environmental Microbiology</i> , 2010, 12, 1061-1074.	1.8	55
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3082	Singlet oxygen, a neglected but important environmental factor: short-term and long-term effects on bacterioplankton composition in a humic lake. <i>Environmental Microbiology</i> , 2010, 12, 3124-3136.	1.8	69
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3085	Determination of DNA amplification conditions for quantitative assessment of basidiomycotal flora. <i>MOKUZAI HOZON (Wood Protection)</i> , 2010, 36, 200-207.	0.1	2
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3094	Physio-chemical characteristics and bacterial diversity in copper mining wastewater based on 16S rRNA gene analysis. African Journal of Biotechnology, 2010, 9, 7891-7899.	0.3	5
3095	Caprylic Acid Reduces Enteric Campylobacter Colonization in Market-Aged Broiler Chickens but Does Not Appear To Alter Cecal Microbial Populations. Journal of Food Protection, 2010, 73, 251-257.	0.8	30
3096	Microbiological and biochemical survey on the transition of fermentative processes in Fukuyama pot vinegar brewing. Journal of General and Applied Microbiology, 2010, 56, 205-211.	0.4	19
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3100	Description of <i>Francisella hispaniensis</i> sp. nov., isolated from human blood, reclassification of <i>Francisella novicida</i> (Larson et al. 1955) Olsufiev et al. 1959 as <i>Francisella tularensis</i> subsp. <i>novicida</i> comb. nov. and emended description of the genus <i>Francisella</i> . International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 1887-1896.	0.8	101
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3108	Productions Diversity of Agriculture Solidwastes Biodegraded. <i>Advanced Materials Research</i> , 2010, 113-116, 51-54.	0.3	0
3109	Microbial diversity in biofilms on water distribution pipes of different materials. <i>Water Science and Technology</i> , 2010, 61, 163-171.	1.2	167
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3111	Evaluation of repetitive extragenic palindromic-polymerase chain reaction and denatured gradient gel electrophoresis in identifying <i>Salmonella</i> serotypes isolated from processed turkeys. <i>Poultry Science</i> , 2010, 89, 1293-1300.	1.5	20
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3113	Different Atmospheric Methane-Oxidizing Communities in European Beech and Norway Spruce Soils. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3228-3235.	1.4	138
3114	Molecular Analysis of Bacterial Community DNA in Sludge Undergoing Autothermal Thermophilic Aerobic Digestion (ATAD): Pitfalls and Improved Methodology to Enhance Diversity Recovery. <i>Diversity</i> , 2010, 2, 505-526.	0.7	33
3115	MUWS (Microbiology in Urban Water Systems) – an interdisciplinary approach to study microbial communities in urban water systems. <i>Drinking Water Engineering and Science</i> , 2010, 3, 91-99.	0.8	2
3116	Ileal and Caecal Microbial Populations in Broilers Given Specific Essential Oil Blends and Probiotics in two Consecutive Grow-Outs. <i>Avian Biology Research</i> , 2010, 3, 157-169.	0.4	15
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3118	<i>Rhodobacter johrii</i> sp. nov., an endospore-producing cryptic species isolated from semi-arid tropical soils. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 2099-2107.	0.8	50
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3122	Soil Microbial Community Responses to Multiple Experimental Climate Change Drivers. <i>Applied and Environmental Microbiology</i> , 2010, 76, 999-1007.	1.4	690
3123	Primary bioreceptivity of limestones used in southern European monuments. <i>Geological Society Special Publication</i> , 2010, 331, 79-92.	0.8	22
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3126	Community Structure of Bacteria Associated with Microcystis Colonies from Cyanobacterial Blooms. Journal of Freshwater Ecology, 2010, 25, 193-203.	0.5	55
3127	Microbial succession in response to 1,4-dioxane exposure in activated sludge reactors: Effect of inoculum source and extra carbon addition. Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering, 2010, 45, 674-681.	0.9	8
3128	The Impact of <i>Spartina alterniflora</i> on the Soil Microbial Assemblages in Jiangsu Coast. , 2010, , .		1
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3452	The effect of lactic acid bacteria administration on growth, digestive enzyme activity and gut microbiota in Persian sturgeon (<i>Acipenser persicus</i>) and beluga (<i>Huso huso</i>) fry. <i>Aquaculture Nutrition</i> , 2011, 17, 488-497.	1.1	83
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3997	The application of bioflocs technology in high-intensive, zero exchange farming systems of <i>Marsupenaeus japonicus</i> . <i>Aquaculture</i> , 2012, 354-355, 97-106.	1.7	118
3998	High temporal variability in bacterial community, silicatein and hsp70 expression during the annual life cycle of <i>Hymeniacidon sinapium</i> (Demospongiae) in China's Yellow Sea. <i>Aquaculture</i> , 2012, 358-359, 262-273.	1.7	16
3999	Treatment of high ethanol concentration wastewater by biological sand filters: Enhanced COD removal and bacterial community dynamics. <i>Journal of Environmental Management</i> , 2012, 109, 54-60.	3.8	24
4000	Sustainable remediation – The application of bioremediated soil for use in the degradation of TNT chips. <i>Journal of Environmental Management</i> , 2012, 110, 69-76.	3.8	26
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4004	Improving oligonucleotide fingerprinting of rRNA genes by implementation of polony microarray technology. <i>Journal of Microbiological Methods</i> , 2012, 90, 235-240.	0.7	1
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4140	Sinus Microbiome Diversity Depletion and <i>Corynebacterium tuberculostearicum</i> Enrichment Mediates Rhinosinusitis. <i>Science Translational Medicine</i> , 2012, 4, 151ra124.	5.8	372
4141	Monitoring bacterial community structure and variability in time scale in full-scale anaerobic digesters. <i>Journal of Environmental Monitoring</i> , 2012, 14, 1893.	2.1	122
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4145	Responses of <i>Cajanus cajan</i> and rhizospheric N-cycling communities to bioinoculants. <i>Plant and Soil</i> , 2012, 358, 143-154.	1.8	18

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4280	Microbial diversity in bovine papillomatous digital dermatitis in Holstein dairy cows from upstate New York. <i>FEMS Microbiology Ecology</i> , 2012, 79, 518-529.	1.3	44
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4321	Abiotic factors influence microbial diversity in permanently cold soil horizons of a maritime-associated Antarctic Dry Valley. <i>FEMS Microbiology Ecology</i> , 2012, 82, 326-340.	1.3	85
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4424	Dynamic Assessment of the Floc Morphology, Bacterial Diversity, and Integron Content of an Activated Sludge Reactor Processing Hospital Effluent. <i>Environmental Science & Technology</i> , 2013, 47, 7909-7917.	4.6	34
4425	Microbial and functional diversity of a subterrestrial high pH groundwater associated to serpentinization. <i>Environmental Microbiology</i> , 2013, 15, 1687-1706.	1.8	136
4426	<i>Seleniivibrio woodruffii</i> gen. nov., sp. nov., a selenate- and arsenate-respiring bacterium in the Deferribacteraceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 3659-3665.	0.8	20
4427	Soil microbial community structure of rangeâ€“expanding plant species differs from coâ€“occurring natives. <i>Journal of Ecology</i> , 2013, 101, 1093-1102.	1.9	39
4428	Culture-Dependent and Independent Studies of Microbial Diversity in Highly Copper-Contaminated Chilean Marine Sediments. <i>Microbial Ecology</i> , 2013, 65, 311-324.	1.4	25
4429	Novel approach for the development of axenic microalgal cultures from environmental samples. <i>Journal of Phycology</i> , 2013, 49, 802-810.	1.0	51
4430	Polyvinyl alcohol biodegradation under denitrifying conditions. <i>International Biodeterioration and Biodegradation</i> , 2013, 84, 21-28.	1.9	53
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4432	Bioremediation of diesel-polluted soil using biostimulation as post-treatment after oxidation with Fenton-like reagents: Assays in a pilot plant. <i>Science of the Total Environment</i> , 2013, 445-446, 347-355.	3.9	92
4433	Biodegradation of aged diesel in diverse soil matrixes: impact of environmental conditions and bioavailability on microbial remediation capacity. <i>Biodegradation</i> , 2013, 24, 487-498.	1.5	42

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4436	The Diversity and Abundance of Bacteria and Oxygenic Phototrophs in Saline Biological Desert Crusts in Xinjiang, Northwest China. <i>Microbial Ecology</i> , 2013, 66, 40-48.	1.4	30
4437	Changes in microbial communities in a hybrid anaerobic reactor with organic loading rate and temperature. <i>Bioresource Technology</i> , 2013, 129, 538-547.	4.8	34
4438	Nitrification in hybrid bioreactors treating simulated domestic wastewater. <i>Journal of Applied Microbiology</i> , 2013, 115, 621-630.	1.4	11
4439	Potential mineralization and nitrification in volcanic grassland soils in Chile. <i>Soil Science and Plant Nutrition</i> , 2013, 59, 380-391.	0.8	18
4440	Flow cytometry, microscopy, and DNA analysis as complementary phytoplankton screening methods in ballast water treatment studies. <i>Journal of Applied Phycology</i> , 2013, 25, 1047-1053.	1.5	17
4441	<i>Lactobacillus acidophilus</i> CRL 1014 improved "œgut health" in the SHIME® reactor. <i>BMC Gastroenterology</i> , 2013, 13, 100.	0.8	58
4442	Soil metagenomics reveals differences under conventional and no-tillage with crop rotation or succession. <i>Applied Soil Ecology</i> , 2013, 72, 49-61.	2.1	124
4443	Acidobacterial community responses to agricultural management of soybean in Amazon forest soils. <i>FEMS Microbiology Ecology</i> , 2013, 83, 607-621.	1.3	228
4444	Specificity and temporal dynamics of complex bacteria" sponge symbiotic interactions. <i>Ecology</i> , 2013, 94, 2781-2791.	1.5	33
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4446	The steady state anaerobic digestion of <i>Laminaria hyperborea</i> " Effect of hydraulic residence on biogas production and bacterial community composition. <i>Bioresource Technology</i> , 2013, 143, 221-230.	4.8	49
4447	The Effect of Biomass Immobilization Support Material and Bed Porosity on Hydrogen Production in an Upflow Anaerobic Packed-Bed Bioreactor. <i>Applied Biochemistry and Biotechnology</i> , 2013, 170, 1348-1366.	1.4	45
4448	Performance and Microbial Diversity of Aerated Trickling Biofilter Used for Treating Cheese Industry Wastewater. <i>Applied Biochemistry and Biotechnology</i> , 2013, 170, 149-163.	1.4	4
4449	Effect of temperature and hydraulic retention time on volatile fatty acid production based on bacterial community structure in anaerobic acidogenesis using swine wastewater. <i>Bioprocess and Biosystems Engineering</i> , 2013, 36, 791-798.	1.7	26
4450	Analysis of microbial diversity in tomato paste wastewater through PCR-DGGE. <i>Biotechnology and Bioprocess Engineering</i> , 2013, 18, 111-118.	1.4	9
4451	The microbiome of North Sea copepods. <i>Helgoland Marine Research</i> , 2013, 67, 757-773.	1.3	29
4452	Aerobic biodegradation of propylene glycol by soil bacteria. <i>Biodegradation</i> , 2013, 24, 603-613.	1.5	14

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4453	Rhizosphere bacterial communities associated with long-lived perennial prairie plants vary in diversity, composition, and structure. <i>Canadian Journal of Microbiology</i> , 2013, 59, 494-502.	0.8	31
4454	Characterization of enriched aerotolerant cellulose-degrading communities for biofuels production using differing selection pressures and inoculum sources. <i>Canadian Journal of Microbiology</i> , 2013, 59, 679-683.	0.8	9
4455	Carbon source " A strong determinant of microbial community structure and performance of an anaerobic reactor. <i>Journal of Biotechnology</i> , 2013, 168, 616-624.	1.9	31
4456	Abundance and diversity of copper resistance genes <i>cusA</i> and <i>copA</i> in microbial communities in relation to the impact of copper on Chilean marine sediments. <i>Marine Pollution Bulletin</i> , 2013, 67, 16-25.	2.3	52
4457	Rhizosphere microbial diversity as influenced by humic substance amendments and chemical composition of rhizodeposits. <i>Journal of Geochemical Exploration</i> , 2013, 129, 82-94.	1.5	54
4458	Enrichment of anaerobic syngas-converting bacteria from thermophilic bioreactor sludge. <i>FEMS Microbiology Ecology</i> , 2013, 86, 590-597.	1.3	48
4459	Ecological Inferences from a deep screening of the <i>C</i> complex <i>B</i> bacterial <i>C</i> consortia associated with the coral, <i>P</i> <i>orites astreoides</i> . <i>Molecular Ecology</i> , 2013, 22, 4349-4362.	2.0	59
4460	<i>Moorella stamsii</i> sp. nov., a new anaerobic thermophilic hydrogenogenic carboxydrotroph isolated from digester sludge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 4072-4076.	0.8	58
4461	Impacts of chloride de-icing salt on bulk soils, fungi, and bacterial populations surrounding the plant rhizosphere. <i>Applied Soil Ecology</i> , 2013, 72, 69-78.	2.1	49
4462	Design and field-scale implementation of an "œon site" bioremediation treatment in PAH-polluted soil. <i>Environmental Pollution</i> , 2013, 181, 190-199.	3.7	39
4463	Molecular diversity and tools for deciphering the methanogen community structure and diversity in freshwater sediments. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 7553-7562.	1.7	26
4464	Proliferation of diversified clostridial species during biological soil disinfection incorporated with plant biomass under various conditions. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 8365-8379.	1.7	55
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4467	Bacterial communities in different sections of a municipal wastewater treatment plant revealed by 16S rDNA 454 pyrosequencing. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 2681-2690.	1.7	253
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4469	Ribosomal Intergenic Spacer Analysis as a Tool for Monitoring Methanogenic Archaea Changes in an Anaerobic Digester. <i>Current Microbiology</i> , 2013, 67, 240-248.	1.0	39
4470	Ex-situ enzyme activity and bacterial community diversity through soil depth profiles in penguin and seal colonies on Vestfold Hills, East Antarctica. <i>Polar Biology</i> , 2013, 36, 1347-1361.	0.5	22

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4472	Comparison of the diversity of root-associated bacteria in <i>Phragmites australis</i> and <i>Typha angustifolia</i> L. in artificial wetlands. <i>World Journal of Microbiology and Biotechnology</i> , 2013, 29, 1499-1508.	1.7	32
4473	Configuration of biological wastewater treatment line and influent composition as the main factors driving bacterial community structure of activated sludge. <i>World Journal of Microbiology and Biotechnology</i> , 2013, 29, 1145-1153.	1.7	17
4474	The ecological roles of bacterial populations in the surface sediments of coastal lagoon environments in Japan as revealed by quantification and qualification of 16S rDNA. <i>World Journal of Microbiology and Biotechnology</i> , 2013, 29, 759-774.	1.7	9
4475	Assessment of the ecological security of immobilized enzyme remediation process with biological indicators of soil health. <i>Environmental Science and Pollution Research</i> , 2013, 20, 5773-5780.	2.7	11
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4477	Applicability of a modified MCE filter method with Button Inhalable Sampler for monitoring personal bioaerosol inhalation exposure. <i>Environmental Science and Pollution Research</i> , 2013, 20, 2963-2972.	2.7	5
4478	Phytoremediation of a PCB-contaminated soil by alfalfa and tall fescue single and mixed plants cultivation. <i>Journal of Soils and Sediments</i> , 2013, 13, 925-931.	1.5	62
4479	Negatively and positively charged bacterial aerosol concentration and diversity in natural environments. <i>Science Bulletin</i> , 2013, 58, 3169-3176.	1.7	8
4480	Spatial variability of cyanobacterial community composition in Sanya Bay as determined by DGGE fingerprinting and multivariate analysis. <i>Science Bulletin</i> , 2013, 58, 1019-1027.	1.7	5
4481	Evaluation of microbial community reproducibility, stability and composition in a human distal gut chemostat model. <i>Journal of Microbiological Methods</i> , 2013, 95, 167-174.	0.7	144
4482	Organic loading rate shock impact on operation and microbial communities in different anaerobic fixed-bed reactors. <i>Bioresource Technology</i> , 2013, 140, 211-219.	4.8	31
4483	Biodegradation of thiocyanate by a novel strain of <i>Burkholderia phytofirmans</i> from soil contaminated by gold mine tailings. <i>Letters in Applied Microbiology</i> , 2013, 57, 368-372.	1.0	21
4484	A hydrocarbon-oxidizing acidophilic thermotolerant bacterial association from sulfur blocks. <i>Microbiology</i> , 2013, 82, 482-489.	0.5	14
4485	Biofilm formation on stainless steel and gold wires for bonded retainers in vitro and in vivo and their susceptibility to oral antimicrobials. <i>Clinical Oral Investigations</i> , 2013, 17, 1209-1218.	1.4	16
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4491	Changes in Bacterial Community Structure and Abundance in Agricultural Soils under Varying Levels of Arsenic Contamination. <i>Geomicrobiology Journal</i> , 2013, 30, 635-644.	1.0	27
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4493	Microbiological and Physicochemical Quality Evaluation of Vacuumâ€Packed Argentine Beef Imported into <sc>I</sc>aly. <i>Journal of Food Quality</i> , 2013, 36, 253-262.	1.4	7
4494	The Combination of Different Carbon Sources Enhances Bacterial Growth Efficiency in Aquatic Ecosystems. <i>Microbial Ecology</i> , 2013, 66, 871-878.	1.4	58
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4497	Increased nitrous oxide accumulation by bioelectrochemical denitrification under autotrophic conditions: Kinetics and expression ofÂDenitrification pathway genes. <i>Water Research</i> , 2013, 47, 7087-7097.	5.3	64
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4501	Thermophilic anaerobic biodegradation test and analysis of eubacteria involved inÂanaerobic biodegradation of four specified biodegradable polyesters. <i>Polymer Degradation and Stability</i> , 2013, 98, 1182-1187.	2.7	71
4502	Changes in Microbial Community Structure During Anaerobic Repeated-Batch Treatment of Cheese-Processing Wastewater. <i>APCBEE Procedia</i> , 2013, 5, 520-526.	0.5	5
4503	How does N deposition affect belowground heathland recovery following wildfire?. <i>Soil Biology and Biochemistry</i> , 2013, 57, 775-783.	4.2	9
4504	Evaluation of thermal, ultrasonic and alkali pretreatments on mixed-microalgal biomass to enhance anaerobic methane production. <i>Bioresource Technology</i> , 2013, 143, 330-336.	4.8	137
4505	Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. <i>Nucleic Acids Research</i> , 2013, 41, e1-e1.	6.5	6,268
4506	A molecular ecological approach to the detection and designation of the etiological agents of a model polymicrobial disease. <i>Journal of Veterinary Diagnostic Investigation</i> , 2013, 25, 467-472.	0.5	1

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4508	Effect of electron donors on anammox coupling with nitrate reduction for removing nitrogen from nitrate and ammonium. <i>Bioresource Technology</i> , 2013, 130, 592-598.	4.8	48
4509	Influence of soil bulk density and matric potential on microbial dynamics, inorganic N transformations, N ₂ O and N ₂ fluxes following urea deposition. <i>Soil Biology and Biochemistry</i> , 2013, 65, 1-11.	4.2	41
4510	Biosynthesis of poly(hydroxybutyrate-hydroxyvalerate) from the acclimated activated sludge and microbial characterization in this process. <i>Bioresource Technology</i> , 2013, 148, 61-69.	4.8	36
4511	CARD-FISH analysis of prokaryotic community composition and abundance along small-scale vegetation gradients in a dry arctic tundra ecosystem. <i>Soil Biology and Biochemistry</i> , 2013, 64, 147-154.	4.2	6
4512	Microbial growth, communities and sensory characteristics of vacuum and modified atmosphere packaged lamb shoulders. <i>Food Microbiology</i> , 2013, 36, 305-315.	2.1	45
4513	Soil microbial communities respond differently to three chemically defined polyphenols. <i>Plant Physiology and Biochemistry</i> , 2013, 72, 190-197.	2.8	27
4514	Autotrophic nitrogen removal from domestic sewage in MBRâ€œCANON system and the biodiversity of functional microbes. <i>Bioresource Technology</i> , 2013, 150, 113-120.	4.8	52
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4518	Temporal variation in airborne microbial populations and microbially-derived allergens in a tropical urban landscape. <i>Atmospheric Environment</i> , 2013, 74, 291-300.	1.9	109
4519	First report of endocarditis by <i>Gluconobacter</i> spp. in a patient with a history of intravenous-drug abuse. <i>Journal of Infection</i> , 2013, 66, 285-287.	1.7	5
4520	A molecular survey of a captive wallaby population for periodontopathogens and the co-incidence of <i>Fusobacterium necrophorum</i> subspecies <i>necrophorum</i> with periodontal diseases. <i>Veterinary Microbiology</i> , 2013, 163, 335-343.	0.8	17
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4522	Successful bioaugmentation of an activated sludge reactor with <i>Rhodococcus</i> sp. YYL for efficient tetrahydrofuran degradation. <i>Journal of Hazardous Materials</i> , 2013, 261, 550-558.	6.5	22
4523	Denaturing Gradient Gel Electrophoresis Detects Bacterial and Cyanobacterial Diversities in Biological Soil Crusts in a Semiarid Desert, China. <i>Advanced Materials Research</i> , 2013, 726-731, 3680-3684.	0.3	0
4524	Soil microbial diversity, site conditions, shelter forest land, saline water dripâ€œirrigation, drift desert. <i>Journal of Basic Microbiology</i> , 2013, 53, 856-867.	1.8	1

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4527	Effects of carbon-nitrogen ratio on nitrogen removal in a sequencing batch reactor enhanced with low-intensity ultrasound. <i>Bioresource Technology</i> , 2013, 148, 128-134.	4.8	9
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4530	Sequencing the human microbiome in health and disease. <i>Human Molecular Genetics</i> , 2013, 22, R88-R94.	1.4	123
4531	The performance of <i>Fraxinus angustifolia</i> as a helper for metal phytoremediation programs and its relation to the endophytic bacterial communities. <i>Geoderma</i> , 2013, 202-203, 171-182.	2.3	18
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4536	Bacterial consortia in iron-deposited colonies formed on paddy soil surface under microaerobic conditions. <i>Soil Science and Plant Nutrition</i> , 2013, 59, 337-346.	0.8	10
4537	Biological control of plant pathogens by microorganisms isolated from agro-industrial composts. <i>Biological Control</i> , 2013, 67, 509-515.	1.4	55
4538	An innovative bioremediation strategy using a bacterial consortium entrapped in chitosan beads. <i>Journal of Environmental Management</i> , 2013, 127, 10-17.	3.8	55
4539	A novel approach to stimulate the biphenyl-degrading potential of bacterial community from PCBs-contaminated soil of e-waste recycling sites. <i>Bioresource Technology</i> , 2013, 146, 27-34.	4.8	50
4540	Diversity of thermophilic bacteria in raw, pasteurized and selectively-cultured milk, as assessed by culturing, PCR-DGGE and pyrosequencing. <i>Food Microbiology</i> , 2013, 36, 103-111.	2.1	86
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4542	Physiological and functional characteristics of <i>Propionibacterium</i> strains of the poultry microbiota and relevance for the development of probiotic products. <i>Anaerobe</i> , 2013, 23, 27-37.	1.0	34

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4544	Enrichment, isolation and identification of sulfur-oxidizing bacteria from sulfide removing bioreactor. <i>Journal of Environmental Sciences</i> , 2013, 25, 1393-1399.	3.2	45
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4549	Bioremediation of high organic load lagoon sediments: Compost addition and priming effects. <i>Chemosphere</i> , 2013, 91, 99-104.	4.2	16
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4552	Exploring microbial succession and diversity during solid-state fermentation of Tianjin duliu mature vinegar. <i>Bioresource Technology</i> , 2013, 148, 325-333.	4.8	78
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4555	Characterization of the Bacterial Community of the Chemically Defended Hawaiian Sacoglossan <i>Elysia rufescens</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 7073-7081.	1.4	37
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4557	Monitoring of the bacterial and fungal biodiversity and dynamics during <i>Massa Medicata Fermentata</i> fermentation. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 9647-9655.	1.7	28
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4560	Effectiveness of Probiotic <i>Phaeobacter</i> Bacteria Grown in Biofilters Against <i>Vibrio anguillarum</i> Infections in the Rearing of Turbot (<i>Psetta maxima</i>) Larvae. <i>Marine Biotechnology</i> , 2013, 15, 726-738.	1.1	19

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4562	Identification of bacteria in enrichment cultures of sulfate reducers in the Cariaco Basin water column employing Denaturing Gradient Gel Electrophoresis of 16S ribosomal RNA gene fragments. <i>Aquatic Biosystems</i> , 2013, 9, 17.	1.8	12
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4570	Enhancement of growth and intestinal flora in grass carp: The effect of exogenous cellulase. <i>Aquaculture</i> , 2013, 416-417, 1-7.	1.7	77
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4586	Transient response of microbial communities in a water well field to application of an impressed current. <i>Water Research</i> , 2013, 47, 672-682.	5.3	7
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4602	Evolution of microbial community diversity and enzymatic activity during composting. <i>Research in Microbiology</i> , 2013, 164, 189-198.	1.0	88
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4604	Comparing Metabolic Functionalities, Community Structures, and Dynamics of Herbicide-Degrading Communities Cultivated with Different Substrate Concentrations. <i>Applied and Environmental Microbiology</i> , 2013, 79, 367-375.	1.4	33
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4706	Microbial community evolution during simulated managed aquifer recharge in response to different biodegradable dissolved organic carbon (BDOC) concentrations. <i>Water Research</i> , 2013, 47, 2421-2430.	5.3	87
4707	Isolation and Characterization of Antagonistic <i>Bacillus</i> Strains Capable to Degrade Ethylenethiourea. <i>Current Microbiology</i> , 2013, 66, 243-250.	1.0	13
4708	Tolerance of Selected Plant Species to Petrogenic Hydrocarbons and Effect of Plant Rhizosphere on the Microbial Removal of Hydrocarbons in Contaminated Soil. <i>Water, Air, and Soil Pollution</i> , 2013, 224, 1.	1.1	37
4709	A microbiology-based multi-parametric approach towards assessing biological stability in drinking water distribution networks. <i>Water Research</i> , 2013, 47, 3015-3025.	5.3	153
4710	Contrasting relationships between biogeochemistry and prokaryotic diversity depth profiles along an estuarine sediment gradient. <i>FEMS Microbiology Ecology</i> , 2013, 85, 143-157.	1.3	20
4711	Role of Thermophilic Microflora in Composting. , 2013, , 137-169.		7
4712	Bacterial and Biochemical Properties of Newly Invented Aerobic, High-Temperature Compost. , 2013, , 119-135.		2
4713	An optimized DNA extraction and purification method from dairy manure compost for genetic diversity analysis. <i>World Journal of Microbiology and Biotechnology</i> , 2013, 29, 815-823.	1.7	7
4714	Shifting Species Interaction in Soil Microbial Community and Its Influence on Ecosystem Functions Modulating. <i>Microbial Ecology</i> , 2013, 65, 700-708.	1.4	28
4715	Detection of <i>Spiroplasma</i> and <i>Wolbachia</i> in the Bacterial Gonad Community of <i>Chorthippus parallelus</i> . <i>Microbial Ecology</i> , 2013, 66, 211-223.	1.4	13
4716	Changes in intestinal morphology and microbiota caused by dietary administration of inulin and <i>Bacillus subtilis</i> in gilthead sea bream (<i>Sparus aurata</i> L.) specimens. <i>Fish and Shellfish Immunology</i> , 2013, 34, 1063-1070.	1.6	156
4717	Oil-bioremediation potential of two hydrocarbonoclastic, diazotrophic <i>Marinobacter</i> strains from hypersaline areas along the Arabian Gulf coasts. <i>Extremophiles</i> , 2013, 17, 463-470.	0.9	48
4720	Effects of vegetative-periodic-induced rhizosphere variation on the uptake and translocation of metals in <i>Phragmites australis</i> (Cav.) Trin ex. Steudel growing in the Sun Island Wetland. <i>Ecotoxicology</i> , 2013, 22, 608-618.	1.1	18
4721	Effects of Age and Strain on the Microbiota Colonization in an Infant Human Flora-Associated Mouse Model. <i>Current Microbiology</i> , 2013, 67, 313-321.	1.0	30
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4726	Dinitrogen-Fixing Prokaryotes. , 2013, , 427-451.		43
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4728	Transgenic Bt rice has adverse impacts on CH ₄ flux and rhizospheric methanogenic archaeal and methanotrophic bacterial communities. <i>Plant and Soil</i> , 2013, 369, 297-316.	1.8	22
4729	Back to the basics: The need for ecophysiological insights to enhance our understanding of microbial behaviour in the rhizosphere. <i>Plant and Soil</i> , 2013, 373, 1-15.	1.8	34
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4732	Effect of galactooligosaccharides and <i>Bifidobacterium animalis</i> Bb-12 on growth of <i>Lactobacillus amylovorus</i> DSM 16698, microbial community structure, and metabolite production in an <i>in vitro</i> colonic model set up with human or pig microbiota. <i>FEMS Microbiology Ecology</i> , 2013, 84, 110-123.	1.3	33
4733	Carrier mounted bacterial consortium facilitates oil remediation in the marine environment. <i>Bioresource Technology</i> , 2013, 134, 107-116.	4.8	25
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4736	Changes in soil microbial properties with no-tillage in Chinese cropping systems. <i>Biology and Fertility of Soils</i> , 2013, 49, 373-377.	2.3	59
4737	Temperature sensitivity of peatland C and N cycling: Does substrate supply play a role?. <i>Soil Biology and Biochemistry</i> , 2013, 61, 109-120.	4.2	68
4738	Artificially applied vanillic acid changed soil microbial communities in the rhizosphere of cucumber (<i>Cucumis sativus</i> L.). <i>Canadian Journal of Soil Science</i> , 2013, 93, 13-21.	0.5	36
4739	Effect of DNA polymerases on PCR-DGGE patterns. <i>International Biodeterioration and Biodegradation</i> , 2013, 84, 244-249.	1.9	19
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4744	Use of denaturing gradient gel electrophoresis to detect Actinobacteria associated with the human faecal microbiota. <i>Anaerobe</i> , 2013, 22, 90-96.	1.0	12
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4746	Evidence for successional development in Antarctic hypolithic bacterial communities. <i>ISME Journal</i> , 2013, 7, 2080-2090.	4.4	93
4747	Enrichment of specific protozoan populations during <i>in situ</i> bioremediation of uranium-contaminated groundwater. <i>ISME Journal</i> , 2013, 7, 1286-1298.	4.4	34
4748	Soil moisture effect on bacterial and fungal community in Beilu River (Tibetan Plateau) permafrost soils with different vegetation types. <i>Journal of Applied Microbiology</i> , 2013, 114, 1054-1065.	1.4	90
4749	Variation in microbial communities colonizing horticultural slow sand filter beds: implications for filter function. <i>Irrigation Science</i> , 2013, 31, 631-642.	1.3	5
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4755	Comparison of commercial kits for the extraction of DNA from paddy soils. <i>Letters in Applied Microbiology</i> , 2013, 56, 222-228.	1.0	49
4756	Mass effects meet species sorting: transformations of microbial assemblages in epiphreatic subsurface karst water pools. <i>Environmental Microbiology</i> , 2013, 15, 2476-2488.	1.8	42
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4758	Indigenous PAH-degrading bacteria from oil-polluted sediments in Caleta Cordova, Patagonia Argentina. <i>International Biodeterioration and Biodegradation</i> , 2013, 82, 207-214.	1.9	72
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4762	Biodiversity and characterization of indigenous coagulase-negative staphylococci isolated from raw milk and cheese of North Italy. <i>Food Microbiology</i> , 2013, 34, 106-111.	2.1	68
4763	Prevention of fungal infestation of rainbow trout (<i>Oncorhynchus mykiss</i>) eggs using UV irradiation of the hatching water. <i>Aquacultural Engineering</i> , 2013, 55, 9-15.	1.4	7
4764	Yeast diversity of traditional alcohol fermentation starters for Hong Qu glutinous rice wine brewing, revealed by culture-dependent and culture-independent methods. <i>Food Control</i> , 2013, 34, 183-190.	2.8	88
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4767	Comparative study of changes in reaction profile and microbial community structure in two anaerobic repeated-batch reactors started up with different seed sludges. <i>Bioresource Technology</i> , 2013, 129, 495-505.	4.8	45
4768	Inoculation with microorganisms of <i>Lolium perenne</i> L.: evaluation of plant growth parameters and endophytic colonization of roots. <i>New Biotechnology</i> , 2013, 30, 695-704.	2.4	30
4769	Comparison of adhesive gut bacteria composition, immunity, and disease resistance in juvenile hybrid tilapia fed two different <i>Lactobacillus</i> strains. <i>Fish and Shellfish Immunology</i> , 2013, 35, 54-62.	1.6	135
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4774	Analysis of Yeast-Like Symbiote Diversity in the Brown Planthopper (BPH), <i>Nilaparvata lugens</i> Stål, Using a Novel Nested PCR-DGGE Protocol. <i>Current Microbiology</i> , 2013, 67, 263-270.	1.0	27
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4777	Bacterial Communities Established in Bauxite Residues with Different Restoration Histories. <i>Environmental Science & Technology</i> , 2013, 47, 7110-7119.	4.6	69
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4780	Inoculating <i>Helianthus annuus</i> (sunflower) grown in zinc and cadmium contaminated soils with plant growth promoting bacteria – Effects on phytoremediation strategies. <i>Chemosphere</i> , 2013, 92, 74-83.	4.2	141
4781	Dynamics of oral microbial community profiling during severe early childhood caries development monitored by PCR-DGGE. <i>Archives of Oral Biology</i> , 2013, 58, 1129-1138.	0.8	31
4782	Enrichment of an anammox bacterial community from a flooded paddy soil. <i>Environmental Microbiology Reports</i> , 2013, 5, 483-489.	1.0	41
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4785	Analysis of polyhydroxyalkanoate (PHA) synthase gene and PHA-producing bacteria in activated sludge that produces PHA containing 3-hydroxydodecanoate. <i>FEMS Microbiology Letters</i> , 2013, 346, 56-64.	0.7	30
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4794	Prebiotics. , 2013, , 25-43.		11
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4819	Diversity of the skin microbiota of fishes: evidence for host species specificity. <i>FEMS Microbiology Ecology</i> , 2013, 85, 483-494.	1.3	166
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4843	Comparative analysis of bacterial community and antibiotic-resistant strains in different developmental stages of the housefly (<i>Musca domestica</i>). <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 1775-1783.	1.7	29
4844	Antibiotic Administration Routes Significantly Influence the Levels of Antibiotic Resistance in Gut Microbiota. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3659-3666.	1.4	173
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4848	Sustainable nitrification in fluidised bed reactor with immobilised sludge pellets. <i>Water S A</i> , 2013, 39, .	0.2	4
4849	PCR-DGGE Analysis of Bacterial Diversity of Intestinal System in Hyperlipidemia Rats. <i>Advanced Materials Research</i> , 2013, 726-731, 898-901.	0.3	0
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4851	Potential for Plant Growth Promotion of Rhizobacteria Associated with <i>Salicornia</i> Growing in Tunisian Hypersaline Soils. <i>BioMed Research International</i> , 2013, 2013, 1-13.	0.9	146

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4861	Prebiotic Content of Bread Prepared with Flour from Immature Wheat Grain and Selected Dextran-Producing Lactic Acid Bacteria. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3779-3785.	1.4	45
4862	A Diet High in Resistant Starch Modulates Microbiota Composition, SCFA Concentrations, and Gene Expression in Pig Intestine. <i>Journal of Nutrition</i> , 2013, 143, 274-283.	1.3	281
4863	White Button Mushrooms Increase Microbial Diversity and Accelerate the Resolution of <i>Citrobacter rodentium</i> Infection in Mice. <i>Journal of Nutrition</i> , 2013, 143, 526-532.	1.3	26
4864	Biodiversity of Polyphosphate Accumulating Bacteria in Eight WWTPs with Different Modes of Operation. <i>Journal of Environmental Engineering, ASCE</i> , 2013, 139, 1089-1098.	0.7	16
4865	Normal Operating Range of Bacterial Communities in Soil Used for Potato Cropping. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1160-1170.	1.4	33
4866	Application of Denaturing High-Performance Liquid Chromatography for Monitoring Sulfate-Reducing Bacteria in Oil Fields. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5186-5196.	1.4	17
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4868	Large cryoconite aggregates on a Svalbard glacier support a diverse microbial community including ammonia-oxidizing archaea. <i>Environmental Research Letters</i> , 2013, 8, 035044.	2.2	48
4869	Biased Diversity Metrics Revealed by Bacterial 16S Pyrotags Derived from Different Primer Sets. <i>PLoS ONE</i> , 2013, 8, e53649.	1.1	167

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4881	Bacterial community composition in a large marine anoxic basin: a Cariaco Basin time-series survey. <i>FEMS Microbiology Ecology</i> , 2013, 84, 625-639.	1.3	18
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4884	Spatiotemporal Variations in Microbial Communities in a Landfill Leachate Plume. <i>Ground Water Monitoring and Remediation</i> , 2013, 33, 69-78.	0.6	10
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4981	Detection of intestinal microflora from mice affected by macrolide antibiotics. <i>African Journal of Microbiology Research</i> , 2013, 7, 1475-1479.	0.4	1
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5130	Toxicity of Nanomaterials to Microorganisms: Mechanisms, Methods, and New Perspectives. <i>Nanomedicine and Nanotoxicology</i> , 2014, , 363-405.	0.1	7
5131	Importance of Saprotrophic Freshwater Fungi for Pollen Degradation. <i>PLoS ONE</i> , 2014, 9, e94643.	1.1	110
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5133	Biohydrogen facilitated denitrification at biocathode in bioelectrochemical system (BES). <i>Bioresource Technology</i> , 2014, 171, 187-192.	4.8	28
5134	Fecal Bacterial Community Changes Associated with Isoflavone Metabolites in Postmenopausal Women after Soy Bar Consumption. <i>PLoS ONE</i> , 2014, 9, e108924.	1.1	89
5135	Diversity of Plant-Growth-Promoting Rhizobacteria Associated with Maize (<i>Zea mays</i> L.). <i>Sustainable Development and Biodiversity</i> , 2014, , 167-189.	1.4	1
5137	Development of a Prokaryotic Universal Primer for Simultaneous Analysis of Bacteria and Archaea Using Next-Generation Sequencing. <i>PLoS ONE</i> , 2014, 9, e105592.	1.1	1,115
5138	Kinetic parameters for nutrient enhanced crude oil biodegradation in intertidal marine sediments. <i>Frontiers in Microbiology</i> , 2014, 5, 160.	1.5	42
5139	Characterization of Intestinal Bacteria in Wild and Domesticated Adult Black Tiger Shrimp (<i>Penaeus</i>) Tj ETQq1 1 0.784314 rgBT/Overbo 1.1 213		
5140	Integrated management of root-knot nematodes on tomato in glasshouse production using nematicides and a biocontrol agent, and their effect on soil microbial communities. <i>Nematology</i> , 2014, 16, 463-473.	0.2	15
5141	Analysis of intestinal bacterial community diversity of adult <i>Dastarcus helophoroides</i> . <i>Journal of Insect Science</i> , 2014, 14, 114.	0.6	7

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5143	Microbial diversity in fecal samples depends on DNA extraction method: easyMag DNA extraction compared to QIAamp DNA stool mini kit extraction. <i>BMC Research Notes</i> , 2014, 7, 50.	0.6	56
5144	Characterization of bacterial community shift in human Ulcerative Colitis patients revealed by Illumina based 16S rRNA gene amplicon sequencing. <i>Gut Pathogens</i> , 2014, 6, 22.	1.6	84
5145	Quantitative analysis of ruminal methanogenic microbial populations in beef cattle divergent in phenotypic residual feed intake (RFI) offered contrasting diets. <i>Journal of Animal Science and Biotechnology</i> , 2014, 5, 41.	2.1	19
5146	Effects of feeding plant-derived agents on the colonization of <i>Campylobacter jejuni</i> in broiler chickens. <i>Poultry Science</i> , 2014, 93, 2337-2346.	1.5	23
5147	A <i>D</i> sp. strain PR reductively dechlorinates both 1,1,1-trichloroethane and chloroform. <i>Environmental Microbiology</i> , 2014, 16, 3387-3397.	1.8	58
5148	Factors Limiting the Spread of the Protective Symbiont <i>Hamiltonella defensa</i> in <i>Aphis craccivora</i> Aphids. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5818-5827.	1.4	58
5149	Assessment of the bacterial community diversity associated with the queen conch <i>Strombus gigas</i> (Linnaeus, 1758) from the Caribbean coast of Colombia using denaturing gradient gel electrophoresis and culturing. <i>Aquaculture Research</i> , 2014, 45, 773-786.	0.9	10
5150	Removal of heavy metal cations by biogenic magnetite nanoparticles produced in Fe(III)-reducing microbial enrichment cultures. <i>Journal of Bioscience and Bioengineering</i> , 2014, 117, 333-335.	1.1	44
5151	Assessment of Anaerobic Biodegradation of Aromatic Hydrocarbons: The Impact of Molecular Biology Approaches. <i>Geomicrobiology Journal</i> , 2014, 31, 276-284.	1.0	9
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5153	Effects of Fish Oil with a High Content of n-3 Polyunsaturated Fatty Acids on Mouse Gut Microbiota. <i>Archives of Medical Research</i> , 2014, 45, 195-202.	1.5	138
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5156	Increased microbial activity contributes to phosphorus immobilization in the rhizosphere of wheat under elevated CO ₂ . <i>Soil Biology and Biochemistry</i> , 2014, 75, 292-299.	4.2	42
5157	Nanomodification of the electrodes in microbial fuel cell: Impact of nanoparticle density on electricity production and microbial community. <i>Applied Energy</i> , 2014, 116, 216-222.	5.1	120
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5159	Genetic diversity of endophytic bacteria of the manganese-hyperaccumulating plant <i>Phytolacca americana</i> growing at a manganese mine. <i>European Journal of Soil Biology</i> , 2014, 62, 15-21.	1.4	29

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5162	Utilization of alkali-tolerant stains in fermentation of excess sludge. Bioresource Technology, 2014, 157, 52-59.	4.8	6
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5165	Molecular evidence for rapid dissolved organic matter turnover in Arctic fjords. Marine Chemistry, 2014, 160, 1-10.	0.9	48
5166	Microbial ecology of meat slicers as determined by denaturing gradient gel electrophoresis. Food Control, 2014, 42, 242-247.	2.8	18
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5171	Kinetic characterization of acetate utilization and response of microbial population in super fast membrane bioreactor. Journal of Membrane Science, 2014, 455, 392-404.	4.1	28
5172	Admixture of alder (Alnus formosana) litter can improve the decomposition of eucalyptus (Eucalyptus) Tj ETQq0 0 0 rBT /Overlock 10 T	4.2	23
5173	Performance of a haloalkaliphilic bioreactor under different ratios. Bioresource Technology, 2014, 153, 216-222.	4.8	27
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5175	Application of rumen microbes to enhance food waste hydrolysis in acidogenic leach-bed reactors. Bioresource Technology, 2014, 168, 64-71.	4.8	41
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5181	Dietary probiotic supplementation (<i>Shewanella putrefaciens</i> Pdp11) modulates gut microbiota and promotes growth and condition in Senegalese sole larviculture. <i>Fish Physiology and Biochemistry</i> , 2014, 40, 295-309.	0.9	61
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5187	Biases for detecting arbuscular mycorrhizal fungal mixture by terminal restriction fragment length polymorphism (T-RFLP). <i>World Journal of Microbiology and Biotechnology</i> , 2014, 30, 77-86.	1.7	1
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5190	Microbial communities analysis assessed by pyrosequencing—a new approach applied to conservation state studies of mural paintings. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 887-895.	1.9	39
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5199	Succession of cable bacteria and electric currents in marine sediment. <i>ISME Journal</i> , 2014, 8, 1314-1322.	4.4	134
5200	Pyrosequencing-based characterization of gastrointestinal bacteria of Atlantic salmon (<i>Salmo</i>) Tj ETQq0 0 0 rgBTJ /Overlock 10 Tf 50	1.4	131
5201	Biofilm models for the food industry: hot spots for plasmid transfer?. <i>Pathogens and Disease</i> , 2014, 70, 332-338.	0.8	35
5202	Efficient removal of antibiotics in surface-flow constructed wetlands, with no observed impact on antibiotic resistance genes. <i>Science of the Total Environment</i> , 2014, 476-477, 29-37.	3.9	85
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5207	Analysis of microbial diversity by pyrosequencing the small-subunit ribosomal RNA without PCR amplification. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 3777-3789.	1.7	16
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5211	Tourmaline combined with <i>Phanerochaete chrysosporium</i> to remediate agricultural soil contaminated with PAHs and OCPs. <i>Journal of Hazardous Materials</i> , 2014, 264, 439-448.	6.5	37
5212	Bio-organic fertilizer application significantly reduces the <i>Fusarium oxysporum</i> population and alters the composition of fungi communities of watermelon <i>Fusarium</i> wilt rhizosphere soil. <i>Biology and Fertility of Soils</i> , 2014, 50, 765-774.	2.3	72
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5216	Spatial and temporal distribution of archaeal diversity in meromictic, hypersaline Ocnei Lake (Transylvanian Basin, Romania). <i>Extremophiles</i> , 2014, 18, 399-413.	0.9	29
5217	Dynamics of ammonia-oxidizing archaea and bacteria in relation to nitrification along simulated dissolved oxygen gradient in sediment-water interface of the Jiulong river estuarine wetland, China. <i>Environmental Earth Sciences</i> , 2014, 72, 2225-2237.	1.3	20
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5221	Quantitative analysis of microbial community structure in two-phase anaerobic digesters treating food wastewater. <i>Korean Journal of Chemical Engineering</i> , 2014, 31, 381-385.	1.2	9
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5225	Microbial contamination of laboratory constructed removable orthodontic appliances. <i>Clinical Oral Investigations</i> , 2014, 18, 2193-2202.	1.4	8
5226	Bacterial diversity within five unexplored freshwater lakes interconnected by surface channels in East Antarctic Dronning Maud Land (Schirmacher Oasis) using amplicon pyrosequencing. <i>Polar Biology</i> , 2014, 37, 359-366.	0.5	7
5227	Dietary Supplementation of Usnic Acid, an Antimicrobial Compound in Lichens, Does Not Affect Rumen Bacterial Diversity or Density in Reindeer. <i>Current Microbiology</i> , 2014, 68, 724-728.	1.0	14
5228	Characteristics of biofilm development in an operating rainwater storage tank. <i>Environmental Earth Sciences</i> , 2014, 72, 1633-1642.	1.3	8
5229	Characterization of Bacterial Communities in Sediments Receiving Various Wastewater Effluents with High-Throughput Sequencing Analysis. <i>Microbial Ecology</i> , 2014, 67, 612-623.	1.4	63
5230	Response of microbial community to petroleum stress and phosphate dosage in sediments of Jiaozhou Bay, China. <i>Journal of Ocean University of China</i> , 2014, 13, 249-256.	0.6	7
5231	Bacterial diversity of gut content in sea cucumber (<i>Apostichopus japonicus</i>) and its habitat surface sediment. <i>Journal of Ocean University of China</i> , 2014, 13, 303-310.	0.6	22

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5233	Microbial community analysis for aerobic granular sludge reactor treating high-level 4-chloroaniline wastewater. <i>International Journal of Environmental Science and Technology</i> , 2014, 11, 1845-1854.	1.8	22
5234	Differential responses of ammonia/ammonium-oxidizing microorganisms in mangrove sediment to amendment of acetate and leaf litter. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 3165-3180.	1.7	20
5235	Bacterial communities in trace metal contaminated lake sediments are dominated by endospore-forming bacteria. <i>Aquatic Sciences</i> , 2014, 76, 33-46.	0.6	28
5236	Standard inocula preparations reduce the bacterial diversity and reliability of regulatory biodegradation tests. <i>Environmental Science and Pollution Research</i> , 2014, 21, 9511-9521.	2.7	40
5237	Diversity and activities of yeasts from different parts of a Stilton cheese. <i>International Journal of Food Microbiology</i> , 2014, 177, 109-116.	2.1	47
5238	Isolation and characterization of a novel <i>Dehalobacter</i> species strain TCP1 that reductively dechlorinates 2,4,6-trichlorophenol. <i>Biodegradation</i> , 2014, 25, 313-323.	1.5	35
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5242	Dynamics of the bacterial community structure in the rhizosphere of a maize cultivar. <i>Soil Biology and Biochemistry</i> , 2014, 68, 392-401.	4.2	346
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5244	Degradation of high concentrations of nonionic surfactant (linear alcohol ethoxylate) in an anaerobic fluidized bed reactor. <i>Science of the Total Environment</i> , 2014, 481, 121-128.	3.9	37
5245	Microbial and endogenous origin of fibrinolytic activity in traditional fermented foods of Northeast India. <i>Food Research International</i> , 2014, 55, 356-362.	2.9	72
5246	Soil fungi rather than bacteria were modified by invasive plants, and that benefited invasive plant growth. <i>Plant and Soil</i> , 2014, 378, 253-264.	1.8	49
5247	Insights into the relationship between antimicrobial residues and bacterial populations in a hospital-urban wastewater treatment plant system. <i>Water Research</i> , 2014, 54, 327-336.	5.3	117
5248	Impact of diatom growth on trace metal dynamics (Mn, Mo, V, U). <i>Journal of Sea Research</i> , 2014, 87, 35-45.	0.6	9
5249	Reducing NO and N ₂ O emission during aerobic denitrification by newly isolated <i>Pseudomonas stutzeri</i> PCN-1. <i>Bioresource Technology</i> , 2014, 162, 80-88.	4.8	110

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5251	Bacterial community structure and dissolved organic matter in repeatedly flooded subsurface karst water pools. <i>FEMS Microbiology Ecology</i> , 2014, 89, 111-126.	1.3	48
5252	Genetic diversity of <i>Rhizobium</i> present in nodules of <i>Phaseolus vulgaris</i> L. cultivated in two soils of the central region in Chile. <i>Applied Soil Ecology</i> , 2014, 80, 60-66.	2.1	8
5253	Antibiotic resistances of intestinal lactobacilli isolated from wild boars. <i>Veterinary Microbiology</i> , 2014, 168, 240-244.	0.8	19
5254	Dynamics and functions of bacterial communities in bark, charcoal and sand filters treating greywater. <i>Water Research</i> , 2014, 54, 21-32.	5.3	40
5255	Anodic microbial community diversity as a predictor of the power output of microbial fuel cells. <i>Bioresource Technology</i> , 2014, 156, 84-91.	4.8	39
5256	Phytomanagement of Cd-contaminated soils using maize (<i>Zea mays</i> L.) assisted by plant growth-promoting rhizobacteria. <i>Environmental Science and Pollution Research</i> , 2014, 21, 9742-9753.	2.7	76
5257	The impact of bioaugmentation on dechlorination kinetics and on microbial dechlorinating communities in subsurface clay till. <i>Environmental Pollution</i> , 2014, 186, 149-157.	3.7	17
5258	Impact of Experimental Hookworm Infection on the Human Gut Microbiota. <i>Journal of Infectious Diseases</i> , 2014, 210, 1431-1434.	1.9	153
5259	Effects of short chain fatty acid producing bacteria on epigenetic regulation of FFAR3 in type 2 diabetes and obesity. <i>Gene</i> , 2014, 537, 85-92.	1.0	257
5260	Improved group-specific primers based on the full SILVA 16S rRNA gene reference database. <i>Environmental Microbiology</i> , 2014, 16, 2389-2407.	1.8	59
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5262	Novel bacteria associated with Arctic seashore lichens have potential roles in nutrient scavenging. <i>Canadian Journal of Microbiology</i> , 2014, 60, 307-317.	0.8	35
5263	Bacteria, phages and pigs: the effects of in-feed antibiotics on the microbiome at different gut locations. <i>ISME Journal</i> , 2014, 8, 1566-1576.	4.4	377
5264	VOC emission of various <i>Serratia</i> species and isolates and genome analysis of <i>Serratia plymuthica</i> 4Rx13. <i>FEMS Microbiology Letters</i> , 2014, 352, 45-53.	0.7	46
5265	Performance of a haloalkaliphilic bioreactor and bacterial community shifts under different COD/SO ₄ ²⁻ ratios and hydraulic retention times. <i>Journal of Hazardous Materials</i> , 2014, 274, 53-62.	6.5	29
5266	Impact of a phytoplankton bloom on the diversity of the active bacterial community in the southern North Sea as revealed by metatranscriptomic approaches. <i>FEMS Microbiology Ecology</i> , 2014, 87, 378-389.	1.3	113
5267	Assessment of core and accessory genetic variation in <i>Rhizobium leguminosarum</i> symbiovar <i>trifolii</i> strains from diverse locations and host plants using PCR-based methods. <i>Letters in Applied Microbiology</i> , 2014, 59, 238-246.	1.0	15

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5268	Impact of abrupt temperature increase on the performance of an anaerobic hybrid bioreactor and its intrinsic microbial community. <i>Bioresource Technology</i> , 2014, 168, 72-79.	4.8	23
5269	Synergistic effects of bioremediation and electrokinetics in the remediation of petroleum-contaminated soil. <i>Chemosphere</i> , 2014, 109, 226-233.	4.2	61
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5316	Influence of Nutrient Concentrations on MPN Quantification and Enrichment of Nitrate-Reducing Fe(II)-Oxidizing and Fe(III)-Reducing Bacteria from Littoral Freshwater Lake Sediments. <i>Geomicrobiology Journal</i> , 2014, 31, 788-801.	1.0	10
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5405	Probing potential microbial coupling of carbon and nitrogen cycling during decomposition of maize residue by ¹³ C-DNA-SIP. <i>Soil Biology and Biochemistry</i> , 2014, 70, 12-21.	4.2	127
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5848	Exploring deep microbial life in coal-bearing sediment down to ~2.5 km below the ocean floor. <i>Science</i> , 2015, 349, 420-424.	6.0	376
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5851	Antibacterial and cytotoxic activity from the extract and fractions of a marine derived bacterium from the <i>Streptomyces</i> genus. <i>Pharmaceutical Biology</i> , 2015, 53, 1826-1830.	1.3	4
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6265	Biominalization of atrazine and analysis of 16S rRNA and catabolic genes of atrazine degraders in a former pesticide mixing site and a machinery washing area. <i>Journal of Soils and Sediments</i> , 2016, 16, 2263-2274.	1.5	10
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6421	Quantification of the Genetic Expression of <i>bgl-A</i> , <i>bgl</i> , and <i>CspA</i> and Enzymatic Characterization of β -Glucosidases from <i>Shewanella</i> sp. G5. <i>Marine Biotechnology</i> , 2016, 18, 396-408.	1.1	3
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6541	Does nutrient enrichment compensate fungicide effects on litter decomposition and decomposer communities in streams?. <i>Aquatic Toxicology</i> , 2016, 174, 169-178.	1.9	17
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6825	Effects of silver nanoparticles on nitrification and associated nitrous oxide production in aquatic environments. <i>Science Advances</i> , 2017, 3, e1603229.	4.7	95
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6827	Bioinformatics for NGS-based metagenomics and the application to biogas research. <i>Journal of Biotechnology</i> , 2017, 261, 10-23.	1.9	84
6828	Effects of polysaccharide from <i>Physalis alkekengi</i> var. <i>francheti</i> on liver injury and intestinal microflora in type-2 diabetic mice. <i>Pharmaceutical Biology</i> , 2017, 55, 2020-2025.	1.3	20
6829	Diversity and screening of lactic acid bacteria in la-baicai made by Korean-Chinese in northeastern China. <i>Food Biotechnology</i> , 2017, 31, 193-209.	0.6	2
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6833	Evaluation of dried yeast and threonine fermentation biomass as partial fish meal replacements in the diet of red drum <i>Sciaenops ocellatus</i> . <i>Animal Feed Science and Technology</i> , 2017, 232, 190-197.	1.1	30
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6846	Molecular estimation of alteration in intestinal microbial composition in Hashimoto's thyroiditis patients. <i>Biomedicine and Pharmacotherapy</i> , 2017, 95, 865-874.	2.5	70
6847	Segment-specific responses of intestinal epithelium transcriptome to in-feed antibiotics in pigs. <i>Physiological Genomics</i> , 2017, 49, 582-591.	1.0	15
6848	Evaluation of biochars from different stock materials as carriers of bacterial strain for remediation of heavy metal-contaminated soil. <i>Scientific Reports</i> , 2017, 7, 12114.	1.6	46
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6850	Introduction of Faba bean in crop rotation: Impacts on soil chemical and biological characteristics. <i>Applied Soil Ecology</i> , 2017, 120, 219-228.	2.1	57
6851	A cross-sectional comparative study of gut bacterial community of Indian and Finnish children. <i>Scientific Reports</i> , 2017, 7, 10555.	1.6	37
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6853	Diversity of Soil Microbial Communities from an Iron Mining Area (Oued Zem, Morocco). <i>Materials and Geoenvironment</i> , 2017, 64, 21-34.	0.4	5
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6867	Differences in free-living and particle-associated bacterial communities and their spatial variation in Kongsfjorden, Arctic. <i>Journal of Basic Microbiology</i> , 2017, 57, 827-838.	1.8	49
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6906	Seasonal variation of bacterial community in biological aerated filter for ammonia removal in drinking water treatment. <i>Water Research</i> , 2017, 123, 668-677.	5.3	63
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7113	Newly isolated bacterium <i>Tenacibaculum</i> sp. strain Pbs-1 from diseased pearl oysters is associated with black-spot shell disease. <i>Aquaculture</i> , 2018, 493, 61-67.	1.7	11
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7115	Perfluoroalkyl phosphonic acids adsorption behaviour and removal by wastewater organisms. <i>Science of the Total Environment</i> , 2018, 636, 273-281.	3.9	5
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7128	Improving in vivo conversion of oleuropein into hydroxytyrosol by oral granules containing probiotic <i>Lactobacillus plantarum</i> 299v and an <i>Olea europaea</i> standardized extract. <i>International Journal of Pharmaceutics</i> , 2018, 543, 73-82.	2.6	20
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7134	Tetracycline resistance genes are more prevalent in wet soils than in dry soils. <i>Ecotoxicology and Environmental Safety</i> , 2018, 156, 337-343.	2.9	9
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7144	Comparison of two bacterial DNA extraction methods from non-polluted and polluted soils. <i>Folia Microbiologica</i> , 2018, 63, 85-92.	1.1	8
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7172	Response of soil microbial abundance and diversity in Sacha Inchi (<i>Plukenetia volubilis</i> L.) farms with different land-use histories in a tropical area of Southwestern China. <i>Archives of Agronomy and Soil Science</i> , 2018, 64, 588-596.	1.3	3
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7250	The Effect of White Rice and White Bread as Staple Foods on Gut Microbiota and Host Metabolism. <i>Nutrients</i> , 2018, 10, 1323.	1.7	15
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7258	Selection of metabolic pathways for continuous hydrogen production under thermophilic and mesophilic temperature conditions in anaerobic fluidized bed reactors. <i>International Journal of Hydrogen Energy</i> , 2018, 43, 18908-18917.	3.8	21
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7316	Soil bacterial networks are less stable under drought than fungal networks. <i>Nature Communications</i> , 2018, 9, 3033.	5.8	992
7317	The effects of increased hay:corn grain ratio on behavior, metabolic health measures, and fecal bacterial communities in four Masai giraffe (<i>Giraffa camelopardalis tippelskirchi</i>) at Cleveland Metroparks Zoo. <i>Zoo Biology</i> , 2018, 37, 320-331.	0.5	4

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7349	Studies of Microbiota Dynamics Reveals Association of <i>Candidatus Liberibacter Asiaticus</i> Infection with Citrus (<i>Citrus sinensis</i>) Decline in South of Iran. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1817.	1.8	12
7350	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. <i>Microbiome</i> , 2018, 6, 90.	4.9	3,159
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7356	Novel Self-assembled Organic Nanoprobe for Molecular Imaging and Treatment of Gram-positive Bacterial Infection. <i>Theranostics</i> , 2018, 8, 1911-1922.	4.6	38
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7370	Rhizobacterial community structure in response to nitrogen addition varied between two Mollisols differing in soil organic carbon. <i>Scientific Reports</i> , 2018, 8, 12280.	1.6	8
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7375	Plant Species and Heavy Metals Affect Biodiversity of Microbial Communities Associated With Metal-Tolerant Plants in Metalliferous Soils. <i>Frontiers in Microbiology</i> , 2018, 9, 1425.	1.5	59
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7381	The Role of the Microbiome in PMI Estimation. , 2018, , 113-131.		4
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7383	The application of rumen simulation technique (RUSITEC) for studying dynamics of the bacterial community and metabolome in rumen fluid and the effects of a challenge with <i>Clostridium perfringens</i> . <i>PLoS ONE</i> , 2018, 13, e0192256.	1.1	36
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7529	Risk assessment and inactivation of invertebrate-internalized bacteria in pilot-scale biological activated carbon filtration. <i>Science of the Total Environment</i> , 2019, 676, 321-332.	3.9	7
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7531	Hydrocarbon degradation potential and competitive persistence of hydrocarbonoclastic bacterium <i>Acinetobacter pittii</i> strain ABC. <i>Archives of Microbiology</i> , 2019, 201, 1129-1140.	1.0	16
7532	Physiological traits and relative abundance of species as explanatory variables of co-occurrence pattern of cultivable bacteria associated with chia seeds. <i>Canadian Journal of Microbiology</i> , 2019, 65, 668-680.	0.8	0
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7536	Effects of size and autoclavation of fruit and vegetable wastes on biohydrogen production by dark dry anaerobic fermentation under mesophilic condition. <i>International Journal of Hydrogen Energy</i> , 2019, 44, 17767-17780.	3.8	24
7537	Characterizing the Intra-Vineyard Variation of Soil Bacterial and Fungal Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 1239.	1.5	31
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7540	The biogeochemistry of gas generation from low-level nuclear waste: Microbiological characterization during 18 years study under in situ conditions. <i>Applied Geochemistry</i> , 2019, 105, 55-67.	1.4	8
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7551	Accelerated biodegradation of PLA/PHB-blended nonwovens by a microbial community. <i>RSC Advances</i> , 2019, 9, 10386-10394.	1.7	22

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7568	The anammox process at typical feast-famine states: Reactor performance, sludge activity and microbial community. <i>Chemical Engineering Journal</i> , 2019, 370, 110-119.	6.6	53
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7609	Tracing Fruits and Vegetables from Farm to Fork: Questions of Novelty and Efficiency. , 2019, , 179-209.		4
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7618	Comparative metagenomics and functional profiling of crude oil-polluted soils in Bodo West Community, Ogoni, with other sites of varying pollution history. <i>Annals of Microbiology</i> , 2019, 69, 495-513.	1.1	33
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7622	Exploration of bacterial contaminants in reservoirs of Palamuru by PCR-DGGE method: household water treatment. <i>Journal of Water Sanitation and Hygiene for Development</i> , 2019, 9, 38-48.	0.7	3
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7650	Isolation and characterization of soil bacteria able to rapidly degrade the organophosphorus nematicide fosthiazate. <i>Letters in Applied Microbiology</i> , 2019, 68, 149-155.	1.0	11
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7652	Effects of supplementation with exhausted myrtle berries on rumen function of dairy sheep. <i>Small Ruminant Research</i> , 2019, 170, 51-61.	0.6	19
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7654	Impact of nanoparticles on transcriptional regulation of catabolic genes of petroleum hydrocarbon-degrading bacteria in contaminated soil microcosms. <i>Journal of Basic Microbiology</i> , 2019, 59, 166-180.	1.8	4
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7657	Diversity and abundance of denitrifiers during cow manure composting. <i>Revista Argentina De Microbiologia</i> , 2019, 51, 191-200.	0.4	11
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7659	Systemic proinflammation after <i>Mycobacterium tuberculosis</i> infection was correlated to the gut microbiome in HIV-uninfected humans. <i>European Journal of Clinical Investigation</i> , 2019, 49, e13068.	1.7	21
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7661	Bioremediation of soil long-term contaminated with PAHs by algal-bacterial synergy of <i>Chlorella</i> sp. MM3 and <i>Rhodococcus wratislaviensis</i> strain 9 in slurry phase. <i>Science of the Total Environment</i> , 2019, 659, 724-731.	3.9	45
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7665	TAK1 Prevents Endothelial Apoptosis and Maintains Vascular Integrity. <i>Developmental Cell</i> , 2019, 48, 151-166.e7.	3.1	26
7666	Impact of turning, pod storage and fermentation time on microbial ecology and volatile composition of cocoa beans. <i>Food Research International</i> , 2019, 119, 477-491.	2.9	56
7667	Preferential flow paths shape the structure of bacterial communities in a clayey till depth profile. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	13
7668	Coupled virus - bacteria interactions and ecosystem function in an engineered microbial system. <i>Water Research</i> , 2019, 152, 264-273.	5.3	31
7669	Oxygen loss from seagrass roots coincides with colonisation of sulphide-oxidising cable bacteria and reduces sulphide stress. <i>ISME Journal</i> , 2019, 13, 707-719.	4.4	89
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7776	Supplemental selenium source on gut health: insights on fecal microbiome and fermentation products of growing puppies. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	29
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7786	Metagenomic data on bacterial diversity profiling of high-microbial-abundance tropical marine sponges <i>Aaptos aaptos</i> and <i>Xestospongia muta</i> from waters off terengganu, South China Sea. <i>Data in Brief</i> , 2020, 31, 105971.	0.5	4
7787	Irrigation of radish (<i>Raphanus sativus</i> L.) with microcystin-enriched water holds low risk for plants and their associated rhizopheric and epiphytic microbiome. <i>Environmental Pollution</i> , 2020, 266, 115208.	3.7	8
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7790	Microbiota composition of captive bluestreak cleaner wrasse <i>Labroides dimidiatus</i> (Valenciennes.) Tj ETQq1 1 0.784314 rgBT ₄ /Overlo	1.7	4
7791	Long-term effect of non-irrigation and irrigation on soil <i>Pythium</i> , <i>Fusarium</i> , and <i>Rhizoctonia</i> communities and their relation with seed-rot, root-rot, and damping-off of soybean. <i>European Journal of Plant Pathology</i> , 2020, 158, 297-314.	0.8	5
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7802	Soil Bacterial and Fungal Richness Forecast Patterns of Early Pine Litter Decomposition. <i>Frontiers in Microbiology</i> , 2020, 11, 542220.	1.5	15
7803	Temporal dynamics of <i>Pinus tabulaeformis</i> litter decomposition under nitrogen addition on the Loess Plateau of China. <i>Forest Ecology and Management</i> , 2020, 476, 118465.	1.4	10
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7805	Renoprotective effects of paramylon, a β -1,3-D-Glucan isolated from <i>Euglena gracilis</i> Z in a rodent model of chronic kidney disease. <i>PLoS ONE</i> , 2020, 15, e0237086.	1.1	8
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8100	Comprehensive characterization of stress tolerant bacteria with plant growth-promoting potential isolated from glyphosate-treated environment. <i>World Journal of Microbiology and Biotechnology</i> , 2021, 37, 94.	1.7	8
8101	Assessment of 16S rRNA Gene-Based Phylogenetic Diversity of Archaeal Communities in Halite-Crystal Salts Processed from Natural Saharan Saline Systems of Southern Tunisia. <i>Biology</i> , 2021, 10, 397.	1.3	7
8103	Metaplasmidome-encoded functions of Siberian low-centered polygonal tundra soils. <i>ISME Journal</i> , 2021, 15, 3258-3270.	4.4	2

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8105	Resuscitation of the microbial seed bank alters plant-soil interactions. <i>Molecular Ecology</i> , 2021, 30, 2905-2914.	2.0	6
8106	Investigation of microbial community changes in petroleum polluted sediments during hydrocarbons degradation. <i>Soil and Sediment Contamination</i> , 2022, 31, 200-219.	1.1	4
8107	A Combined Application of Molecular Microbial Ecology and Elemental Analyses Can Advance the Understanding of Decomposition Dynamics. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	0
8109	The effects of vehicular emissions on the activity and diversity of the roadside soil microbial community. <i>Environmental Pollution</i> , 2021, 277, 116744.	3.7	11
8110	Mixed plantations of <i>Metasequoia glyptostroboides</i> and <i>Bischofia polycarpa</i> change soil fungal and archaeal communities and enhance soil phosphorus availability in Shanghai, China. <i>Ecology and Evolution</i> , 2021, 11, 7239-7249.	0.8	8
8111	Biochar alters soil microbial communities and potential functions 3-4 years after amendment in a double rice cropping system. <i>Agriculture, Ecosystems and Environment</i> , 2021, 311, 107291.	2.5	57
8112	Bioconversion of potato solid waste into antifungals and biopigments using <i>Streptomyces</i> spp.. <i>PLoS ONE</i> , 2021, 16, e0252113.	1.1	9
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8114	Valorization of pineapple peel and poultry manure for clean energy generation. <i>Food and Energy Security</i> , 2022, 11, e228.	2.0	11
8116	Cow manure stabilizes anaerobic digestion of cocoa waste. <i>Waste Management</i> , 2021, 126, 508-516.	3.7	14
8117	Synergistic effects of <i>Bacillus pumilus</i> and exogenous protease on Nile tilapia (<i>Oreochromis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf Feed Science and Technology, 2021, 275, 114892.	1.1	26
8118	Efficacy of a woodchip-sediment integrated system in nitrate elimination from wastewater with low C/N condition. <i>Journal of Soils and Sediments</i> , 2021, 21, 3392-3404.	1.5	2
8119	A comparison of the gut microbiota among adult patients with drug-responsive and drug-resistant epilepsy: An exploratory study. <i>Epilepsy Research</i> , 2021, 172, 106601.	0.8	27
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8129	Purification effect evaluation of the designed new volcanic soil adsorption material containing bioreactor for eutrophic water treatment. <i>Environmental Science and Pollution Research</i> , 2021, 28, 59821-59833.	2.7	4
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8131	Long-term phytoremediation using the symbiotic <i>Pongamia pinnata</i> reshaped soil micro-ecological environment. <i>Science of the Total Environment</i> , 2021, 774, 145112.	3.9	9
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8135	Mass-immigration determines the assembly of activated sludge microbial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	48
8136	Organic fertilization improves soil aggregation through increases in abundance of eubacteria and products of arbuscular mycorrhizal fungi. <i>Scientific Reports</i> , 2021, 11, 12548.	1.6	22
8137	Soil and temperature effects on nitrification and denitrification modified N ₂ O mitigation by 3,4-dimethylpyrazole phosphate. <i>Soil Biology and Biochemistry</i> , 2021, 157, 108224.	4.2	28
8138	Broad diversity of bacteria degrading 17 β -estradiol-3-sulfate isolated from river sediment and biofilm at a wastewater treatment plant discharge. <i>Archives of Microbiology</i> , 2021, 203, 4209-4219.	1.0	2
8139	Stable colonization of native plants and early invaders by arbuscular mycorrhizal fungi after exposure to recent invaders from the Asteraceae family. <i>Invasive Plant Science and Management</i> , 2021, 14, 147-155.	0.5	4
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8141	Metabolically Active Prokaryotes and Actively Transcribed Antibiotic Resistance Genes in Sewer Systems: Implications for Public Health and Microbially Induced Corrosion. <i>Microbial Ecology</i> , 2022, 83, 583-595.	1.4	3
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8146	GC-MS Metabolomics and Antifungal Characteristics of Autochthonous <i>Lactobacillus</i> Strains. <i>Dairy</i> , 2021, 2, 326-335.	0.7	8
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8149	Microbiological Attributes and Performance of the Bacterial Community in Brazilian Cerrado Soil with Different Cover Crops. <i>Sustainability</i> , 2021, 13, 8318.	1.6	0
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8152	Microbial functions and soil nitrogen mineralisation processes in the soil of a cool temperate forest in northern Japan. <i>Biogeochemistry</i> , 2021, 155, 359-379.	1.7	10
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8154	Oily Bilge Wastes Harbor a Set of Persistent Hydrocarbonoclastic Bacteria Accompanied by a Variable <i>alkB</i> Gene Composition in Marine Vessel Samples from Southwestern Atlantic Port of Mar del Plata, Argentina. <i>Water, Air, and Soil Pollution</i> , 2021, 232, 1.	1.1	4
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8160	Assessment of total bacterial diversity in whiteleg shrimps and its aquaculture environment in Pangkajene and Banyuwangi, Indonesia. <i>Asia-Pacific Journal of Molecular Biology and Biotechnology</i> , 0, , 26-37.	0.2	0
8161	Biodegradable mulching vs traditional polyethylene film for sustainable solarization: Chemical properties and microbial community response to soil management. <i>Applied Soil Ecology</i> , 2021, 163, 103921.	2.1	33
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8173	Halophilic Prokaryotes in Urmia Salt Lake, a Hypersaline Environment in Iran. <i>Current Microbiology</i> , 2021, 78, 3230-3238.	1.0	7
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8180	Genotypic variation in maize (<i>Zea mays</i>) influences rates of soil organic matter mineralization and gross nitrification. <i>New Phytologist</i> , 2021, 231, 2015-2028.	3.5	16
8181	The Novel Interplay between Commensal Gut Bacteria and Metabolites in Diet-Induced Hyperlipidemic Rats Treated with Simvastatin. <i>Journal of Proteome Research</i> , 2021, , .	1.8	5
8182	Community level physiological profiling of microorganisms in the rhizosphere of transgenic plants â€“ A review. <i>Nova Biotechnologica Et Chimica</i> , 2021, 10, .	0.1	0
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8195	Analysis of microflora in dentinal tubule by denaturing gradient gel electrophoresis. <i>World Journal of Advanced Research and Reviews</i> , 2021, 11, 085-092.	0.1	0
8196	UV treatment in RAS influences the rearing water microbiota and reduces the survival of European lobster larvae (<i>Homarus gammarus</i>). <i>Aquacultural Engineering</i> , 2021, 94, 102176.	1.4	11
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8198	Estuarine benthic nitrate reduction rates: Potential role of microalgae?. <i>Estuarine, Coastal and Shelf Science</i> , 2021, 257, 107394.	0.9	4
8199	Degradation of antibiotic resistance genes and mobile gene elements in dairy manure anaerobic digestion. <i>PLoS ONE</i> , 2021, 16, e0254836.	1.1	11
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8225	Decomposition of peatland DOC affected by root exudates is driven by specific r and K strategic bacterial taxa. <i>Scientific Reports</i> , 2021, 11, 18677.	1.6	10
8226	Periphytic Microbial Response to Environmental Phosphate (P) Bioavailability and Its Relevance to P Management in Paddy Fields. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0120121.	1.4	4
8227	Impact of Hinoki Cypress Wood on Diversity of Microflora: A Case Study from Owase City Hall. <i>Diversity</i> , 2021, 13, 473.	0.7	2
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8231	Effects of iron-carbon materials on microbial-catalyzed reductive dechlorination of polychlorinated biphenyls in Taihu Lake sediment microcosms: Enhanced chlorine removal, detoxification and shifts of microbial community. <i>Science of the Total Environment</i> , 2021, 792, 148454.	3.9	11
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8241	Culture-dependent PCR-DGGE-based fingerprinting to trace fishing origin or storage history of gilthead seabream. <i>Food Control</i> , 2021, 130, 108398.	2.8	0
8242	Comparative characterization of microbial communities that inhabit PFAS-rich contaminated sites: A case-control study. <i>Journal of Hazardous Materials</i> , 2022, 423, 126941.	6.5	27
8243	Molecular techniques and current research approaches. , 2022, , 195-229.		1
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9741	Effects of anthropogenic stress on hosts and their microbiomes: Treated wastewater alters performance and gut microbiome of a key detritivore (<i>Asellus aquaticus</i>). <i>Evolutionary Applications</i> , 2023, 16, 824-848.	1.5	0
9742	Responses of Soil Microbial Community to Herbicide Atrazine Contamination. <i>Water, Air, and Soil Pollution</i> , 2023, 234, .	1.1	5
9743	PATHOGENIC POLLUTION OF CROPS CAUSING BY CHIKEN MANURE BASED FERTILIZERS. , 2022, , .		0
9744	Soil Suppressiveness Against <i>Pythium ultimum</i> and <i>Rhizoctonia solani</i> in Two Land Management Systems and Eleven Soil Health Treatments. <i>Microbial Ecology</i> , 0, , .	1.4	1
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9746	Rumen microbial community and milk quality in Holstein lactating cows fed olive oil pomace as part in a sustainable feeding strategy. <i>Animal</i> , 2023, 17, 100815.	1.3	1
9747	Acclimation, manganese removal, and backwash impact on full-scale drinking water biofilter microbiome. <i>AWWA Water Science</i> , 2023, 5, .	1.0	0
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9773	Microbial Biofilms in Wastewater Remediation. , 2023, , 101-118.		0
9829	Microbial aerosols: analytical methods, dispersal mechanisms and health risk assessment. , 2024, , 35-62.		0
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9884	NGS profiling of water and soil microbial DNA in forensic science. , 2024, , 375-385.		0
9891	Development of microbial biotechnology products for phytopathogen management. , 2024, , 105-130.		0

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9910	Granular Sludgeâ€™State of the Art. Springer Theses, 2024, , 37-163.	0.0	0
9911	Use of PCR-DGGE-Based Molecular Methods to Analyze Nematode Community Diversity. Methods in Molecular Biology, 2024, , 247-255.	0.4	0