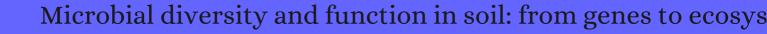
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1341	Genomic signature tags (GSTs): a system for profiling genomic DNA. 2002 , 12, 1756-65		26
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1339	Structure and mechanism of a bacterial haloalcohol dehalogenase: a new variation of the short-chain dehydrogenase/reductase fold without an NAD(P)H binding site. 2003 , 22, 4933-44		89
1338	Diversity of Actinoplanes and related genera isolated from an Italian soil. 2003, 45, 362-72		22
1337	A rhizospheric Burkholderia cepacia complex population: genotypic and phenotypic diversity of Burkholderia cenocepacia and Burkholderia ambifaria. 2003 , 46, 179-87		24
1336	Microbial diversity and functional characterization of sediments from reservoirs of different trophic state. 2003 , 46, 331-47		113
1335	Sampling strategy in molecular microbial ecology: influence of soil sample size on DNA fingerprinting analysis of fungal and bacterial communities. 2003 , 5, 1111-20		192
1334	Functional gene diversity analysis in BTEX contaminated soils by means of PCR-SSCP DNA fingerprinting: comparative diversity assessment against bacterial isolates and PCR-DNA clone libraries. 2004 , 6, 95-110		73
1333	Genomics tools in environmental impact assessment. 2003 , 37, 356A-363A		23
1332	Amplified functional DNA restriction analysis to determine catechol 2,3-dioxygenase gene diversity in soil bacteria. 2003 , 55, 697-708		36
1331	Resolving functional diversity in relation to microbial community structure in soil: exploiting genomics and stable isotope probing. <i>Current Opinion in Microbiology</i> , 2003 , 6, 295-301	7.9	115
1330	Metagenome survey of biofilms in drinking-water networks. 2003 , 69, 7298-309		156
1329	Prospecting for novel biocatalysts in a soil metagenome. 2003 , 69, 6235-42		239
1328	Improved efficacy of whole genome amplification from bacterial cells. 2004 , 37, 40, 42, 44		12
1327	. 2004,		20
1326	Development of negative feedback during successive growth cycles of black cherry. 2004 , 271, 317-24		51
1325	Denaturing gradient gel electrophoretic analysis of ammonia-oxidizing bacterial community structure in the lower Seine River: impact of Paris wastewater effluents. 2004 , 70, 6726-37		99

1324	GigaMatrix🛮An Ultra High-Throughput Tool for Accessing Biodiversity. 2004 , 9, 200-208	10
1323	Enzyme production-based approach for determining the functions of microorganisms within a community. 2004 , 70, 3329-37	19
1322	Amazonian Dark Earths Biological Measurements. 2003 , 287-332	1
1321	Pharmacogenomic strategies against resistance development in microbial infections. 2004 , 5, 361-79	8
1320	Assessment of intra-species diversity among strains of Acinetobacter baumannii isolated from sites contaminated with petroleum hydrocarbons. 2004 , 50, 405-14	23
1319	Spatial and temporal changes in microbial community structure associated with recharge-influenced chemical gradients in a contaminated aquifer. 2004 , 6, 438-48	70
1318	Suppressive subtractive hybridization as a tool for identifying genetic diversity in an environmental metagenome: the rumen as a model. 2004 , 6, 928-37	77
1317	Identification and phylogenetic sorting of bacterial lineages with universally conserved genes and proteins. 2004 , 6, 754-9	183
1316	Quantifying the accessibility of the metagenome by random expression cloning techniques. 2004 , 6, 879-86	182
1315	Characterization of large-insert DNA libraries from soil for environmental genomic studies of Archaea. 2004 , 6, 970-80	88
1314	Microbial diversity in soil: selection microbial populations by plant and soil type and implications for disease suppressiveness. 2004 , 42, 243-70	923
1313	The soil metagenomea rich resource for the discovery of novel natural products. 2004 , 15, 199-204	236
1312	Genetic diversity of bacterial communities of serpentine soil and of rhizosphere of the nickel-hyperaccumulator plant Alyssum bertolonii. 2004 , 48, 209-17	44
1311	Soil water content and organic carbon availability are major determinants of soil microbial community composition. 2004 , 48, 424-30	377
1310	Spatial variation in Streptomyces genetic composition and diversity in a prairie soil. 2004 , 48, 601-12	36
1309	Environmental genomics: exploring the unmined richness of microbes to degrade xenobiotics. 2004 , 66, 123-30	87
1308	Screening for novel lipolytic enzymes from uncultured soil microorganisms. 2004 , 65, 720-6	128
1307	Prospecting for biocatalysts and drugs in the genomes of non-cultured microorganisms. 2004 , 15, 285-90	82

1306	Novel Biocatalysts by Identification and Design. 2004 , 22, 141-146	19
1305	Degradation of polycyclic aromatic hydrocarbons by a newly discovered enteric bacterium, Leclercia adecarboxylata. 2004 , 70, 3163-6	76
1304	Rhizosphere bacterial signalling: a love parade beneath our feet. 2004 , 30, 205-40	379
1303	Metagenomics: application of genomics to uncultured microorganisms. 2004 , 68, 669-85	1494
1302	References. 2004 , 327-373	
1301	Bacterial communities and enzyme activities of PAHs polluted soils. 2004 , 57, 401-12	220
1300	Unravelling rhizosphere-microbial interactions: opportunities and limitations. 2004 , 12, 386-93	335
1299	Genomics for the ecological toolbox. 2004 , 19, 439-45	76
1298	Immunological method for direct assessment of the functionality of a denitrifying strain of Pseudomonas fluorescens in soil. 2004 , 58, 13-21	10
1297	Proteomics as a Tool to Study Microbial Interactions. 2004 , 1, 27-34	6
1296	Microbial Biomass, Abundance and Community Diversity Determined by Terminal Restriction Fragment Length Polymorphism Analysis in Soil at Varying Periods after Occurrence of Forest Fire. 2004 , 19, 154-162	8
1295	Microbial Diversity and Genomics. 2005 , 21-40	1
1294	Characterization of a deep-sea microbial mat from an active cold seep at the Milano mud volcano in the Eastern Mediterranean Sea. 2005 , 54, 47-56	45
1293	Microbial enzymes mined from the Urania deep-sea hypersaline anoxic basin. 2005 , 12, 895-904	134
1292	Diversity of functional genes of methanogens, methanotrophs and sulfate reducers in deep-sea hydrothermal environments. 2005 , 7, 118-32	86
1291	Analysis of the distribution and diversity in recent Hawaiian volcanic deposits of a putative carbon monoxide dehydrogenase large subunit gene. 2005 , 7, 1405-12	19
1290	The metagenomics of soil. 2005 , 3, 470-8	540
1289	Community analysis of a full-scale anaerobic bioreactor treating paper mill wastewater. 2005 , 28, 175-85	170

(2005-2005)

1288 Accessing microbial diversity for bioremediation and environmental restoration. 2005 , 23, 135-42		198
1287 Metagenomic gene discovery: past, present and future. 2005 , 23, 321-9		214
1286 "In-gel patch electrophoresis:" a new method for environmental DNA purification. 2005 , 26, 3055-61		12
$_{1285}$ Characterization of fungal community structure on a weathered pegmatitic granite. 2005 , 50, 360-8		95
Microbial community structure and density under different tree species in an acid forest soil (Morvan, France). 2005 , 50, 614-25		89
Effect of carbon and nitrogen input on the bacterial community structure of Neocaledonian nickel mine spoils. 2005 , 51, 333-40		12
Molecular detection of Fusarium oxysporum f. sp. niveum and Mycosphaerella melonis in infected plant tissues and soil. 2005 , 249, 39-47		82
Phospholipases: Occurrence and production in microorganisms, assay for high-throughput screening, and gene discovery from natural and man-made diversity. 2005 , 82, 691-705		24
1280 Promising Strategies for the Mineralisation of 2,4,6-trinitrotoluene. 2005 , 4, 39-60		33
1279 References. 2005 , 499-574		
1278 BACTERIA Soil. 2005 , 115-122		
Molecular diversity and biomass of epilithic biofilms from intertidal rocky shores in the Gulf of Mexico. 2005 , 2, 93-103		10
1276 Marker Genes in Soil Microbiology. 2005 , 359-382		
Contribution of nanosized bacteria to the total biomass and activity of a soil microbial community. 2005 , 57, 245-96		36
Design of long oligonucleotide probes for functional gene detection in a microbial community. 2005 , 21, 4092-100		24
1273 Microorganisms in Soils: Roles in Genesis and Functions. 2005 ,		7
Characterization of a forest soil metagenome clone that confers indirubin and indigo production on Escherichia coli. 2005 , 71, 7768-77		111
Microbial diversitythe bright and promising future of microbial manufacturing. <i>Current Opinion in Microbiology</i> , 2005 , 8, 229-33	7.9	5

1270	Semi-automated genetic analyses of soil microbial communities: comparison of T-RFLP and RISA based on descriptive and discriminative statistical approaches. 2005 , 61, 349-60	92
1269	High molecular weight DNA recovery from soils prerequisite for biotechnological metagenomic library construction. 2005 , 62, 1-11	101
1268	Microbial gene expression in soil: methods, applications and challenges. 2005 , 63, 1-19	102
1267	Methods of microbial community profiling and their application to forest soils. 2005 , 220, 88-106	130
1266	The use of microorganisms in ecological soil classification and assessment concepts. 2005 , 62, 230-48	183
1265	Linking species richness, biodiversity and ecosystem function in soil systems. 2005 , 49, 479-497	133
1264	Soil feedbacks of plant diversity on soil microbial communities and subsequent plant growth. 2005 , 7, 27-49	170
1263	Molecular approaches to the assessment of biodiversity in aquatic microbial communities. 2005 , 39, 2207-18	89
1262	Bacterial activity in cystic fibrosis lung infections. 2005 , 6, 49	69
1261	EFFECTS OF GRAZING ON MICROBIAL FUNCTIONAL GROUPS INVOLVED IN SOIL N DYNAMICS. 2005 , 75, 65-80	164
1260	Extreme environments as a resource for microorganisms and novel biocatalysts. 2005 , 96, 219-62	69
1259	Immune Mechanisms in Inflammatory Bowel Disease. 2006,	6
1258	Do microorganisms influence seed-bank dynamics?. 2006 , 54, 575-587	101
1257	Accessing the black box of microbial diversity and ecophysiology: recent advances through polyphasic experiments. 2006 , 41, 897-922	33
1256	Environment arrays: a possible approach for predicting changes in waterborne bacterial disease potential. 2006 , 40, 7150-6	12
1255	Influence of planting papaya ringspot virus resistant transgenic papaya on soil microbial biodiversity. 2006 , 54, 130-7	19
1254	Polyphasic characterization of the bacterial community in an urban soil profile with in situ and culture-dependent methods. 2006 , 31, 267-279	35
1253	Community structures and substrate utilization of bacteria in soils from organic and conventional farming systems of the DOK long-term field experiment. 2006 , 33, 294-307	89

(2006-2006)

1252	Isolation of the non-fastidious microalga with astaxanthin-accumulating property and its potential for application to aquaculture. 2006 , 261, 285-293	17
1251	Evaluation of quantitative and qualitative recovery of bacterial communities from different soil types by density gradient centrifugation. 2006 , 42, 65-73	64
1250	Archaeal habitatsfrom the extreme to the ordinary. 2006 , 52, 73-116	165
1249	The Structure and Function of Microbial Communities. 2006 , 299-327	4
1248	Use of functional genes to quantify denitrifiers in the environment. 2006 , 34, 101-3	34
1247	Development and validation of a prototype 16S rRNA-based taxonomic microarray for Alphaproteobacteria. 2006 , 8, 289-307	82
1246	Structural diversity of bacterial communities in a heavy metal mineralized granite outcrop. 2006 , 8, 383-93	24
1245	Soil biota and invasive plants. 2006 , 170, 445-57	501
1244	Diagnostic microbial microarrays in soil ecology. 2006 , 171, 719-35	73
1243	Thauera and Azoarcus as functionally important genera in a denitrifying quinoline-removal bioreactor as revealed by microbial community structure comparison. 2006 , 55, 274-86	131
1242	The influence of synthetic sheep urine on ammonia oxidizing bacterial communities in grassland soil. 2006 , 56, 444-54	33
1241	Molecular detection of Phytophthora capsici in infected plant tissues, soil and water. 2006 , 55, 770-775	34
1240	Investigating microbial community structure in soils by physiological, biochemical and molecular fingerprinting methods. 2006 , 57, 72-82	83
1239	Exploration of soil bacterial communities for their potential as bioresource. 2006 , 97, 2217-24	36
1238	Antibiotika als Umweltkontaminanten Œffekte auf Bodenbakterien. 2006 , 18, 110-118	4
1237	Gene Detection, Expression and Related Enzyme Activity in Soil. 2006 , 217-255	9
1236	Potential Inoculum Sources of in South African Grapevine Nurseries. 2006 , 115, 331-339	41
1235	Cyanobacterial flora from polluted marine shores. 2006 , 120, 407-14	9

1234	Cyanobacterial flora from polluted industrial effluents. 2006 , 116, 91-102	7
1233	Rationalizing molecular analysis of field-collected roots for assessing diversity of arbuscular mycorrhizal fungi: to pool, or not to pool, that is the question. 2006 , 16, 525-531	42
1232	Relationships between microbial community structure and soil processes under elevated atmospheric carbon dioxide. 2006 , 51, 302-14	47
1231	Characterization of bacterial community structure on a weathered pegmatitic granite. 2006 , 51, 526-34	92
1230	Microarray applications in microbial ecology research. 2006 , 52, 159-75	155
1229	Microbial community structure in three deep-sea carbonate crusts. 2006 , 52, 451-62	30
1228	The influence of tropical plant diversity and composition on soil microbial communities. 2006 , 52, 226-38	95
1227	FeeM, an N-acyl amino acid synthase from an uncultured soil microbe: structure, mechanism, and acyl carrier protein binding. 2006 , 14, 1425-35	31
1226	Influence of plant diversity and elevated atmospheric carbon dioxide levels on belowground bacterial diversity. 2006 , 6, 68	56
1225	Natural Pseudomonas sp. strain N3 in artificial soil microcosms. 2006 , 72, 2385-9	21
1224	Variation in dissolved organic matter controls bacterial production and community composition. 2006 , 87, 2068-79	217
1223	Plant-associated bacteria: survey, molecular phylogeny, genomics and recent advances. 2007 , 1-56	30
1222	Molecular Techniques for Understanding the Microbial Community Structure in Mycorrhizosphere. 2006 , 173-198	1
1221	Variations of bacterial community structure in flooded paddy soil contaminated with herbicide quinclorac. 2006 , 41, 821-32	12
122 0	Microbial Activity in the Rhizoshere. 2006,	33
1219	Quantitative assessment of protein function prediction from metagenomics shotgun sequences. 2007 , 104, 13913-8	66
1218	A fast and flexible approach to oligonucleotide probe design for genomes and gene families. 2007 , 23, 1195-202	28
1217	Molecular microbial community structure of the Regenerative Enclosed Life Support Module Simulator air system. 2007 , 6, 131-145	17

1216	Soil Microbial Community Analysis Using Denaturing Gradient Gel Electrophoresis. 2007, 71, 562-571	95
1215	Species richness and phylogenetic diversity comparisons of soil microbial communities affected by nickel-mining and revegetation efforts in New Caledonia. 2007 , 43, 130-139	39
1214	Molecular cloning and functional characterization of a novel decarboxylase from uncultured microorganisms. 2007 , 357, 421-6	21
1213	Bacterial community structure in soils contaminated by polycyclic aromatic hydrocarbons. 2007 , 68, 1535-41	62
1212	Biogeochemistry in Mineral Exploration. 2007 , 9, xiii-460	49
1211	Accessing the mobile metagenome of the human gut microbiota. 2007 , 3, 749-58	21
121 0	Advanced Techniques in Soil Microbiology. 2007,	6
1209	Applications of molecular ecology to IPM: what impact?. 469-521	
1208	Extraction of inhibitor-free metagenomic DNA from polluted sediments, compatible with molecular diversity analysis using adsorption and ion-exchange treatments. 2007 , 98, 761-8	86
1207	Genome-wide high-throughput mining of natural-product biosynthetic gene clusters by phage display. 2007 , 14, 303-12	49
1206	Physical constraints affecting bacterial habitats and activity in unsaturated porous media 🗈 review. 2007 , 30, 1505-1527	424
1205	Impact of a new biopesticide produced by Paenibacillus sp. strain B2 on the genetic structure and density of soil bacterial communities. 2007 , 63, 269-75	10
1204	Visualization, modelling and prediction in soil microbiology. 2007 , 5, 689-99	122
1203	Impact of elevated carbon dioxide on the rhizosphere communities of Carex arenaria and Festuca rubra. 2007 , 13, 2396-2410	64
1202	Relationships between temperature responses and bacterial community structure along seasonal and altitudinal gradients. 2007 , 59, 418-27	111
1201	Single particle analysis reveals that bacterial community structures are semi-specific to the type of soil particle. 2007 , 53, 740-743	9
12 00	Ecological impact of application of wastewater biosolids to agricultural soil. 2007, 21, 34-40	8
1199	Nano-scale secondary ion mass spectrometry [A new analytical tool in biogeochemistry and soil ecology: A review article. 2007 , 39, 1835-1850	152

1198	Long-term exposure to Zn-spiked sewage sludge alters soil community structure. 2007 , 39, 2576-2586	31
1197	Detection and Diversity of Fungi from Environmental Samples: Traditional Versus Molecular Approaches. 2007 , 1-15	21
1196	Analysis of diurnal and vertical microbial diversity of a hypersaline microbial mat. 2007, 188, 137-46	27
1195	Protein extraction and fingerprinting optimization of bacterial communities in natural environment. 2007 , 53, 426-34	37
1194	Relationships between soil organic status and microbial community density and genetic structure in two agricultural soils submitted to various types of organic management. 2007 , 53, 650-63	53
1193	Use of 16S rRNA gene based clone libraries to assess microbial communities potentially involved in anaerobic methane oxidation in a Mediterranean cold seep. 2007 , 53, 384-98	71
1192	Metaproteomics: a new approach for studying functional microbial ecology. 2007 , 53, 486-93	173
1191	Growth on dichlorobiphenyls with chlorine substitution on each ring by bacteria isolated from contaminated African soils. 2007 , 74, 484-92	22
1190	Comparison of methods for total community DNA extraction and purification from compost. 2007 , 74, 918-25	69
1189	Metagenomics, biotechnology with non-culturable microbes. 2007 , 75, 955-62	225
	Metagenomics, biotechnology with non-culturable microbes. 2007, 75, 955-62 DNA extraction method affects microbial community profiles from soils and sediment. 2007, 77, 955-64	225
1188	DNA extraction method affects microbial community profiles from soils and sediment. 2007 , 77, 955-64 Isolation and characterization of two new microbial strains capable of degradation of the naturally	
1188	DNA extraction method affects microbial community profiles from soils and sediment. 2007 , 77, 955-64 Isolation and characterization of two new microbial strains capable of degradation of the naturally occurring organophosphonate - ciliatine. 2007 , 18, 223-31	121 7
1188 1187 1186	DNA extraction method affects microbial community profiles from soils and sediment. 2007, 77, 955-64 Isolation and characterization of two new microbial strains capable of degradation of the naturally occurring organophosphonate - ciliatine. 2007, 18, 223-31 The rhizosphere: complex by design. 2008, 312, 1-6 Characterizing cultivable soil microbial communities from copper fungicide-amended olive orchard and vineyard soils. 2008, 24, 309-318	121 7 65
1188 1187 1186	DNA extraction method affects microbial community profiles from soils and sediment. 2007, 77, 955-64 Isolation and characterization of two new microbial strains capable of degradation of the naturally occurring organophosphonate - ciliatine. 2007, 18, 223-31 The rhizosphere: complex by design. 2008, 312, 1-6 Characterizing cultivable soil microbial communities from copper fungicide-amended olive orchard and vineyard soils. 2008, 24, 309-318	7 65 32
1188 1187 1186 1185	DNA extraction method affects microbial community profiles from soils and sediment. 2007, 77, 955-64 Isolation and characterization of two new microbial strains capable of degradation of the naturally occurring organophosphonate - ciliatine. 2007, 18, 223-31 The rhizosphere: complex by design. 2008, 312, 1-6 Characterizing cultivable soil microbial communities from copper fungicide-amended olive orchard and vineyard soils. 2008, 24, 309-318 Molecular diversity of 16S rRNA and gyrB genes in copper mines. 2008, 189, 101-10 The modulating role of dissolved organic matter on spatial patterns of microbial metabolism in	121 7 65 32 33

1180	Fungal Taxa Target Different Carbon Sources in Forest Soil. 2008 , 11, 1157-1167	141
1179	Effect of 2,4,6-trinitrotoluene on soil bacterial communities. 2008 , 35, 225-36	32
1178	New insights into polylactide biodegradation from molecular ecological techniques. 2008 , 8, 304-15	54
1177	Molecular Mechanisms of Plant and Microbe Coexistence. 2008,	25
1176	Effect of elevated CO2 and drought on soil microbial communities associated with Andropogon gerardii. 2008 , 50, 1406-15	21
1175	Differences in vegetation composition and plant species identity lead to only minor changes in soil-borne microbial communities in a former arable field. 2008 , 63, 372-82	107
1174	Comparison of deep-sea sediment microbial communities in the Eastern Mediterranean. 2008 , 64, 362-77	58
1173	Local adaptation of microbial communities to heavy metal stress in polluted sediments of Lake Erie. 2008 , 65, 156-68	66
1172	High aromatic ring-cleavage diversity in birch rhizosphere: PAH treatment-specific changes of I.E.3 group extradiol dioxygenases and 16S rRNA bacterial communities in soil. 2008 , 2, 968-81	79
1171	Molecular eco-systems biology: towards an understanding of community function. 2008 , 6, 693-9	284
1170	High temporal resolution tracing of photosynthate carbon from the tree canopy to forest soil microorganisms. 2008 , 177, 220-228	285
1169	Fruiting body and soil rDNA sampling detects complementary assemblage of Agaricomycotina (Basidiomycota, Fungi) in a hemlock-dominated forest plot in southern Ontario. 2008 , 17, 3037-50	6 7
1168	Isolation of a low-temperature adapted lipolytic enzyme from uncultivated micro-organism. 2008 , 105, 116-23	42
1167	Microbial DNA profiling by multiplex terminal restriction fragment length polymorphism for forensic comparison of soil and the influence of sample condition. 2008 , 105, 813-21	32
1166	Gene prediction in metagenomic fragments: a large scale machine learning approach. 2008, 9, 217	66
1165	Predicting biological networks from genomic data. 2008 , 582, 1251-8	33
1164	Emerging high-throughput approaches to analyze bioremediation of sites contaminated with hazardous and/or recalcitrant wastes. 2008 , 26, 561-75	54
1163	Differences in the composition and diversity of bacterial communities from agricultural and forest soils. 2008 , 40, 1294-1305	81

1162	Assessment of fungal communities in soil and tomato roots subjected to diverse land and crop management systems. 2008 , 40, 1967-1970	20
1161	Quantitative assessment of the fungal contribution to microbial tissue in soil. 2008 , 40, 2977-2991	415
1160	Biodiversity, chemical diversity and drug discovery. 2008 , 65, 141, 143-74	21
1159	Effects of Root Exudates in Microbial Diversity and Activity in Rhizosphere Soils. 2008, 339-365	46
1158	FEATHER-DEGRADING BACTERIA: A NEW FRONTIER IN AVIAN AND HOSTPARASITE RESEARCH?. 2008 , 125, 972-979	59
1157	Molecular Methods for Studying Microbial Ecology in the Soil and Rhizosphere. 2008, 411-436	1
1156	Natural Compounds as Drugs Volume I. 2008 ,	5
1155	Understanding the Biomass Decay Community. 454-479	3
1154	Chapter 21 Microbial activities, monitoring and application as part of a management strategy for heavy metal-contaminated soil and ground water. 2008 , 32, 521-559	3
1153	CE-SSCP and CE-FLA, simple and high-throughput alternatives for fungal diversity studies. 2008 , 72, 42-53	26
1152	A novel retrieval system for nearly complete microbial genomic fragments from soil samples. 2008 , 72, 197-205	10
1151	Influence of irrigated agriculture on soil microbial diversity. 2008, 40, 146-154	26
1150	Protein and DNA fingerprinting of a soil bacterial community inoculated into three different sterile soils. 2008 , 159, 231-6	11
1149	Colloquium paper: resistance, resilience, and redundancy in microbial communities. 2008 , 105 Suppl 1, 11512-9	1594
1148	Novel weapons: invasive plant suppresses fungal mutualists in America but not in its native Europe. 2008 , 89, 1043-55	381
1147	Past, present and future of soil quality indices: A biological perspective. 2008 , 147, 159-171	413
1146	Microbial PAH degradation. 2008, 65, 27-66	47
1145	Soil health in agricultural systems. 2008 , 363, 685-701	494

(2009-2008)

1144	geochemically variable soil profile. 2008 , 74, 1620-33	341
1143	Development of microbial genome-probing microarrays using digital multiple displacement amplification of uncultivated microbial single cells. 2008 , 42, 6058-64	23
1142	Experimental approach for deep proteome measurements from small-scale microbial biomass samples. 2008 , 80, 9517-25	27
1141	Microarray-based characterization of microbial community functional structure and heterogeneity in marine sediments from the Gulf of Mexico. 2008 , 74, 4516-29	87
1140	Development of a water state index to assess the severity of impacts on and changes in natural water resources. 2008 , 58, 1595-600	
1139	Short-term response of soil bacteria to carbon enrichment in different soil microsites. 2008 , 74, 5589-92	16
1138	Diversity and Potential of Nonsymbiotic Diazotrophic Bacteria in Promoting Plant Growth. 81-109	9
1137	Global sequencing: a review of current molecular data and new methods available to assess microbial diversity. 2008 , 23, 253-68	58
1136	MODERN APPROACHES FOR THE STUDY OF s-TRIAZINE HERBICIDE BIOREMEDIATION IN AGRICULTURAL SOILS. 2008 , 8,	
1135	Temporal Shifts in Microbial Communities in Nonpregnant African-American Women with and without Bacterial Vaginosis. 2008 , 2008, 181253	15
1135	without Bacterial Vaginosis. 2008, 2008, 181253	15
	without Bacterial Vaginosis. 2008, 2008, 181253	
1134	without Bacterial Vaginosis. 2008, 2008, 181253 . 2008, Inference in incidence, infection, and impact: co-infection of multiple hosts by multiple pathogens.	18
1134	without Bacterial Vaginosis. 2008, 2008, 181253 . 2008, Inference in incidence, infection, and impact: co-infection of multiple hosts by multiple pathogens. 2009, 4, Linking sequence to function in soil bacteria: sequence-directed isolation of novel bacteria	18
1134 1133 1132	. 2008, Inference in incidence, infection, and impact: co-infection of multiple hosts by multiple pathogens. 2009, 4, Linking sequence to function in soil bacteria: sequence-directed isolation of novel bacteria contributing to soilborne plant disease suppression. 2009, 75, 915-24	18 6 53
1134 1133 1132 1131	. 2008, Inference in incidence, infection, and impact: co-infection of multiple hosts by multiple pathogens. 2009, 4, Linking sequence to function in soil bacteria: sequence-directed isolation of novel bacteria contributing to soilborne plant disease suppression. 2009, 75, 915-24 Bioremediation of Polluted Soil. 2009, 103-121	18 6 53 6
1134 1133 1132 1131 1130	without Bacterial Vaginosis. 2008, 2008, 181253 . 2008, Inference in incidence, infection, and impact: co-infection of multiple hosts by multiple pathogens. 2009, 4, Linking sequence to function in soil bacteria: sequence-directed isolation of novel bacteria contributing to soilborne plant disease suppression. 2009, 75, 915-24 Bioremediation of Polluted Soil. 2009, 103-121 DNA-based stable isotope probing: a link between community structure and function. 2009, 407, 3611-9	18 6 53 6 67

1126	Identifying natural product biosynthetic genes from a soil metagenome by using T7 phage selection. 2009 , 10, 2599-606	10
1125	Identifying the Relative Importance of Leaf versus Shredder Species Loss on Litter Decomposition in Streams. 2009 , 94, 452-471	7
1124	Optimization of metagenomic DNA extraction from activated sludge samples. 2009 , 4, 780-786	6
1123	Diversity and functional responses of nitrogen-fixing microbes to three wetland invasions. 2009 , 11, 225-239	25
1122	The trade-off between growth rate and yield in microbial communities and the consequences for under-snow soil respiration in a high elevation coniferous forest. 2009 , 95, 23-35	89
1121	Dynamics of microbial growth and coexistence on variably saturated rough surfaces. 2009 , 58, 262-75	32
1120	Enhancement of the microbial community biomass and diversity during air sparging bioremediation of a soil highly contaminated with kerosene and BTEX. 2009 , 82, 565-77	50
1119	Chemical characterization of soil extract as growth media for the ecophysiological study of bacteria. 2009 , 83, 161-73	69
1118	Diversity of total, nitrogen-fixing and denitrifying bacteria in an acid forest soil. 2009 , 60, 883-894	14
1117	Soil metaproteomics: a review of an emerging environmental science. Significance, methodology and perspectives. 2009 , 60, 845-859	88
1116	Microbial leaf degraders in boreal streams: bringing together stochastic and deterministic regulators of community composition. 2009 , 54, 2276-2289	12
1115	Comparison of DNA- and RNA-based bacterial community structures in soil exposed to 2,4-dichlorophenol. 2009 , 107, 1883-93	22
1114	Evaluation of the effect of late blight-resistant potato plants on the structure of bacterial associations in soil. 2009 , 45, 194-198	3
1113	A plasmid RK2-based broad-host-range cloning vector useful for transfer of metagenomic libraries to a variety of bacterial species. 2009 , 296, 149-58	77
1112	Integrative approaches for assessing the ecological sustainability of in situ bioremediation. 2009 , 33, 324-75	123
1111	Systemic approaches to biodegradation. 2009 , 33, 98-108	47
1110	Effect of continuous olive mill wastewater applications, in the presence and absence of nitrogen fertilization, on the structure of rhizosphere-soil fungal communities. 2009 , 70, 388-401	21
1109	Bacterial community dynamics during bioremediation of phenanthrene- and fluoranthene-amended soil. 2009 , 63, 52-56	45

(2009-2009)

1108	Characterization of the bottom sediments contaminated with polychlorinated biphenyls: Evaluation of ecotoxicity and biodegradability. 2009 , 63, 440-449	19
1107	Complementary cooperation between two syntrophic bacteria in pesticide degradation. 2009 , 256, 644-54	38
1106	Bacterial phylogenetic diversity in a Spartina marsh in China. 2009 , 35, 529-535	7
1105	Biochemical characterization of a metagenome-derived decarboxylase. 2009 , 45, 58-63	7
1104	Assessment of the bacterial diversity in soils: Evolution of approaches and methods. 2009 , 42, 1138-1147	8
1103	Terrestrial ecotoxicological effects of the antimicrobial agent triclosan. 2009 , 72, 86-92	88
1102	Inoculation of wheat with Azospirillum brasilense and Pseudomonas fluorescens: Impact on the production and culturable rhizosphere microflora. 2009 , 45, 44-51	82
1101	Enhanced removal of 1,2-dichloroethane by anodophilic microbial consortia. 2009 , 43, 2936-46	99
1100	Use of the frc gene as a molecular marker to characterize oxalate-oxidizing bacterial abundance and diversity structure in soil. 2009 , 76, 120-7	21
1099	Functional principal component data analysis: a new method for analysing microbial community fingerprints. 2009 , 79, 89-95	19
1098	Factors Affecting the Variation of Microbial Communities in Different Agro-Ecosystems. 2009 , 301-324	7
1097	Bacterial Communities in Natural Ecosystems. 2009 , 347-356	1
1096	Advances in Applied Bioremediation. 2009,	36
1095	Bacterial diversity analysis of Huanglongbing pathogen-infected citrus, using PhyloChip arrays and 16S rRNA gene clone library sequencing. 2009 , 75, 1566-74	106
1094	Assessment of bias associated with incomplete extraction of microbial DNA from soil. 2009 , 75, 5428-33	225
1093	Gene-centric metagenomics of the fiber-adherent bovine rumen microbiome reveals forage specific glycoside hydrolases. 2009 , 106, 1948-53	495
1092	Application of the 50-mer Oligonucleotide Arrays Hybridization for Profiling Microbial Community in Acid Mine Drainage Sediment. 2009 ,	1
1091	Spatial and temporal diversity of methanotrophs in a landfill cover soil are differentially related to soil abiotic factors. 2009 , 1, 398-407	30

1090	Microbial activity in contrasting conditions of soil C and N availability in a tropical dry forest. 2009 , 25, 401-413	7
1089	Volatile Organic Metabolites as Indicators of Soil Microbial Activity and Community Composition Shifts. 2009 , 73, 579-588	50
1088	Effects of Treated Municipal Wastewater Irrigation on Soil Microbiology. 2010 , 351-381	
1087	Current taxonomy of common foodborne bacteria. 2010 , 39, 471-487	2
1086	Comparative analysis of acidobacterial genomic fragments from terrestrial and aquatic metagenomic libraries, with emphasis on acidobacteria subdivision 6. 2010 , 76, 6769-77	24
1085	Microbial community diversity of moonmilk deposits at Ballynamintra Cave, Co. Waterford, Ireland. 2010 , 60, 753-61	20
1084	Bioaugmentation of a sequencing batch reactor with Pseudomonas putida ONBA-17, and its impact on reactor bacterial communities. 2010 , 176, 20-6	34
1083	An improved method for extracting bacteria from soil for high molecular weight DNA recovery and BAC library construction. 2010 , 48, 728-33	26
1082	Effects of elevated CO2, water stress, and inoculation with Glomus intraradices or Pseudomonas mendocina on lettuce dry matter and rhizosphere microbial and functional diversity under growth chamber conditions. 2010 , 10, 1585-1597	25
1081	Soil microbial population dynamics along a chronosequence of moist evergreen broad-leaved forest succession in southwestern China. 2010 , 7, 327-338	9
1080	Microbial community structure and diversity in a native forest wood-decomposed hollow-stump ecosystem. 2010 , 26, 233-240	14
1079	Effect of monospecific and mixed Cunninghamia lanceolata plantations on microbial community and two functional genes involved in nitrogen cycling. 2010 , 327, 413-428	18
1078	Bacterial soil community in a Brazilian sugarcane field. 2010 , 336, 337-349	15
1077	Not a peripheral issue: secretion in plant-microbe interactions. 2010 , 13, 378-87	76
1076	Shifts in bacterial community structure associated with inputs of low molecular weight carbon compounds to soil. 2010 , 42, 896-903	316
1075	Size Does Matter: Application-driven Approaches for Soil Metagenomics. 2010 , 42, 1911-1923	84
1074	Long-term no-till management affects microbial biomass but not community composition in Canadian prairie agroecosytems. 2010 , 42, 2192-2202	82
1073	Detecting variants with Metabolic Design, a new software tool to design probes for explorative functional DNA microarray development. 2010 , 11, 478	10

1072 Assessment of fatty acid as a differentiator of usages of urban soils. 2010 , 81, 968-75	9
Effectiveness of inoculation with isolated Geobacillus strains in the thermophilic stage of vegetable waste composting. 2010 , 101, 2892-5	47
1070 Use of metagenomic approaches to isolate lipolytic genes from activated sludge. 2010 , 101, 8323-9	36
Comparison of bioclogging effects in saturated porous media within one- and two-dimensional flow systems. 2010 , 36, 176-196	110
1068 Global ecological patterns in uncultured Archaea. 2010 , 4, 182-90	312
1067 Identifying active phage lysins through functional viral metagenomics. 2010 , 76, 7181-7	34
The large-scale organization of the bacterial network of ecological co-occurrence interactions. 2010 , 38, 3857-68	193
1065 Low pore connectivity increases bacterial diversity in soil. 2010 , 76, 3936-42	181
1064 FragGeneScan: predicting genes in short and error-prone reads. 2010 , 38, e191	535
Molecular Characterization of the Archaeal Diversity in Vlasa Hot Spring, Bulgaria, by using 16S rRNA and Glycoside Hydrolase Family 4 Genes. 2010 , 24, 1979-1985	3
1062 Unlocking Environmental DNA Derived Gene Clusters Using a Metagenomics Approach. 2010 , 455-47	74 1
Impacts of Forest Conversion to Agriculture on Microbial Communities and Microbial Function. 2010 , 45-63	6
Biogeography of soil microbial communities: a review and a description of the ongoing french national initiative. 2010 , 30, 359-365	53
Molecular characterization and in situ detection of bacterial communities associated with rhizosphere soil of high altitude native Poaceae from the Andean Puna region. 2010 , 74, 1177-1185	10
1058 Bacterial soil communities affected by water-repellency. 2010 , 158, 343-351	19
1057 Anaerobic Eury- and Crenarchaeota inhabit ectomycorrhizas of boreal forest Scots pine. 2010 , 46, 35	5 6-364 20
Screening for hydrocarbon biodegraders in a metagenomic clone library derived from Brazilian petroleum reservoirs. 2010 , 41, 675-681	38
Reprint of: Screening for hydrocarbon biodegraders in a metagenomic clone library derived from Brazilian petroleum reservoirs. 2010 , 41, 1067-1073	7

1054	Exploring research frontiers in microbiology: the challenge of metagenomics in soil microbiology. 2010 , 161, 497-505	82
1053	Systematic study of the effect of operating variables on reactor performance and microbial diversity in laboratory-scale activated sludge reactors. 2010 , 44, 1341-52	64
1052	Olive mill wastewater affects the structure of soil bacterial communities. 2010 , 45, 101-111	55
1051	Soil Biology and Agriculture in the Tropics. 2010 ,	3
1050	Bioremediation Technology. 2010 ,	13
1049	Soil Microbiology and Sustainable Crop Production. 2010 ,	10
1048	Genomics Approach to Bioremediation. 2010 , 206-244	0
1047	Meter-Scale Diversity of Microbial Communities on a Weathered Pegmatite Granite Outcrop in the Wicklow Mountains, Ireland; Evidence for Mineral Induced Selection?. 2010 , 27, 1-14	44
1046	Responses of the bacterial community to chronic gamma radiation in a rice paddy ecosystem. 2011 , 87, 663-72	4
1045	Fermentation Improvement of Processes Yielding Natural Products for Industry. 2011 , 601-629	
1044	Population Genomics Informs Our Understanding of the Bacterial Species Concept. 2011 , 75-82	
1043	Application of Phylogenetic Oligonucleotide Microarrays in Microbial Analysis. 2011 , 551-566	1
1042	Targeting Major Soil-Borne Bacterial Lineages Using Large-Insert Metagenomic Approaches. 2011 , 135-141	
1041	Molecular Approaches to the Study of Biological Phosphorus Cycling. 2011 , 93-111	3
1040	Nitric Oxide as a Signal Molecule in Intracellular and Extracellular Bacteria-plant Interactions. 2011 , 397-420	4
1039	Discovery and characterization of heme enzymes from unsequenced bacteria: application to microbial lignin degradation. 2011 , 133, 18006-9	84
1038	Soil Biota, Soil Health and Global Change. 2011 , 155-177	5
1037	Molecular Techniques to Assess Microbial Community Structure, Function, and Dynamics in the Environment. 2011 , 29-57	115

1036	Microbes and Microbial Technology. 2011 ,	35
1035	Endospore-forming Soil Bacteria. 2011 ,	13
1034	Assessment of soil quality using microbial properties and attributes of ecological relevance. 2011 , 49, 1-4	64
1033	Soil microbial diversity: Methodological strategy, spatial overview and functional interest. 2011 , 334, 403-11	8o
1032	Functional diversity of terrestrial microbial decomposers and their substrates. 2011 , 334, 393-402	54
1031	From pattern to process: species and functional diversity in fungal endophytes of Abies beshanzuensis. 2011 , 115, 197-213	51
1030	Molecular analyses of Eglucosidase diversity and function in soil. 2011 , 47, 1-8	36
1029	Diversity of Endophytic Bacteria in Forest Trees. 2011 , 95-105	15
1028	Inter-laboratory evaluation of the ISO standard 11063 "Soil quality - Method to directly extract DNA from soil samples". 2011 , 84, 454-60	86
1027	Microbial Community Structure and Enzyme Activities in a Sequence of Copper-Polluted Soils. 2011 , 21, 164-169	30
1026	Physical disturbance to ecological niches created by soil structure alters community composition of methanotrophs. 2011 , 3, 613-21	14
1025	Ecological physiology of diet and digestive systems. 2011 , 73, 69-93	205
1024	Longitudinal Metagenomic Analysis of the Water and Soil from Gulf of Mexico Beaches Affected by the Deep Water Horizon Oil Spill. 2011 ,	3
1023	Species-specific detection of Dickeya sp. (Pectobacterium chrysanthemi) in infected banana tissues, soil and water. 2011 , 10,	1
1022	EmissB de gases do efeito estufa em diferentes usos da terra no bioma Cerrado. 2011 , 35, 63-76	29
1021	Mikrobiolgiai indikEorok alkalmazsa a talajminsg EtkelsBen. 1. Milszerek. 2011 , 60, 273-286	4
1020	Symbiotic effectiveness of rhizobial mutualists varies in interactions with native Australian legume genera. 2011 , 6, e23545	40
1019	Environmental Antibiotic Resistome: New Insights from Culture-Independent Approaches. 2011 , 123-148	2

1018	Microbial metabolomics. 2011 , 12, 391-403	121
1017	Innovation and productivity in dryland agriculture: a return-risk analysis for Australia. 2011 , 149, 77-89	23
1016	Assessing biodiversity in arable farmland by means of indicators: an overview. 2011 , 18, 137-144	16
1015	Biogeographical patterns of soil molecular microbial biomass as influenced by soil characteristics and management. 2011 , 20, 641-652	156
1014	A survey of the cellular responses in Pseudomonas putida KT2440 growing in sterilized soil by microarray analysis. 2011 , 78, 220-32	15
1013	Functional gene diversity of soil microbial communities from five oil-contaminated fields in China. 2011 , 5, 403-13	161
1012	Transcriptional and antagonistic responses of Pseudomonas fluorescens Pf0-1 to phylogenetically different bacterial competitors. 2011 , 5, 973-85	135
1011	Reproducibility and quantitation of amplicon sequencing-based detection. 2011 , 5, 1303-13	294
1010	The importance and ecology of yeasts in soil. 2011 , 43, 1-8	157
1009	Microbial ecology of autothermal thermophilic aerobic digester (ATAD) systems for treating waste activated sludge. 2011 , 34, 127-38	25
1008	Performance and mechanisms of a microbial-earthworm ecofilter for removing organic matter and nitrogen from synthetic domestic wastewater. 2011 , 195, 245-53	73
1007	Evidence for shifts in the structure and abundance of the microbial community in a long-term PCB-contaminated soil under bioremediation. 2011 , 195, 254-60	43
1006	Spatial and temporal changes in microbial diversity of the Marmara Sea sediments. 2011 , 62, 2384-94	23
1005	Effect of surfactants on PAH biodegradation by a bacterial consortium and on the dynamics of the bacterial community during the process. 2011 , 102, 9438-46	64
1004	Molecular Methods of Studying Microbial Diversity in Soil Environments. 2011 , 83-89	2
1003	Microbially Mediated Degradation of Common Pharmaceuticals and Personal Care Products in Soil Under Aerobic and Reduced Oxygen Conditions. 2011 , 216, 633-642	47
1002	Functional genomics analysis of plant growth-promoting rhizobacterial traits involved in rhizosphere competence. 2011 , 47, 729-743	139
1001	Cloning and functional characterization of a novel endo-日,4-glucanase gene from a soil-derived metagenomic library. 2011 , 89, 1083-92	59

1000	An improved protocol for DNA extraction from alkaline soil and sediment samples for constructing metagenomic libraries. 2011 , 165, 454-64	29
999	Isolation of xylose isomerases by sequence- and function-based screening from a soil metagenomic library. 2011 , 4, 9	34
998	CLOTU: an online pipeline for processing and clustering of 454 amplicon reads into OTUs followed by taxonomic annotation. 2011 , 12, 182	57
997	Functional Metagenomics as a Technique for the Discovery of Novel Enzymes and Natural Products. 2011 , 1-39	
996	Isolation of soil bacteria able to hydrolyze both organophosphate and carbamate pesticides. 2011 , 102, 3184-92	58
995	Effects of low-molecular-weight organic ligands and phosphate on adsorption of Pseudomonas putida by clay minerals and iron oxide. 2011 , 82, 147-51	38
994	An introduction to and a reflection on the Ecogenomics promise 2011, 8, 23-38	4
993	Computer and Computing Technologies in Agriculture IV. 2011,	2
992	Genomic and functional analyses of Rhodococcus equi phages ReqiPepy6, ReqiPoco6, ReqiPine5, and ReqiDocB7. 2011 , 77, 669-83	38
991	Beneficial Microorganisms in Multicellular Life Forms. 2011 ,	11
990	Molecular analysis of microbial diversity in corrosion samples from energy transmission towers. 2011 , 27, 435-47	10
989	Soil microbial community successional patterns during forest ecosystem restoration. 2011 , 77, 6158-64	
		162
988	Structure and evolution of Streptomyces interaction networks in soil and in silico. 2011 , 9, e1001184	131
988 987	Structure and evolution of Streptomyces interaction networks in soil and in silico. 2011 , 9, e1001184 Enhancing Soil Quality and Plant Health Through Suppressive Organic Amendments. 2012 , 4, 475-491	
		131
987	Enhancing Soil Quality and Plant Health Through Suppressive Organic Amendments. 2012 , 4, 475-491	131 98
987 986	Enhancing Soil Quality and Plant Health Through Suppressive Organic Amendments. 2012 , 4, 475-491 Primary malignant melanoma in the pineal region treated without chemotherapy. 2012 , 3, 123	131 98 7

982	Distribution of microbial biomass and potential for anaerobic respiration in Hanford Site 300 Area subsurface sediment. 2012 , 78, 759-67	37
981	Metagenomics to Unveil Microbiome of Human Body. 2012 , 04,	
980	Antimicrobial activity of filamentous fungi isolated from highly antibiotic-contaminated river sediment. 2012 , 2,	18
979	Pesticide Degradation in Water. 2012 , 96-147	1
978	Effect of rainfall-induced soil geochemistry dynamics on grassland soil microbial communities. 2012 , 78, 7587-95	41
977	On-farm biopurification systems for the depuration of pesticide wastewaters: recent biotechnological advances and future perspectives. 2012 , 23, 787-802	68
976	Detecting unknown sequences with DNA microarrays: explorative probe design strategies. 2012 , 14, 356-71	31
975	Vaginal microbiome: rethinking health and disease. 2012 , 66, 371-89	424
974	Influence of geogenic factors on microbial communities in metallogenic Australian soils. 2012, 6, 2107-18	54
973	Taxonomic and functional characterization of microbial communities in Technosols constructed for remediation of a contaminated industrial wasteland. 2012 , 12, 1396-1406	22
972	Bayesian model averaging for estimating the number of classes: applications to the total number of species in metagenomics. 2012 , 39, 1489-1504	1
971	Microbial community structure stability, a key parameter in monitoring the development of constructed wetland mesocosms during start-up. 2012 , 163, 28-35	38
970	Unique soil microbial assemblages associated with grassland ant species with different nesting and foraging strategies. 2012 , 55, 33-40	24
969	Plant Root Secretions and Their Interactions with Neighbors. 2012 , 1-26	7
968	Cross-taxa congruence, indicators and environmental gradients in soils under agricultural and extensive land management. 2012 , 49, 55-62	24
967	Interactions of vegetation succession, soil bio-chemical properties and microbial communities in a Karst ecosystem. 2012 , 51, 1-7	62
966	Natural zinc enrichment in peatlands: Biogeochemistry of ZnS formation. 2012 , 84, 165-176	25
965	Engineered nanoparticles in the soil and their potential implications to microbial activity. 2012 , 173-174, 19-27	195

(2012-2012)

964	Rhizosphere Microbial Communities: Isolation, Characterization, and Value Addition for Substrate Development. 2012 , 169-194	7
963	Fluctuations in the population density of Gram-negative bacteria in a chernozem in the course of a succession initiated by moistening and chitin and cellulose introduction. 2012 , 45, 958-967	
962	The Potential of Rhizosphere Microorganisms to Promote the Plant Growth in Disturbed Soils. 2012 , 35-64	26
961	Methods for the study of endophytic microorganisms from traditional Chinese medicine plants. 2012 , 517, 3-21	9
960	Genome Enabled Technologies in Green Chemistry. 2012 , 611-626	
959	Impact of fungicides on the diversity and function of non-target ammonia-oxidizing microorganisms residing in a litter soil cover. 2012 , 64, 692-701	31
958	Microbial community diversity and composition across a gradient of soil acidity in spruce fi r forests of the southern Appalachian Mountains. 2012 , 61, 60-68	29
957	Prokaryotes in salt marsh sediments of Ria de Aveiro: Effects of halophyte vegetation on abundance and diversity. 2012 , 110, 61-68	19
956	Soil structural responses to alterations in soil microbiota induced by the dilution method and mycorrhizal fungal inoculation. 2012 , 55, 271-281	15
955	Comparisons of direct extraction methods of microbial DNA from different paddy soils. 2012 , 19, 337-42	15
954	Improved real-time PCR estimation of gene copy number in soil extracts using an artificial reference. 2012 , 91, 38-44	31
953	Discovery of Enzymes. 2012 , 67-87	1
952	Isolation of a gene encoding a cellulolytic enzyme from swamp buffalo rumen metagenomes and its cloning and expression in Escherichia coli. 2012 , 23, 261-77	19
951	Evaluation of the ISO standard 11063 DNA extraction procedure for assessing soil microbial abundance and community structure. 2012 , 7, e44279	86
950	Effects of Monoculture, Crop Rotation, and Soil Moisture Content on Selected Soil Physicochemical and Microbial Parameters in Wheat Fields. 2012 , 2012, 1-13	11
949	Relating Phylogenetic and Functional Diversity among Denitrifiers and Quantifying their Capacity to Predict Community Functioning. 2012 , 3, 209	45
948	Soil nitrate reducing processes - drivers, mechanisms for spatial variation, and significance for nitrous oxide production. 2012 , 3, 407	118
	Molecular detection of Cylindrocarpon destructans in infected Chinese ginseng roots and soil. 2012	

946	Patterns in the distribution of soil bacterial 16S rRNA gene sequences from different regions of Antarctica. 2012 , 181-182, 45-55	34
945	Diversity analysis of type I ketosynthase in rhizosphere soil of cucumber. 2012 , 52, 224-31	6
944	Bacterial Eglucosidase function and metabolic activity depend on soil management in semiarid rainfed agriculture. 2012 , 2, 727-31	7
943	Microbial Communities Associated with Potato Common Scab-Suppressive Soil Determined by Pyrosequencing Analyses. 2012 , 96, 718-725	134
942	Changes in bacterial community structure of agricultural land due to long-term organic and chemical amendments. 2012 , 64, 450-60	189
941	Biotreatment of o-nitrobenzaldehyde manufacturing wastewater and changes in activated sludge flocs in a sequencing batch reactor. 2012 , 104, 228-34	11
940	Application of metagenomic techniques in mining enzymes from microbial communities for biofuel synthesis. 2012 , 30, 920-9	75
939	Molecular biomass and MetaTaxogenomic assessment of soil microbial communities as influenced by soil DNA extraction procedure. 2012 , 5, 135-41	95
938	Characterization of a new Acidobacteria-derived moderately thermostable lipase from a Brazilian Atlantic Forest soil metagenome. 2012 , 81, 386-94	27
937	Modeling microbial community structure and functional diversity across time and space. 2012 , 332, 91-8	33
936	Adsorption of Pseudomonas putida on soil particle size fractions: effects of solution chemistry and organic matter. 2012 , 12, 143-149	33
935	Impact of root exudates and plant defense signaling on bacterial communities in the rhizosphere. A review. 2012 , 32, 227-243	378
934	Response of induced perturbation on replicating Eproteobacterial ammonia-oxidizing populations in soil. 2012 , 63, 701-9	4
933	The great screen anomalya new frontier in product discovery through functional metagenomics. 2012 , 93, 1005-20	116
932	Soil bacterial community composition and diversity respond to cultivation in Karst ecosystems. 2012 , 28, 205-13	19
931	Effects of wetland degradation on bacterial community in the Zoige Wetland of Qinghai-Tibetan Plateau (China). 2012 , 28, 649-57	24
930	The effect of tetrahydrofuran on the enzymatic activity and microbial community in activated sludge from a sequencing batch reactor. 2012 , 21, 56-65	14
929	Taxonomic and functional assignment of cloned sequences from high Andean forest soil metagenome. 2012 , 101, 205-15	14

(2013-2013)

928	Drivers of cyanobacterial diversity and community composition in mangrove soils in south-east Brazil. 2013 , 15, 1103-14	27
927	Host plant genus-level diversity is the best predictor of ectomycorrhizal fungal diversity in a Chinese subtropical forest. 2013 , 22, 3403-14	88
926	Soil microbial diversity affects soil organic matter decomposition in a silty grassland soil. 2013 , 114, 201-212	64
925	Modern clinical microbiology: new challenges and solutions. 2013 , 11, 574-85	220
924	Geochip-based analysis of microbial communities in alpine meadow soils in the Qinghai-Tibetan plateau. 2013 , 13, 72	24
923	Spatial heterogeneity of a microbial community in a sandy soil ecosystem. 2013 , 56, 195-203	2
922	Rhizosphere bacterial communities associated with long-lived perennial prairie plants vary in diversity, composition, and structure. 2013 , 59, 494-502	25
921	Effect of land use on the abundance and diversity of autotrophic bacteria as measured by ribulose-1,5-biphosphate carboxylase/oxygenase (RubisCO) large subunit gene abundance in soils. 2013 , 49, 609-616	34
920	Effects of land utilization patterns on soil microbial communities in an acid red soil based on DNA and PLFA analyses. 2013 , 13, 1223-1231	19
919	Changes of bacterioplankton apparent species richness in two ornamental fish aquaria. 2013 , 2, 66	11
918	Isolation of an organic solvent-tolerant lipolytic enzyme from uncultivated microorganism. 2013 , 171, 1750-8	5
917	Arimetamycin A: improving clinically relevant families of natural products through sequence-guided screening of soil metagenomes. 2013 , 52, 11063-7	45
916	Microbial succession and metabolite changes during fermentation of saeu-jeot: traditional Korean salted seafood. 2013 , 34, 360-8	90
915	Soil microbial diversity and C turnover modified by tillage and cropping in Laos tropical grassland. 2013 , 11, 391-398	18
914	Differential response of archaeal groups to land use change in an acidic red soil. 2013 , 461-462, 742-9	18
913	Arable weeds, cover crops, and tillage drive soil microbial community composition in organic cropping systems. 2013 , 72, 232-241	40
912	Frequent-wildfires with shortened time-since-fire affect soil microbial functional stability to drying and rewetting events. 2013 , 57, 663-674	17
911	Analysis of the bacterial community in the two typical intertidal sediments of Bohai Bay, China by pyrosequencing. 2013 , 72, 181-7	59

910	Bioprospecting microbial metagenome for natural products. 2013 , 68, 1079-1086	13
909	Review: soil biological properties as indicators of soil quality in Australian viticulture. 2013, 19, n/a-n/a	13
908	GeoChip-based analysis of the functional gene diversity and metabolic potential of soil microbial communities of mangroves. 2013 , 97, 7035-48	58
907	Stable isotope probing in the metagenomics era: a bridge towards improved bioremediation. 2013 , 31, 154-65	102
906	Speedy speciation in a bacterial microcosm: new species can arise as frequently as adaptations within a species. 2013 , 7, 1080-91	52
905	Leaf litter is the main driver for changes in bacterial community structures in the rhizosphere of ash and beech. 2013 , 72, 150-160	33
904	Toward conceptual clarity: PLFA in warmed soils. 2013 , 57, 769-774	55
903	Conjugative Plasmids in Anthropogenic Soils. 2013 , 215-247	
902	Recent Advances and Perspectives in Metagenomic Studies of Soil Microbial Communities. 2013, 141-166	10
901	Estimation of metagenome size and structure in an experimental soil microbiota from low coverage next-generation sequence data. 2013 , 114, 141-51	19
900	Structure and Function of Microbial Communities. 2013, 3-30	2
899	Molecular Fingerprinting of Fungal Communities in Soil. 2013 , 349-356	
898	Hydration dynamics promote bacterial coexistence on rough surfaces. 2013, 7, 395-404	65
897	Toward the development of microbial indicators for wetland assessment. 2013 , 47, 1711-25	95
896	Microbial diversity and PAH catabolic genes tracking spatial heterogeneity of PAH concentrations. 2013 , 65, 91-100	18
895	Biofilm Formation in the Rhizosphere: Multispecies Interactions and Implications for Plant Growth. 2013 , 701-712	13
894	Recovery of soil unicellular eukaryotes: an efficiency and activity analysis on the single cell level. 2013 , 95, 463-9	13
893	Phylogenetic and functional changes in the microbial community of long-term restored soils under semiarid climate. 2013 , 65, 12-21	68

(2013-2013)

892	Bacteria distribution and dynamics in constructed wetlands based on modelling results. 2013 , 461-462, 430-40	50
891	Enumeration of Bacteria from Landfill Bioreactor Leachates Using Culture-Independent Molecular and Classical Culture-Dependent Microbiological Methods. 2013 , 39, 87-100	
890	The root microbiotall fingerprint in the soil?. 2013 , 370, 671-686	65
889	Impact of logging and forest conversion to oil palm plantations on soil bacterial communities in Borneo. 2013 , 79, 7290-7	82
888	Microbial community diversity in a 21-year-old temperate alley cropping system. 2013, 87, 1031-1041	15
887	Genomic Sequence Fragment Identification using Quasi-Alignment. 2013,	1
886	A Modified Protocol for Microbial DNA Extraction and Purification in Crude Oil-Spilled Marsh Soil. 2013 , 340, 353-357	О
885	Phosphate solubilizing microbes: sustainable approach for managing phosphorus deficiency in agricultural soils. 2013 , 2, 587	894
884	Bacterial chitinolytic communities respond to chitin and pH alteration in soil. 2013 , 79, 263-72	56
883	Microbial diversity in the era of omic technologies. 2013 , 2013, 958719	45
882	Ion Torrent PGM as tool for fungal community analysis: a case study of endophytes in Eucalyptus grandis reveals high taxonomic diversity. 2013 , 8, e81718	69
881	Characterization of depth-related changes in bacterial community compositions and functions of a paddy soil profile. 2013 , 347, 33-42	22
880	Diversity of the chlorite dismutase gene in low and high organic carbon rhizosphere soil colonized by perchlorate-reducing bacteria. 2013 , 15, 830-43	1
879	The Good, the Bad, and the Ugly: Tales of Mold-Ripened Cheese. 2013 , 1,	11
878	Arimetamycin A: Improving Clinically Relevant Families of Natural Products through Sequence-Guided Screening of Soil Metagenomes. 2013 , 125, 11269-11273	5
877	The development and suppressive activity of soil microbial communities under compost amendment. 2013 , 0-0	13
876	Hydrocarbon Biodegradation Potential of Native and Exogenous Microbial Inocula in Mexican Tropical Soils. 2013 ,	7
875	The role of microorganisms at different stages of ecosystem development for soil formation. 2013 , 10, 3983-3996	140

874	Molecular Identification of Fungal Communities in a Soil Cultivated with Vegetables and Soil Suppressiveness toRhizoctonia solani. 2013 , 2013, 1-7	8
873	Identification and characterization of four bacterial strains isolated from a bioaugmented sequencing batch reactor. 2013 , 59, 251-6	1
872	Dynamics of soil bacterial communities in response to repeated application of manure containing sulfadiazine. 2014 , 9, e92958	90
871	Bioinformatic approaches reveal metagenomic characterization of soil microbial community. 2014 , 9, e93445	38
870	Soil-borne microbial functional structure across different land uses. 2014 , 2014, 216071	5
869	Effect of CuO Nanoparticles over Isolated Bacterial Strains from Agricultural Soil. 2014 , 2014, 1-13	38
868	Seasonal effects in a lake sediment archaeal community of the Brazilian Savanna. 2014 , 2014, 957145	9
867	Bacterial microbiome of lungs in COPD. 2014 , 9, 229-38	63
866	Emerging strategies and integrated systems microbiology technologies for biodiscovery of marine bioactive compounds. 2014 , 12, 3516-59	54
865	Soil fauna and soil functions: a jigsaw puzzle. 2014 , 2,	93
86 ₅	Soil fauna and soil functions: a jigsaw puzzle. 2014, 2, The Effect of Industrial Heavy Metal Pollution on Microbial Abundance and Diversity in Soils IA Review. 2014,	93
	The Effect of Industrial Heavy Metal Pollution on Microbial Abundance and Diversity in Soils [A	
864	The Effect of Industrial Heavy Metal Pollution on Microbial Abundance and Diversity in Soils [A Review. 2014, Thermal characteristics and bacterial diversity of forest soil in the Haean basin of Korea. 2014,	27
864	The Effect of Industrial Heavy Metal Pollution on Microbial Abundance and Diversity in Soils IA Review. 2014 , Thermal characteristics and bacterial diversity of forest soil in the Haean basin of Korea. 2014 , 2014, 247401	27
864 863 862	The Effect of Industrial Heavy Metal Pollution on Microbial Abundance and Diversity in Soils IA Review. 2014, Thermal characteristics and bacterial diversity of forest soil in the Haean basin of Korea. 2014, 2014, 247401 Aplicals da biodiversidade bacteriana do solo para a sustentabilidade da agricultura. 2014, 3, 56	27 1 6
864863862861	The Effect of Industrial Heavy Metal Pollution on Microbial Abundance and Diversity in Soils IA Review. 2014, Thermal characteristics and bacterial diversity of forest soil in the Haean basin of Korea. 2014, 2014, 247401 Aplicals da biodiversidade bacteriana do solo para a sustentabilidade da agricultura. 2014, 3, 56 mVOC: a database of microbial volatiles. 2014, 42, D744-8 Removal of pharmaceuticals and personal care products during water recycling: microbial	27 1 6
864863862861860	The Effect of Industrial Heavy Metal Pollution on Microbial Abundance and Diversity in Soils IA Review. 2014, Thermal characteristics and bacterial diversity of forest soil in the Haean basin of Korea. 2014, 2014, 247401 Aplicals da biodiversidade bacteriana do solo para a sustentabilidade da agricultura. 2014, 3, 56 mVOC: a database of microbial volatiles. 2014, 42, D744-8 Removal of pharmaceuticals and personal care products during water recycling: microbial community structure and effects of substrate concentration. 2014, 80, 2440-50 Application of Molecular Techniques for the Assessment of Microbial Communities in	27 1 6 221 32

856	Novel Molecular Tools to Assess Microbial Activity in Contaminated Environments. 2014 , 17-35	1
855	Determinants of the pathways of litter chemical decomposition in a tropical region. 2014 , 203, 873-82	24
854	Droplet-based microfluidics platform for ultra-high-throughput bioprospecting of cellulolytic microorganisms. 2014 , 21, 1722-32	65
853	Microbial community structure varies across soil organic matter aggregate pools during tropical land cover change. 2014 , 77, 292-303	138
852	Composting for Sustainable Agriculture. 2014 ,	9
851	Biodiversity and multifunctionality in a microbial community: a novel theoretical approach to quantify functional redundancy. 2014 , 281, 20132498	60
850	Multisubstrate isotope labeling and metagenomic analysis of active soil bacterial communities. 2014 , 5, e01157-14	89
849	Proceedings of the 2013 A.S.P.E.N. Research workshop: the interface between nutrition and the gut microbiome: implications and applications for human health [corrected]. 2014 , 38, 167-78	12
848	Trends and Prospects of Microbial Diversity in Rhizosphere. 2014 , 1-22	3
847	Cropping Systems to Improve Soil Biodiversity and Ecosystem Services: The Outlook and Lines of Research. 2014 , 117-158	5
846	Ecology in the age of DNA barcoding: the resource, the promise and the challenges ahead. 2014 , 14, 221-32	80
845	Community composition and cellulase activity of cellulolytic bacteria from forest soils planted with broad-leaved deciduous and evergreen trees. 2014 , 98, 1449-58	39
844	Tag-encoded pyrosequencing analysis of bacterial diversity within different alpine grassland ecosystems of the Qinghai-Tibet Plateau, China. 2014 , 72, 779-786	16
843	An affinity-effect relationship for microbial communities in plant-soil feedback loops. 2014 , 67, 866-76	12
842	Cryptic diversity within morphospecies of testate amoebae (Amoebozoa: Arcellinida) in New England bogs and fens. 2014 , 165, 196-207	27
841	Land use type significantly affects microbial gene transcription in soil. 2014 , 67, 919-30	26
840	The composition and stability of the vaginal microbiota of normal pregnant women is different from that of non-pregnant women. 2014 , 2, 4	447
839	Effects of super-absorbent polymers on a soilwheat (Triticum aestivum L.) system in the field. 2014 , 73, 58-63	37

838	Biochar enhances the microbial and chemical transformation of pentachlorophenol in paddy soil. 2014 , 70, 142-150	132
837	POGO-DBa database of pairwise-comparisons of genomes and conserved orthologous genes. 2014 , 42, D625-32	19
836	Diffuse symbioses: roles of plant-plant, plant-microbe and microbe-microbe interactions in structuring the soil microbiome. 2014 , 23, 1571-83	94
835	An efficient and economical method for extraction of DNA amenable to biotechnological manipulations, from diverse soils and sediments. 2014 , 116, 923-33	17
834	Impact of short-term storage temperature on determination of microbial community composition and abundance in aerated forest soil and anoxic pond sediment samples. 2014 , 37, 570-7	10
833	Microbial community structure during fluoranthene degradation in the presence of plants. 2014 , 117, 74-84	29
832	Adhesion of Pseudomonas putida onto kaolinite at different growth phases. 2014 , 390, 1-8	27
831	Loss of microbial diversity in soils is coincident with reductions in some specialized functions. 2014 , 16, 2408-20	164
830	Microbial population and functional dynamics associated with surface potential and carbon metabolism. 2014 , 8, 963-78	108
829	Biogeographic patterns in below-ground diversity in New York City's Central Park are similar to those observed globally. 2014 , 281,	201
828	The Importance and Application of Bacterial Diversity in Sustainable Agricultural Crop Production Ecosystems. 2014 , 341-367	1
827	Bacteria-phage interactions in natural environments. 2014 , 89, 135-83	93
826	Effects of organic and conventional management of sugar cane crop on soil physicochemical characteristics and phosphomonoesterase activity. 2014 , 62, 1456-63	5
825	Soil and plant changing after invasion: the case of Acacia dealbata in a Mediterranean ecosystem. 2014 , 497-498, 491-498	63
824	Radionuclide Contamination and Remediation Through Plants. 2014,	11
823	Bioelectricity production from soil using microbial fuel cells. 2014 , 173, 2287-96	11
822	Impact of long-term N, P, K, and NPK fertilization on the composition and potential functions of the bacterial community in grassland soil. 2014 , 90, 195-205	136
821	Bacterial community composition and diversity of five different permafrost-affected soils of Northeast Greenland. 2014 , 89, 426-41	51

820	Remarkable recovery and colonization behaviour of methane oxidizing bacteria in soil after disturbance is controlled by methane source only. 2014 , 68, 259-70	17
819	Bacterial Diversity in Sustainable Agriculture. 2014 ,	5
818	Microbial Activity and Culturable Bacterial Diversity in Sediments of the Great Rann of Kachchh, Western India. 2014 , 24, 45-55	8
817	Changes in extracellular enzyme activity and microbial community structure with soil depth at the Luquillo Critical Zone Observatory. 2014 , 75, 237-247	174
816	Fate of 14C-labeled dissolved organic matter in paddy and upland soils in responding to moisture. 2014 , 488-489, 268-74	17
815	Characterization and high-level expression of a metagenome-derived alkaline pectate lyase in recombinant Escherichia coli. 2014 , 49, 69-76	26
814	Accessing Microbial Communities Relevant to Biofuels Production. 2014 , 565-576	
813	Molecular Methods To Study Complex Microbial Communities. 2014 , 323-345	
812	Gene finding in metatranscriptomic sequences. 2014 , 15 Suppl 9, S8	22
811	Optimization of isolation and cultivation of bacterial endophytes through addition of plant extract to nutrient media. 2015 , 8, 707-15	66
810	Antimicrobial compounds from rhizosphere bacteria and their role in plant disease management. 2015 , 371-386	
809	Identification and Characterization of Two Novel Esterases from a Metagenomic Library. 2015 , 21, 649-657	8
808	Diversity of key players in the microbial ecosystems of the human body. 2015 , 5, 15920	19
807	The influence of surface soil physicochemistry on the edaphic bacterial communities in contrasting terrain types of the Central Namib Desert. 2015 , 13, 494-505	18
806	Diversity Study of Nitrate Reducing Bacteria from Soil Samples-A Metagenomics Approach. 2015 , 8,	
805	Microbial Diversity and Interactions in Natural Ecosystems. 2015, 441-460	4
804	Microbial Diversity: Relevance and Relationship Between Environmental Conservation And Human Health. 2015 , 58, 137-145	21
803	Applications of Natural Products from Soil Microbes. 2015 , 51-77	1

802	Cigarette butt decomposition and associated chemical changes assessed by 13C CPMAS NMR. 2015 , 10, e0117393	40
801	Soil Biology with an Emphasis on Symbiotic Nitrogen Fixation. 2015 , 171-209	
800	The interdisciplinary nature of <i>SOIL</i>. 2015 , 1, 117-129	414
799	Sampling, metadata and DNA extraction - important steps in metagenomic studies. 2015 , 62, 151-60	28
798	Application of substrate utilization patterns and terminal restriction fragment length polymorphism analysis to characterize the oral bacterial community of healthy subjects and patients with periodontitis. 2015 , 9, 2013-2017	
797	Microbial Forensic Analysis of Bacterial Fingerprint by Sequence Comparison of 16S rRNA Gene. 2015 , 06,	1
796	Screening, identification, and characterization of a GH43 family Ekylosidase/Earabinofuranosidase from a compost microbial metagenome. 2015 , 99, 8943-54	37
795	Organic amendments to avocado crops induce suppressiveness and influence the composition and activity of soil microbial communities. 2015 , 81, 3405-18	28
794	Irrigation with Treated Wastewater: Potential Impacts on Microbial Function and Diversity in Agricultural Soils. 2015 , 105-128	3
793	Diversity, Dynamics and Functional Role of Actinomycetes on European Smear Ripened Cheeses. 2015 ,	1
79²	Microbiomics: An Approach to Community Microbiology. 2015 , 633-653	
791	Molecular Approaches to Studying the Soil Biota. 2015 , 151-185	2
79°	Understanding and managing soil biodiversity: a major challenge in agroecology. 2015 , 35, 67-81	63
789	Effects of land-use change and fungicide application on soil respiration in playa wetlands and adjacent uplands of the U.S. High Plains. 2015 , 514, 290-7	18
788	Bacterial Community Features Are Shaped by Geographic Location, Physicochemical Properties, and Oil Contamination of Soil in Main Oil Fields of China. 2015 , 70, 380-9	42
787	Identification of response classes from heavy metal-tolerant soil microbial communities by highly resolved concentration-dependent screenings in a microfluidic system. 2015 , 6, 600-609	6
786	Salt marsh sediment characteristics as key regulators on the efficiency of hydrocarbons bioremediation by Juncus maritimus rhizospheric bacterial community. 2015 , 22, 450-62	9
785	Impact of engineered nanoparticles on the activity, abundance, and diversity of soil microbial communities: a review. 2015 , 22, 13710-23	183

(2015-2015)

784	A rapid flow cytometry method to assess bacterial abundance in agricultural soil. 2015 , 88, 60-68	24
783	Isolation of oxygenase genes for indigo-forming activity from an artificially polluted soil metagenome by functional screening using Pseudomonas putida strains as hosts. 2015 , 99, 4453-70	39
782	Microbial functional diversity enhances predictive models linking environmental parameters to ecosystem properties. 2015 , 96, 1985-93	54
781	New insights into the fungal community from the raw genomic sequence data of fig wasp Ceratosolen solmsi. 2015 , 15, 27	3
780	Bacterial community composition and function along a river to reservoir transition. 2015 , 747, 201-215	11
779	Nanoscale copper in the soil-plant system - toxicity and underlying potential mechanisms. 2015 , 138, 306-25	102
778	Soils, microbes, and forest health: A qualitative analysis of social and institutional factors affecting genomic technology adoption. 2015 , 43, 1-9	10
777	Sex and Gender Differences in Infection and Treatments for Infectious Diseases. 2015 ,	8
776	Farm management, not soil microbial diversity, controls nutrient loss from smallholder tropical agriculture. 2015 , 6, 90	24
775	Optimization of biostimulant for bioremediation of contaminated coastal sediment by response surface methodology (RSM) and evaluation of microbial diversity by pyrosequencing. 2015 , 98, 235-46	12
774	Soil conditions and land use intensification effects on soil microbial communities across a range of European field sites. 2015 , 88, 403-413	101
773	Isolation of previously uncultivable bacteria from a nickel contaminated soil using a diffusion-chamber-based approach. 2015 , 95, 115-127	5
772	Fate of faecal indicator organisms and bacterial diversity dynamics in a series of continuously fed aerated tank reactors treating dairy manure. 2015 , 81, 363-372	
771	Community structure, diversity, and species dominance of bacteria, fungi, and nematodes from naturally and conventionally farmed soil: a case study on Japanese apple orchards. 2015 , 5, 11-28	11
770	Feather bacterial load shapes the trade-off between preening and immunity in pigeons. 2015 , 15, 60	13
769	Parental material and cultivation determine soil bacterial community structure and fertility. 2015 , 91, 1-10	25
768	Diversity and Spatial Structure of Soil Fungi and Arbuscular Mycorrhizal Fungi in Forest Litter Contaminated with Copper Smelter Emissions. 2015 , 226, 1	12
767	From patterns to causal understanding: Structural equation modeling (SEM) in soil ecology. 2015 , 58, 65-72	199

766	Distribution, diversity and abundance of bacterial laccase-like genes in different particle size fractions of sediments in a subtropical mangrove ecosystem. 2015 , 24, 1508-16	3
765	Microbial phospholipid biomarkers and stable isotope methods help reveal soil functions. 2015 , 86, 98-107	39
764	A comparative study of macrophytes influence on wastewater treatment through subsurface flow hybrid constructed wetland. 2015 , 81, 62-69	52
763	Effect of digestate and fly ash applications on soil functional properties and microbial communities. 2015 , 71, 1-12	35
762	Adaptation in Natural Microbial Populations. 2015 , 46, 503-522	30
761	Microbial Fuel Cells: From Fundamentals to Wastewater Treatment Applications. 2015 , 163-189	
760	Shifts in microbial diversity through land use intensity as drivers of carbon mineralization in soil. 2015 , 90, 204-213	104
759	Phenotypic Diversity as a Mechanism to Exit Cellular Dormancy. 2015 , 25, 2272-7	40
75 ⁸	Bacterial diversity of Murlen National Park located in Indo-Burman Biodiversity hotspot region: A metagenomic approach. 2015 , 5, 25-6	7
757	Soil aggregate size mediates the impacts of cropping regimes on soil carbon and microbial communities. 2015 , 91, 169-181	107
756	Migration and horizontal gene transfer divide microbial genomes into multiple niches. 2015, 6, 8924	70
755	Salt effects on the soil microbial decomposer community and their role in organic carbon cycling: A review. 2015 , 81, 108-123	227
754	Effect of the accuracy of pH control on hydrogen fermentation. 2015 , 179, 595-601	46
753	Wastewater reuse in irrigation: a microbiological perspective on implications in soil fertility and human and environmental health. 2015 , 75, 117-35	264
752	Metagenomic analysis reveals microbial functional redundancies and specificities in a soil under different tillage and crop-management regimes. 2015 , 86, 106-112	58
751	Fungal communities are more sensitive indicators to non-extreme soil moisture variations than bacterial communities. 2015 , 86, 158-164	98
75°	Bio-Organo-Phos: A Sustainable Approach for Managing Phosphorus Deficiency in Agricultural Soils. 2016 ,	8
749	Microbial activity promoted with organic carbon accumulation in macroaggregates of paddy soils under long-term rice cultivation. 2016 , 13, 6565-6586	17

(2016-2016)

748	Uso de filtros de carvid ativado granular associado a microrganismos para remoid de filmacos no tratamento de gua de abastecimento. 2016 , 21, 709-720	10
747	Microbial Profiling of a Suppressiveness-Induced Agricultural Soil Amended with Composted Almond Shells. 2016 , 7, 4	28
746	Microbes as Engines of Ecosystem Function: When Does Community Structure Enhance Predictions of Ecosystem Processes?. 2016 , 7, 214	321
745	Wheat and Rice Growth Stages and Fertilization Regimes Alter Soil Bacterial Community Structure, But Not Diversity. 2016 , 7, 1207	58
744	Molecular Detection and Environment-Specific Diversity of Glycosyl Hydrolase Family 1 EGlucosidase in Different Habitats. 2016 , 7, 1597	11
743	Community Composition and Abundance of Bacterial, Archaeal and Nitrifying Populations in Savanna Soils on Contrasting Bedrock Material in Kruger National Park, South Africa. 2016 , 7, 1638	25
742	Characterization of Uncultured Genome Fragment from Soil Metagenomic Library Exposed Rare Mismatch of Internal Tetranucleotide Frequency. 2016 , 7, 2081	8
741	Biosynthetic Functional Gene Analysis of Bis-Indole Metabolites from 25D7, a Clone Derived from a Deep-Sea Sediment Metagenomic Library. 2016 , 14,	3
740	Bioprospecting Red Sea Coastal Ecosystems for Culturable Microorganisms and Their Antimicrobial Potential. 2016 , 14,	24
739	Microbial ecology of the salmon necrobiome: evidence salmon carrion decomposition influences aquatic and terrestrial insect microbiomes. 2016 , 18, 1511-22	43
738	An ecological and ecotoxicological perspective on fine particulate organic matter in streams. 2016 , 61, 2063-2074	50
737	Long-term effects of vegetational restoration on soil microbial communities on the Loess Plateau of China. 2016 , 24, 794-804	24
736	Performance Evaluation of Integrated Constructed Wetland for Domestic Wastewater Treatment. 2016 , 88, 280-7	12
735	Beyond the Cell: Using Multiscalar Topics to Bring Interdisciplinarity into Undergraduate Cellular Biology Courses. 2016 , 15,	6
734	Urban-development-induced Changes in the Diversity and Composition of the Soil Bacterial Community in Beijing. 2016 , 6, 38811	37
733	Soil Microbial Metabolomics. 2016 , 147-198	6
732	Microbial Metabolomics. 2016,	12
731	Discovering novel enzymes by functional screening of plurigenomic libraries from alga-associated Flavobacteriia and Gammaproteobacteria. 2016 , 186-187, 52-61	22

730	Dynamics of the microbial community and Fe(III)-reducing and dechlorinating microorganisms in response to pentachlorophenol transformation in paddy soil. 2016 , 312, 97-105	22
729	The combination of quarry restoration strategies in semiarid climate induces different responses in biochemical and microbiological soil properties. 2016 , 107, 33-47	38
728	Reductive soil disinfestations combined or not with Trichoderma for the treatment of a degraded and Rhizoctonia solani infested greenhouse soil. 2016 , 206, 51-61	19
727	Assessment of non-cultured aquatic fungal diversity from different habitats in Mexico. 2016 , 87, 18-28	3
726	Efficacy of Biofertilizers: Challenges to Improve Crop Production. 2016 , 17-40	44
725	Screening, identification, and characterization of Exylosidase from a soil metagenome. 2016 , 122, 393-9	22
724	Self-Driven Jamming in Growing Microbial Populations. 2016 , 12, 762-766	78
723	Deterministic assembly processes govern bacterial community structure in the Fynbos, South Africa. 2016 , 72, 313-23	15
722	Modeling Soil Processes: Review, Key Challenges, and New Perspectives. 2016 , 15, vzj2015.09.0131	311
721	Contribution of soil respiration to the global carbon equation. 2016 , 203, 16-28	68
720	Ecotoxicity Analyses of Nanomaterials. 2016 , 367-392	1
719	The importance of C, N and P as driver for bacterial community structure in German beech dominated forest soils. 2016 , 179, 472-480	15
718	Soil microbial community profiles and functional diversity in limestone cedar glades. 2016 , 147, 216-224	9
717	Life Inside an Acorn: How Microclimate and Microbes Influence Nest Organization in Temnothorax Ants. 2016 , 122, 790-797	18
716	CRISPR© as System: A new Paradigm for Bacterial Stress Response Through Genome Rearrangement. 2016 , 146-160	2
715	Development of a method for detection and quantification of B. brongniartii and B. bassiana in soil. 2016 , 6, 22933	25
714	Volatile Gas Production by Methyl Halide Transferase: An In Situ Reporter Of Microbial Gene Expression In Soil. 2016 , 50, 8750-9	10

(2016-2016)

712	Environmental Change and Human Health: Can Environmental Proxies Inform the Biodiversity Hypothesis for Protective Microbial Human Contact?. 2016 , 66, 1023-1034	16
711	Using community analysis to explore bacterial indicators for disease suppression of tobacco bacterial wilt. 2016 , 6, 36773	53
710	Pampered inside, pestered outside? Differences and similarities between plants growing in controlled conditions and in the field. 2016 , 212, 838-855	242
709	Responsiveness of soil nitrogen fractions and bacterial communities to afforestation in the Loess Hilly Region (LHR) of China. 2016 , 6, 28469	38
708	Phylogenetic distribution of extracellular guanyl-preferring ribonucleases renews taxonomic status of two Bacillus strains. 2016 , 62, 181-8	15
707	Effect of pH on soil bacterial diversity. 2016 , 40,	34
706	Yucatīl in black and red: Linking edaphic analysis and pyrosequencing-based assessment of bacterial and fungal community structures in the two main kinds of soil of Yucatīl State. 2016 , 188-189, 23-33	7
705	Factors that affect bacterial ecology in hydrogen-producing anaerobic reactors. 2016 , 9, 1260-1271	20
704	Carbon and phosphorus exchange may enable cooperation between an arbuscular mycorrhizal fungus and a phosphate-solubilizing bacterium. 2016 , 210, 1022-32	160
703	Microbial siderophores and their potential applications: a review. 2016 , 23, 3984-99	333
702	Aerobic biofilm reactor for treating a commercial formulation of the herbicides 2,4-D and dicamba: Biodegradation kinetics and biofilm bacterial diversity. 2016 , 107, 123-131	27
701	Challenges and opportunities in harnessing soil disease suppressiveness for sustainable pasture production. 2016 , 95, 100-111	24
700	Classification and valuation of soil ecosystem services. 2016 , 145, 24-38	79
699	Effects of Bacillus amyloliquefaciens ZM9 on bacterial wilt and rhizosphere microbial communities of tobacco. 2016 , 103, 1-12	51
698	Estimates of Soil Bacterial Ribosome Content and Diversity Are Significantly Affected by the Nucleic Acid Extraction Method Employed. 2016 , 82, 2595-2607	21
697	Microbial genetic and enzymatic responses to an anthropogenic phosphorus gradient within a subtropical peatland. 2016 , 268, 119-127	21
696	Exposure of Cucurbita pepo to DDE-contamination alters the endophytic community: A cultivation dependent vs a cultivation independent approach. 2016 , 209, 147-54	20
695	Biofilms on Hospital Shower Hoses: Characterization and Implications for Nosocomial Infections. 2016 , 82, 2872-2883	54

694	Functional and structural responses of bacterial and fungal communities from paddy fields following long-term rice cultivation. 2016 , 16, 1460-1471	25
693	Impact of soil compaction on soil biodiversity ldoes it matter in urban context?. 2016 , 19, 1163-1178	7
692	Coal mining practices reduce the microbial biomass, richness and diversity of soil. 2016 , 98, 195-203	75
691	Comparison between cultivated and total bacterial communities associated with Cucurbita pepo using cultivation-dependent techniques and 454 pyrosequencing. 2016 , 39, 58-66	19
690	A soil bacterium Rhizobium borbori and its potential for citrinin-degrading application. 2016 , 66, 807-816	9
689	Microbial Diversity in Caves. 2016 , 33, 20-38	57
688	One step forwards for the routine use of high-throughput DNA sequencing in environmental monitoring. An efficient and standardizable method to maximize the detection of environmental bacteria. 2017 , 6, e00421	18
687	Trends in Taxonomic and Functional Composition of Soil Microbiome Along a Precipitation Gradient in Israel. 2017 , 74, 168-176	28
686	Nanomaterial Effects on Soil Microorganisms. 2017 , 137-200	5
685	Influence of agricultural activities in the structure and metabolic functionality of paramo soil samples in Colombia studied using a metagenomics analysis in dynamic state. 2017 , 351, 63-76	6
684	Soil bacteria as trace evidence. 2017 , 339-357	1
683	Approaches and considerations for forensic microbiology decomposition research. 2017 , 56-71	1
682	Increasing soil carbon storage: mechanisms, effects of agricultural practices and proxies. A review. 2017 , 37, 1	170
681	The microbially mediated soil organic carbon loss under degenerative succession in an alpine meadow. 2017 , 26, 3676-3686	12
68o	The 'known' genetic potential for microbial communities to degrade organic phosphorus is reduced in low-pH soils. 2017 , 6, e00474	16
679	Bioresources and Bioprocess in Biotechnology. 2017 ,	1
678	Differential responses of soil bacteria, fungi, archaea and protists to plant species richness and plant functional group identity. 2017 , 26, 4085-4098	99
677	Mycorrhiza: Creating Good Spaces for Interactions. 2017 , 39-60	4

676 Metagenomic Approaches for Novel Active Metabolites. **2017**, 275-302

Ammonia oxidizer populations vary with nitrogen cycling across a tropical montane mean annual temperature gradient. 2017 , 98, 1896-1907 Phytoremediation of Petroleum-Contaminated Soil in Association with Soil Bacteria. 2017 , 77-99 Towards the co-ordination of terrestrial ecosystem protocols across European research infrastructures. 2017 , 7, 3967-3975	17
Towards the co-ordination of terrestrial ecosystem protocols across European research	
673	2
	9
Phytostabilization of salt accumulated soil using plant and biofertilizers: Field application. 2017 , 124, 188-195	9
Microbial functionality as affected by experimental warming of a temperate mountain forest soil metaproteomics survey. 2017 , 117-118, 196-202	39
Carbon-driven enrichment of the crucial nitrate-reducing bacteria in limed peat soil microcosms. 2017 , 65, 159-164	5
Methanotrophic bacterial diversity in two diverse soils under varying land-use practices as determined by high-throughput sequencing of the pmoA gene. 2017 , 119, 35-45	28
High-throughput amplicon sequencing and stream benthic bacteria: identifying the best taxonomic level for multiple-stressor research. 2017 , 7, 44657	26
Emerging Culture-Independent Tools to Enhance Our Understanding of Soil Microbial Ecology. 2017 , 207-225	
Scientific Opinion addressing the state of the science on risk assessment of plant protection products for in-soil organisms. 2017 , 15, e04690	40
665 Antimicrobial Resistance Genes in Pigeons from Public Parks in Costa Rica. 2017 , 64, e23-e30	14
Coupled molecular and isotopic evidence for denitrifier controls over terrestrial nitrogen availability. 2017 , 11, 727-740	11
663 Depth-dependent influence of different land-use systems on bacterial biogeography. 2017 , 93,	27
Spatial Heterogeneity of SOM Concentrations Associated with White-rot Versus Brown-rot Wood Decay. 2017 , 7, 13758	10
661 Siderophores: Augmentation of Soil Health and Crop Productivity. 2017 , 291-312	17
Impact of Agricultural Land Management on Soil Bacterial Community: A Case Study in the Mediterranean Area. 2017 , 77-95	4
659 Strength of Microbes in Nutrient Cycling: A Key to Soil Health. 2017 , 69-86	15

658	Agriculturally Important Microbes for Sustainable Agriculture. 2017,	4
657	Enhancing Functional Metagenomics of Complex Microbial Communities Using Stable Isotopes. 2017 , 139-150	1
656	Understanding Host-Microbiome Interactions - An Omics Approach. 2017,	9
655	Short-term exclusion of degraded pasture in the permafrost zone: aspects of soil microbial community. 2017 , 7, 184-190	
654	Effects of microcystins contamination on soil enzyme activities and microbial community in two typical lakeside soils. 2017 , 231, 134-142	26
653	Embracing the unknown: disentangling the complexities of the soil microbiome. 2017 , 15, 579-590	1106
652	Rhizosphere Microbiota and Microbiome of Medicinal Plants: From Molecular Biology to Omics Approaches. 2017 , 9, 199-217	13
651	Impact of the Nanomaterials on Soil Bacterial Biodiversity. 2017 , 173-190	
650	nirS-type denitrifying bacterial assemblages respond to environmental conditions of a shallow estuary. 2017 , 9, 766-778	5
649	Improving de novo metatranscriptome assembly via machine learning algorithms. 2017, 10, 91	1
648	Unravelling diversity and metabolic potential of microbial consortia at each stage of leather sewage treatment. 2017 , 7, 41727-41737	8
647	Metagenomics of Plant Rhizosphere Microbiome. 2017 , 193-205	17
646	Metagenome of Rhizosphere and Endophytic Ecosystem. 2017 , 125-156	3
645	9. Artificial Soils as Tools for Microbial Ecology. 2017 , 159-180	Ο
644	Biofilms: An Overview of Their Significance in Plant and Soil Health. 2017 , 1-25	4
643	Abundance and diversity of carbon monoxide dehydrogenase genes from BMS clade bacteria in different vegetated soils. 2017 , 81, 94-99	7
642	Biophysical processes supporting the diversity of microbial life in soil. 2017 , 41, 599-623	184
641	Bacterial Community Response to Hydrocarbon Contamination in Soils and Marine Sediments: A Critical Review of Case Studies. 2017 , 185-226	1

640	CONSERVATION AGRICULTURE FOR CLIMATE CHANGE RESILIENCE. 2017 , 165-190	3
639	Understanding the variation of microbial community in heavy metals contaminated soil using high throughput sequencing. 2017 , 144, 300-306	122
638	Optimization of high-yielding protocol for DNA extraction from the forest rhizosphere microbes. 2017 , 7, 91	4
637	Increasing crop diversity increased soil microbial activity, nitrogen-sourcing and crop nitrogen, but not soil microbial diversity. 2017 , 34, 371-378	6
636	Mikrofluidik நோல் Potenzial in kleinen Tropfen. 2017 , 23, 394-397	
635	Preservation of nucleic acids by freeze-drying for next generation sequencing analyses of soil microbial communities. 2017 , 10, 81-90	27
634	Rapid and efficient method to extract metagenomic DNA from estuarine sediments. 2017 , 7, 182	7
633	Characterizing bacterial communities in tilapia pond surface sediment and their responses to pond differences and temporal variations. 2017 , 33, 1	58
632	Human Land-Use and Soil Change. 2017 , 351-371	2
631	Functional diversity and dominant populations of bacteria in banana plantation soils as influenced by long-term organic and conventional farming. 2017 , 110, 21-33	16
630	Soil microbial abundance and community structure vary with altitude and season in the coniferous forests, China. 2017 , 17, 2318-2328	10
629	Can biochar alleviate soil compaction stress on wheat growth and mitigate soil N2O emissions?. 2017 , 104, 8-17	69
628	Enzymatic Biocatalysis in Chemical Transformations. 2017 , 347-403	15
627	Screening, identification, and characterization of a novel saccharide-stimulated Eglycosidase from a soil metagenomic library. 2017 , 101, 633-646	28
626	Application of Bioorganic Fertilizer Significantly Increased Apple Yields and Shaped Bacterial Community Structure in Orchard Soil. 2017 , 73, 404-416	51
625	The effect of heavy metal contamination on the bacterial community structure at Jiaozhou Bay, China. 2017 , 48, 71-78	32
624	Managing clubroot disease (caused by Plasmodiophora brassicae Wor.) by exploiting the interactions between calcium cyanamide fertilizer and soil microorganisms. 2017 , 155, 527-543	8
623	The Soils of the USA. 2017 ,	4

622	Microbial Interactions and Perspectives for Bioremediation of Pesticides in the Soils. 2017, 649-671	3
621	Functional Diversity of Soil Microbial Communities in Different-age Rubber Plantations IA Case Study of Hainan Province, China. 2017 , 20, 168-181	O
620	Phylogenetic and Functional Diversity of Faecal Microbiome of Pack Animals. 2017,	1
619	Nutrient Cycling and Soil Biology in Row Crop Systems under Intensive Tillage. 2017 , 231-255	5
618	Effects of Short-Term Set-Aside Management Practices on Soil Microorganism and Enzyme Activity in China. 2017 , 14,	4
617	Metatranscriptomics Reveals the Active Bacterial and Eukaryotic Fibrolytic Communities in the Rumen of Dairy Cow Fed a Mixed Diet. 2017 , 8, 67	66
616	Bacterial Communities in Boreal Forest Mushrooms Are Shaped Both by Soil Parameters and Host Identity. 2017 , 8, 836	38
615	Estimating Herd Immunity to Amphibian Chytridiomycosis in Madagascar Based on the Defensive Function of Amphibian Skin Bacteria. 2017 , 8, 1751	24
614	Linking the Gut Microbial Ecosystem with the Environment: Does Gut Health Depend on Where We Live?. 2017 , 8, 1935	73
613	Resolving Species Level Changes in a Representative Soil Bacterial Community Using Microfluidic Quantitative PCR. 2017 , 8, 2017	23
612	Exogenous Nitrogen Addition Reduced the Temperature Sensitivity of Microbial Respiration without Altering the Microbial Community Composition. 2017 , 8, 2382	12
611	A broad pH range and processive chitinase from a metagenome library. 2017 , 50, e5658	15
610	Temporal dynamics in microbial soil communities at anthrax carcass sites. 2017 , 17, 206	5
609	Functional diversity of microbial communities in pristine aquifers inferred by PLFA- and sequencing-based approaches. 2017 , 14, 2697-2714	41
608	Temperature, pH and carbon source affect drastically indole acetic acid production of plant growth promoting yeasts. 2017 , 34, 429-438	10
607	Diversity and distribution of the endophytic fungal community in eucalyptus leaves. 2017 , 11, 92-105	7
606	Formulation of Novel Surface Sterilization Method and Culture Media for the Isolation of Endophytic Actinomycetes from Medicinal Plants and its Antibacterial Activity. 2017 , 08,	1
605	Screening of active antimicrobial and biological enzymes of microbial isolated from soil in Thailand. 2017 , 10, 73	1

604	Optimal Tree Canopy Cover during Ecological Restoration: A Case Study of Possible Ecological Thresholds in Changting, China. 2017 , biw157	5
603	References. 2018 , 313-359	
602	Distribution of prokaryotic communities throughout the Chernozem profiles under different land uses for over a century. 2018 , 127, 8-18	29
601	DmicsDools in Soil Microbiology: The State of the Art. 2018 , 35-64	12
600	Impacts of anaerobic soil disinfestation and chemical fumigation on soil microbial communities in field tomato production system. 2018 , 126, 165-173	18
599	Long-term nitrogen fertilization decreases bacterial diversity and favors the growth of Actinobacteria and Proteobacteria in agro-ecosystems across the globe. 2018 , 24, 3452-3461	187
598	The restoration age of Robinia pseudoacacia plantation impacts soil microbial biomass and microbial community structure in the Loess Plateau. 2018 , 165, 192-200	35
597	Soil quality 🖪 critical review. 2018 , 120, 105-125	801
596	External immunity in ant societies: sociality and colony size do not predict investment in antimicrobials. 2018 , 5, 171332	9
595	Impact of Soil Heterogeneity on Forest Structure and Diversity of Tree Species in the Central Congo Basin. 2018 , 179, 198-208	Ο
594	Bacterial and Fungal Community Composition and Functional Activity Associated with Lake Wetland Water Level Gradients. 2018 , 8, 760	24
593	Diversity, Functions, and Stress Responses of Soil Microorganisms. 2018 , 1-19	3
592	Dominant plant species shape soil bacterial community in semiarid sandy land of northern China. 2018 , 8, 1693-1704	16
591	The control of Fusarium oxysporum in soil treated with organic material under anaerobic condition is affected by liming and sulfate content. 2018 , 54, 295-307	18
590	Scaling up: A guide to high-throughput genomic approaches for biodiversity analysis. 2018 , 27, 313-338	140
589	Microorganisms reveal what plants do not: wheat growth and rhizosphere microbial communities after Azospirillum brasilense inoculation and nitrogen fertilization under field conditions. 2018 , 424, 405-417	32
588	Ambient soil cation exchange capacity inversely associates with infectious and parasitic disease risk in regional Australia. 2018 , 626, 117-125	18
587	Testing association between soil bacterial diversity and soil carbon storage on the Loess Plateau. 2018 , 626, 48-58	29

586	Phylogeny, novel bacterial lineage and enzymatic potential of haloalkaliphilic bacteria from the saline coastal desert of Little Rann of Kutch, Gujarat, India. 2018 , 8, 53	17
585	Effects of short-term fallow managements on soil microbial properties: A case study in China. 2018 , 125, 128-137	6
584	Functional and phylogenetic diversity assessment of microbial communities at Gulf of Kachchh, India: An ecological footprint. 2018 , 93, 65-75	9
583	Root Exudates Dominate the Colonization of Pathogen and Plant Growth-Promoting Rhizobacteria. 2018 , 167-180	6
582	Continuous application of inorganic and organic fertilizers over 47 years in paddy soil alters the bacterial community structure and its influence on rice production. 2018 , 262, 65-75	62
581	Endophyte-enhanced phytoremediation of DDE-contaminated using Cucurbita pepo: A field trial. 2018 , 20, 301-310	8
580	A hierarchical Bayesian model to incorporate uncertainty into methods for diversity partitioning. 2018 , 99, 947-956	7
579	Reactive Transport Modeling and Biogeochemical Cycling. 2018 , 485-510	3
578	Evaluation of the natural attenuation capacity of urban residential soils with ecosystem-service performance index (EPX) and entropy-weight methods. 2018 , 238, 222-229	33
577	Long-term fire management history affects N-fertilization sensitivity, but not seasonality, of grassland soil microbial communities. 2018 , 121, 231-239	16
576	Decreasing soil microbial diversity is associated with decreasing microbial biomass under nitrogen addition. 2018 , 120, 126-133	190
575	Surface-Enhanced Raman Scattering (SERS) in Microbiology: Illumination and Enhancement of the Microbial World. 2018 , 72, 987-1000	43
574	Integrated network analysis reveals the importance of microbial interactions for maize growth. 2018 , 102, 3805-3818	42
573	Effect of nanoparticles on crops and soil microbial communities. 2018 , 18, 2179-2187	94
572	Effects of reclamation years on composition and diversity of soil bacterial communities in Northwest China. 2018 , 64, 28-40	13
571	Profiling of heavy metal(loid)-resistant bacterial community structure by metagenomic-DNA fingerprinting using PCRDGGE for monitoring and bioremediation of contaminated environment. 2018 , 3, 102-109	11
57°	Assessment of derelict soil quality: Abiotic, biotic and functional approaches. 2018 , 613-614, 990-1002	19
569	Fate of potential indicator antimicrobial resistance genes (ARGs) and bacterial community diversity in simulated manure-soil microcosms. 2018 , 147, 817-823	39

(2018-2018)

568	Humusica 2, article 17: techno humus systems and global change Ithree crucial questions. 2018 , 122, 237-253	7
567	Response of soil microbial community dynamics to Robinia pseudoacacia L. afforestation in the loess plateau: a chronosequence approach. 2018 , 423, 327-338	46
566	Metagenomic analysis of the bacterial communities and their functional profiles in water and sediments of the Apies River, South Africa, as a function of land use. 2018 , 616-617, 326-334	53
565	Evaluation of two types of superabsorbent polymer on soil water and some soil microbial properties. 2018 , 16, 143-152	5
564	Correlation Model Analysis of Nitrogen Addition and Tan Sheep Grazing Effects on Soil Bacterial Community in the Loess Plateau, China. 2018 ,	
563	. 2018,	5
562	. 2018,	1
561	Plant Immunity Is Compartmentalized and Specialized in Roots. 2018 , 9, 1692	35
560	The Evolution of Living Beings Started with Prokaryotes and in Interaction with Prokaryotes. 2018 , 241-338	1
559	Ecotoxicity of Metal Nanoparticles on Microorganisms. 2018, 77-93	
558	Life in the Soil: From Taxonomy to Ecological Integration. 2018 , 1-15	
557	Biodiversity and Ecological Functioning of Soils. 2018, 39-56	
556	Prokaryotes and Evolution. 2018,	2
555	Effects of soil type, temperature, moisture, application dose, fertilizer, and organic amendments on chemical properties and biodegradation of dimethyl disulfide in soil. 2018 , 29, 4282-4290	14
554	The Local Ecological Memory of Soil: Majority and Minority Components of Bacterial Communities in Prehistorical Urns from Schps (Germany). 2018 , 12, 575-584	3
553	Adaptation limits ecological diversification and promotes ecological tinkering during the competition for substitutable resources. 2018 , 115, E10407-E10416	15
552	Long-term effects of environmentally relevant concentrations of silver nanoparticles on major soil bacterial phyla of a loamy soil. 2018 , 30, 31	20
551	Model Microbial Consortia as Tools for Understanding Complex Microbial Communities. 2018 , 19, 723-733	13

550	Effect of different inoculation treatments on AM fungal communities and the sustainability of soil remediation in Daliuta coal mining subsidence area in northwest China. 2018 , 132, 107-113	15
549	Endophytic fungal community of Dysphania ambrosioides from two heavy metal-contaminated sites: evaluated by culture-dependent and culture-independent approaches. 2018 , 11, 1170-1183	12
548	Effects of organic substitution for synthetic N fertilizer on soil bacterial diversity and community composition: A 10-year field trial in a tea plantation. 2018 , 268, 124-132	52
547	Characterization of microbial communities of soils from gold mine tailings and identification of mercury-resistant strain. 2018 , 165, 182-193	25
546	Organic and Biofertilization on Crop Production in Semiarid Regions. 2018, 235-263	1
545	Toward the Unculturable Microbes for Sustainable Agricultural Production. 2018 , 107-123	12
544	Diversity and Applications of Penicillium spp. in Plant-Growth Promotion. 2018, 261-276	4
543	Linking Nitrogen Load to the Structure and Function of Wetland Soil and Rhizosphere Microbial Communities. 2018 , 3,	39
542	Functional activity and functional gene diversity of a Cu-contaminated soil remediated by aided phytostabilization using compost, dolomitic limestone and a mixed tree stand. 2018 , 242, 229-238	18
541	Improving understanding of soil organic matter dynamics by triangulating theories, measurements, and models. 2018 , 140, 1-13	42
540	Genetic correlation network prediction of forest soil microbial functional organization. 2018, 12, 2492-2505	40
539	Anaerobic Fungi in Gorilla (Gorilla gorilla) Feces: an Adaptation to a High-Fiber Diet?. 2018 , 39, 567-580	2
538	The Green Roof Microbiome: Improving Plant Survival for Ecosystem Service Delivery. 2018, 6,	19
537	Mining Novel Constitutive Promoter Elements in Soil Metagenomic Libraries in. 2018 , 9, 1344	13
536	Enhanced Tolerance to Cadmium in Bacterial-Fungal Co-Cultures as a Strategy for Metal Biorecovery from e-Waste. 2018 , 8, 121	2
535	Synthetic Biology to Improve the Production of Lipases and Esterases (Review). 2018 , 1835, 229-242	2
534	Analysis of soil microbial dynamics at a cropland-grassland interface in an agro-pastoral zone in a temperate steppe in northern China. 2018 , 170, 257-265	7
533	A Ready-to-Use Single- and Duplex-TaqMan-qPCR Assay to Detect and Quantify the Biocontrol Agents and. 2018 , 9, 2073	10

532	Variation in microbial community structure correlates with heavy-metal contamination in soils decades after mining ceased. 2018 , 126, 57-63	63
531	Impact of Microbial Diversity on Environmental Stability. 2018 , 81-91	1
530	Soil Properties Drive Microbial Community Structure in a Large Scale Transect in South Eastern Australia. 2018 , 8, 11725	89
529	Long-term and high-concentration heavy-metal contamination strongly influences the microbiome and functional genes in Yellow River sediments. 2018 , 637-638, 1400-1412	118
528	Soil Carbon in the World: Ecosystem Services Linked to Soil Carbon in Forest and Agricultural Soils. 2018 , 1-38	5
527	Microbial Control of Soil Carbon Turnover. 2018 , 165-194	5
526	Biodegradation of biodiesel and toluene under nitrate-reducing conditions and the impact on bacterial community structure. 2019 , 19, 439-450	5
525	An in vitro protocol for rapidly assessing the effects of antimicrobial compounds on the unculturable bacterial plant pathogen, Liberibacter asiaticus. 2019 , 15, 85	1
524	Diversity and function of soil bacterial communities in response to long-term intensive management in a subtropical bamboo forest. 2019 , 354, 113894	25
523	Metagenomic Approach in Relation to Microbe Microbe and Plant Microbiome Interactions. 2019, 507-534	2
522	Applications of the Soil, Plant and Rumen Microbiomes in Pastoral Agriculture. 2019, 6, 107	16
521	SoilMicrobesPlants: Interactions and Ecological Diversity. 2019 , 145-176	4
520	Loss of soil microbial diversity exacerbates spread of antibiotic resistance. 2019 , 1, 3-13	33
519	Single-Cell Metagenomics. 2019 , 199-213	
518	A methodological framework to embrace soil biodiversity. 2019 , 136, 107536	47
517	Direct and indirect linkages between soil aggregates and soil bacterial communities under tillage methods. 2019 , 354, 113879	18
516	Soil functionality produced by soil mixing: The role of inoculum and substrate. 2019 , 34, 600-611	1
515	Microbial Community Structures and Important Associations Between Soil Nutrients and the Responses of Specific Taxa to Rice-Frog Cultivation. 2019 , 10, 1752	15

514	Analysis of Soil Properties, Bacterial Community Composition, and Metabolic Diversity in Fluvisols of a Floodplain Area. 2019 , 11, 3929	7
513	Effects of phosphate-solubilizing bacteria on phosphorous release and sorption on montmorillonite. 2019 , 181, 105227	11
512	Dystric Cambisol properties at windthrow sites with secondary succession developed after 12 years under different conditions in Tatra National Park. 2019 , 74, 1099-1114	1
511	Antibiotic Pollution in the Environment: From Microbial Ecology to Public Policy. 2019 , 7,	271
510	Spatial and temporal succession of bacterial communities in three artificial fishponds. 2019 , 50, 2793-2801	2
509	Environmental filtering: A case of bacterial community assembly in soil. 2019 , 136, 107531	11
508	Soil Microbiomes Promising Strategy for Contaminated Soil Remediation: A Review. 2019 , 29, 283-297	34
507	Profiling the Functional Diversity of Termite Mound Soil Bacteria as Revealed by Shotgun Sequencing. 2019 , 10,	14
506	Toxin-mediated competition in weakly motile bacteria. 2019 , 480, 205-217	
505	Inhibitory interaction networks among coevolved Streptomyces populations from prairie soils. 2019 , 14, e0223779	2
504	Evaluation of microbial shifts caused by a silver nanomaterial: comparison of four test systems. 2019 , 31,	4
503	Diversity, Ecology, and Prevalence of Antimicrobials in Nature. 2019 , 10, 2518	21
502	Does Soil Contribute to the Human Gut Microbiome?. 2019 , 7,	43
501	Exploring bacterial diversity: from cell to sequence. 2019 , 263-306	4
500	Impact of silver nanoparticles (AgNP) on soil microbial community depending on functionalization, concentration, exposure time, and soil texture. 2019 , 31,	29
499	Functional Diversity: An Epistemic Roadmap. 2019 , 69, 800-811	10
498	Effect of acclimation on inoculum functioning and dynamics within a microbial community. 2019 , 128, 105312	5
497	Bacterial community structure and function in soils from tidal freshwater wetlands in a Chinese delta: Potential impacts of salinity and nutrient. 2019 , 696, 134029	38

496	Redox-active humics support interspecies syntrophy and shift microbial community. 2019 , 62, 1695-1702	5
495	A comparative metagenomic and spectroscopic analysis of soils from an international point of entry between the US and Mexico. 2019 , 123, 558-566	11
494	Changes in the Active, Dead, and Dormant Microbial Community Structure across a Pleistocene Permafrost Chronosequence. 2019 , 85,	36
493	Soil Functions: Connecting Earth's Critical Zone. 2019 , 47, 333-359	31
492	Bacterial communities associated to Chilean altiplanic native plants from the Andean grasslands soils. 2019 , 9, 1042	16
491	Plant beneficial endophytic bacteria: Mechanisms, diversity, host range and genetic determinants. 2019 , 221, 36-49	210
490	Genome mining for ribosomally synthesised and post-translationally modified peptides (RiPPs) reveals undiscovered bioactive potentials of actinobacteria. 2019 , 112, 1477-1499	13
489	Technologies for the Selection, Culture and Metabolic Profiling of Unique Rhizosphere Microorganisms for Natural Product Discovery. 2019 , 24,	8
488	Microbial community composition of saltern soils from Ramnagar, West Bengal, India. 2019 , 12, 100040	3
487	Use of heavy metals resistant bacteria-a strategy for arsenic bioremediation. 2019 , 103, 6007-6021	33
486	Probing the active fraction of soil microbiomes using BONCAT-FACS. 2019 , 10, 2770	53
485	Detoxification of toxic heavy metals by serine protease inhibitor isolated from polluted soil. 2019 , 143, 104718	6
484	When Is A Lineage A Species? A Case Study In Myxacorys gen. nov. (Synechococcales: Cyanobacteria) With The Description of Two New Species From The Americas. 2019 , 55, 976-996	24
483	Pseudomonas strains isolated from different environmental niches exhibit different antagonistic ability. 2019 , 31, 399-420	3
482	Effect of Long-Term Farming Practices on Agricultural Soil Microbiome Members Represented by Metagenomically Assembled Genomes (MAGs) and Their Predicted Plant-Beneficial Genes. 2019 , 10,	31
481	Biodegradation of compostable polymers in various environments. 2019 , 255-292	4
480	Changes in soil taxonomic and functional diversity resulting from gamma irradiation. 2019 , 9, 7894	8
479	The First Report of Indigenous Free-Living Diazotroph Kosakonia sacchari Isolated from Himalayan Alder-Based Shifting Cultivation System in Nagaland, India. 2019 , 19, 574-579	4

478	Cobalt-dependent inhibition of nitrite oxidation in Nitrobacter winogradskyi. 2019, 128, 463-467	O
477	Separate and joint eco-toxicological effects of sulfadimidine and copper on soil microbial biomasses and ammoxidation microorganisms abundances. 2019 , 228, 556-564	17
476	Effect of Organic Carbon and Nitrogen on the Interactions of spp. and Bacteria Dispersing on Their Mycelium. 2019 , 10, 124	6
475	Soil health indicator responses on Missouri claypan soils affected by landscape position, depth, and management practices. 2019 , 74, 126-137	14
474	Phosphorus addition alters the response of soil organic carbon decomposition to nitrogen deposition in a subtropical forest. 2019 , 133, 119-128	24
473	Differences in Distribution of Potassium-Solubilizing Bacteria in Forest and Plantation Soils in Myanmar. 2019 , 16,	17
472	A soil bacterium alters sex determination and rhizoid development in gametophytes of the fern. 2019 , 11, plz012	5
471	Disentangling carbon flow across microbial kingdoms in the rhizosphere of maize. 2019 , 134, 122-130	21
470	Microbial community composition and network analyses in arid soils of the Patagonian Monte under grazing disturbance reveal an important response of the community to soil particle size. 2019 , 138, 223-232	19
469	High proportions of bacteria are culturable across major biomes. 2019 , 13, 2125-2128	66
468	CRISPR evolution and bacteriophage persistence in the context of population bottlenecks. 2019 , 16, 588-594	6
467	Microbial communities are sensitive indicators for freshwater sediment copper contamination. 2019 , 247, 1028-1038	18
466	Redox traits characterize the organization of global microbial communities. 2019 , 116, 3630-3635	27
465	Soil Bacterial Communities From the Chilean Andean Highlands: Taxonomic Composition and Culturability. 2019 , 7, 10	24
464	Nanotoxicity of engineered nanomaterials (ENMs) to environmentally relevant beneficial soil bacteria - a critical review. 2019 , 13, 392-428	37
463	Functional diversity of microorganisms in metal- and alkali-contaminated soils of Central and North-eastern Slovakia. 2019 , 14, 32-39	7
462	Nanotechnology for Agriculture. 2019 ,	3
461	7. Techniques and approaches to quantify microbial diversity in extreme environments. 2019 , 151-166	

460	Rhizosphere Metagenomics of L. (Kodo Millet) Reveals Rhizobiome Multifunctionalities. 2019 , 7,	10
459	Changes in Functional Response of Soil Microbial Community along Chronosequence of Spontaneous Succession on Post Mining Forest Sites Evaluated by Biolog and SIR Methods. 2019 , 10, 1005	4
458	Steering soil microbiome to enhance soil system resilience. 2019 , 45, 743-753	14
457	Soil pH is the primary factor driving the distribution and function of microorganisms in farmland soils in northeastern China. 2019 , 69, 1461-1473	42
456	Impacts of DNA extraction and PCR on DNA metabarcoding estimates of soil biodiversity. 2019 , 10, 120-133	27
455	Diet composition and gut microbiome of 0-group European plaice Pleuronectes platessa L Strong homogeneity and subtle spatial and temporal differences. 2019 , 144, 67-77	4
454	The microbiota of technosols resembles that of a nearby forest soil three years after their establishment. 2019 , 220, 600-610	7
453	Consumption of florfenicol-medicated feed alters the composition of the channel catfish intestinal microbiota including enriching the relative abundance of opportunistic pathogens. 2019 , 501, 111-118	24
452	Using proteins to study how microbes contribute to soil ecosystem services: The current state and future perspectives of soil metaproteomics. 2019 , 198, 50-58	33
45 ¹	Environmental and spatial variables determine the taxonomic but not functional structure patterns of microbial communities in alpine grasslands. 2019 , 654, 960-968	3
450	Recent advances in microfluidic devices for bacteria and fungus research. 2019, 112, 175-195	32
449	Microbial growth and carbon use efficiency in soil: Links to fungal-bacterial dominance, SOC-quality and stoichiometry. 2019 , 131, 195-205	82
448	Optimization of combined phytoremediation for heavy metal contaminated mine tailings by a field-scale orthogonal experiment. 2019 , 168, 1-8	44
447	Soil pH rather than elevation determines bacterial phylogenetic community assembly on Mt. Norikura. 2019 , 95,	11
446	Evaluating the impact of the biocontrol agent Trichoderma harzianum ITEM 3636 on indigenous microbial communities from field soils. 2019 , 126, 608-623	9
445	Comprehensive insights into the key components of bacterial assemblages in pharmaceutical wastewater treatment plants. 2019 , 651, 2148-2157	19
444	Functional Microbial Diversity in Context to Agriculture. 2019 , 347-358	5
443	Apple rootstocks of different nitrogen tolerance affect the rhizosphere bacterial community composition. 2019 , 126, 595-607	7

442	Living and labouring soils: Metagenomic ecology and a new agricultural revolution?. 2019, 14, 393-415	14
441	Functional Microbial Diversity in Contaminated Environment and Application in Bioremediation. 2019 , 359-385	19
440	Fungal mycobiota and mycotoxin risk for traditional artisan Italian cave cheese. 2019 , 78, 62-72	22
439	Metagenomic Achievements in Microbial Diversity Determination in Croplands. 2019, 15-35	6
438	Microbial Diversity of Thermophiles Through the Lens of Next Generation Sequencing. 2019, 217-226	2
437	A New Antifungal Antibiotic from Bacillus sp. KM5 Isolated from Rice Rhizospheric Soil. 2019 , 89, 333-344	
436	Omics in traditional vegetable fermented foods and beverages. 2020 , 60, 791-809	36
435	Introduction. 2020 , 1-4	
434	Soil Health Restoration and Management. 2020 ,	1
433	Species of Cryphonectriaceae occupy an endophytic niche in the Melastomataceae and are putative latent pathogens of Eucalyptus. 2020 , 156, 273-283	4
432	Impact of short-term application of seaweed fertilizer on bacterial diversity and community structure, soil nitrogen contents, and plant growth in maize rhizosphere soil. 2020 , 65, 591-603	7
431	The influence of transplanted trees on soil microbial diversity in coal mine subsidence areas in the Loess Plateau of China. 2020 , 21, e00877	5
430	Assessment of microbial diversity and enumeration of metal tolerant autochthonous bacteria from tailings of magnesite and bauxite mines. 2020 , 33, 4391-4401	5
429	Functional gene categories differentiate maize leaf drought-related microbial epiphytic communities. 2020 , 15, e0237493	2
428	Phytomanagement Reduces Metal Availability and Microbial Metal Resistance in a Metal Contaminated Soil. 2020 , 11, 1899	2
427	Microbial dynamics in traditional eco-knowledge vis-Bvis chemical-intensive agri-amendment systems of stress prone semi-arid tropics. 2020 , 155, 103668	3
426	Exogenously applied ferulic acid and p-coumaric acid differentially affect cucumber rhizosphere Trichoderma spp. community structure and abundance. 2020 , 66, 461-467	4
425	Microbial Communities in Soils Under Natural Reforestation. 2020 , 219-235	

(2020-2020)

424	The incidence of antibiotic resistance within and beyond the agricultural ecosystem: A concern for public health. 2020 , 9, e1035	31
423	Geobiochemistry characteristics of rare earth elements in soil and ground water: a case study in Baotou, China. 2020 , 10, 11740	10
422	Bacterial diversity on an abandoned, industrial wasteland contaminated by polychlorinated biphenyls, dioxins, furans and trace metals. 2020 , 748, 141242	7
421	Distribution and Control of Bacterial Community Composition in Marian Cove Surface Waters, King George Island, Antarctica during the Summer of 2018. 2020 , 8,	4
420	Subsoil Microbial Diversity and Stability in Rotational Cotton Systems. 2020, 4, 44	3
419	Correlations of Soil Fungi, Soil Structure and Tree Vigour on an Apple Orchard with Replant Soil. 2020 , 4, 70	3
418	Discovery of Novel Biosynthetic Gene Cluster Diversity From a Soil Metagenomic Library. 2020 , 11, 585398	5
417	MPN Drop Agar Method for Determination of Heterotrophic Microorganisms in Soil and Water Samples Using Tissue Plate as a Carrier. 2020 , 12, 8252	
416	Screening of Heavy Metal-Immobilizing Bacteria and Its Effect on Reducing Cd and Pb Concentrations in Water Spinach (Forsk.). 2020 , 17,	2
415	It takes three to tango: the importance of microbes, host plant, and soil management to elucidate manipulation strategies for the plant microbiome. 2020 , 66, 413-433	18
414	Optimal biochar amendment rate reduced the yield-scaled NO emissions from Ultisols in an intensive vegetable field in South China. 2020 , 723, 138161	9
413	Microbial Ecosystems in Central Andes Extreme Environments. 2020,	6
412	Bacterial community dissimilarity in soils is driven by long-term land-use practices. 2020 , 3, e20031	6
411	Comparative Analysis of Sample Extraction and Library Construction for Shotgun Metagenomics. 2020 , 14, 1177932220915459	3
410	Soil Ecosystems Services. 2020 ,	
409	High-Throughput Sequencing Reveals the Diversity and Community Structure in Rhizosphere Soils of Three Endangered Plants in Western Ordos, China. 2020 , 77, 2713-2723	4
408	Key factors controlling microbial community responses after a fire: Importance of severity and recurrence. 2020 , 741, 140363	9
	Introductory Chapter: Metagenomics and Metagenomic Approaches. 2020 ,	

406	Language of plant-microbe-microbe interactions in rhizospheric ecosystems. 2020 , 59-76	1
405	Microbial diversity and functional response to the redox dynamics of pyrite-rich sediment and the impact of preload surcharge. 2020 , 192, 226	O
404	Agriculturally important microbial biofilms: Biodiversity, ecological significances, and biotechnological applications. 2020 , 221-265	20
403	Random sampling in metagenomic sequencing leads to overestimated spatial scaling of microbial diversity. 2020 , 22, 2140-2149	1
402	High-Throughput Isolation of Nucleic Acids from Soil. 2020 , 4, 3	3
401	Medicago sativa and soil microbiome responses to Trichoderma as a biofertilizer in alkaline-saline soils. 2020 , 153, 103573	6
400	The Structure and Diversity of Nitrogen Functional Groups from Different Cropping Systems in Yellow River Delta. 2020 , 8,	7
399	Microbial biofilms: Functional annotation and potential applications in agriculture and allied sectors. 2020 , 283-301	15
398	Nitrogen and Phosphorus Absorption and Yield of Tomato Increased by Regulating the Bacterial Community under Greenhouse Conditions via the Alternate Drip Irrigation Method. 2020 , 10, 315	3
397	Complex study of glyphosate and metabolites influence on enzymatic activity and microorganisms association in soil enriched with Pseudomonas fluorescens and sewage sludge. 2020 , 393, 122443	11
396	Cow manure application effectively regulates the soil bacterial community in tea plantation. 2020 , 20, 190	14
395	Land rehabilitation improves edaphic conditions and increases soil microbial biomass and abundance. 2020 , 2, 145-156	2
394	The effects of warming and soil chemistry on bacterial community structure in Arctic tundra soils. 2020 , 148, 107882	13
393	Distinct temporal diversity profiles for nitrogen cycling genes in a hyporheic microbiome. 2020 , 15, e0228165	7
392	Antioxidant and cytotoxic activity of endophytic bacteria isolated from mangrove species. 2020 , 439, 012051	
391	Bioremediation: an emerging effective approach towards environment restoration. 2020 , 3, 91-103	28
390	Comparison of different media for the detection of denitrifying and nitrate reducing bacteria in mesotrophic aquatic environments by the most probable number method. 2020 , 168, 105808	3
389	Addition of fructose to the maize hyphosphere increases phosphatase activity by changing bacterial community structure. 2020 , 142, 107724	9

(2021-2020)

	Prevalence of unclassified bacteria in the soil bacterial community from floodplain meadows (fluvisols) under simulated flood conditions revealed by a metataxonomic approachss. 2020 , 188, 104448	14
387	Organic mulching positively regulates the soil microbial communities and ecosystem functions in tea plantation. 2020 , 20, 103	16
386	Arbuscular mycorrhizal fungal communities in the rhizospheric soil of litchi and mango orchards as affected by geographic distance, soil properties and manure input. 2020 , 152, 103593	16
385	Effects of lead (Pb) in stormwater runoff on the microbial characteristics and organics removal in bioretention systems. 2020 , 253, 126721	16
384	Responses of Bacterial Community, Root-Soil Interaction and Tomato Yield to Different Practices in Subsurface Drip Irrigation. 2020 , 12, 2338	2
383	Soil Quality and Heavy Metal Pollution Assessment of Iron Ore Mines in Nizna Slana (Slovakia). 2020 , 12, 2549	27
382	Long-term effects of stump removal and tree species composition on the diversity and structure of soil fungal communities. 2020 , 96,	4
381	Complementary Metagenomic Approaches Improve Reconstruction of Microbial Diversity in a Forest Soil. 2020 , 5,	26
380	Bacterial Community Selection of Mycosphere Soil. 2020 , 11, 347	4
379	Rhizobacteria and its biofilm for sustainable agriculture: A concise review. 2020 , 165-175	0
2/9	Kilizobacceria aliu its bioritii for sustailiabte agriculture. A concise review. 2020, 103-173	8
378	Composition and diversity of prokaryotes at an iron ore post-mining site revealed the natural resilience 10 years after mining exploitation. 2021 , 32, 256-269	1
	Composition and diversity of prokaryotes at an iron ore post-mining site revealed the natural	
378	Composition and diversity of prokaryotes at an iron ore post-mining site revealed the natural resilience 10 years after mining exploitation. 2021 , 32, 256-269 Monitoring soil microbial communities using molecular tools: DNA extraction methods may offset	
37 ⁸ 377	Composition and diversity of prokaryotes at an iron ore post-mining site revealed the natural resilience 10 years after mining exploitation. 2021 , 32, 256-269 Monitoring soil microbial communities using molecular tools: DNA extraction methods may offset long-term management effects. 2021 , 72, 1026-1041 Microbial diversity and functionality of traditional fermented milk products of India: Current	1
378 377 376	Composition and diversity of prokaryotes at an iron ore post-mining site revealed the natural resilience 10 years after mining exploitation. 2021, 32, 256-269 Monitoring soil microbial communities using molecular tools: DNA extraction methods may offset long-term management effects. 2021, 72, 1026-1041 Microbial diversity and functionality of traditional fermented milk products of India: Current scenario and future perspectives. 2021, 114, 104941	1 2 7
378 377 376 375	Composition and diversity of prokaryotes at an iron ore post-mining site revealed the natural resilience 10 years after mining exploitation. 2021, 32, 256-269 Monitoring soil microbial communities using molecular tools: DNA extraction methods may offset long-term management effects. 2021, 72, 1026-1041 Microbial diversity and functionality of traditional fermented milk products of India: Current scenario and future perspectives. 2021, 114, 104941 Microbial metabolic noise. 2021, 13, e1512 Soil organic matter and salinity as critical factors affecting the bacterial community and function of	1 2 7
378 377 376 375 374	Composition and diversity of prokaryotes at an iron ore post-mining site revealed the natural resilience 10 years after mining exploitation. 2021, 32, 256-269 Monitoring soil microbial communities using molecular tools: DNA extraction methods may offset long-term management effects. 2021, 72, 1026-1041 Microbial diversity and functionality of traditional fermented milk products of India: Current scenario and future perspectives. 2021, 114, 104941 Microbial metabolic noise. 2021, 13, e1512 Soil organic matter and salinity as critical factors affecting the bacterial community and function of Phragmites australis dominated riparian and coastal wetlands. 2021, 762, 143156 The Impact of Different Techniques of Soil Management on Soil Fertility and the Associated	1 2 7 4

370	Stronger impacts of long-term relative to short-term exposure to carbon nanomaterials on soil bacterial communities. 2021 , 410, 124550	4
369	The Effects of Soil Depth on the Structure of Microbial Communities in Agricultural Soils in Iowa, USA. 2020 ,	16
368	Impact of a Nature-Inspired Engineered Soil Structure on Microbial Diversity and Community Composition in the Bulk Soil and Rhizosphere of Tomato Grown Under Saline Irrigation Water. 2021 , 21, 173-186	0
367	How the 'kitome' influences the characterization of bacterial communities in lepidopteran samples with low bacterial biomass. 2021 , 130, 1780-1793	2
366	Effects of perennial aromatic grass species richness and microbial consortium on soil properties of marginal lands and on biomass production. 2021 , 32, 1008-1021	2
365	Rhizosphere Biology: Interactions Between Microbes and Plants. 2021 ,	1
364	Forest conversion alters the structure and functional processes of tropical forest soil microbial communities. 2021 , 32, 613-627	6
363	Management of Soil-Microorganism: Interphase for Sustainable Soil Fertility Management and Enhanced Food Security. 2021 , 475-494	O
362	Effect of nanoparticles on crop growth. 2021 , 183-201	O
361	Microbial Endophytes: Sustainable Approach for Managing Phosphorus Deficiency in Agricultural Soils. 2021 , 35-75	2
360	Biopolymer production by halotolerant bacteria isolated from Caatinga biome. 2021 , 52, 547-559	1
359	Effects of Simulated Nitrogen Deposition on the Bacterial Community of Urban Green Spaces. 2021 , 11, 918	O
358	Magnetic-Particle-Encapsulated Alginate Beads for Aqueous-Based Bacteria Culturing and Manipulation. 2021 , 1-1	
357	Research Progress on Environmental Behavior and Biological Effects of Metal Nanoparticles. 2021 , 11, 100-108	
356	Engineered Nanoparticles in Smart Agricultural Revolution: An Enticing Domain to Move Carefully. 2021 , 3-18	
355	Influence of land use change on native microbial community and their response to the variations in micro environment. 2021 , 325-340	1
354	Next-generation omics technologies to explore microbial diversity. 2021 , 541-563	
353	Relevance of Metatranscriptomics in Symbiotic Associations Between Plants and Rhizosphere Microorganisms. 2021 , 59-90	

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352	Manoeuvring Soil Microbiome and Their Interactions: A Resilient Technology for Conserving Soil and Plant Health. 2021 , 405-433	
351	Changes in soil available cadmium and bacterial communities after fallowing depend on contamination levels. 2021 , 21, 1408-1419	4
350	Change: Risks and Predictability. 2021 , 181-193	
349	Molecular identification and relative abundance of microorganisms in douchi koji and salted egg white sufu during processing. 2021 , 92, e13567	O
348	Significance of Belowground Microbial-Rhizosphere Interactions. 2021 , 295-310	
347	Metabarcoding and Metagenomics in Soil Ecology Research: Achievements, Challenges, and Prospects. 2021 , 11, 40-53	12
346	Metatranscriptomics: A Promising Tool to Depict Dynamics of Microbial Community Structure and Function. 2021 , 471-491	0
345	The proficiency of the original host species determines community-level plasmid dynamics. 2021 , 97,	5
344	Glucose confers protection to Escherichia coli against contact killing by Vibrio cholerae. 2021 , 11, 2935	5
343	Global projections of the soil microbiome in the Anthropocene. 2021 , 30, 987-999	7
342	Soil quality and fertility in sustainable agriculture, with a contribution to the biological classification of agricultural soils.	3
342		3
	of agricultural soils. Do size and shape matter? Exploring the interactions and the metabolome of the soil isolate	3
341	of agricultural soils. Do size and shape matter? Exploring the interactions and the metabolome of the soil isolate Hylemonella gracilis. Recent advances in the bioprospection and applications of chitinolytic bacteria for valorization of	
341	of agricultural soils. Do size and shape matter? Exploring the interactions and the metabolome of the soil isolate Hylemonella gracilis. Recent advances in the bioprospection and applications of chitinolytic bacteria for valorization of waste chitin. 2021, 203, 1953-1969 Bacterial diversity and bio-chemical properties in the rhizosphere soils of Cumin and Coriander.	3
34 ¹ 34 ⁰ 339	of agricultural soils. Do size and shape matter? Exploring the interactions and the metabolome of the soil isolate Hylemonella gracilis. Recent advances in the bioprospection and applications of chitinolytic bacteria for valorization of waste chitin. 2021, 203, 1953-1969 Bacterial diversity and bio-chemical properties in the rhizosphere soils of Cumin and Coriander. 2021, 62, 368-376 Metagenomic Analysis of Microbial Community Affiliated with Termitarium Reveals High	3
341 340 339 338	of agricultural soils. Do size and shape matter? Exploring the interactions and the metabolome of the soil isolate Hylemonella gracilis. Recent advances in the bioprospection and applications of chitinolytic bacteria for valorization of waste chitin. 2021, 203, 1953-1969 Bacterial diversity and bio-chemical properties in the rhizosphere soils of Cumin and Coriander. 2021, 62, 368-376 Metagenomic Analysis of Microbial Community Affiliated with Termitarium Reveals High Lignocellulolytic Potential. 2021, 78, 1551-1565	3

334	Keystone species affect the relationship between soil microbial diversity and ecosystem function under land use change in subtropical China. 2021 , 35, 1159-1170	6
333	Soil microbial DNA concentration is a powerful indicator for estimating soil microbial biomass C and N across arid and semi-arid regions in northern China. 2021 , 160, 103869	3
332	Elucidating the effect of biofertilizers on bacterial diversity in maize rhizosphere soil. 2021 , 16, e0249834	2
331	Active metabolic pathways of anaerobic methane oxidation in paddy soils. 2021 , 156, 108215	7
330	Global Simulation and Evaluation of Soil Organic Matter and Microbial Carbon and Nitrogen Stocks Using the Microbial Decomposition Model ORCHIMIC v2.0. 2021 , 35, e2020GB006836	4
329	Scale-dependent tipping points of bacterial colonization resistance.	O
328	Effects of Flurochloridone Application on Rhizosphere Soil Fungal Community and Composition in Potato Growing Areas of the Qinghai-Tibet Plateau. 2021 , 7,	0
327	Non-Specific Immunity Associated Gut Microbiome in under Different Rearing Strategies. 2021 , 12,	O
326	Wastewater reuse for crop irrigation: Crop yield, soil and human health implications based on giardiasis epidemiology. 2021 , 775, 145833	22
325	Genomics as a potential tool to unravel the rhizosphere microbiome interactions on plant health. 2021 , 185, 106215	5
324	Coupled DNA-labeling and sequencing approach enables the detection of viable-but-non-culturable Vibrio spp. in irrigation water sources in the Chesapeake Bay watershed. 2021 , 16, 13	0
323	Edaphic variables are better indicators of soil microbial functional structure than plant-related ones in subtropical broad-leaved forests. 2021 , 773, 145630	2
322	Unraveling bacterial community structure and function and their links with natural salinity gradient in the Yellow River Delta. 2021 , 773, 145673	8
321	Deciphering edaphic bacterial community and function potential in a Chinese delta under exogenous nutrient input and salinity stress. 2021 , 201, 105212	2
320	Organic management practices shape the structure and associations of soil bacterial communities in tea plantations. 2021 , 163, 103975	6
319	Microbial functions and soil nitrogen mineralisation processes in the soil of a cool temperate forest in northern Japan. 2021 , 155, 359-379	2
318	Growth kinetic and transport of mixed microbial cultures in subsurface environments. 2021 , 153, 103929	2
317	Meta-omic evaluation of bacterial microbial community structure and activity for the environmental assessment of soils: overcoming protein extraction pitfalls. 2021 , 23, 4706-4725	O

316	Influence of plants and environmental variables on the diversity of soil microbial communities in the Yellow River Delta Wetland, China. 2021 , 274, 129967	17
315	A small-scale test for rapid assessment of the soil development potential in post-mining soils. 2021 , 211, 105016	О
314	Misdiagnosed tuberculosis being corrected as Nocardia farcinica infection by metagenomic sequencing: a case report. 2021 , 21, 754	3
313	Small-scale variation in a pristine montane cloud forest: evidence on high soil fungal diversity and biogeochemical heterogeneity. 2021 , 9, e11956	О
312	The role of soils in provision of genetic, medicinal and biochemical resources. 2021 , 376, 20200183	3
311	Shifts in arbuscular mycorrhizal fungal community composition and edaphic variables during reclamation chronosequence of an open-cast coal mining dump. 2021 , 203, 105301	2
310	Indigenous bacterial community and function in phenanthrene-polluted coastal wetlands: Potential for phenanthrene degradation and relation with soil properties. 2021 , 199, 111357	5
309	Longitudinal patterns in sediment type and quality during daily flow regimes and following natural hazards in an urban estuary: a Hurricane Harvey retrospective. 2021 , 1	1
308	Can We Estimate Functionality of Soil Microbial Communities from Structure-Derived Predictions? A Reality Test in Agricultural Soils. 2021 , 9, e0027821	0
307	Decreased growth of wild soil microbes after 15 years of transplant-induced warming in a montane meadow. 2022 , 28, 128-139	2
306	Phospholipid fatty acid (PLFA) analysis as a tool to estimate absolute abundances from compositional 16S rRNA bacterial metabarcoding data. 2021 , 188, 106271	5
305	Liming alters microbial community composition and its co-occurrence patterns in Cd- and Pb-contaminated agricultural soil. 2021 , 166, 104064	7
304	Viral abundance, community structure and correlation with bacterial community in soils of different cover plants. 2021 , 168, 104138	2
303	Changes in the root fungal microbiome of strawberry following application of residues of the biofumigant oilseed radish. 2021 , 168, 104116	1
302	Soil bacterial diversity related to soil compaction and aggregates sizes in potato cropping systems. 2021 , 168, 104147	O
301	Characterization of growth promoting bacterial endophytes isolated from Artemisia annua L 2021 , 143, 238-247	1
300	Metagenomics for mining of thermoalkalophilic enzymes. 2022 , 259-274	
299	Soil Microbiome for Plant Growth and Bioremediation. 2021 , 158-180	1

298	Plant Growth-Promoting Rhizobacteria and Their Application in Sustainable Crop Production. 2021, 217-234	1
297	Multiparameter analysis of immunogenetic mechanisms in clinical diagnosis and management of inflammatory bowel disease. 2006 , 579, 209-18	9
296	Biological Assessment and Remediation of Contaminated Sediments. 2006, 179-238	3
295	Advances and Challenges in Studying Cave Microbial Diversity. 2013 , 1-34	6
294	Plant Growth-Promoting Rhizobacteria (PGPR) as Protagonists of Ever-Sustained Agriculture: An Introduction. 2019 , 1-10	3
293	Culture Independent Diversity Analysis of Soil Microbial Community and their Significance. 2014, 305-340	2
292	Principles of Compost-based Plant Diseases Control and Innovative New Developments. 2014 , 151-171	2
291	StructureHunction Relationships of Microbial Communities. 2015, 167-184	1
290	Reproductive Tract Infections in Women. 2015 , 313-335	1
289	Application of Terminal-Restriction Fragment Length Polymorphism for MolecularAnalysis of Soil Bacterial Communities. 2007 , 295-305	3
288	Extreme Views on Prokaryote Evolution. 2008 , 45-70	21
287	Plant-Microbe Partnerships. 2010 , 2545-2574	4
286	Soil Bacteria and Bacteriophages. 2011 , 67-112	6
285	Soil-Borne Pathogens and Their Interactions with the Soil Environment. 2010 , 197-271	18
284	The Impact of Land-Use Practices on Soil Microbes. 2010 , 273-295	2
283	Biogeography of Soil Microbial Communities: A Review and a Description of the Ongoing French National Initiative. 2011 , 857-865	1
282	Soils Supporting Biodiversity. 2014 , 27-58	11
281	Modeling in Microbial Ecology. 2015 , 847-882	1

280	Impacts of Nitrogen Deposition on Forest Ecosystems in China. 2020 , 185-213	4
279	Soil Erosion and Management Strategies. 2019 , 73-122	7
278	Role of Soil Microbiome and Enzyme Activities in Plant Growth Nutrition and Ecological Restoration of Soil Health. 2019 , 99-132	2
277	Nanoparticles and Their Fate in Soil Ecosystem. 2020 , 221-245	1
276	Bacterial Endophytes: Diversity, Functional Importance, and Potential for Manipulation. 2021, 1-49	3
275	Rhizosphere Microbiome and Soil-Borne Diseases. 2021 , 155-168	1
274	Soil Microbiomes for Healthy Nutrient Recycling. 2021 , 1-21	24
273	Soil Ecological Pros and Cons of Nanomaterials: Impact on Microorganisms and Soil Health. 2019 , 145-159	1
272	Self-Driven Jamming in Growing Microbial Populations.	2
271	Towards an Ecological Trait-data Standard.	1
270	Study of Oak Ridge soils using BONCAT-FACS-Seq reveals that a large fraction of the soil microbiome is active.	3
269	Changes in the Active, Dead, and Dormant Microbial Community Structure Across a Pleistocene Permafrost Chronosequence.	1
268	Sugars dominate the seagrass rhizosphere.	3
267	Gene copy normalization of the 16S rRNA gene cannot outweigh the methodological biases of sequencing.	2
266	Metagenomic Methods for the Identification of Active Microorganisms and Genes in Biodegradation Processes. 2007 , 1079-1088	1
265	Soil microbial communities of Japanese apricot (Prunus mume) orchard under organic and conventional management. 2019 , 62,	2
264	Fungal Communities of Seaweeds. 2005 , 533-579	27
263	Comparative metagenomics reveals host specific metavirulomes and horizontal gene transfer elements in the chicken cecum microbiome. 2008 , 3, e2945	202

262	New detection systems of bacteria using highly selective media designed by SMART: selective medium-design algorithm restricted by two constraints. 2011 , 6, e16512	21
261	Validation and application of a PCR primer set to quantify fungal communities in the soil environment by real-time quantitative PCR. 2011 , 6, e24166	145
260	Soil bacterial diversity screening using single 16S rRNA gene V regions coupled with multi-million read generating sequencing technologies. 2012 , 7, e42671	67
259	Fungal diversity is not determined by mineral and chemical differences in serpentine substrates. 2012 , 7, e44233	22
258	Development and biotechnological application of a novel endoxylanase family GH10 identified from sugarcane soil metagenome. 2013 , 8, e70014	23
257	Manure refinement affects apple rhizosphere bacterial community structure: a study in sandy soil. 2013 , 8, e76937	24
256	Regime shift in sandy beach microbial communities following Deepwater Horizon oil spill remediation efforts. 2014 , 9, e102934	18
255	How does conversion of natural tropical rainforest ecosystems affect soil bacterial and fungal communities in the Nile river watershed of Uganda?. 2014 , 9, e104818	13
254	Mycobiome of the bat white nose syndrome affected caves and mines reveals diversity of fungi and local adaptation by the fungal pathogen Pseudogymnoascus (Geomyces) destructans. 2014 , 9, e108714	24
253	Influence of soil type, cultivar and Verticillium dahliae on the structure of the root and rhizosphere soil fungal microbiome of strawberry. 2014 , 9, e111455	35
252	Aminobacter MSH1-Mineralisation of BAM in Sand-Filters Depends on Biological Diversity. 2015 , 10, e01288.	38 6
251	Land Use History Shifts In Situ Fungal and Bacterial Successions following Wheat Straw Input into the Soil. 2015 , 10, e0130672	45
250	Individual-Based Model of Microbial Life on Hydrated Rough Soil Surfaces. 2016 , 11, e0147394	25
249	Turing Patterning Using Gene Circuits with Gas-Induced Degradation of Quorum Sensing Molecules. 2016 , 11, e0153679	13
248	Inferring interactions in complex microbial communities from nucleotide sequence data and environmental parameters. 2017 , 12, e0173765	11
247	The preservation of microbial DNA in archived soils of various genetic types. 2017 , 12, e0173901	10
246	The rhizospheric microbial community structure and diversity of deciduous and evergreen forests in Taihu Lake area, China. 2017 , 12, e0174411	29
245	Contrasting bacterial communities in two indigenous Chionochloa (Poaceae) grassland soils in New Zealand. 2017 , 12, e0179652	10

244	Analysis of Microbial Composition Associated with Freshwater and Seawater. 2016 , 22, 150-159	25
243	The Method of Microbiological Soil Investigations within the Framework of the Project Microbiome of Russia (2017, 100-113)	2
242	TAXONOMIC STRUCTURE OF PROKARYOTIC COMMUNITIES IN SOILS OF DIFFERENT BIOCLIMATIC ZONES. 2018 , 125-153	3
241	Isolation of Bacterial Endophytes from and their Potential in Diclofenac and Sulfamethoxazole Degradation. 2018 , 67, 321-331	13
240	DNA Sequencing: Strategies for Soil Microbiology. 2007 , 71, 592-600	23
239	Metabolic Modeling of Microbial Community Interactions for Health, Environmental and Biotechnological Applications. 2018 , 19, 712-722	13
238	Cultivation Effect of Chitinase-Transgenic Cotton on Functional Bacteria and Fungi in Rhizosphere and Bulk Soil. 2019 , 17, e1982	2
237	Metagenomic analysis of soil microbial communities. 2010 , 62, 559-564	19
236	Diversity of soil bacteria complexes associated with summer truffle (Tuber aestivum). 2020 , 62, 114-127	2
235	Functional diversity of soil microorganisms in the conditions of an ecological farming system. 2019 , 46, 146-152	2
234	Characterization of Microbial Diversity and Community Structure in Fermentation Pit Mud of Different Ages for Production of Strong-Aroma Baijiu. 2020 , 69, 1-14	3
233	Microbial community structure and dynamics in restored subtropical seagrass sediments. 2015 , 74, 43-57	10
232	Effects of different organic fertilizers on soil microbial biomass and yield of peanut. 2009, 17, 235-238	3
231	Microbial community diversity in tea root zone soils at different elevations. 2010 , 18, 866-871	1
230	Antibiotic production by intertidal sedimentary and porewater bacteria and the characterization of their prevalence in situ. 2019 , 14, 197-205	1
229	The Metagenome Approach: A New Resource for Glycosidases. 2019 , 31, E15-E20	1
228	Simultaneous Growth of <i>Chaetoceros muelleri</i> and Bacteria in Batch Cultures. 2014 , 04, 1025-1032	1
227	Assessment of the Influence of Oil Palm and Rubber Plantations in Tropical Peat Swamp Soils Using Microbial Diversity and Activity Analysis. 2016 , 05, 53-65	2

226	Can Changes in Soil Properties in Organic Banana Production Suppress Fusarium Wilt?. 2015 , 06, 181-195	6
225	Towards a Comprehensive Search of Putative Chitinases Sequences in Environmental Metagenomic Databases. 2014 , 06, 323-337	3
224	Reviews and syntheses: The mechanisms underlying carbon storage in soil. 2020 , 17, 5223-5242	27
223	The role of microorganisms and plants at different stages of ecosystem development for soil formation.	2
222	Influence of hydrological fluxes on bio-geochemical processes in a peatland.	1
221	Editorial "The Interdisciplinary Nature of SOIL".	5
220	Metagenome, the Untapped Microbial Genome, toward Discovery of Novel Microbial Resources and Application into the Plant Pathology. 2005 , 21, 93-98	3
219	First Isolation and Molecular Characterization of Bacteriophages Infecting , the Causal Agent of Bacterial Fruit Blotch. 2018 , 34, 59-64	9
218	Metagenomic Profiling of the Bacterial Community Changes from Koji to Mash Stage in the Brewing of Soy Sauce. 2017 , 66, 537-541	5
217	Bacterial community dynamics with rhizosphere of Calotropis procera and Senna alexandrina desert plants in Saudi Arabia. 2020 , 16, 567-578	3
216	Successive DNA extractions improve characterization of soil microbial communities. 2017, 5, e2915	11
215	A survey on cultivable heterotrophic bacteria inhabiting a thermally unstratified water column in an Atlantic Rainforest lake. 2014 , 2, e478	4
214	Long-read viral metagenomics captures abundant and microdiverse viral populations and their niche-defining genomic islands. 2019 , 7, e6800	68
213	Seasonal dynamics of microbial diversity in the rhizosphere of L. var. in a steppe desert area of Northern China. 2019 , 7, e7526	6
212	The effects of humic substances on DNA isolation from soils. 2020 , 8, e9378	7
211	KEYLINK: towards a more integrative soil representation for inclusion in ecosystem scale models. I. review and model concept. 2020 , 8, e9750	8
210	Effects of Reducing Nitrogen Fertilizer and Improving Organic Fertilizer on Crop Yield, Soil Quality and Microbial Community in Five Years Wheat-Rice Rotation Field. 2021 , 15, 449-458	0
209	Analysis of Microbial Diversity in Various Forest Communities by Biolog Ecoplate Method: Yenice Hot Spot.	

208	Microbiome of Pukzing Cave in India shows high antimicrobial activity against plant and animal pathogens. 2021 , 113, 4098-4108	1
207	Shaping of soil microbial communities by plants does not translate into specific legacy effects on organic carbon mineralization. 2021 , 163, 108449	O
206	21st Century Guidebook to Fungi. 2000 , 3-17	
205	Introduction and Overview: Soil, Rhizosphere, and Phyllosphere. 2007, 595-596	
204	Diversity and Functions of Soil Microflora in Development of Plants. 2008 , 71-98	1
203	The Environment and the Tools in Rhizo- and Bioremediation of Contaminated Soil. 2009, 315-338	
202	Detection and Characterization of Uncultivated Microorganisms Using Microarrays. 2009, 179-202	
201	Design of 16 S rRNA-based Oligonucleotide Array Using Group-specific Non-unique Probes in Large Scale Bacteria Detection*. 2009 , 36, 1025-1034	
200	Exploiting Microbial Diversity: The Challenges and the Means. 2010 , 2435-2458	
199	Population and Comparative Genomics Inform Our Understanding of Bacterial Species Diversity in the Soil. 2011 , 283-292	
198	Studying the Life Cycle of Aerobic Endospore-forming Bacteria in Soil. 2011 , 115-133	
197	Toward the Educated Design of Bacterial Communities. 2012 , 177-188	
196	Assessment of Korean Paddy Soil Microbial Community Structure by Use of Quantitative Real-time PCR Assays. 2011 , 30, 367-376	
195	Metagenomic profiles of soil microbiota under two different cropping systems detected by STRs-based PCR. 2012 , 03, 98-103	1
194	Complex Microbial Communities as Part of Fermented Food Ecosystems and Beneficial Properties. 2012 ,	
193	Application of Amplicon Pyrosequencing in Soil Microbial Ecology. 2012 , 45, 1073-1085	
192	Seasonal Variation of Bacterial Community in the Seawater of Gwangyang Bay Estimated by Amplified Ribosomal DNA Restriction Analysis. 2013 , 23, 770-778	
191	Concluding Perspectives of Sequelae and Long-Term Consequences of Infectious DiseasesIWhat's Next?. 487-493	

190	Application of Microbial Source Tracking to Human Health and National Security. 211-234	1
189	The Good, The Bad, and the Ugly: Tales of Mold-Ripened Cheese. 95-131	1
188	Toluene Biodegradation by Novel Bacteria Isolated from Polluted Soil Surrounding Car Body Repair and Spray Painting Workshops. 2015 , 06, 1417-1429	3
187	Clonacifi, expresifi y caracterizacifi de una nueva esterasa derivada de metagenomas de suelos agrfiolas colombianos. 2016 , 18, 48	1
186	Terrestrial Microbial Diversity. 2016 , 37-56	
185	Functional gene categories differentiate maize leaf drought-related microbial epiphytic communities.	3
184	Advancement in Bioremediation of Pharmaceutical and Personal Care Products. 2017, 451-469	
183	Rhizoremediation in Cold Climates. 2017 , 661-685	
182	Heavy Metals Contamination, Inauspicious Wallop on Microbial Diversity and their Possible Remediation for Environmental Restoration. 2017 , 5,	
181	Rehabilitation of Biological Characteristics in Mine Tailings. 2017 , 75-94	
180	Linking nitrogen load to the structure and function of wetland soil and rhizosphere microbial communities.	
	communicies.	
179	Assessing and characterising the repertoire of constitutive promoter elements in soil metagenomic libraries in Escherichia coli.	
179 178	Assessing and characterising the repertoire of constitutive promoter elements in soil metagenomic	2
	Assessing and characterising the repertoire of constitutive promoter elements in soil metagenomic libraries in Escherichia coli. Characterization and Comparison of Microbial Soil Diversity in Two Andean Peatlands in Different	2
178	Assessing and characterising the repertoire of constitutive promoter elements in soil metagenomic libraries in Escherichia coli. Characterization and Comparison of Microbial Soil Diversity in Two Andean Peatlands in Different States of Conservation-Vega Tocorpuri. 2018, 06, 194-210 Directional selection limits ecological diversification and promotes ecological tinkering during the	
178 177	Assessing and characterising the repertoire of constitutive promoter elements in soil metagenomic libraries in Escherichia coli. Characterization and Comparison of Microbial Soil Diversity in Two Andean Peatlands in Different States of Conservation-Vega Tocorpuri. 2018, 06, 194-210 Directional selection limits ecological diversification and promotes ecological tinkering during the competition for substitutable resources. Application of Molecular and Sequencing Techniques in Analysis of Microbial Diversity in	
178 177 176	Assessing and characterising the repertoire of constitutive promoter elements in soil metagenomic libraries in Escherichia coli. Characterization and Comparison of Microbial Soil Diversity in Two Andean Peatlands in Different States of Conservation-Vega Tocorpuri. 2018, 06, 194-210 Directional selection limits ecological diversification and promotes ecological tinkering during the competition for substitutable resources. Application of Molecular and Sequencing Techniques in Analysis of Microbial Diversity in Agroecosystem. 2019, 21-44	Ο

Relevance of Microbial Diversity in Implicating Soil Restoration and Health Management. **2020**, 161-202

171	Temporal dynamics of nitrogen cycle gene diversity in a hyporheic microbiome.	O
170	Development of Methodology for Vulnerability Assessment of Chemical Accident in Terrestrial Ecosystem:(1) Focusing on the Trees. 2020 , 42, 229-238	1
169	Glucose promotes resistance of human commensal Escherichia coli against contact-killing by pandemic Vibrio cholerae.	
168	Effect of heavy metals on soil microbial quality of an abandoned mining area Sidi Kamber, North-East of Algeria. 2020 , 9, 254-263	1
167	Pollution impact on microbial communities composition in natural and anthropogenically modified soils of Southern Russia. 2022 , 254, 126913	4
166	Novel species (Mucoromycetes, Mucoraceae) from northern Thailand. 2021 , 84, 57-78	1
165	Salinity Drives Functional and Taxonomic Diversities in Global Water Metagenomes. 2021 , 12, 719725	2
164	Metabolism of Nitroaromatic Compounds by Microbes and Study of Chemotaxis Toward These Compounds. 2020 , 303-325	
163	From Aerial Spaces to Litter Layers. 2020 , 10-40	
162	Resonating Farms and Vital Spaces. 2020 , 137-168	
161	References. 2020 , 197-212	
160	Development of Methodology for Vulnerability Assessment of Chemical Accident in Terrestrial Ecosystem: (2) Focusing on the Herbs. 2020 , 42, 610-622	
159	Molecular characterization of local cyanobacterial isolates using 16S rRNA, rpoB, and nif H biomarkers. 2022 , 307-334	
158	Simulated root exudates stimulate the abundance of Saccharimonadales to improve the alkaline phosphatase activity in maize rhizosphere. 2022 , 170, 104274	2
157	Advancement in Bioremediation of Pharmaceutical and Personal Care Products. 2020 , 1150-1168	2
156	Composition and Diversity of Soil Bacterial Communities along an Environmental Gradient in the Sudano-Sahelian Region of Senegal. 2020 , 10, 58-89	
155	The Theater of Life is Also a Stage of Death. 2020 , 41-69	

154	Dissecting Structure and Function of Plant Rhizomicrobiome: A Genomic Approach. 2020, 73-103	
153	Microbial Characterization of Andean Peatland⊠ Soil. 2020 , 87-93	Ο
152	Introduction. 2020 , 1-9	
151	Characteristics of Microbial Community and Enzyme Activities in Higher Altitude Regions. 2020 , 201-226	
150	Designing and Evaluation of Metagenomics 16S rRNA Gene Primers.	1
149	Decomposition as Life Politics. 2020 , 105-136	
148	Microbiome of post-technogenic soils of quarries in the Republic of Bashkortostan (Russia). 2020 , 5, 529-538	1
147	Notes. 2020 , 183-195	
146	Which Soils? Where Soils? Why Soils?. 2020 , 169-181	
145	Partial Alliances among Minor Practices. 2020 , 70-104	
144	The effects of soil depth on the structure of microbial communities in agricultural soils in Iowa, USA.	
143	Effect of Chicken Manure-Based Fertiliser on Bacterial Communities and Diversity of Tomato Endosphere Microbiota. 2021 , 67, 144-154	O
142	Stable Soil Microbial Functional Structure Responding to Biodiversity Loss Based on Metagenomic Evidences. 2021 , 12, 716764	1
141	Biostimulants in Agricultural and Horticultural Production. 2022 , 35-95	О
140	Evolution and Origin of Virulence Isolates. 2006 , 21-30	
139	The proficiency of the original host species determines community-level plasmid dynamics.	
138	21st Century Guidebook to Fungi. 2020 , 1-14	
137	The use of molecular tools to characterize functional microbial communities in contaminated areas. 2022 , 55-68	0

136	Induction of plant defense response by endophytic microorganisms. 2022, 89-115	O
135	Interactions of Muscovy duck reovirus, gut microbiota, and host innate immunity: Transcriptome and gut microbiota analysis. 2021 , 264, 109286	O
134	Effect of fertilizer management on the soil bacterial community in agroecosystems across the globe. 2022 , 326, 107795	3
133	Smart soils to observe hidden rhizosphere processes.	
132	Biostimulation of Bacteria in Liquid Culture for Identification of New Antimicrobial Compounds 2021 , 14,	1
131	Soil Microbial and Nematode Community Response to the Field Application of Recycled Bio-Based Fertilisers in Irish Grassland. 2021 , 13, 12342	O
130	Soil Bacterial Biogeography at the Scale of France. 2021 , 165-192	
129	Improvement of eukaryotic proteins prediction from soil metagenomes.	
128	Effects of Seven-Year Fertilization Reclamation on Bacterial Community in a Coal Mining Subsidence Area in Shanxi, China. 2021 , 18,	О
127	Monoterpene Enrichments Have Positive Impacts on Soil Bacterial Communities and the Potential of Application in Bioremediation. 2021 , 10,	1
126	Anthropogenic impacts on phytosociological features and soil microbial health of Colchicum luteum L. an endangered medicinal plant of North Western Himalaya 2022 , 29, 2856-2866	2
125	Construction of a TRFIC strip for rapid and sensitive detection of Ralstoniasolanacearum 2021 , 239, 123139	
124	Mechanism of salicylic acid in promoting the rhizosphere benzo[a]pyrene biodegradation as revealed by DNA-stable isotope probing. 2021 , 152202	О
123	If the combination of straw interlayer and irrigation water reduction maintained sunflower yield by boosting soil fertility and improving bacterial community in arid and saline areas. 2022 , 262, 107424	
122	Succession of soil bacterial community along a 46-year choronsequence artificial revegetation in an arid oasis-desert ecotone 2021 , 152496	1
121	Changing thermal sensitivity of bacterial communities and soil enzymes in a bog peat in spring, summer and autumn. 2022 , 173, 104382	O
120	Responses of Bacterial Taxonomical Diversity Indicators to Pollutant Loadings in Experimental Wetland Microcosms. 2022 , 14, 251	0
119	Teamwork to Survive in Hostile Soils: Use of Plant Growth-Promoting Bacteria to Ameliorate Soil Salinity Stress in Crops 2022 , 10,	1

118	Metagenomic monitoring of soil bacterial community after the construction of a crude oil flowline 2022 , 194, 48	О
117	Global diversity and distribution of mushroom-inhabiting bacteria 2022,	1
116	Significance of the Diversification of Wheat Species for the Assembly and Functioning of the Root-Associated Microbiome 2021 , 12, 782135	1
115	Microbial Communities Influence Soil Dissolved Organic Carbon Concentration by Altering Metabolite Composition 2021 , 12, 799014	1
114	Scale-dependent tipping points of bacterial colonization resistance 2022, 119,	1
113	Converting tropical rainforest to native rubber plantations alters soil bacterial and fungal communities. 2022 , 2, 1-6	
112	Bacterial Community Diversity of a Congolese Traditional Fermented Food, P andé Revealed by Illumina Miseq<sup>TM</sup> Sequencing of 16S rRNA Gene. 2022 , 12, 387-405	
111	Biodiversity and Metabolic Potential of Bacteria in Bulk Soil from the Peri-Root Zone of Black Alder (), Silver Birch () and Scots Pine () 2022 , 23,	O
110	Database-independent analysis of probable post-translational modifications of soil proteins across ecosystems.	
109	Spatial Metagenomic Analysis in Understanding the Microbial Diversity of Thar Desert 2022 , 11,	1
108	Plant growth promoting rhizobacterial diversity in potato grown soil in the Gwalior region of India 2022 , 33, e00713	О
107	Environmental and Human Microbiome for Health 2022 , 12,	O
106	Linking Soil Microbial Diversity to Modern Agriculture Practices: A Review 2022, 19,	1
105	Metagenomic insights to the functional potential of sediment microbial communities in freshwater lakes. 6,	1
104	Lower functional redundancy in Barrowlthan Broadlfunctions in global soil metagenomics. 2022 , 8, 297-308	O
103	The associations between intestinal bacteria of Eospalax cansus and soil bacteria of its habitat 2022 , 18, 129	
102	Microbial functional genes influenced by short-term experimental drought across European agricultural fields. 2022 , 168, 108650	О
101	Changes in soil microbial community following the conversion of wasteland to cotton land in saline-sodic region of Northwest China. 2022 , 174, 104424	O

(2020-2021)

100	Diversity and functions of microbes in surface sediments under heavy metal pollution of western Chaohu Lake. 2021 ,	O
99	Soil enzymes as indicators of soil function: A step toward greater realism in microbial ecological modeling 2021 ,	O
98	Cross inoculation of rhizobiome from a congeneric ruderal plant imparts drought tolerance in maize (Zea mays) through changes in root morphology and proteome 2022 ,	O
97	Temporal Dynamics of Bacterial Communities along a Gradient of Disturbance in a U.S. Southern Plains Agroecosystem 2022 , e0382921	
96	A sustainable approach for bioremediation of secondary salinized soils: Studying remediation efficiency and soil nitrate transformation by bioaugmentation 2022 , 134580	3
95	Data_Sheet_1.docx. 2019,	
94	Data_Sheet_1.pdf. 2018 ,	
93	Data_Sheet_1.pdf. 2019 ,	
92	lmage_1.TIF. 2018 ,	
91	Table_1.docx. 2018 ,	
90	Data_Sheet_1.docx. 2020 ,	
89	Data_Sheet_1.PDF. 2020 ,	
88	lmage_1.TIF. 2020 ,	
87	Image_2.TIF. 2020 ,	
86	Image_3.TIF. 2020 ,	
85	Image_4.TIF. 2020 ,	
84	lmage_5.TIF. 2020 ,	
83	Table_1.DOCX. 2020 ,	

82	Table_2.DOCX. 2020 ,
81	Table_3.DOCX. 2020 ,
80	Table_4.DOCX. 2020 ,
79	Table_1.XLSX. 2020 ,
78	Table_2.XLSX. 2020 ,
77	Table_3.XLSX. 2020 ,
76	Table_4.XLSX. 2020 ,
75	Consequences of Climate Change Over Soil Dynamics: An Update. 2022 , 101-111
74	Analyzing the Capabilities of Actinobacteria for Remediation Through Metagenomic Analysis of Contaminated Habitats. 2022 , 471-487
73	Links Among Crop Diversification, Microbial Diversity, and Soil Organic Carbon: Mini Review and Case Studies 2022 , 13, 854247
72	Sugars dominate the seagrass rhizosphere 2022,
71	Temporal variation in bacterial community profile on patients' bedsheets in a primary healthcare unit 2022 , 204, 308
70	Functional diversity of bacterial communities in the rhizosphere of maize grown on a soil under organic and inorganic fertilization. 2022 , 16, e01212
69	Protein sequence databases generated from metagenomics and public databases produced similar soil metaproteomic results of microbial taxonomic and functional changes. 2022 , 32, 507-520
68	??????????????????. 2018 , 8, 164-167
67	[Review] Isolation and Characterization of Novel Glycosidases Using Culture-dependent and Culture-independent Metagenomic Approaches. 2018 , 8, 206-210
66	Sequestration of Molecular and Mass Spectra Characterized Metallophilic Cadmium Tolerant Bacteria for Sustainable Agriculture 2022 , 13, 845853
65	Role of microorganisms in climate-smart agriculture. 2022 , 29-43

64	In vitro functional characterization predicts the impact of bacterial root endophytes on plant growth.	1
63	Microbiological Analysis and Metagenomic Profiling of the Bacterial Community of an Anthropogenic Soil Modified from Typic Haploxererts. 2022 , 11, 748	O
62	Effect of weather conditions, substrate pH, biochar amendment and plant species on two plant growth-promoting microbes on vegetated roofs and facades. 2022 , 8, e09560	О
61	Impact of long-term application of manure and inorganic fertilizers on common soil bacteria in different soil types. 2022 , 337, 108044	O
60	Impacts of land-use change on soil microbial communities and their function in the Amazon Rainforest. 2022 ,	
59	Improvement of eukaryotic protein predictions from soil metagenomes. 2022, 9,	
58	Legumes for eco-friendly weed management in agroecosystem. 2022 , 133-154	Ο
57	Importance of diverse soil microbial community in crop rotation for sustainable agriculture. 2022 , 113-145	
56	Evaluating the Antagonistic Potential of Actinomycete Strains Isolated From Sudan Soils Against Phytophthora infestans. 13,	Ο
55	Long-Term OrganicIhorganic Fertilization Regimes Alter Bacterial and Fungal Communities and Rice Yields in Paddy Soil. 13,	Ο
54	MdNRT2.4 interacts with rhizosphere bacteria to enhance nitrate uptake in apple rootstocks.	
53	Current Techniques to Study Beneficial Plant-Microbe Interactions. 2022 , 10, 1380	2
52	Microbial diversity as an indicator of a diversified cropping system for luvisoils in a moderate climate. Case study \mathbf{L} ong term experiments from Poland. 2022 , 141, 109133	O
51	Dynamics of fungal and bacterial communities in different types of soil ageing with different dosages of cadmium. 2022 , 242, 113860	O
50	Rhizosphere Soil Microbial Survival States and N-Related Process during Riparian Plant Dormancy: Influences of Plant Locations and Plant Species. 2022 , 14, 611	
49	Propagation of Recombinant Genes through Complex Microbiomes with Synthetic Mini-RP4 Plasmid Vectors. 2022 , 2022, 1-15	O
48	Opportunities and limits in imaging microorganisms and their activities in soil microhabitats. 2022 , 108807	1
47	The network perspective: Vertical connections linking organizational levels. 2022 , 473, 110112	Ο

46	The importance of system complexity in understanding plant responses to engineered nanoparticles: direct versus indirect effects. 2022 , 151-170	1
45	Dynamics of Soil Microbiome and Its Role in Sustainable Agriculture. 2022 , 27-55	O
44	Soil Microbiome: Characteristics, Impact of Climate Change and Resilience. 2022, 285-313	O
43	Impact of Pharmaceutical Compounds on the Microbial Ecology of Surface Water Resources. 2022 , 323-343	O
42	Metagenomics, Microbial Diversity, and Environmental Cleanup. 2022, 47-72	O
41	Land-Use Change and Management Intensification Is Associated with Shifts in Composition of Soil Microbial Communities and Their Functional Diversity in Coffee Agroecosystems. 2022 , 10, 1763	O
40	Genomic features predict bacterial life history strategies in soil, as identified by metagenomic stable isotope probing.	O
39	Random sampling associated with microbial profiling leads to overestimated stochasticity inference in community assembly. 13,	O
38	Exploring the Rhizosphere Microbiome for Sustainable Agriculture Production. 2022, 63-87	O
37	Actinobacteria in Natural Product Research: Avenues and Challenges. 2022 , 171-193	O
37 36	Actinobacteria in Natural Product Research: Avenues and Challenges. 2022, 171-193 Influence of Biochar on Soil Nutrients and Associated Rhizobacterial Communities of Mountainous Apple Trees in Northern Loess Plateau China. 2022, 10, 2078	0
	Influence of Biochar on Soil Nutrients and Associated Rhizobacterial Communities of Mountainous	
36	Influence of Biochar on Soil Nutrients and Associated Rhizobacterial Communities of Mountainous Apple Trees in Northern Loess Plateau China. 2022 , 10, 2078 Seasonal Shifts in Soil Microbiome Structure Are Associated with the Cultivation of the Local	0
36 35	Influence of Biochar on Soil Nutrients and Associated Rhizobacterial Communities of Mountainous Apple Trees in Northern Loess Plateau China. 2022, 10, 2078 Seasonal Shifts in Soil Microbiome Structure Are Associated with the Cultivation of the Local Runner Bean Variety around the Lake Mikri Prespa. 2022, 11, 1595 Divergent Changes in Bacterial Functionality as Affected by Root-Zone Ecological Restoration in an	0
36 35 34	Influence of Biochar on Soil Nutrients and Associated Rhizobacterial Communities of Mountainous Apple Trees in Northern Loess Plateau China. 2022, 10, 2078 Seasonal Shifts in Soil Microbiome Structure Are Associated with the Cultivation of the Local Runner Bean Variety around the Lake Mikri Prespa. 2022, 11, 1595 Divergent Changes in Bacterial Functionality as Affected by Root-Zone Ecological Restoration in an Aged Peach Orchard. 2022, 10, 2127	0 0
36 35 34 33	Influence of Biochar on Soil Nutrients and Associated Rhizobacterial Communities of Mountainous Apple Trees in Northern Loess Plateau China. 2022, 10, 2078 Seasonal Shifts in Soil Microbiome Structure Are Associated with the Cultivation of the Local Runner Bean Variety around the Lake Mikri Prespa. 2022, 11, 1595 Divergent Changes in Bacterial Functionality as Affected by Root-Zone Ecological Restoration in an Aged Peach Orchard. 2022, 10, 2127 Membrane lipid adaptation of soil Gram-negative bacteria isolates to temperature and pH. Bioprospecting and Challenges of Plant Microbiome Research for Sustainable Agriculture, a Review	o o o
36 35 34 33 32	Influence of Biochar on Soil Nutrients and Associated Rhizobacterial Communities of Mountainous Apple Trees in Northern Loess Plateau China. 2022, 10, 2078 Seasonal Shifts in Soil Microbiome Structure Are Associated with the Cultivation of the Local Runner Bean Variety around the Lake Mikri Prespa. 2022, 11, 1595 Divergent Changes in Bacterial Functionality as Affected by Root-Zone Ecological Restoration in an Aged Peach Orchard. 2022, 10, 2127 Membrane lipid adaptation of soil Gram-negative bacteria isolates to temperature and pH. Bioprospecting and Challenges of Plant Microbiome Research for Sustainable Agriculture, a Review on Soybean Endophytic Bacteria. Long-term adoption of reduced tillage and green manure improves soil physicochemical properties and increases the abundance of beneficial bacteria in a Mediterranean rainfed almond orchard.	0 0 0

28	Distinct Changes in Abundance of Culturable Microbial Community and Respiration Activities in Response to Mineral (Drganic Mixture Application in Contaminated Soil. 2022, 14, 15004	О
27	Characterization of bacterial diversity between two coastal regions with heterogeneous soil texture. 2022 , 12,	O
26	Boreal forest soil biotic communities are affected by harvesting, site preparation with no additional effects of higher biomass removal 5 years post-harvest. 2023 , 528, 120636	О
25	LC-MS analysis of D2O-labelled soil suggests a large fraction of membrane lipid exists within slow growing microbes. 2023 , 177, 108912	0
24	Exploring the Interspecific Interactions and the Metabolome of the Soil Isolate Hylemonella gracilis.	О
23	Identification of Novel Viruses and Their Microbial Hosts from Soils with Long-Term Nitrogen Fertilization and Cover Cropping Management. 2022 , 7,	O
22	A brief account on enzyme mining using metagenomic approach. 2,	О
21	Functions of Soil Microbes Under Stress Environment. 2022 , 373-381	О
20	Implications of Plant Invasion on the Soil Microbial Diversity and Ecosystem Sustainability: Evidence from a Tropical Biodiversity Hot Spot. 2023 , 161-182	О
19	Effect of Long-Term Inorganic Fertilization on Diversity and Abundance of Bacterial and Archaeal Communities at Tillage in Irrigated Rice Field. 2023 , 14, 18-33	О
18	Distribution characteristics of soil microbial communities and their responses to environmental factors in the sea buckthorn forest in the water-wind erosion crisscross region. 13,	1
17	Soil pH determines arsenic-related functional gene and bacterial diversity in natural forests on the Taibai Mountain. 2023 , 220, 115181	1
16	Genomics of microbial communities in African lakes. 2023 , 73-95	О
15	Impact of petroleum refinery on aquatic ecosystem of Skikda Bay (Algeria): Diversity and abundance of viable bacterial strains. 2023 , 188, 114704	О
14	New perspective: Symbiotic pattern and assembly mechanism of Cantharellus cibarius-associated bacteria. 14,	О
13	The Role of Metagenomic Approaches in the Analysis of Microbial Community in Extreme Environment.	O
12	Changes of Soil Dissolved Organic Matter and Its Relationship with Microbial Community along the Hailuogou Glacier Forefield Chronosequence. 2023 , 57, 4027-4038	О
11	Fine-scale evaluation of two standard 16S rRNA gene amplicon primer pairs for analysis of total prokaryotes and archaeal nitrifiers in differently managed soils. 14,	O

10	Membrane lipid adaptation of soil Bacteroidetes isolates to temperature and pH. 14,	O
9	Genomic Features Predict Bacterial Life History Strategies in Soil, as Identified by Metagenomic Stable Isotope Probing.	O
8	The rotation of Phallus impudicus benefits the soil microenvironment via improving the soil microbiome structure and soil properties.	O
7	Garden soil bacteria transiently colonize gardeners' skin after direct soil contact. 2023 , 8, 1-22	O
6	Soil Health Management and Microorganisms: Recent Development. 2023, 437-493	O
5	The rotation of Phallus impudicus benefits the microenvironment via improving the soil microbial structure and soil properties.	O
4	Metagenomics Provides a Deeper Assessment of the Diversity of Bacterial Communities in Polar Soils Than Metabarcoding. 2023 , 14, 812	O
3	The Spreading of Antibiotic-Resistant Bacteria in Terrestrial Ecosystems and the Formation of Soil Resistome. 2023 , 12, 769	O
2	Relationship of environmental factors in pond water and dynamic changes of gut microbes of sea bass Lateolabrax japonicus. 14,	0
1	Exploring the short-term in-field performance of Recovered Nitrogen from Manure (RENURE) materials to substitute synthetic nitrogen fertilisers. 2023 , 5, 100043	O