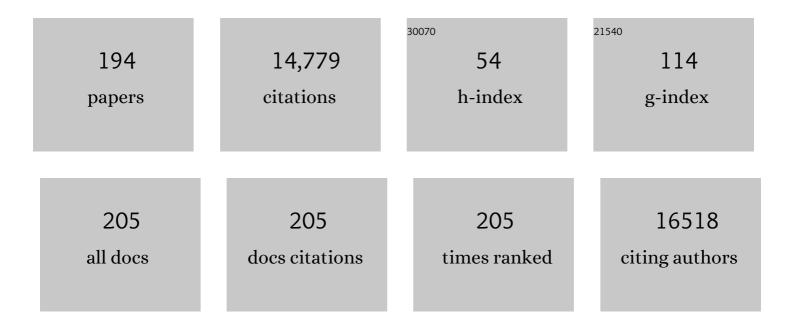
Michael Schloter

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Archaea predominate among ammonia-oxidizing prokaryotes in soils. Nature, 2006, 442, 806-809.	27.8	2,144
2	Microbiome definition re-visited: old concepts and new challenges. Microbiome, 2020, 8, 103.	11.1	903
3	Land use intensification alters ecosystem multifunctionality via loss of biodiversity and changes to functional composition. Ecology Letters, 2015, 18, 834-843.	6.4	578
4	Indicators for evaluating soil quality. Agriculture, Ecosystems and Environment, 2003, 98, 255-262.	5.3	554
5	Unraveling the plant microbiome: looking back and future perspectives. Frontiers in Microbiology, 2014, 5, 148.	3.5	498
6	Niche specialization of terrestrial archaeal ammonia oxidizers. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 21206-21211.	7.1	402
7	Microbial indicators for soil quality. Biology and Fertility of Soils, 2018, 54, 1-10.	4.3	312
8	Life in leaf litter: novel insights into community dynamics of bacteria and fungi during litter decomposition. Molecular Ecology, 2016, 25, 4059-4074.	3.9	297
9	Submicron structures provide preferential spots for carbon and nitrogen sequestration in soils. Nature Communications, 2014, 5, 2947.	12.8	288
10	Dynamics and functional relevance of ammoniaâ€oxidizing archaea in two agricultural soils. Environmental Microbiology, 2009, 11, 446-456.	3.8	276
11	Influence of Freeze-Thaw Stress on the Structure and Function of Microbial Communities and Denitrifying Populations in Soil. Applied and Environmental Microbiology, 2006, 72, 2148-2154.	3.1	245
12	Activity profiling of ectomycorrhiza communities in two forest soils using multiple enzymatic tests. New Phytologist, 2005, 167, 309-319.	7.3	244
13	Climate extremes initiate ecosystemâ€regulating functions while maintaining productivity. Journal of Ecology, 2011, 99, 689-702.	4.0	243
14	Phosphorus depletion in forest soils shapes bacterial communities towards phosphorus recycling systems. Environmental Microbiology, 2016, 18, 1988-2000.	3.8	212
15	Enumeration of total bacteria and bacteria with genes for proteolytic activity in pure cultures and in environmental samples by quantitative PCR mediated amplification. Journal of Microbiological Methods, 2002, 49, 235-245.	1.6	202
16	Analysis of soil microbial communities based on amplicon sequencing of marker genes. Biology and Fertility of Soils, 2017, 53, 485-489.	4.3	197
17	The role of microorganisms at different stages of ecosystem development for soil formation. Biogeosciences, 2013, 10, 3983-3996.	3.3	189
18	Multiple forest attributes underpin the supply of multiple ecosystem services. Nature Communications, 2018, 9, 4839.	12.8	182

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19	Microbial Colonization of Beech and Spruce Litter—Influence of Decomposition Site and Plant Litter Species on the Diversity of Microbial Community. Microbial Ecology, 2006, 52, 127-135.	2.8	181
20	Abundances and potential activities of nitrogen cycling microbial communities along a chronosequence of a glacier forefield. ISME Journal, 2011, 5, 1025-1037.	9.8	174
21	Transitory microbial habitat in the hyperarid Atacama Desert. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2670-2675.	7.1	172
22	Soil phosphorus supply controls P nutrition strategies of beech forest ecosystems in Central Europe. Biogeochemistry, 2017, 136, 5-29.	3.5	171
23	Tree girdling provides insight on the role of labile carbon in nitrogen partitioning between soil microorganisms and adult European beech. Soil Biology and Biochemistry, 2009, 41, 1622-1631.	8.8	167
24	Land-use intensity alters networks between biodiversity, ecosystem functions, and services. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 28140-28149.	7.1	164
25	Making big data smart—how to use metagenomics to understand soil quality. Biology and Fertility of Soils, 2017, 53, 479-484.	4.3	160
26	Nitrogen turnover in soil and global change. FEMS Microbiology Ecology, 2011, 78, 3-16.	2.7	159
27	The plant microbiome and its importance for plant and human health. Frontiers in Microbiology, 2014, 5, 491.	3.5	128
28	Rhizosphere microbiomes of potato cultivated in the High Andes show stable and dynamic core microbiomes with different responses to plant development. FEMS Microbiology Ecology, 2017, 93, fiw242.	2.7	114
29	Influence of the nitrification inhibitor 3,4-dimethylpyrazole phosphate (DMPP) on ammonia-oxidizing bacteria and archaea in rhizosphere and bulk soil. Chemosphere, 2011, 84, 182-186.	8.2	110
30	Molecular characterisation of the diazotrophic bacterial community in uninoculated and inoculated field-grown sugarcane (Saccharum sp.). Plant and Soil, 2012, 356, 83-99.	3.7	105
31	Oral administration of antibiotics increased the potential mobility of bacterial resistance genes in the gut of the fish Piaractus mesopotamicus. Microbiome, 2019, 7, 24.	11.1	98
32	Apple Replant Disease: Causes and Mitigation Strategies. Current Issues in Molecular Biology, 2019, 30, 89-106.	2.4	98
33	pH as a Driver for Ammonia-Oxidizing Archaea in Forest Soils. Microbial Ecology, 2015, 69, 879-883.	2.8	95
34	Changes in Diversity and Functional Gene Abundances of Microbial Communities Involved in Nitrogen Fixation, Nitrification, and Denitrification in a Tidal Wetland versus Paddy Soils Cultivated for Different Time Periods. Applied and Environmental Microbiology, 2011, 77, 6109-6116.	3.1	94
35	Decoupled carbon and nitrogen mineralization in soil particle size fractions of a forest topsoil. Soil Biology and Biochemistry, 2014, 78, 263-273.	8.8	91
36	Abundance and Diversity of CO2-fixing Bacteria in Grassland Soils Close to Natural Carbon Dioxide Springs. Microbial Ecology, 2009, 58, 1-9.	2.8	88

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37	Long-term effects of environmentally relevant concentrations of silver nanoparticles on microbial biomass, enzyme activity, and functional genes involved in the nitrogen cycle of loamy soil. Journal of Environmental Sciences, 2018, 69, 12-22.	6.1	87
38	Accumulation of nitrogen and microbial residues during 2000Âyears of rice paddy and non-paddy soil development in the Yangtze River Delta, China. Global Change Biology, 2011, 17, 3405-3417.	9.5	85
39	Cowpea Nodules Harbor Non-rhizobial Bacterial Communities that Are Shaped by Soil Type Rather than Plant Genotype. Frontiers in Plant Science, 2016, 7, 2064.	3.6	85
40	Dynamics of Bacterial Communities during the Ripening Process of Different Croatian Cheese Types Derived from Raw Ewe's Milk Cheeses. PLoS ONE, 2013, 8, e80734.	2.5	83
41	Novel oligonucleotide primers reveal a high diversity of microbes which drive phosphorous turnover in soil. Journal of Microbiological Methods, 2016, 125, 91-97.	1.6	80
42	Spatial and temporal dynamics of nitrogen fixing, nitrifying and denitrifying microbes in an unfertilized grassland soil. Soil Biology and Biochemistry, 2017, 109, 214-226.	8.8	80
43	Integrated microbiota and metabolite profiles link Crohn's disease to sulfur metabolism. Nature Communications, 2020, 11, 4322.	12.8	79
44	Soil biotic processes remain remarkably stable after 100-year extreme weather events in experimental grassland and heath. Plant and Soil, 2008, 308, 175-188.	3.7	77
45	Microbial response to exudates in the rhizosphere of young beech trees (Fagus sylvatica L.) after dormancy. Soil Biology and Biochemistry, 2009, 41, 1976-1985.	8.8	76
46	Pollution from azithromycin-manufacturing promotes macrolide-resistance gene propagation and induces spatial and seasonal bacterial community shifts in receiving river sediments. Environment International, 2019, 123, 501-511.	10.0	74
47	Denitrifying pathways dominate nitrous oxide emissions from managed grassland during drought and rewetting. Science Advances, 2021, 7, .	10.3	71
48	Dominant Groups of Potentially Active Bacteria Shared by Barley Seeds become Less Abundant in Root Associated Microbiome. Frontiers in Plant Science, 2017, 8, 1005.	3.6	70
49	The Microbiome of Endophytic, Wood Colonizing Bacteria from Pine Trees as Affected by Pine Wilt Disease. Scientific Reports, 2017, 7, 4205.	3.3	69
50	Climate change amplifies gross nitrogen turnover in montane grasslands of Central Europe in both summer and winter seasons. Global Change Biology, 2016, 22, 2963-2978.	9.5	68
51	Improved protocol for the simultaneous extraction and column-based separation of DNA and RNA from different soils. Journal of Microbiological Methods, 2011, 84, 406-412.	1.6	67
52	Abundance of Microbes Involved in Nitrogen Transformation in the Rhizosphere of Leucanthemopsis alpina (L.) Heywood Grown in Soils from Different Sites of the Damma Glacier Forefield. Microbial Ecology, 2010, 60, 762-770.	2.8	66
53	Potential of Wheat Straw, Spruce Sawdust, and Lignin as High Organic Carbon Soil Amendments to Improve Agricultural Nitrogen Retention Capacity: An Incubation Study. Frontiers in Plant Science, 2018, 9, 900.	3.6	64
54	Patterns and processes of initial terrestrialâ€ecosystem development. Journal of Plant Nutrition and Soil Science, 2011, 174, 229-239.	1.9	61

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55	The Influence of Land Use Intensity on the Plant-Associated Microbiome of Dactylis glomerata L Frontiers in Plant Science, 2017, 8, 930.	3.6	57
56	Optimized assay and storage conditions for enzyme activity profiling of ectomycorrhizae. Mycorrhiza, 2011, 21, 589-600.	2.8	56
57	Changes induced by heavy metals in the plant-associated microbiome of Miscanthus x giganteus. Science of the Total Environment, 2020, 711, 134433.	8.0	56
58	The Microbiome and Preterm Birth: A Change in Paradigm with Profound Implications for Pathophysiologic Concepts and Novel Therapeutic Strategies. BioMed Research International, 2018, 2018, 1-12.	1.9	55
59	A long-term field experiment demonstrates the influence of tillage on the bacterial potential to produce soil structure-stabilizing agents such as exopolysaccharides and lipopolysaccharides. Environmental Microbiomes, 2019, 14, 1.	5.0	54
60	DNAâ€based stable isotope probing enables the identification of active bacterial endophytes in potatoes. New Phytologist, 2009, 181, 802-807.	7.3	53
61	Different Land Use Intensities in Grassland Ecosystems Drive Ecology of Microbial Communities Involved in Nitrogen Turnover in Soil. PLoS ONE, 2013, 8, e73536.	2.5	52
62	Effects of drought on nitrogen turnover and abundances of ammonia-oxidizers in mountain grassland. Biogeosciences, 2014, 11, 6003-6015.	3.3	51
63	Community structure of prokaryotes and their functional potential in subsoils is more affected by spatial heterogeneity than by temporal variations. Soil Biology and Biochemistry, 2014, 75, 197-201.	8.8	51
64	Organic Amendments in a Long-term Field Trial—Consequences for the Bulk Soil Bacterial Community as Revealed by Network Analysis. Microbial Ecology, 2018, 76, 226-239.	2.8	51
65	Climate change alters temporal dynamics of alpine soil microbial functioning and biogeochemical cycling via earlier snowmelt. ISME Journal, 2021, 15, 2264-2275.	9.8	51
66	Effects of genetically modified starch metabolism in potato plants on photosynthate fluxes into the rhizosphere and on microbial degraders of root exudates. FEMS Microbiology Ecology, 2011, 76, 564-575.	2.7	50
67	Estimation by PLFA of Microbial Community Structure Associated with the Rhizosphere of Lygeum spartum and Piptatherum miliaceum Growing in Semiarid Mine Tailings. Microbial Ecology, 2010, 60, 265-271.	2.8	49
68	Bacterial potentials for uptake, solubilization and mineralization of extracellular phosphorus in agricultural soils are highly stable under different fertilization regimes. Environmental Microbiology Reports, 2018, 10, 320-327.	2.4	49
69	Pro-Inflammatory versus Immunomodulatory Effects of Silver Nanoparticles in the Lung: The Critical Role of Dose, Size and Surface Modification. Nanomaterials, 2017, 7, 300.	4.1	48
70	Origin of volatile organic compound emissions from subarctic tundra under global warming. Global Change Biology, 2020, 26, 1908-1925.	9.5	46
71	Changes in microbial community structure in soil as a result of different amounts of nitrogen fertilization. Biology and Fertility of Soils, 2008, 44, 1103-1106.	4.3	45
72	Biological Soil Crusts from Different Soil Substrates Harbor Distinct Bacterial Groups with the Potential to Produce Exopolysaccharides and Lipopolysaccharides. Microbial Ecology, 2020, 79, 326-341.	2.8	43

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73	Towards the development of general rules describing landscape heterogeneity–multifunctionality relationships. Journal of Applied Ecology, 2019, 56, 168-179.	4.0	42
74	Effect of Sulfadiazine on Abundance and Diversity of Denitrifying Bacteria by Determining nirK and nirS Genes in Two Arable Soils. Microbial Ecology, 2010, 60, 703-707.	2.8	41
75	Comparison of Barley Succession and Take-All Disease as Environmental Factors Shaping the Rhizobacterial Community during Take-All Decline. Applied and Environmental Microbiology, 2010, 76, 4703-4712.	3.1	41
76	Dynamics of microbial communities during decomposition of litter from pioneering plants in initial soil ecosystems. Biogeosciences, 2013, 10, 5115-5124.	3.3	41
77	Impact of fertilization on the abundance of nitrifiers and denitrifiers at the root–soil interface of plants with different uptake strategies for nitrogen. Biology and Fertility of Soils, 2015, 51, 57-64.	4.3	40
78	Cholesterol metabolism promotes B ell positioning during immune pathogenesis of chronic obstructive pulmonary disease. EMBO Molecular Medicine, 2018, 10, .	6.9	39
79	Metagenomic analyses reveal no differences in genes involved in cellulose degradation under different tillage treatments. FEMS Microbiology Ecology, 2015, 91, fiv069.	2.7	38
80	Influence of difloxacin-contaminated manure on microbial community structure and function in soils. Biology and Fertility of Soils, 2011, 47, 177-186.	4.3	37
81	N2O and NOx emissions by reactions of nitrite with soil organic matter of a Norway spruce forest. Biogeochemistry, 2017, 132, 325-342.	3.5	37
82	Changes of Diversity Pattern of Proteolytic Bacteria over Time and Space in an Agricultural Soil. Microbial Ecology, 2009, 57, 391-401.	2.8	36
83	Development of a Stable Lung Microbiome in Healthy Neonatal Mice. Microbial Ecology, 2018, 75, 529-542.	2.8	36
84	Winter warming is ecologically more relevant than summer warming in a cool-temperate grassland. Scientific Reports, 2019, 9, 14632.	3.3	36
85	Development of a simple root model to study the effects of single exudates on the development of bacterial community structure. Journal of Microbiological Methods, 2013, 94, 30-36.	1.6	35
86	Spatial variability of hydrolytic and oxidative potential enzyme activities in different subsoil compartments. Biology and Fertility of Soils, 2015, 51, 517-521.	4.3	33
87	Land use as a driver for protist community structure in soils under agricultural use across Europe. Science of the Total Environment, 2020, 717, 137228.	8.0	33
88	Pre-digest of unprotected DNA by Benzonase improves the representation of living skin bacteria and efficiently depletes host DNA. Microbiome, 2021, 9, 123.	11.1	33
89	Influence of lung CT changes in chronic obstructive pulmonary disease (COPD) on the human lung microbiome. PLoS ONE, 2017, 12, e0180859.	2.5	33
90	Characterization of Enterococcal Community Isolated from an Artisan Istrian Raw Milk Cheese: Biotechnological and Safety Aspects. Food Technology and Biotechnology, 2017, 55, 368-380.	2.1	33

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91	Effects of genetically modified amylopectin-accumulating potato plants on the abundance of beneficial and pathogenic microorganisms in the rhizosphere. Plant and Soil, 2010, 335, 413-422.	3.7	32
92	Development of a molecular approach to describe the composition of Trichoderma communities. Journal of Microbiological Methods, 2010, 80, 63-69.	1.6	32
93	Hypoxia and Inactivity Related Physiological Changes (Constipation, Inflammation) Are Not Reflected at the Level of Gut Metabolites and Butyrate Producing Microbial Community: The PlanHab Study. Frontiers in Physiology, 2017, 8, 250.	2.8	32
94	Early life determinants induce sustainable changes in the gut microbiome of six-year-old children. Scientific Reports, 2019, 9, 12675.	3.3	32
95	Low resistance of montane and alpine grasslands to abrupt changes in temperature and precipitation regimes. Arctic, Antarctic, and Alpine Research, 2019, 51, 215-231.	1.1	32
96	Microevolution of Anthrax from a Young Ancestor (M.A.Y.A.) Suggests a Soil-Borne Life Cycle of Bacillus anthracis. PLoS ONE, 2015, 10, e0135346.	2.5	32
97	Influence of chronic ozone stress on carbon translocation pattern into rhizosphere microbial communities of beech trees (Fagus sylvatica L.) during a growing season. Plant and Soil, 2009, 323, 85-95.	3.7	31
98	More than 2500Âyears of oil exposure shape sediment microbiomes with the potential for syntrophic degradation of hydrocarbons linked to methanogenesis. Microbiome, 2017, 5, 118.	11.1	31
99	Shifts in reclamation management strategies shape the role of exopolysaccharide and lipopolysaccharideâ€producing bacteria during soil formation. Microbial Biotechnology, 2020, 13, 584-598.	4.2	31
100	Development of Microbiome Biobanks – Challenges and Opportunities. Trends in Microbiology, 2021, 29, 89-92.	7.7	31
101	Bacterial communities associated with the production of artisanal Istrian cheese. International Journal of Food Microbiology, 2010, 142, 19-24.	4.7	29
102	Climate Change Induces Shifts in Abundance and Activity Pattern of Bacteria and Archaea Catalyzing Major Transformation Steps in Nitrogen Turnover in a Soil from a Mid-European Beech Forest. PLoS ONE, 2014, 9, e114278.	2.5	29
103	A review of the importance of mineral nitrogen cycling in the plant-soil-microbe system of permafrost-affected soils—changing the paradigm. Environmental Research Letters, 2022, 17, 013004.	5.2	29
104	A continuous labelling approach to recover photosynthetically fixed carbon in plant tissue and rhizosphere organisms of young beech trees (Fagus sylvatica L.) using 13C depleted CO2. Plant and Soil, 2009, 323, 21-29.	3.7	27
105	Influence of different litter quality on the abundance of genes involved in nitrification and denitrification after freezing and thawing of an arable soil. Biology and Fertility of Soils, 2010, 46, 537-541.	4.3	27
106	Diverse Viruses Carrying Genes for Microbial Extremotolerance in the Atacama Desert Hyperarid Soil. MSystems, 2021, 6, .	3.8	27
107	Biological inhibition of soil nitrification by forest tree species affects <scp><i>Nitrobacter</i></scp> populations. Environmental Microbiology, 2020, 22, 1141-1153.	3.8	26
108	Accumulation of NO ₂ ^{â^'} during periods of drying stimulates soil N ₂ O emissions during subsequent rewetting. European Journal of Soil Science, 2018, 69, 936-946.	3.9	25

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109	Intestinal Metagenomes and Metabolomes in Healthy Young Males: Inactivity and Hypoxia Generated Negative Physiological Symptoms Precede Microbial Dysbiosis. Frontiers in Physiology, 2018, 9, 198.	2.8	25
110	Soil Bacterial Diversity Is Positively Correlated with Decomposition Rates during Early Phases of Maize Litter Decomposition. Microorganisms, 2021, 9, 357.	3.6	25
111	Effects of industrial effluents containing moderate levels of antibiotic mixtures on the abundance of antibiotic resistance genes and bacterial community composition in exposed creek sediments. Science of the Total Environment, 2020, 706, 136001.	8.0	24
112	A comparative study of most probable number (MPN)-PCR vs. real-time-PCR for the measurement of abundance and assessment of diversity of alkB homologous genes in soil. Journal of Microbiological Methods, 2010, 80, 295-298.	1.6	23
113	Soil pH and plant diversity drive co-occurrence patterns of ammonia and nitrite oxidizer in soils from forest ecosystems. Biology and Fertility of Soils, 2017, 53, 691-700.	4.3	23
114	N2 Gas Flushing Alleviates the Loss of Bacterial Diversity and Inhibits Psychrotrophic Pseudomonas during the Cold Storage of Bovine Raw Milk. PLoS ONE, 2016, 11, e0146015.	2.5	23
115	Comparison of lipid biomarker and gene abundance characterizing the archaeal ammonia-oxidizing community in flooded soils. Biology and Fertility of Soils, 2011, 47, 839-843.	4.3	22
116	Influence of Land Use Intensity on the Diversity of Ammonia Oxidizing Bacteria and Archaea in Soils from Grassland Ecosystems. Microbial Ecology, 2014, 67, 161-166.	2.8	22
117	Reduced microbial potential for the degradation of phenolic compounds in the rhizosphere of apple plantlets grown in soils affected by replant disease. Environmental Microbiomes, 2019, 14, 8.	5.0	22
118	Denitrification in a vertisol under long-term tillage and no-tillage management in dryland agricultural systems: Key genes and potential rates. Applied Soil Ecology, 2011, 47, 221-225.	4.3	21
119	Bacteria utilizing plantâ€derived carbon in the rhizosphere of <i>Triticum aestivum</i> change in different depths of an arable soil. Environmental Microbiology Reports, 2017, 9, 729-741.	2.4	21
120	Hypoxia and inactivity related physiological changes precede or take place in absence of significant rearrangements in bacterial community structure: The PlanHab randomized trial pilot study. PLoS ONE, 2017, 12, e0188556.	2.5	20
121	Effects of Elevated Atmospheric CO2 on Microbial Community Structure at the Plant-Soil Interface of Young Beech Trees (Fagus sylvatica L.) Grown at Two Sites with Contrasting Climatic Conditions. Microbial Ecology, 2015, 69, 867-878.	2.8	19
122	Influence of rewetting on microbial communities involved in nitrification and denitrification in a grassland soil after a prolonged drought period. Scientific Reports, 2019, 9, 2280.	3.3	19
123	Carbohydrate depletion in roots impedes phosphorus nutrition in young forest trees. New Phytologist, 2021, 229, 2611-2624.	7.3	19
124	Microbial Hotspots in Lithic Microhabitats Inferred from DNA Fractionation and Metagenomics in the Atacama Desert. Microorganisms, 2021, 9, 1038.	3.6	19
125	The Impact of the Diurnal Cycle on the Microbial Transcriptome in the Rhizosphere of Barley. Microbial Ecology, 2018, 75, 830-833.	2.8	18
126	Management versus site effects on the abundance of nitrifiers and denitrifiers in European mountain grasslands. Science of the Total Environment, 2019, 648, 745-753.	8.0	18

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127	Bacterial diversity of naturally fermented game meat sausages: Sources of new starter cultures. LWT - Food Science and Technology, 2020, 118, 108782.	5.2	18
128	Site-Specific Conditions Change the Response of Bacterial Producers of Soil Structure-Stabilizing Agents Such as Exopolysaccharides and Lipopolysaccharides to Tillage Intensity. Frontiers in Microbiology, 2020, 11, 568.	3.5	18
129	<i>Dechloromonas</i> and close relatives prevail during hydrogenotrophic denitrification in stimulated microcosms with oxic aquifer material. FEMS Microbiology Ecology, 2021, 97, .	2.7	18
130	Influence of Commonly Used Primer Systems on Automated Ribosomal Intergenic Spacer Analysis of Bacterial Communities in Environmental Samples. PLoS ONE, 2015, 10, e0118967.	2.5	18
131	Leave no stone unturned: individually adapted xerotolerant Thaumarchaeota sheltered below the boulders of the Atacama Desert hyperarid core. Microbiome, 2021, 9, 234.	11.1	18
132	Effect of the Nursing Mother on the Gut Microbiome of the Offspring During Early Mouse Development. Microbial Ecology, 2019, 78, 517-527.	2.8	17
133	Dinitrogen (N2) pulse emissions during freeze-thaw cycles from montane grassland soil. Biology and Fertility of Soils, 2020, 56, 959-972.	4.3	17
134	Correlation of the abundance of bacteria catalyzing phosphorus and nitrogen turnover in biological soil crusts of temperate forests of Germany. Biology and Fertility of Soils, 2021, 57, 179-192.	4.3	17
135	The Potato Yam Phyllosphere Ectosymbiont Paraburkholderia sp. Msb3 Is a Potent Growth Promotor in Tomato. Frontiers in Microbiology, 2020, 11, 581.	3.5	16
136	National Forest Inventories capture the multifunctionality of managed forests in Germany. Forest Ecosystems, 2021, 8, .	3.1	16
137	Microbiome profiling reveals that <i>Pseudomonas</i> antagonises parasitic nodule colonisation of cheater rhizobia in <i>Lotus</i> . New Phytologist, 2022, 234, 242-255.	7.3	16
138	Diversity of proteolytic community encoding for subtilisin in an arable field: spatial and temporal variability. Biology and Fertility of Soils, 2008, 45, 185-191.	4.3	15
139	An inter-laboratory comparison of gaseous and liquid fumigation based methods for measuring microbial phosphorus (P mic) in forest soils with differing P stocks. Journal of Microbiological Methods, 2016, 128, 66-68.	1.6	15
140	Bacterial Colonization within the First Six Weeks of Life and Pulmonary Outcome in Preterm Infants <1000 g. Journal of Clinical Medicine, 2020, 9, 2240.	2.4	15
141	Microbial Key Players Involved in P Turnover Differ in Artificial Soil Mixtures Depending on Clay Mineral Composition. Microbial Ecology, 2021, 81, 897-907.	2.8	14
142	Manure contaminated with the antibiotic sulfadiazine impairs the abundance of nirK- and nirS-type denitrifiers in the gut of the earthworm Eisenia fetida. Biology and Fertility of Soils, 2010, 46, 415-418.	4.3	13
143	Effects of multiple but low pesticide loads on aquatic fungal communities colonizing leaf litter. Journal of Environmental Sciences, 2016, 46, 116-125.	6.1	13
144	Field-Scale Pattern of Denitrifying Microorganisms and N2O Emission Rates Indicate a High Potential for Complete Denitrification in an Agriculturally Used Organic Soil. Microbial Ecology, 2017, 74, 765-770.	2.8	13

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145	Characterization of Extracellular Biosurfactants Expressed by a Pseudomonas putida Strain Isolated from the Interior of Healthy Roots from Sida hermaphrodita Grown in a Heavy Metal Contaminated Soil. Current Microbiology, 2019, 76, 1320-1329.	2.2	13
146	52Âyears of ecological restoration following a major disturbance by opencast lignite mining does not reassemble microbiome structures of the original arable soils. Science of the Total Environment, 2020, 745, 140955.	8.0	13
147	Metadata harmonization–Standards are the key for a better usage of omics data for integrative microbiome analysis. Environmental Microbiomes, 2022, 17, .	5.0	13
148	Abundance of bacterial genes encoding for proteases and chitinases in the rhizosphere of three different potato cultivars. Biology and Fertility of Soils, 2010, 46, 649-652.	4.3	12
149	Drivers for ammonia-oxidation along a land-use gradient in grassland soils. Soil Biology and Biochemistry, 2014, 69, 179-186.	8.8	12
150	Long-Read Amplicon Sequencing of Nitric Oxide Dismutase (nod) Genes Reveal Diverse Oxygenic Denitrifiers in Agricultural Soils and Lake Sediments. Microbial Ecology, 2020, 80, 243-247.	2.8	12
151	Longâ€term ferrocyanide application via deicing salts promotes the establishment of Actinomycetales assimilating ferrocyanideâ€derived carbon in soil. Microbial Biotechnology, 2016, 9, 502-513.	4.2	11
152	Response of Barley Plants to Drought Might Be Associated with the Recruiting of Soil-Borne Endophytes. Microorganisms, 2020, 8, 1414.	3.6	11
153	Short term effects of climate change and intensification of management on the abundance of microbes driving nitrogen turnover in montane grassland soils. Science of the Total Environment, 2021, 780, 146672.	8.0	11
154	Effect of triple superphosphate and biowaste compost on mycorrhizal colonization and enzymatic P mobilization under maize in a longâ€ŧerm field experiment. Journal of Plant Nutrition and Soil Science, 2019, 182, 167-174.	1.9	10
155	Strategies to Overcome Intermediate Accumulation During in situ Nitrate Remediation in Groundwater by Hydrogenotrophic Denitrification. Frontiers in Microbiology, 2021, 12, 610437.	3.5	10
156	Shrub expansion modulates belowground impacts of changing snow conditions in alpine grasslands. Ecology Letters, 2022, 25, 52-64.	6.4	10
157	The role of microbes in the increase of organic phosphorus availability in the rhizosheath of cover crops. Plant and Soil, 2022, 476, 353-373.	3.7	10
158	Alder-induced stimulation of soil gross nitrogen turnover in a permafrost-affected peatland of Northeast China. Soil Biology and Biochemistry, 2022, 172, 108757.	8.8	9
159	Effect of slope orientation on microbial community composition in different particle size fractions from soils obtained from desert ecosystems. Biology and Fertility of Soils, 2015, 51, 507-510.	4.3	8
160	Nitrate induction and physiological responses of two maize lines differing in nitrogen use efficiency: effects on N availability, microbial diversity and enzyme activity in the rhizosphere. Plant and Soil, 2018, 422, 331-347.	3.7	8
161	Precipitation of enzymes and organic matter by aluminum—Impacts on carbon mineralization. Journal of Plant Nutrition and Soil Science, 2008, 171, 900-907.	1.9	7
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