George A Kowalchuk

List of Publications by Year
in descending order

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156

papers

19,503

citations

13099

68

h-index

11607

135

g-index

163

all docs

163

docs citations

163

times ranked

17385

citing authors

#	Article	IF	Citations
1	Reciprocal Rewards Stabilize Cooperation in the Mycorrhizal Symbiosis. Science, 2011, 333, 880-882.	12.6	1,373
2	Ammonia-Oxidizing Bacteria: A Model for Molecular Microbial Ecology. Annual Review of Microbiology, 2001, 55, 485-529.	7.3	1,143
3	The minimum information about a genome sequence (MIGS) specification. Nature Biotechnology, 2008, 26, 541-547.	17.5	1,069
4	The Ecology of Acidobacteria: Moving beyond Genes and Genomes. Frontiers in Microbiology, 2016, 7, 744.	3.5	762
5	Analysis of ammonia-oxidizing bacteria of the beta subdivision of the class Proteobacteria in coastal sand dunes by denaturing gradient gel electrophoresis and sequencing of PCR-amplified 16S ribosomal DNA fragments. Applied and Environmental Microbiology, 1997, 63, 1489-1497.	3.1	711
6	Nitrification in acid soils: micro-organisms and mechanisms. Soil Biology and Biochemistry, 2001, 33, 853-866.	8.8	644
7	Effects of above-ground plant species composition and diversity on the diversity of soil-borne microorganisms. Antonie Van Leeuwenhoek, 2002, 81, 509-520.	1.7	520
8	Micro-scale determinants of bacterial diversity in soil. FEMS Microbiology Reviews, 2013, 37, 936-954.	8.6	418
9	Shifting carbon flow from roots into associated microbial communities in response to elevated atmospheric CO ₂. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10938-10942.	7.1	390
10	Root exudates drive the soil-borne legacy of aboveground pathogen infection. Microbiome, 2018, 6, 156.	11.1	354
11	Soil characteristics more strongly influence soil bacterial communities than land-use type. FEMS Microbiology Ecology, 2012, 79, 12-24.	2.7	347
12	Initial soil microbiome composition and functioning predetermine future plant health. Science Advances, 2019, 5, eaaw0759.	10.3	314
13	Positive effects of organic farming on belowâ€ground mutualists: largeâ€scale comparison of mycorrhizal fungal communities in agricultural soils. New Phytologist, 2010, 186, 968-979.	7.3	301
14	Patterns of bacterial diversity across a range of Antarctic terrestrial habitats. Environmental Microbiology, 2007, 9, 2670-2682.	3.8	267
15	Analysis of Bacterial Communities in the Rhizosphere of Chrysanthemum via Denaturing Gradient Gel Electrophoresis of PCR-Amplified 16S rRNA as Well as DNA Fragments Coding for 16S rRNA. Applied and Environmental Microbiology, 2001, 67, 172-178.	3.1	259
16	Shifts in soil microorganisms in response to warming are consistent across a range of Antarctic environments. ISME Journal, 2012, 6, 692-702.	9.8	258
17	Unlocking the potential of metagenomics through replicated experimental design. Nature Biotechnology, 2012, 30, 513-520.	17.5	250
18	Effect of Toxic Metals on Indigenous Soil Î²-Subgroup Proteobacterium Ammonia Oxidizer Community Structure and Protection against Toxicity by Inoculated Metal-Resistant Bacteria. Applied and Environmental Microbiology, 1999, 65, 95-101.	3.1	249

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19	Analysis of Î²-Subgroup Proteobacterial Ammonia Oxidizer Populations in Soil by Denaturing Gradient Gel Electrophoresis Analysis and Hierarchical Phylogenetic Probing. Applied and Environmental Microbiology, 1998, 64, 2958-2965.	3.1	245
20	Functional microarray analysis of nitrogen and carbon cycling genes across an Antarctic latitudinal transect. ISME Journal, 2007, 1, 163-179.	9.8	232
21	Molecular Analysis of Ammonia-Oxidizing Bacteria of the Î² Subdivision of the Class <i>Proteobacteria</i> in Compost and Composted Materials. Applied and Environmental Microbiology, 1999, 65, 396-403.	3.1	228
22	Climate change goes underground: effects of elevated atmospheric CO2 on microbial community structure and activities in the rhizosphere. Biology and Fertility of Soils, 2008, 44, 667-679.	4.3	223
23	Microvariation Artifacts Introduced by PCR and Cloning of Closely Related 16S rRNA Gene Sequences. Applied and Environmental Microbiology, 2001, 67, 469-472.	3.1	219
24	Bio-fertilizer application induces soil suppressiveness against Fusarium wilt disease by reshaping the soil microbiome. Soil Biology and Biochemistry, 2017, 114, 238-247.	8.8	216
25	Protists: Puppet Masters of the Rhizosphere Microbiome. Trends in Plant Science, 2019, 24, 165-176.	8.8	215
26	Community assembly, species richness and nestedness of arbuscular mycorrhizal fungi in agricultural soils. Molecular Ecology, 2012, 21, 2341-2353.	3.9	203
27	Size and structure of bacterial, fungal and nematode communities along an Antarctic environmental gradient. FEMS Microbiology Ecology, 2006, 59, 436-451.	2.7	202
28	Comparative Diversity of Ammonia Oxidizer 16S rRNA Gene Sequences in Native, Tilled, and Successional Soils. Applied and Environmental Microbiology, 1999, 65, 2994-3000.	3.1	200
29	Soil protist communities form a dynamic hub in the soil microbiome. ISME Journal, 2018, 12, 634-638.	9.8	184
30	Bio-organic fertilizers stimulate indigenous soil Pseudomonas populations to enhance plant disease suppression. Microbiome, 2020, 8, 137.	11.1	181
31	Responses of Antarctic soil microbial communities and associated functions to temperature and freezeâ€“thaw cycle frequency. Environmental Microbiology, 2008, 10, 2223-2235.	3.8	177
32	Community analysis of arbuscular mycorrhizal fungi associated with Ammophila arenaria in Dutch coastal sand dunes. Molecular Ecology, 2002, 11, 571-581.	3.9	175
33	Differential responses of soil bacteria, fungi, archaea and protists to plant species richness and plant functional group identity. Molecular Ecology, 2017, 26, 4085-4098.	3.9	173
34	Detection and characterization of fungal infections of Ammophila arenaria (marram grass) roots by denaturing gradient gel electrophoresis of specifically amplified 18s rDNA. Applied and Environmental Microbiology, 1997, 63, 3858-3865.	3.1	170
35	Rhizosphere bacterial community composition in natural stands of Carex arenaria (sand sedge) is determined by bulk soil community composition. Soil Biology and Biochemistry, 2005, 37, 349-357.	8.8	157
36	Environmental microarray analyses of Antarctic soil microbial communities. ISME Journal, 2009, 3, 340-351.	9.8	156

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37	Rhizosphere protists are key determinants of plant health. Microbiome, 2020, 8, 27.	11.1	156
38	Nitrogen Cycling and Community Structure of Proteobacterial Î²-Subgroup Ammonia-Oxidizing Bacteria within Polluted Marine Fish Farm Sediments. Applied and Environmental Microbiology, 1999, 65, 213-220.	3.1	153
39	Changes in the community structure of ammonia-oxidizing bacteria during secondary succession of calcareous grasslands. Environmental Microbiology, 2000, 2, 99-110.	3.8	152
40	Root exudates drive soilâ€microbeâ€nutrient feedbacks in response to plant growth. Plant, Cell and Environment, 2021, 44, 613-628.	5.7	150
41	Community analysis of ammonia-oxidising bacteria, in relation to oxygen availability in soils and root-oxygenated sediments, using PCR, DGGE and oligonucleotide probe hybridisation. FEMS Microbiology Ecology, 1998, 27, 339-350.	2.7	149
42	Microbial Community Composition Affects Soil Fungistasis. Applied and Environmental Microbiology, 2003, 69, 835-844.	3.1	147
43	Bacteria, not archaea, restore nitrification in a zinc-contaminated soil. ISME Journal, 2009, 3, 916-923.	9.8	138
44	Molecular analysis of ammonia-oxidising bacteria in soil of successional grasslands of the Drentsche A (The Netherlands). FEMS Microbiology Ecology, 2000, 31, 207-215.	2.7	137
45	Effects of genetically modified plants on microbial communities and processes in soil. Biology and Fertility of Soils, 2003, 37, 329-337.	4.3	132
46	Differences in vegetation composition and plant species identity lead to only minor changes in soil-borne microbial communities in a former arable field. FEMS Microbiology Ecology, 2008, 63, 372-382.	2.7	132
47	Summer warming accelerates subâ€arctic peatland nitrogen cycling without changing enzyme pools or microbial community structure. Global Change Biology, 2012, 18, 138-150.	9.5	125
48	Collimonas fungivorans gen. nov., sp. nov., a chitinolytic soil bacterium with the ability to grow on living fungal hyphae. International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 857-864.	1.7	122
49	Fungistasis and general soil biostasis â€“ A new synthesis. Soil Biology and Biochemistry, 2011, 43, 469-477.	8.8	122
50	Microbial modulation of plant ethylene signaling: ecological and evolutionary consequences. Microbiome, 2018, 6, 52.	11.1	121
51	Back to the Future of Soil Metagenomics. Frontiers in Microbiology, 2016, 7, 73.	3.5	120
52	Temperature adaptation of soil bacterial communities along an Antarctic climate gradient: predicting responses to climate warming. Global Change Biology, 2009, 15, 2615-2625.	9.5	119
53	Variation in local carrying capacity and the individual fate of bacterial colonizers in the phyllosphere. ISME Journal, 2012, 6, 756-765.	9.8	114
54	Phylogenetic diversity of <i>Acidobacteria</i> in a former agricultural soil. ISME Journal, 2009, 3, 378-382.	9.8	110

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55	A Comparison of rpoB and 16S rRNA as Markers in Pyrosequencing Studies of Bacterial Diversity. PLoS ONE, 2012, 7, e30600.	2.5	109
56	Shifts in the dominant populations of ammonia-oxidizing b-subclass Proteobacteria along the eutrophic Schelde estuary. Aquatic Microbial Ecology, 2001, 23, 225-236.	1.8	105
57	Assessing responses of soil microorganisms to GM plants. Trends in Ecology and Evolution, 2003, 18, 403-410.	8.7	101
58	Soil and plant factors driving the community of soil-borne microorganisms across chronosequences of secondary succession of chalk grasslands with a neutral pH. FEMS Microbiology Ecology, 2011, 77, 285-294.	2.7	101
59	INTERPLAY BETWEENSENECIO JACOBAEAAND PLANT, SOIL, AND ABOVEGROUND INSECT COMMUNITY COMPOSITION. Ecology, 2006, 87, 2002-2013.	3.2	97
60	Impacts of 3Âyears of elevated atmospheric <scp><scp>CO</scp></scp>₂ on rhizosphere carbon flow and microbial community dynamics. Global Change Biology, 2013, 19, 621-636.	9.5	93
61	SOIL FEEDBACK OF EXOTIC SAVANNA GRASS RELATES TO PATHOGEN ABSENCE AND MYCORRHIZAL SELECTIVITY. Ecology, 2007, 88, 978-988.	3.2	91
62	Phylogenetic analysis of aerobic freshwater and marine enrichment cultures efficient in hydrocarbon degradation: effect of profiling method. Journal of Microbiological Methods, 2000, 40, 19-31.	1.6	84
63	Specific rhizosphere bacterial and fungal groups respond differently to elevated atmospheric CO2. ISME Journal, 2009, 3, 1204-1217.	9.8	83
64	Impact of Metal Pollution and <i>Thlaspi caerulescens</i> Growth on Soil Microbial Communities. Applied and Environmental Microbiology, 2010, 76, 7843-7853.	3.1	80
65	Bacterial diversity amplifies nutrientâ€based plantâ€“soil feedbacks. Functional Ecology, 2015, 29, 1341-1349.	3.6	78
66	Spatiotemporal stability of an ammonia-oxidizing community in a nitrogen-saturated forest soil. Microbial Ecology, 2001, 42, 35-45.	2.8	75
67	Impact of elevated carbon dioxide on the rhizosphere communities of <i>Carex arenaria</i> and <i>Festuca rubra</i>. Global Change Biology, 2007, 13, 2396-2410.	9.5	73
68	Microbial secondary succession in a chronosequence of chalk grasslands. ISME Journal, 2010, 4, 711-715.	9.8	73
69	Root exudates mediate plant defense against foliar pathogens by recruiting beneficial microbes. Soil Ecology Letters, 2021, 3, 42-51.	4.5	71
70	Protists as main indicators and determinants of plant performance. Microbiome, 2021, 9, 64.	11.1	71
71	Growth of Chitinolytic Dune Soil Î²-Subclass Proteobacteria in Response to Invading Fungal Hyphae. Applied and Environmental Microbiology, 2001, 67, 3358-3362.	3.1	69
72	Rhizosphere microbiome functional diversity and pathogen invasion resistance build up during plant development. Environmental Microbiology, 2020, 22, 5005-5018.	3.8	69

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73	Contrasting patterns of evolutionary divergence within the Acinetobacter calcoaceticus pca operon. Gene, 1994, 146, 23-30.	2.2	68
74	PCR-Denaturing Gradient Gel Electrophoresis Profiling of Inter- and Intraspecies 18S rRNA Gene Sequence Heterogeneity Is an Accurate and Sensitive Method To Assess Species Diversity of Arbuscular Mycorrhizal Fungi of the Genus Gigaspora. Applied and Environmental Microbiology, 2004, 70, 1413-1424.	3.1	68
75	Finding the Needles in the Metagenome Haystack. Microbial Ecology, 2007, 53, 475-485.	2.8	68
76	Temperature sensitivity of peatland C and N cycling: Does substrate supply play a role?. Soil Biology and Biochemistry, 2013, 61, 109-120.	8.8	68
77	Quantitative multiplex detection of plant pathogens using a novel ligation probe-based system coupled with universal, high-throughput real-time PCR on OpenArraysâ„¢. BMC Genomics, 2007, 8, 276.	2.8	67
78	Impact of Matric Potential and Pore Size Distribution on Growth Dynamics of Filamentous and Non-Filamentous Soil Bacteria. PLoS ONE, 2013, 8, e83661.	2.5	67
79	Plant biomass, soil microbial community structure and nitrogen cycling under different organic amendment regimes; a 15N tracer-based approach. Applied Soil Ecology, 2016, 107, 251-260.	4.3	67
80	Competitive PCRâ€"DGGE analysis of bacterial mixtures. Journal of Microbiological Methods, 2000, 40, 111-123.	1.6	64
81	Rhizosphere fungal communities are influenced by Senecio jacobaea pyrrolizidine alkaloid content and composition. Soil Biology and Biochemistry, 2006, 38, 2852-2859.	8.8	61
82	Resource availability modulates biodiversityâ€invasion relationships by altering competitive interactions. Environmental Microbiology, 2017, 19, 2984-2991.	3.8	61
83	Structural and functional variation in soil fungal communities associated with litter bags containing maize leaf. FEMS Microbiology Ecology, 2013, 84, 519-531.	2.7	59
84	Trophic interactions between predatory protists and pathogen-suppressive bacteria impact plant health. ISME Journal, 2022, 16, 1932-1943.	9.8	57
85	Influences of space, soil, nematodes and plants on microbial community composition of chalk grassland soils. Environmental Microbiology, 2010, 12, 2096-2106.	3.8	54
86	Testing Potential Effects of Maize Expressing the Bacillus thuringiensis Cry1Ab Endotoxin (Bt Maize) on Mycorrhizal Fungal Communities via DNA- and RNA-Based Pyrosequencing and Molecular Fingerprinting. Applied and Environmental Microbiology, 2012, 78, 7384-7392.	3.1	52
87	ACC deaminaseâ€producing rhizosphere bacteria modulate plant responses to flooding. Journal of Ecology, 2017, 105, 979-986.	4.0	51
88	Root-associated microorganisms reprogram plant life history along the growthâ€"stress resistance tradeoff. ISME Journal, 2019, 13, 3093-3101.	9.8	51
89	A global overview of the trophic structure within microbiomes across ecosystems. Environment International, 2021, 151, 106438.	10.0	48
90	Unusual G + C content and codon usage in catIJF, a segment of the bencat supra-operonic cluster in the Acinetobacter calcoaceticus chromosome. Gene, 1994, 138, 59-65.	2.2	47

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91	A survey of 16S rRNA andamoAgenes related to autotrophic ammonia-oxidizing bacteria of the Î²-subdivision of the class proteobacteria in contaminated groundwater. Canadian Journal of Microbiology, 2000, 46, 1012-1020.	1.7	46
92	Bacterial and fungal communities associated with<i>Tuber magnatum</i>â€productive niches. Plant Biosystems, 2010, 144, 323-332.	1.6	45
93	Nitrosomonas europaea-like bacteria detected as the dominant Î²-subclass Proteobacteria ammonia oxidisers in reference and limed acid forest soils. Soil Biology and Biochemistry, 2002, 34, 1047-1050.	8.8	41
94	Enzymology under global change: organic nitrogen turnover in alpine and sub-Arctic soils. Biochemical Society Transactions, 2011, 39, 309-314.	3.4	39
95	New perspectives towards analysing fungal communities in terrestrial environments. Current Opinion in Biotechnology, 1999, 10, 247-251.	6.6	37
96	Microbial community responses to disease management soil treatments used in flower bulb cultivation. Biology and Fertility of Soils, 2003, 37, 55-63.	4.3	34
97	Effect of land use and soil organic matter quality on the structure and function of microbial communities in pastoral soils: Implications for disease suppression. PLoS ONE, 2018, 13, e0196581.	2.5	34
98	Toward a Standards-Compliant Genomic and Metagenomic Publication Record. OMICS A Journal of Integrative Biology, 2008, 12, 157-160.	2.0	33
99	Molecular trait indicators: moving beyond phylogeny in arbuscular mycorrhizal ecology. New Phytologist, 2010, 185, 67-82.	7.3	33
100	Challenges and opportunities in harnessing soil disease suppressiveness for sustainable pasture production. Soil Biology and Biochemistry, 2016, 95, 100-111.	8.8	33
101	Optimization of plant hormonal balance by microorganisms prevents plant heavy metal accumulation. Journal of Hazardous Materials, 2019, 379, 120787.	12.4	33
102	Microbial amendments alter protist communities within the soil microbiome. Soil Biology and Biochemistry, 2019, 135, 379-382.	8.8	32
103	Ecotrons: Powerful and versatile ecosystem analysers for ecology, agronomy and environmental science. Global Change Biology, 2021, 27, 1387-1407.	9.5	32
104	Indirect reduction of <i>Ralstonia solanacearum</i> via pathogen helper inhibition. ISME Journal, 2022, 16, 868-875.	9.8	32
105	Morphological, ontogenetic and molecular characterization of Scutellospora reticulata (Glomeromycota). Mycological Research, 2005, 109, 697-706.	2.5	31
106	Comparative Analysis of Acidobacterial Genomic Fragments from Terrestrial and Aquatic Metagenomic Libraries, with Emphasis on <i>Acidobacteria</i> Subdivision 6. Applied and Environmental Microbiology, 2010, 76, 6769-6777.	3.1	31
107	Succession of the Resident Soil Microbial Community in Response to Periodic Inoculations. Applied and Environmental Microbiology, 2021, 87, .	3.1	30
108	Introduction of probiotic bacterial consortia promotes plant growth via impacts on the resident rhizosphere microbiome. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20211396.	2.6	29

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109	Shifts in the phylogenetic structure and functional capacity of soil microbial communities follow alteration of native tussock grassland ecosystems. Soil Biology and Biochemistry, 2013, 57, 675-682.	8.8	28
110	No effects of experimental warming but contrasting seasonal patterns for soil peptidase and glycosidase enzymes in a sub-arctic peat bog. Biogeochemistry, 2014, 117, 55-66.	3.5	26
111	Singleâ€cell versus populationâ€level reproductive success of bacterial immigrants to preâ€colonized leaf surfaces. Environmental Microbiology Reports, 2013, 5, 387-392.	2.4	25
112	Targeted plant hologenome editing for plant trait enhancement. New Phytologist, 2021, 229, 1067-1077.	7.3	25
113	Tracking Fungal Community Responses to Maize Plants by DNA- and RNA-Based Pyrosequencing. PLoS ONE, 2013, 8, e69973.	2.5	25
114	The ISME Journal: Multidisciplinary Journal of Microbial Ecology. ISME Journal, 2007, 1, 1-3.	9.8	24
115	Accurate Quantification of Microorganisms in PCR-Inhibiting Environmental DNA Extracts by a Novel Internal Amplification Control Approach Using Biotrove OpenArrays. Applied and Environmental Microbiology, 2009, 75, 7253-7260.	3.1	24
116	Bad News for Soil Carbon Sequestration?. Science, 2012, 337, 1049-1050.	12.6	24
117	Biocontrol Traits Correlate With Resistance to Predation by Protists in Soil Pseudomonads. Frontiers in Microbiology, 2020, 11, 614194.	3.5	24
118	Robust Detection and Identification of Multiple Oomycetes and Fungi in Environmental Samples by Using a Novel Cleavable Padlock Probe-Based Ligation Detection Assay. Applied and Environmental Microbiology, 2009, 75, 4185-4193.	3.1	23
119	Phylogenetic and metagenomic analysis of VerrucomicrobiaÃ¢Â€Âƒin former Ã¢Â€Âƒagricultural grassland soil. FEMS Microbiology Ecology, 2010, 71, 23-33.	2.7	23
120	Modulation of Litter Decomposition by the Soil Microbial Food Web Under Influence of Land Use Change. Frontiers in Microbiology, 2018, 9, 2860.	3.5	23
121	Impacts of long-term plant residue management on soil organic matter quality, Pseudomonas community structure and disease suppressiveness. Soil Biology and Biochemistry, 2019, 135, 396-406.	8.8	22
122	Compositional Stability of the Bacterial Community in a Climate-Sensitive Sub-Arctic Peatland. Frontiers in Microbiology, 2017, 8, 317.	3.5	20
123	Optimizing cover crop and fertilizer timing for high maize yield and nitrogen cycle control. Geoderma, 2022, 405, 115423.	5.1	20
124	Silver Toxicity Thresholds for Multiple Soil Microbial Biomarkers. Environmental Science & Technology, 2018, 52, 8745-8755.	10.0	19
125	Alternative transient states and slow plant community responses after changed flooding regimes. Global Change Biology, 2019, 25, 1358-1367.	9.5	19
126	The Earth Microbiome Project: The Meeting Report for the 1st International Earth Microbiome Project Conference, Shenzhen, China, June 13th-15th 2011. Standards in Genomic Sciences, 2011, 5, 243-247.	1.5	18

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127	Microbes orchestrate life on Earth. ISME Journal, 2008, 2, 795-796.	9.8	16
128	Nucleotide sequences transferred by gene conversion in the bacterium Acinetobacter calcoaceticus. Gene, 1995, 153, 111-115.	2.2	15
129	Assessing Bacterial and Fungal Community Structure in Soil Using Ribosomal RNA and Other Structural Gene Markers. Soil Biology, 2006, , 159-188.	0.8	15
130	Microbial community assembly in soil aggregates: A dynamic interplay of stochastic and deterministic processes. Applied Soil Ecology, 2021, 163, 103911.	4.3	15
131	Protist feeding patterns and growth rate are related to their predatory impacts on soil bacterial communities. FEMS Microbiology Ecology, 2022, 98, .	2.7	14
132	Trichoderma-amended biofertilizer stimulates soil resident Aspergillus population for joint plant growth promotion. Npj Biofilms and Microbiomes, 2022, 8, .	6.4	14
133	Increased microbial activity and nitrogen mineralization coupled to changes in microbial community structure in the rhizosphere of Bt corn. Applied Soil Ecology, 2013, 68, 46-56.	4.3	13
134	Soil-Borne Microbial Functional Structure across Different Land Uses. Scientific World Journal, The, 2014, 2014, 1-8.	2.1	11
135	Early colonizers of unoccupied habitats represent a minority of the soil bacterial community. FEMS Microbiology Ecology, 2015, 91, .	2.7	11
136	Microbial inoculants modulate growth traits, nutrients acquisition and bioactive compounds accumulation of Cyclocarya paliurus (Batal.) Iljinskaja under degraded field condition. Forest Ecology and Management, 2021, 482, 118897.	3.2	11
137	Recent developments and potential of robotics in plant eco-phenotyping. Emerging Topics in Life Sciences, 2021, 5, 289-300.	2.6	11
138	Resource stoichiometry shapes community invasion resistance via productivity-mediated species identity effects. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20182035.	2.6	10
139	Towards meaningful scales in ecosystem microbiome research. Environmental Microbiology, 2021, 23, 1-4.	3.8	10
140	SRU_D: A simple nonâ€destructive method for accurate quantification of plant diversity dynamics. Journal of Ecology, 2019, 107, 2155-2166.	4.0	9
141	Links between pseudometallophytes and rhizosphere microbial communities in a metalliferous soil. Pedobiologia, 2012, 55, 219-225.	1.2	7
142	The northward shifting neophyte<i>Tragopogon dubius</i>is just as effective in forming mycorrhizal associations as the native<i>T. pratensis</i>. Plant Ecology and Diversity, 2014, 7, 533-539.	2.4	7
143	Local Functioning, Landscape Structuring: Drivers of Soil Microbial Community Structure and Function in Peatlands. Frontiers in Microbiology, 2018, 9, 2060.	3.5	7
144	Microbial Functional Diversity in Vineyard Soils: Sulfur Metabolism and Links With Grapevine Plants and Wine Quality. Frontiers in Environmental Science, 2020, 8, .	3.3	7

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145	Molecular analysis of ammonia-oxidising bacteria in soil of successional grasslands of the Drentsche A (The Netherlands). FEMS Microbiology Ecology, 2000, 31, 207-215.	2.7	7
146	A survey of 16S rRNA and <i>amoA</i> genes related to autotrophic ammonia-oxidizing bacteria of the Î²-subdivision of the class proteobacteria in contaminated groundwater. Canadian Journal of Microbiology, 2000, 46, 1012-1020.	1.7	7
147	Community analysis of ammonia-oxidising bacteria, in relation to oxygen availability in soils and root-oxygenated sediments, using PCR, DGGE and oligonucleotide probe hybridisation. FEMS Microbiology Ecology, 1998, 27, 339-350.	2.7	6
148	Effects of probiotic consortia on plant metabolites are associated with soil indigenous microbiota and fertilization regimes. Industrial Crops and Products, 2022, 185, 115138.	5.2	6
149	Influence of fungal-bacterial interactions on bacterial conjugation in the residuesphere. FEMS Microbiology Ecology, 2000, 31, 39-45.	2.7	5
150	Chapter 12 Valid Recovery of Nucleic Acid Sequence Information from High Contamination Risk Samples â€“ Ancient DNA and Environmental DNA. Perspectives in Bioanalysis, 2007, , 357-371.	0.3	5
151	Microbial Environmental Genomics. Microbial Ecology, 2007, 53, 367-368.	2.8	5
152	Fast and furious: Early differences in growth rate drive shortâ€term plant dominance and exclusion under eutrophication. Ecology and Evolution, 2020, 10, 10116-10129.	1.9	5
153	Rapid evolution of trait correlation networks during bacterial adaptation to the rhizosphere. Evolution; International Journal of Organic Evolution, 2021, 75, 1218-1229.	2.3	5
154	Stem traits, compartments and tree species affect fungal communities on decaying wood. Environmental Microbiology, 2022, 24, 3625-3639.	3.8	4
155	Five Groups in the Genus Allovahlkampfia and the Description of the New Species Vahlkampfia bulbosis n.sp.. Protist, 2022, 173, 125870.	1.5	4
156	ISMEJ turns 10: tracking rapid progress in microbial ecology. ISME Journal, 2017, 11, 1059-1060.	9.8	0