George A Kowalchuk

List of Publications by Year
in descending order

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156

papers

19,503

citations

13099

68

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11607

135

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163

all docs

163

docs citations

163

times ranked

17385

citing authors

#	ARTICLE	IF	CITATIONS
1	Optimizing cover crop and fertilizer timing for high maize yield and nitrogen cycle control. Geoderma, 2022, 405, 115423.	5.1	20
2	Indirect reduction of <i>Ralstonia solanacearum</i> via pathogen helper inhibition. ISME Journal, 2022, 16, 868-875.	9.8	32
3	Stem traits, compartments and tree species affect fungal communities on decaying wood. Environmental Microbiology, 2022, 24, 3625-3639.	3.8	4
4	Five Groups in the Genus Allovahlkampfia and the Description of the New Species Vahlkampfia bulbosis n.sp.. Protist, 2022, 173, 125870.	1.5	4
5	Trophic interactions between predatory protists and pathogen-suppressive bacteria impact plant health. ISME Journal, 2022, 16, 1932-1943.	9.8	57
6	Protist feeding patterns and growth rate are related to their predatory impacts on soil bacterial communities. FEMS Microbiology Ecology, 2022, 98, .	2.7	14
7	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
8	Trichoderma-amended biofertilizer stimulates soil resident Aspergillus population for joint plant growth promotion. Npj Biofilms and Microbiomes, 2022, 8, .	6.4	14
9	Root exudates mediate plant defense against foliar pathogens by recruiting beneficial microbes. Soil Ecology Letters, 2021, 3, 42-51.	4.5	71
10	Targeted plant hologenome editing for plant trait enhancement. New Phytologist, 2021, 229, 1067-1077.	7.3	25
11	Towards meaningful scales in ecosystem microbiome research. Environmental Microbiology, 2021, 23, 1-4.	3.8	10
12	Ecotrons: Powerful and versatile ecosystem analysers for ecology, agronomy and environmental science. Global Change Biology, 2021, 27, 1387-1407.	9.5	32
13	Root exudates drive soilâ€microbeâ€nutrient feedbacks in response to plant growth. Plant, Cell and Environment, 2021, 44, 613-628.	5.7	150
14	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
15	Protists as main indicators and determinants of plant performance. Microbiome, 2021, 9, 64.	11.1	71
16	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
17	Succession of the Resident Soil Microbial Community in Response to Periodic Inoculations. Applied and Environmental Microbiology, 2021, 87, .	3.1	30
18	Recent developments and potential of robotics in plant eco-phenotyping. Emerging Topics in Life Sciences, 2021, 5, 289-300.	2.6	11

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19	A global overview of the trophic structure within microbiomes across ecosystems. Environment International, 2021, 151, 106438.	10.0	48
20	Microbial community assembly in soil aggregates: A dynamic interplay of stochastic and deterministic processes. Applied Soil Ecology, 2021, 163, 103911.	4.3	15
21	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
22	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
23	Bio-organic fertilizers stimulate indigenous soil Pseudomonas populations to enhance plant disease suppression. Microbiome, 2020, 8, 137.	11.1	181
24	Rhizosphere microbiome functional diversity and pathogen invasion resistance build up during plant development. Environmental Microbiology, 2020, 22, 5005-5018.	3.8	69
25	Rhizosphere protists are key determinants of plant health. Microbiome, 2020, 8, 27.	11.1	156
26	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
27	Biocontrol Traits Correlate With Resistance to Predation by Protists in Soil Pseudomonads. Frontiers in Microbiology, 2020, 11, 614194.	3.5	24
28	Root-associated microorganisms reprogram plant life history along the growthâ€"stress resistance tradeoff. ISME Journal, 2019, 13, 3093-3101.	9.8	51
29	Initial soil microbiome composition and functioning predetermine future plant health. Science Advances, 2019, 5, eaaw0759.	10.3	314
30	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
31	Optimization of plant hormonal balance by microorganisms prevents plant heavy metal accumulation. Journal of Hazardous Materials, 2019, 379, 120787.	12.4	33
32	Microbial amendments alter protist communities within the soil microbiome. Soil Biology and Biochemistry, 2019, 135, 379-382.	8.8	32
33	SRU_D: A simple nonâ€destructive method for accurate quantification of plant diversity dynamics. Journal of Ecology, 2019, 107, 2155-2166.	4.0	9
34	Protists: Puppet Masters of the Rhizosphere Microbiome. Trends in Plant Science, 2019, 24, 165-176.	8.8	215
35	Alternative transient states and slow plant community responses after changed flooding regimes. Global Change Biology, 2019, 25, 1358-1367.	9.5	19
36	Microbial modulation of plant ethylene signaling: ecological and evolutionary consequences. Microbiome, 2018, 6, 52.	11.1	121

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37	Soil protist communities form a dynamic hub in the soil microbiome. ISME Journal, 2018, 12, 634-638.	9.8	184
38	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
39	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
40	Local Functioning, Landscape Structuring: Drivers of Soil Microbial Community Structure and Function in Peatlands. Frontiers in Microbiology, 2018, 9, 2060.	3.5	7
41	Root exudates drive the soil-borne legacy of aboveground pathogen infection. Microbiome, 2018, 6, 156.	11.1	354
42	Silver Toxicity Thresholds for Multiple Soil Microbial Biomarkers. Environmental Science & Technology, 2018, 52, 8745-8755.	10.0	19
43	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
44	Resource availability modulates biodiversityâ€invasion relationships by altering competitive interactions. Environmental Microbiology, 2017, 19, 2984-2991.	3.8	61
45	ISMEJ turns 10: tracking rapid progress in microbial ecology. ISME Journal, 2017, 11, 1059-1060.	9.8	0
46	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
47	ACC deaminaseâ€producing rhizosphere bacteria modulate plant responses to flooding. Journal of Ecology, 2017, 105, 979-986.	4.0	51
48	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
49	Compositional Stability of the Bacterial Community in a Climate-Sensitive Sub-Arctic Peatland. Frontiers in Microbiology, 2017, 8, 317.	3.5	20
50	Back to the Future of Soil Metagenomics. Frontiers in Microbiology, 2016, 7, 73.	3.5	120
51	The Ecology of Acidobacteria: Moving beyond Genes and Genomes. Frontiers in Microbiology, 2016, 7, 744.	3.5	762
52	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
53	Challenges and opportunities in harnessing soil disease suppressiveness for sustainable pasture production. Soil Biology and Biochemistry, 2016, 95, 100-111.	8.8	33
54	Early colonizers of unoccupied habitats represent a minority of the soil bacterial community. FEMS Microbiology Ecology, 2015, 91, .	2.7	11

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55	Bacterial diversity amplifies nutrientâ€based plantâ€“soil feedbacks. Functional Ecology, 2015, 29, 1341-1349.	3.6	78
56	Soil-Borne Microbial Functional Structure across Different Land Uses. Scientific World Journal, The, 2014, 2014, 1-8.	2.1	11
57	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
58	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
59	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
60	Micro-scale determinants of bacterial diversity in soil. FEMS Microbiology Reviews, 2013, 37, 936-954.	8.6	418
61	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
62	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
63	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
64	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
65	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
66	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
67	Tracking Fungal Community Responses to Maize Plants by DNA- and RNA-Based Pyrosequencing. PLoS ONE, 2013, 8, e69973.	2.5	25
68	Bad News for Soil Carbon Sequestration?. Science, 2012, 337, 1049-1050.	12.6	24
69	Variation in local carrying capacity and the individual fate of bacterial colonizers in the phyllosphere. ISME Journal, 2012, 6, 756-765.	9.8	114
70	Links between pseudometallophytes and rhizosphere microbial communities in a metalliferous soil. Pedobiologia, 2012, 55, 219-225.	1.2	7
71	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
72	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

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73	A Comparison of rpoB and 16S rRNA as Markers in Pyrosequencing Studies of Bacterial Diversity. PLoS ONE, 2012, 7, e30600.	2.5	109
74	Soil characteristics more strongly influence soil bacterial communities than land-use type. FEMS Microbiology Ecology, 2012, 79, 12-24.	2.7	347
75	Unlocking the potential of metagenomics through replicated experimental design. Nature Biotechnology, 2012, 30, 513-520.	17.5	250
76	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
77	Community assembly, species richness and nestedness of arbuscular mycorrhizal fungi in agricultural soils. Molecular Ecology, 2012, 21, 2341-2353.	3.9	203
78	Reciprocal Rewards Stabilize Cooperation in the Mycorrhizal Symbiosis. Science, 2011, 333, 880-882.	12.6	1,373
79	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
80	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
81	Fungistasis and general soil biostasis â€“ A new synthesis. Soil Biology and Biochemistry, 2011, 43, 469-477.	8.8	122
82	Enzymology under global change: organic nitrogen turnover in alpine and sub-Arctic soils. Biochemical Society Transactions, 2011, 39, 309-314.	3.4	39
83	Influences of space, soil, nematodes and plants on microbial community composition of chalk grassland soils. Environmental Microbiology, 2010, 12, 2096-2106.	3.8	54
84	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
85	Molecular trait indicators: moving beyond phylogeny in arbuscular mycorrhizal ecology. New Phytologist, 2010, 185, 67-82.	7.3	33
86	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
87	Phylogenetic and metagenomic analysis of VerrucomicrobiaÃ¢Â€Âƒin former Ã¢Â€Âƒagricultural grassland soil. FEMS Microbiology Ecology, 2010, 71, 23-33.	2.7	23
88	Microbial secondary succession in a chronosequence of chalk grasslands. ISME Journal, 2010, 4, 711-715.	9.8	73
89	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
90	Bacterial and fungal communities associated with<i>Tuber magnatum</i>â€productive niches. Plant Biosystems, 2010, 144, 323-332.	1.6	45

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91	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
92	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
93	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
94	Environmental microarray analyses of Antarctic soil microbial communities. ISME Journal, 2009, 3, 340-351.	9.8	156
95	Phylogenetic diversity of <i>Acidobacteria</i> in a former agricultural soil. ISME Journal, 2009, 3, 378-382.	9.8	110
96	Bacteria, not archaea, restore nitrification in a zinc-contaminated soil. ISME Journal, 2009, 3, 916-923.	9.8	138
97	Specific rhizosphere bacterial and fungal groups respond differently to elevated atmospheric CO2. ISME Journal, 2009, 3, 1204-1217.	9.8	83
98	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
99	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
100	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
101	Microbes orchestrate life on Earth. ISME Journal, 2008, 2, 795-796.	9.8	16
102	The minimum information about a genome sequence (MIGS) specification. Nature Biotechnology, 2008, 26, 541-547.	17.5	1,069
103	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
104	Toward a Standards-Compliant Genomic and Metagenomic Publication Record. OMICS A Journal of Integrative Biology, 2008, 12, 157-160.	2.0	33
105	SOIL FEEDBACK OF EXOTIC SAVANNA GRASS RELATES TO PATHOGEN ABSENCE AND MYCORRHIZAL SELECTIVITY. Ecology, 2007, 88, 978-988.	3.2	91
106	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
107	The ISME Journal: Multidisciplinary Journal of Microbial Ecology. ISME Journal, 2007, 1, 1-3.	9.8	24
108	Functional microarray analysis of nitrogen and carbon cycling genes across an Antarctic latitudinal transect. ISME Journal, 2007, 1, 163-179.	9.8	232

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109	Patterns of bacterial diversity across a range of Antarctic terrestrial habitats. Environmental Microbiology, 2007, 9, 2670-2682.	3.8	267
110	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
111	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
112	Finding the Needles in the Metagenome Haystack. Microbial Ecology, 2007, 53, 475-485.	2.8	68
113	Microbial Environmental Genomics. Microbial Ecology, 2007, 53, 367-368.	2.8	5
114	Assessing Bacterial and Fungal Community Structure in Soil Using Ribosomal RNA and Other Structural Gene Markers. Soil Biology, 2006, , 159-188.	0.8	15
115	Size and structure of bacterial, fungal and nematode communities along an Antarctic environmental gradient. FEMS Microbiology Ecology, 2006, 59, 436-451.	2.7	202
116	Rhizosphere fungal communities are influenced by Senecio jacobaea pyrrolizidine alkaloid content and composition. Soil Biology and Biochemistry, 2006, 38, 2852-2859.	8.8	61
117	INTERPLAY BETWEENSENECIO JACOBAEAAND PLANT, SOIL, AND ABOVEGROUND INSECT COMMUNITY COMPOSITION. Ecology, 2006, 87, 2002-2013.	3.2	97
118	Morphological, ontogenetic and molecular characterization of Scutellospora reticulata (Glomeromycota). Mycological Research, 2005, 109, 697-706.	2.5	31
119	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
120	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
121	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
122	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
123	Effects of genetically modified plants on microbial communities and processes in soil. Biology and Fertility of Soils, 2003, 37, 329-337.	4.3	132
124	Assessing responses of soil microorganisms to GM plants. Trends in Ecology and Evolution, 2003, 18, 403-410.	8.7	101
125	Microbial Community Composition Affects Soil Fungistasis. Applied and Environmental Microbiology, 2003, 69, 835-844.	3.1	147
126	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

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127	Community analysis of arbuscular mycorrhizal fungi associated with Ammophila arenaria in Dutch coastal sand dunes. Molecular Ecology, 2002, 11, 571-581.	3.9	175
128	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
129	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
130	Nitrification in acid soils: micro-organisms and mechanisms. Soil Biology and Biochemistry, 2001, 33, 853-866.	8.8	644
131	Spatiotemporal stability of an ammonia-oxidizing community in a nitrogen-saturated forest soil. Microbial Ecology, 2001, 42, 35-45.	2.8	75
132	Ammonia-Oxidizing Bacteria: A Model for Molecular Microbial Ecology. Annual Review of Microbiology, 2001, 55, 485-529.	7.3	1,143
133	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
134	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
135	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
136	Changes in the community structure of ammonia-oxidizing bacteria during secondary succession of calcareous grasslands. Environmental Microbiology, 2000, 2, 99-110.	3.8	152
137	Influence of fungal-bacterial interactions on bacterial conjugation in the residuesphere. FEMS Microbiology Ecology, 2000, 31, 39-45.	2.7	5
138	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
139	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
140	Competitive PCRâ€“DGGE analysis of bacterial mixtures. Journal of Microbiological Methods, 2000, 40, 111-123.	1.6	64
141	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
142	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
143	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
144	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

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145	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
146	New perspectives towards analysing fungal communities in terrestrial environments. Current Opinion in Biotechnology, 1999, 10, 247-251.	6.6	37
147	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
148	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
149	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
150	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
151	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
152	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
153	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
154	Nucleotide sequences transferred by gene conversion in the bacterium Acinetobacter calcoaceticus. Gene, 1995, 153, 111-115.	2.2	15
155	Contrasting patterns of evolutionary divergence within the Acinetobacter calcoaceticus pca operon. Gene, 1994, 146, 23-30.	2.2	68
156	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