

Andrew Steven Whiteley

List of Publications by Year in descending order

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118
papers

10,364
citations

61984

43
h-index

36028

97
g-index

126
all docs

126
docs citations

126
times ranked

13672
citing authors

#	ARTICLE	IF	CITATIONS
1	Rapid Method for Coextraction of DNA and RNA from Natural Environments for Analysis of Ribosomal DNA- and rRNA-Based Microbial Community Composition. <i>Applied and Environmental Microbiology</i> , 2000, 66, 5488-5491.	3.1	1,422
2	The bacterial biogeography of British soils. <i>Environmental Microbiology</i> , 2011, 13, 1642-1654.	3.8	753
3	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	17.5	608
4	Aerobic proteobacterial methylotrophs in Movile Cave: genomic and metagenomic analyses. <i>Microbiome</i> , 2018, 6, 1.	11.1	541
5	RNA Stable Isotope Probing, a Novel Means of Linking Microbial Community Function to Phylogeny. <i>Applied and Environmental Microbiology</i> , 2002, 68, 5367-5373.	3.1	527
6	Unravelling rhizosphere microbial interactions: opportunities and limitations. <i>Trends in Microbiology</i> , 2004, 12, 386-393.	7.7	426
7	Shifting carbon flow from roots into associated microbial communities in response to elevated atmospheric CO ₂ . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10938-10942.	7.1	390
8	Raman Microscopic Analysis of Single Microbial Cells. <i>Analytical Chemistry</i> , 2004, 76, 4452-4458.	6.5	371
9	Advances in restoration ecology: rising to the challenges of the coming decades. <i>Ecosphere</i> , 2015, 6, 1-25.	2.2	361
10	Raman-FISH: combining stable-isotope Raman spectroscopy and fluorescence in situ hybridization for the single cell analysis of identity and function. <i>Environmental Microbiology</i> , 2007, 9, 1878-1889.	3.8	305
11	Microbial 16S rRNA Ion Tag and community metagenome sequencing using the Ion Torrent (PGM) Platform. <i>Journal of Microbiological Methods</i> , 2012, 91, 80-88.	1.6	187
12	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	13.3	184
13	Bacterial Community Structure and Physiological State within an Industrial Phenol Bioremediation System. <i>Applied and Environmental Microbiology</i> , 2000, 66, 2400-2407.	3.1	178
14	Influence of depth and sampling time on bacterial community structure in an upland grassland soil. <i>FEMS Microbiology Ecology</i> , 2003, 43, 35-43.	2.7	170
15	Physiological and Community Responses of Established Grassland Bacterial Populations to Water Stress. <i>Applied and Environmental Microbiology</i> , 2003, 69, 6961-6968.	3.1	167
16	N-acyl-L-homoserine lactones (AHLs) affect microbial community composition and function in activated sludge. <i>Environmental Microbiology</i> , 2004, 6, 424-433.	3.8	154
17	Minimizing errors in RT-PCR detection and quantification of SARS-CoV-2 RNA for wastewater surveillance. <i>Science of the Total Environment</i> , 2022, 805, 149877.	8.0	153
18	Resolving Genetic Functions within Microbial Populations: In Situ Analyses Using rRNA and mRNA Stable Isotope Probing Coupled with Single-Cell Raman-Fluorescence In Situ Hybridization. <i>Applied and Environmental Microbiology</i> , 2009, 75, 234-241.	3.1	128

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19	Technical considerations for RNA-based stable isotope probing: an approach to associating microbial diversity with microbial community function. <i>Rapid Communications in Mass Spectrometry</i> , 2002, 16, 2179-2183.	1.5	125
20	The response of marine picoplankton to ocean acidification. <i>Environmental Microbiology</i> , 2012, 14, 2293-2307.	3.8	124
21	Quantitative in situ assay of salicylic acid in tobacco leaves using a genetically modified biosensor strain of <i>Acinetobacter</i> sp. ADP1. <i>Plant Journal</i> , 2006, 46, 1073-1083.	5.7	115
22	Raman tweezers sorting of single microbial cells. <i>Environmental Microbiology Reports</i> , 2009, 1, 44-49.	2.4	115
23	Active microbial RNA turnover in a grassland soil estimated using a $^{13}\text{CO}_2$ spike. <i>Soil Biology and Biochemistry</i> , 2003, 35, 877-885.	8.8	113
24	RNA stable-isotope probing. <i>Nature Protocols</i> , 2007, 2, 838-844.	12.0	109
25	Vegetation Affects the Relative Abundances of Dominant Soil Bacterial Taxa and Soil Respiration Rates in an Upland Grassland Soil. <i>Microbial Ecology</i> , 2010, 59, 335-343.	2.8	107
26	Chromosomally located gene fusions constructed in <i>Acinetobacter</i> sp. ADP1 for the detection of salicylate. <i>Environmental Microbiology</i> , 2005, 7, 1339-1348.	3.8	99
27	Unlocking the "microbial black box"™ using RNA-based stable isotope probing technologies. <i>Current Opinion in Biotechnology</i> , 2006, 17, 67-71.	6.6	93
28	Taxon-specific responses of soil bacteria to the addition of low level C inputs. <i>Soil Biology and Biochemistry</i> , 2010, 42, 1624-1631.	8.8	90
29	Plant community composition affects the biomass, activity and diversity of microorganisms in limestone grassland soil. <i>European Journal of Soil Science</i> , 2003, 54, 671-678.	3.9	88
30	Bacterial community structure and function in a metal-working fluid. <i>Environmental Microbiology</i> , 2003, 5, 453-461.	3.8	83
31	Whole cell immobilised biosensors for toxicity assessment of a wastewater treatment plant treating phenolics-containing waste. <i>Analytica Chimica Acta</i> , 2003, 487, 61-74.	5.4	80
32	Soil Carbon-Fixation Rates and Associated Bacterial Diversity and Abundance in Three Natural Ecosystems. <i>Microbial Ecology</i> , 2017, 73, 645-657.	2.8	80
33	Functional and compositional comparison of two activated sludge communities remediating coking effluent. <i>Environmental Microbiology</i> , 2005, 7, 715-722.	3.8	73
34	$^{13}\text{CO}_2$ pulse labelling of plants in tandem with stable isotope probing: methodological considerations for examining microbial function in the rhizosphere. <i>Journal of Microbiological Methods</i> , 2004, 58, 119-129.	1.6	70
35	Temporal dynamics and degradation activity of an bacterial inoculum for treating waste metal-working fluid. <i>Environmental Microbiology</i> , 2004, 6, 254-263.	3.8	67
36	Comparison of Bacterioneuston and Bacterioplankton Dynamics during a Phytoplankton Bloom in a Fjord Mesocosm. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7173-7181.	3.1	63

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37	Microbial Functional Capacity Is Preserved Within Engineered Soil Formulations Used In Mine Site Restoration. <i>Scientific Reports</i> , 2017, 7, 564.	3.3	61
38	Protists have divergent effects on bacterial diversity along a productivity gradient. <i>Biology Letters</i> , 2010, 6, 639-642.	2.3	60
39	Effects of sieving, drying and rewetting upon soil bacterial community structure and respiration rates. <i>Journal of Microbiological Methods</i> , 2010, 83, 69-73.	1.6	58
40	Dissolved organic carbon and bacterial populations in the gelatinous surface microlayer of a Norwegian fjord mesocosm. <i>FEMS Microbiology Letters</i> , 2009, 299, 248-254.	1.8	54
41	The characterisation of eukaryotic microbial communities on sandstone buildings in Belfast, UK, using TRFLP and 454 pyrosequencing. <i>International Biodeterioration and Biodegradation</i> , 2013, 82, 124-133.	3.9	51
42	Marine bacterial communities are resistant to elevated carbon dioxide levels. <i>Environmental Microbiology Reports</i> , 2014, 6, 574-582.	2.4	47
43	Cropping systems modulate the rate and magnitude of soil microbial autotrophic CO ₂ fixation in soil. <i>Frontiers in Microbiology</i> , 2015, 6, 379.	3.5	47
44	Bacterial Physiological Adaptations to Contrasting Edaphic Conditions Identified Using Landscape Scale Metagenomics. <i>MBio</i> , 2017, 8, .	4.1	46
45	Analysis of the microbial functional diversity within water-stressed soil communities by flow cytometric analysis and CTC+ cell sorting. <i>Journal of Microbiological Methods</i> , 2003, 54, 257-267.	1.6	45
46	The sensitivity of a forest soil microbial community to acute gamma-irradiation. <i>Applied Soil Ecology</i> , 2007, 37, 1-9.	4.3	43
47	Weekly flow cytometric analysis of riverine phytoplankton to determine seasonal bloom dynamics. <i>Environmental Sciences: Processes and Impacts</i> , 2014, 16, 594.	3.5	42
48	The Bacterial Microbiome Associated With Arid Biocrusts and the Biogeochemical Influence of Biocrusts Upon the Underlying Soil. <i>Frontiers in Microbiology</i> , 2019, 10, 2143.	3.5	42
49	Single-Cell Raman Spectral Profiles of <i>Pseudomonas fluorescens</i> SBW25 Reflects in vitro and in planta Metabolic History. <i>Microbial Ecology</i> , 2007, 53, 414-425.	2.8	41
50	Ecological and physiological analyses of <i>Pseudomonad</i> species within a phenol remediation system. <i>Journal of Microbiological Methods</i> , 2001, 44, 79-88.	1.6	40
51	Salivary nitrate ? an ecological factor in reducing oral acidity. <i>Oral Microbiology and Immunology</i> , 2007, 22, 67-71.	2.8	40
52	Grassland management influences spatial patterns of soil microbial communities. <i>Soil Biology and Biochemistry</i> , 2013, 61, 61-68.	8.8	39
53	Plant soil interactions alter carbon cycling in an upland grassland soil. <i>Frontiers in Microbiology</i> , 2013, 4, 253.	3.5	39
54	What can stable isotope probing do for bioremediation?. <i>International Biodeterioration and Biodegradation</i> , 2004, 54, 163-166.	3.9	38

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55	Hydrocarbon utilization within a diesel-degrading bacterial consortium. FEMS Microbiology Letters, 2010, 303, 116-122.	1.8	38
56	Humus-Rich Compost Increases Lettuce Growth, Nutrient Uptake, Mycorrhizal Colonisation, and Soil Fertility. Pedosphere, 2019, 29, 170-179.	4.0	38
57	Bioaugmentation Strategies for Remediating Mixed Chemical Effluents. Biotechnology Progress, 2008, 19, 1156-1161.	2.6	33
58	Response of Wheat to a Multiple Species Microbial Inoculant Compared to Fertilizer Application. Frontiers in Plant Science, 2018, 9, 1601.	3.6	33
59	Reconditioning Degraded Mine Site Soils With Exogenous Soil Microbes: Plant Fitness and Soil Microbiome Outcomes. Frontiers in Microbiology, 2019, 10, 1617.	3.5	33
60	Land coverage influences the bacterial community composition in the critical zone of a sub-Arctic basaltic environment. FEMS Microbiology Ecology, 2013, 86, 381-393.	2.7	30
61	Acylated homoserine lactones in the environment: chameleons of bioactivity. Philosophical Transactions of the Royal Society B: Biological Sciences, 2007, 362, 1235-1240.	4.0	28
62	Insights into the fate of a ¹³ C labelled phenol pulse for stable isotope probing (SIP) experiments. Journal of Microbiological Methods, 2007, 69, 340-344.	1.6	27
63	Characterizing the regulation of the <i>Pu<i>i</i></i> promoter in <i>Acinetobacter baylyi</i> ADP1. Environmental Microbiology, 2008, 10, 1668-1680.	3.8	27
64	Fourier transform infrared spectroscopy as a metabolite fingerprinting tool for monitoring the phenotypic changes in complex bacterial communities capable of degrading phenol. Environmental Microbiology, 2010, 12, 3253-3263.	3.8	27
65	Chemical fixation methods for Raman spectroscopy-based analysis of bacteria. Journal of Microbiological Methods, 2015, 109, 79-83.	1.6	27
66	An improved method of cell cycle synchronisation for the heterotrophic dinoflagellate <i>Cryptocodinium cohnii</i> Biecheler analyzed by flow cytometry. Journal of Experimental Marine Biology and Ecology, 1996, 197, 91-99.	1.5	26
67	Development of bespoke bioluminescent reporters with the potential for in situ deployment within a phenolic-remediating wastewater treatment system. Journal of Microbiological Methods, 2003, 55, 667-677.	1.6	26
68	Abundance and Diversity of CO ₂ -Assimilating Bacteria and Algae Within Red Agricultural Soils Are Modulated by Changing Management Practice. Microbial Ecology, 2015, 70, 971-980.	2.8	25
69	Evidence for Phenotypic Plasticity among Multihost <i>Campylobacter jejuni</i> and <i>C. coli</i> Lineages, Obtained Using Ribosomal Multilocus Sequence Typing and Raman Spectroscopy. Applied and Environmental Microbiology, 2013, 79, 965-973.	3.1	24
70	Microbial analysis of soil and groundwater from a gasworks site and comparison with a sequenced biological reactive barrier remediation process. Journal of Applied Microbiology, 2007, 102, 1227-1238.	3.1	23
71	Transcriptional activities of methanogens and methanotrophs vary with methane emission flux in rice soils under chronic nutrient constraints of phosphorus and potassium. Biogeosciences, 2016, 13, 6507-6518.	3.3	21
72	Examining assumptions of soil microbial ecology in the monitoring of ecological restoration. Ecological Solutions and Evidence, 2020, 1, e12031.	2.0	20

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73	The functions and components of the Sourhope soil microbiota. <i>Applied Soil Ecology</i> , 2006, 33, 114-126.	4.3	19
74	Abundance of microbial CO ₂ -fixing genes during the late rice season in a long-term management paddy field amended with straw and straw-derived biochar. <i>Canadian Journal of Soil Science</i> , 2018, 98, 306-316.	1.2	19
75	SYTO16 labelling and flow cytometry of <i>Mycobacterium avium</i> . <i>Letters in Applied Microbiology</i> , 1997, 25, 437-441.	2.2	17
76	Microbial phylogenetic and functional responses within acidified wastewater communities exhibiting enhanced phosphate uptake. <i>Bioresource Technology</i> , 2016, 220, 55-61.	9.6	17
77	Polymer-coated rock mineral fertilizer has potential to substitute soluble fertilizer for increasing growth, nutrient uptake, and yield of wheat. <i>Biology and Fertility of Soils</i> , 2020, 56, 381-394.	4.3	17
78	Effect of phosphorus amendments on rice rhizospheric methanogens and methanotrophs in a phosphorus deficient soil. <i>Geoderma</i> , 2020, 368, 114312.	5.1	17
79	Functional analysis of pristine estuarine marine sediments. <i>Science of the Total Environment</i> , 2021, 781, 146526.	8.0	16
80	Metaproteomic and metagenomic analyses of defined oceanic microbial populations using microwave cell fixation and flow cytometric sorting. <i>FEMS Microbiology Ecology</i> , 2010, 74, 10-18.	2.7	15
81	Microbial inoculation to improve plant performance in mine waste substrates: A test using pigeon pea (<i>Cajanus cajan</i>). <i>Land Degradation and Development</i> , 2022, 33, 497-511.	3.9	15
82	Density gradient separation of active and non-active cells from natural environments. <i>Antonie Van Leeuwenhoek</i> , 2000, 77, 173-177.	1.7	12
83	Influence of Sustainability and Immigration in Assembling Bacterial Populations of Known Size and Function. <i>Microbial Ecology</i> , 2007, 53, 348-354.	2.8	12
84	Non-destructive sampling of rock-dwelling microbial communities using sterile adhesive tape. <i>Journal of Microbiological Methods</i> , 2012, 91, 391-398.	1.6	12
85	Field scale molecular analysis for the monitoring of bacterial community structures during on-site diesel bioremediation. <i>Bioresource Technology</i> , 2010, 101, 5235-5241.	9.6	11
86	Abundance and diversity of carbon monoxide dehydrogenase genes from BMS clade bacteria in different vegetated soils. <i>European Journal of Soil Biology</i> , 2017, 81, 94-99.	3.2	10
87	Stable Isotope Probing: A Critique of Its Role in Linking Phylogeny and Function. , 2006, , 205-216.		8
88	Monitoring Bioremediation. , 0, , 237-268.		8
89	Novel Primer Sets for Next Generation Sequencing-Based Analyses of Water Quality. <i>PLoS ONE</i> , 2017, 12, e0170008.	2.5	8
90	Small investments with big returns: environmental genomic bioprospecting of microbial life. <i>Critical Reviews in Microbiology</i> , 2022, 48, 641-655.	6.1	7

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91	Genomic Structure of the Luciferase Gene from the Bioluminescent Beetle, <i>Nyctophila</i> cf. <i>Caucasica</i> . <i>Journal of Insect Science</i> , 2006, 6, 1-8.	1.5	5
92	Phospholipid Fatty Acid Stable Isotope Probing Techniques in Microbial Ecology. , 0, , 37-71.		5
93	Wastewater Toxicity Assessment by Whole Cell Biosensor. <i>Handbook of Environmental Chemistry</i> , 2004, , 165-225.	0.4	4
94	Nano-Secondary Ions Mass Spectrometry (nanoSIMS) Coupled with In Situ Hybridization for Ecological Research. , 2014, , 295-303.		4
95	Draft Genome Sequence of the Methane-Oxidizing Bacterium <i>Candidatus</i> <i>Methylomonas</i> sp. LWB-1 Isolated from Movile Cave. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
96	Developing Bioprospecting Strategies for Bioplastics Through the Large-Scale Mining of Microbial Genomes. <i>Frontiers in Microbiology</i> , 2021, 12, 697309.	3.5	4
97	DNA Stable Isotope Probing. , 0, , 1-24.		4
98	From rags to enriched: metagenomic insights into ammonia-oxidizing archaea following ammonia enrichment of a denuded oligotrophic soil ecosystem. <i>Environmental Microbiology</i> , 2022, 24, 3097-3110.	3.8	4
99	Mesophilic Mineral-Weathering Bacteria Inhabit the Critical-Zone of a Perennially Cold Basaltic Environment. <i>Geomicrobiology Journal</i> , 2016, 33, 52-62.	2.0	3
100	RNA Stable Isotope Probing (RNA-SIP). <i>Methods in Molecular Biology</i> , 2019, 2046, 31-44.	0.9	3
101	Temporal Microbial Community Dynamics Within a Unique Acid Saline Lake. <i>Frontiers in Microbiology</i> , 2021, 12, 649594.	3.5	3
102	RNA Stable Isotope Probing. , 0, , 25-36.		3
103	Calibration and deployment of custom-designed bioreporters for protecting biological remediation consortia from toxic shock. <i>Environmental Microbiology</i> , 2005, 7, 260-269.	3.8	2
104	Fish-Microautoradiography and Isotope Arrays for Monitoring the Ecophysiology of Microbes Within Their Natural Environment. , 2014, , 305-316.		2
105	Stable Isotope Probing Techniques Using H ₂ ¹⁸ O. , 0, , 115-128.		2
106	Stable Isotope Probing and Plants. , 0, , 149-163.		2
107	Stable Isotope Probing Techniques Using ¹⁵ N. , 0, , 129-147.		1
108	Raman-Fluorescence in Situ Hybridization. , 0, , 277-294.		1

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109	RNA-Radioisotope Probing for Studying Carbon Metabolism in Soils. , 0, , 317-332.		1
110	Stable Isotope Probing Techniques and Bioremediation. , 0, , 165-201.		1
111	Stable Isotope Probing and the Human Gut. , 0, , 233-257.		1
112	DNA stable Isotope Probing and Gene Mining. , 0, , 259-276.		0
113	Single Cell Microbial Ecophysiology with Raman-FISH. Springer Protocols, 2015, , 65-76.	0.3	0
114	Protein Stable Isotope Probing. , 0, , 73-95.		0
115	Trophic Interactions in Microbial Communities and Food Webs Traced by Stable Isotope Probing of Nucleic Acids. , 0, , 203-232.		0
116	A Glance Toward the Future: Where Do We Go from Here?. , 0, , 333-336.		0
117	Stable Isotope Probing and Metagenomics. , 0, , 97-114.		0
118	Establishing a regional microbial blueprint of metabolic function in sediment collected from pristine tropical estuarine systems. , 2022, , 337-357.		0