Andrew Steven Whiteley

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1322740/publications.pdf

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118 papers 10,364 citations

43 h-index 97 g-index

126 all docs

126 docs citations

times ranked

126

13672 citing authors

#	Article	IF	CITATIONS
1	Minimizing errors in RT-PCR detection and quantification of SARS-CoV-2 RNA for wastewater surveillance. Science of the Total Environment, 2022, 805, 149877.	8.0	153
2	Microbial inoculation to improve plant performance in mineâ€waste substrates: A test using pigeon pea (<i>Cajanus cajan</i>). Land Degradation and Development, 2022, 33, 497-511.	3.9	15
3	Small investments with big returns: environmental genomic bioprospecting of microbial life. Critical Reviews in Microbiology, 2022, 48, 641-655.	6.1	7
4	From rags to enriched: metagenomic insights into ammoniaâ€oxidizing archaea following ammonia enrichment of a denuded oligotrophic soil ecosystem. Environmental Microbiology, 2022, 24, 3097-3110.	3.8	4
5	Establishing a regional microbial blueprint of metabolic function in sediment collected from pristine tropical estuarine systems., 2022,, 337-357.		O
6	Temporal Microbial Community Dynamics Within a Unique Acid Saline Lake. Frontiers in Microbiology, 2021, 12, 649594.	3. 5	3
7	Developing Bioprospecting Strategies for Bioplastics Through the Large-Scale Mining of Microbial Genomes. Frontiers in Microbiology, 2021, 12, 697309.	3.5	4
8	Functional analysis of pristine estuarine marine sediments. Science of the Total Environment, 2021, 781, 146526.	8.0	16
9	Polymer-coated rock mineral fertilizer has potential to substitute soluble fertilizer for increasing growth, nutrient uptake, and yield of wheat. Biology and Fertility of Soils, 2020, 56, 381-394.	4.3	17
10	Examining assumptions of soil microbial ecology in the monitoring of ecological restoration. Ecological Solutions and Evidence, 2020, 1, e12031.	2.0	20
11	Effect of phosphorus amendments on rice rhizospheric methanogens and methanotrophs in a phosphorus deficient soil. Geoderma, 2020, 368, 114312.	5.1	17
12	RNA Stable Isotope Probing (RNA-SIP). Methods in Molecular Biology, 2019, 2046, 31-44.	0.9	3
13	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. Nature Microbiology, 2019, 4, 1727-1736.	13.3	184
14	Reconditioning Degraded Mine Site Soils With Exogenous Soil Microbes: Plant Fitness and Soil Microbiome Outcomes. Frontiers in Microbiology, 2019, 10, 1617.	3.5	33
15	Humus-Rich Compost Increases Lettuce Growth, Nutrient Uptake, Mycorrhizal Colonisation, and Soil Fertility. Pedosphere, 2019, 29, 170-179.	4.0	38
16	The Bacterial Microbiome Associated With Arid Biocrusts and the Biogeochemical Influence of Biocrusts Upon the Underlying Soil. Frontiers in Microbiology, 2019, 10, 2143.	3.5	42
17	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. Canadian Journal of Soil Science, 2018, 98, 306-316.	1.2	19
18	Response of Wheat to a Multiple Species Microbial Inoculant Compared to Fertilizer Application. Frontiers in Plant Science, 2018, 9, 1601.	3.6	33

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19	Aerobic proteobacterial methylotrophs in Movile Cave: genomic and metagenomic analyses. Microbiome, 2018, 6, 1.	11.1	541
20	Microbial Functional Capacity Is Preserved Within Engineered Soil Formulations Used In Mine Site Restoration. Scientific Reports, 2017, 7, 564.	3.3	61
21	Draft Genome Sequence of the Methane-Oxidizing Bacterium " <i>Candidatus</i> Methylomonas sp. LWB―Isolated from Movile Cave. Genome Announcements, 2017, 5, .	0.8	4
22	Bacterial Physiological Adaptations to Contrasting Edaphic Conditions Identified Using Landscape Scale Metagenomics. MBio, 2017, 8, .	4.1	46
23	Abundance and diversity of carbon monoxide dehydrogenase genes from BMS clade bacteria in different vegetated soils. European Journal of Soil Biology, 2017, 81, 94-99.	3.2	10
24	Soil Carbon-Fixation Rates and Associated Bacterial Diversity and Abundance in Three Natural Ecosystems. Microbial Ecology, 2017, 73, 645-657.	2.8	80
25	Novel Primer Sets for Next Generation Sequencing-Based Analyses of Water Quality. PLoS ONE, 2017, 12, e0170008.	2.5	8
26	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
27	Microbial phylogenetic and functional responses within acidified wastewater communities exhibiting enhanced phosphate uptake. Bioresource Technology, 2016, 220, 55-61.	9.6	17
28	Mesophilic Mineral-Weathering Bacteria Inhabit the Critical-Zone of a Perennially Cold Basaltic Environment. Geomicrobiology Journal, 2016, 33, 52-62.	2.0	3
29	Single Cell Microbial Ecophysiology with Raman-FISH. Springer Protocols, 2015, , 65-76.	0.3	O
30	Advances in restoration ecology: rising to the challenges of the coming decades. Ecosphere, 2015, 6, 1-25.	2.2	361
31	Cropping systems modulate the rate and magnitude of soil microbial autotrophic CO2 fixation in soil. Frontiers in Microbiology, 2015, 6, 379.	3.5	47
32	Chemical fixation methods for Raman spectroscopy-based analysis of bacteria. Journal of Microbiological Methods, 2015, 109, 79-83.	1.6	27
33	Abundance and Diversity of CO2-Assimilating Bacteria and Algae Within Red Agricultural Soils Are Modulated by Changing Management Practice. Microbial Ecology, 2015, 70, 971-980.	2.8	25
34	Marine bacterial communities are resistant to elevated carbon dioxide levels. Environmental Microbiology Reports, 2014, 6, 574-582.	2.4	47
35	Weekly flow cytometric analysis of riverine phytoplankton to determine seasonal bloom dynamics. Environmental Sciences: Processes and Impacts, 2014, 16, 594.	3.5	42
36	Nano-Secondary lons Mass Spectrometry (nanoSIMS) Coupled with In Situ Hybridization for Ecological Research., 2014,, 295-303.		4

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37	Fish-Microautoradiography and Isotope Arrays for Monitoring the Ecophysiology of Microbes Within Their Natural Environment., 2014,, 305-316.		2
38	The characterisation of eukaryotic microbial communities onÂsandstone buildings in Belfast, UK, using TRFLP and 454 pyrosequencing. International Biodeterioration and Biodegradation, 2013, 82, 124-133.	3.9	51
39	Evidence for Phenotypic Plasticity among Multihost Campylobacter jejuni and C. coli Lineages, Obtained Using Ribosomal Multilocus Sequence Typing and Raman Spectroscopy. Applied and Environmental Microbiology, 2013, 79, 965-973.	3.1	24
40	Grassland management influences spatial patterns of soil microbial communities. Soil Biology and Biochemistry, 2013, 61, 61-68.	8.8	39
41	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
42	Plant soil interactions alter carbon cycling in an upland grassland soil. Frontiers in Microbiology, 2013, 4, 253.	3.5	39
43	Microbial 16S rRNA lon Tag and community metagenome sequencing using the lon Torrent (PGM) Platform. Journal of Microbiological Methods, 2012, 91, 80-88.	1.6	187
44	Non-destructive sampling of rock-dwelling microbial communities using sterile adhesive tape. Journal of Microbiological Methods, 2012, 91, 391-398.	1.6	12
45	The response of marine picoplankton to ocean acidification. Environmental Microbiology, 2012, 14, 2293-2307.	3.8	124
46	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. Nature Biotechnology, 2011, 29, 415-420.	17.5	608
47	The bacterial biogeography of British soils. Environmental Microbiology, 2011, 13, 1642-1654.	3.8	753
48	Vegetation Affects the Relative Abundances of Dominant Soil Bacterial Taxa and Soil Respiration Rates in an Upland Grassland Soil. Microbial Ecology, 2010, 59, 335-343.	2.8	107
49	Taxon-specific responses of soil bacteria to the addition of low level C inputs. Soil Biology and Biochemistry, 2010, 42, 1624-1631.	8.8	90
50	Field scale molecular analysis for the monitoring of bacterial community structures during on-site diesel bioremediation. Bioresource Technology, 2010, 101, 5235-5241.	9.6	11
51	Metaproteomic and metagenomic analyses of defined oceanic microbial populations using microwave cell fixation and flow cytometric sorting. FEMS Microbiology Ecology, 2010, 74, 10-18.	2.7	15
52	Hydrocarbon utilization within a diesel-degrading bacterial consortium. FEMS Microbiology Letters, 2010, 303, 116-122.	1.8	38
53	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
54	Protists have divergent effects on bacterial diversity along a productivity gradient. Biology Letters, 2010, 6, 639-642.	2.3	60

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55	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
56	Effects of sieving, drying and rewetting upon soil bacterial community structure and respiration rates. Journal of Microbiological Methods, 2010, 83, 69-73.	1.6	58
57	Comparison of Bacterioneuston and Bacterioplankton Dynamics during a Phytoplankton Bloom in a Fjord Mesocosm. Applied and Environmental Microbiology, 2009, 75, 7173-7181.	3.1	63
58	Dissolved organic carbon and bacterial populations in the gelatinous surface microlayer of a Norwegian fjord mesocosm. FEMS Microbiology Letters, 2009, 299, 248-254.	1.8	54
59	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. Applied and Environmental Microbiology, 2009, 75, 234-241.	3.1	128
60	Raman tweezers sorting of single microbial cells. Environmental Microbiology Reports, 2009, 1, 44-49.	2.4	115
61	Bioaugmentation Strategies for Remediating Mixed Chemical Effluents. Biotechnology Progress, 2008, 19, 1156-1161.	2.6	33
62	Characterizing the regulation of the <i>Pu</i> promoter in <i>Acinetobacter baylyi</i> ADP1. Environmental Microbiology, 2008, 10, 1668-1680.	3.8	27
63	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
64	The sensitivity of a forest soil microbial community to acute gamma-irradiation. Applied Soil Ecology, 2007, 37, 1-9.	4.3	43
65	Insights into the fate of a 13C labelled phenol pulse for stable isotope probing (SIP) experiments. Journal of Microbiological Methods, 2007, 69, 340-344.	1.6	27
66	RNA stable-isotope probing. Nature Protocols, 2007, 2, 838-844.	12.0	109
67	Salivary nitrate? an ecological factor in reducing oral acidity. Oral Microbiology and Immunology, 2007, 22, 67-71.	2.8	40
68	Raman-FISH: combining stable-isotope Raman spectroscopy and fluorescence in situ hybridization for the single cell analysis of identity and function. Environmental Microbiology, 2007, 9, 1878-1889.	3.8	305
69	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
70	Single-Cell Raman Spectral Profiles of Pseudomonas fluorescens SBW25 Reflects in vitro and in planta Metabolic History. Microbial Ecology, 2007, 53, 414-425.	2.8	41
71	Influence of Sustainability and Immigration in Assembling Bacterial Populations of Known Size and Function. Microbial Ecology, 2007, 53, 348-354.	2.8	12
72	Genomic Structure of the Luciferase Gene from the Bioluminescent Beetle, <i>Nyctophila </i> Caucasica Journal of Insect Science, 2006, 6, 1-8.	1.5	5

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7 3	The functions and components of the Sourhope soil microbiota. Applied Soil Ecology, 2006, 33, 114-126.	4.3	19
74	Quantitativein situassay of salicylic acid in tobacco leaves using a genetically modified biosensor strain of Acinetobactersp. ADP1. Plant Journal, 2006, 46, 1073-1083.	5.7	115
75	Stable Isotope Probing: A Critique of Its Role in Linking Phylogeny and Function. , 2006, , 205-216.		8
76	Unlocking the â€~microbial black box' using RNA-based stable isotope probing technologies. Current Opinion in Biotechnology, 2006, 17, 67-71.	6.6	93
77	Calibration and deployment of custom-designed bioreporters for protecting biological remediation consortia from toxic shock. Environmental Microbiology, 2005, 7, 260-269.	3.8	2
78	Functional and compositional comparison of two activated sludge communities remediating coking effluent. Environmental Microbiology, 2005, 7, 715-722.	3.8	73
79	Chromosomally located gene fusions constructed in Acinetobacter sp. ADP1 for the detection of salicylate. Environmental Microbiology, 2005, 7, 1339-1348.	3 . 8	99
80	Temporal dynamics and degradation activity of an bacterial inoculum for treating waste metal-working fluid. Environmental Microbiology, 2004, 6, 254-263.	3.8	67
81	N-acyl-l-homoserine lactones (AHLs) affect microbial community composition and function in activated sludge. Environmental Microbiology, 2004, 6, 424-433.	3.8	154
82	What can stable isotope probing do for bioremediation?. International Biodeterioration and Biodegradation, 2004, 54, 163-166.	3.9	38
83	Unravelling rhizosphere–microbial interactions: opportunities and limitations. Trends in Microbiology, 2004, 12, 386-393.	7.7	426
84	13CO2 pulse labelling of plants in tandem with stable isotope probing: methodological considerations for examining microbial function in the rhizosphere. Journal of Microbiological Methods, 2004, 58, 119-129.	1.6	70
85	Raman Microscopic Analysis of Single Microbial Cells. Analytical Chemistry, 2004, 76, 4452-4458.	6.5	371
86	Wastewater Toxicity Assessment by Whole Cell Biosensor. Handbook of Environmental Chemistry, 2004, , 165-225.	0.4	4
87	Whole cell immobilised biosensors for toxicity assessment of a wastewater treatment plant treating phenolics-containing waste. Analytica Chimica Acta, 2003, 487, 61-74.	5 . 4	80
88	Bacterial community structure and function in a metal-working fluid. Environmental Microbiology, 2003, 5, 453-461.	3.8	83
89	Plant community composition affects the biomass, activity and diversity of microorganisms in limestone grassland soil. European Journal of Soil Science, 2003, 54, 671-678.	3.9	88
90	Influence of depth and sampling time on bacterial community structure in an upland grassland soil. FEMS Microbiology Ecology, 2003, 43, 35-43.	2.7	170

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91	Active microbial RNA turnover in a grassland soil estimated using a 13CO2 spike. Soil Biology and Biochemistry, 2003, 35, 877-885.	8.8	113
92	Analysis of the microbial functional diversity within water-stressed soil communities by flow cytometric analysis and CTC+ cell sorting. Journal of Microbiological Methods, 2003, 54, 257-267.	1.6	45
93	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
94	Physiological and Community Responses of EstablishedGrassland Bacterial Populations to WaterStress. Applied and Environmental Microbiology, 2003, 69, 6961-6968.	3.1	167
95	RNA Stable Isotope Probing, a Novel Means of Linking Microbial Community Function to Phylogeny. Applied and Environmental Microbiology, 2002, 68, 5367-5373.	3.1	527
96	Technical considerations for RNA-based stable isotope probing: an approach to associating microbial diversity with microbial community function. Rapid Communications in Mass Spectrometry, 2002, 16, 2179-2183.	1.5	125
97	Ecological and physiological analyses of Pseudomonad species within a phenol remediation system. Journal of Microbiological Methods, 2001, 44, 79-88.	1.6	40
98	Density gradient separation of active and non-active cells from natural environments. Antonie Van Leeuwenhoek, 2000, 77, 173-177.	1.7	12
99	Bacterial Community Structure and Physiological State within an Industrial Phenol Bioremediation System. Applied and Environmental Microbiology, 2000, 66, 2400-2407.	3.1	178
100	Rapid Method for Coextraction of DNA and RNA from Natural Environments for Analysis of Ribosomal DNA- and rRNA-Based Microbial Community Composition. Applied and Environmental Microbiology, 2000, 66, 5488-5491.	3.1	1,422
101	SYTO16 labelling and flow cytometry of Mycobacterium avium. Letters in Applied Microbiology, 1997, 25, 437-441.	2.2	17
102	An improved method of cell cycle synchronisation for the heterotrophic dinoflagellate Crypthecodinium cohnii Biecheler analyzed by flow cytometry. Journal of Experimental Marine Biology and Ecology, 1996, 197, 91-99.	1.5	26
103	Monitoring Bioremediation. , 0, , 237-268.		8
104	Phospholipid Fatty Acid Stable Isotope Probing Techniques in Microbial Ecology., 0,, 37-71.		5
105	Stable Isotope Probing Techniques Using ¹⁵ N., 0,, 129-147.		1
106	DNA stable Isotope Probing and Gene Mining. , 0, , 259-276.		0
107	DNA Stable Isotope Probing. , 0, , 1-24.		4
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	RNA Stable Isotope Probing., 0,, 25-36.		3
111	Stable Isotope Probing Techniques Using H2 18O. , 0, , 115-128.		2
112	Stable Isotope Probing and Plants. , 0, , 149-163.		2
113	Stable Isotope Probing Techniques and Bioremediation. , 0, , 165-201.		1
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.		O
116	A Glance Toward the Future: Where Do We Go from Here?., 0,, 333-336.		0
117	Stable Isotope Probing and the Human Gut. , 0, , 233-257.		1
118	Stable Isotope Probing and Metagenomics. , 0, , 97-114.		0