

Donald A Cowan

List of Publications by Year in descending order

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Version: 2024-02-01

329
papers

16,199
citations

23879

60
h-index

29333

108
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346
all docs

346
docs citations

346
times ranked

17295
citing authors

#	ARTICLE	IF	CITATIONS
1	Differences in Precipitation Regime Shape Microbial Community Composition and Functional Potential in Namib Desert Soils. <i>Microbial Ecology</i> , 2022, 83, 689-701.	1.4	18
2	Novel lichen-dominated hypolithic communities in the Namib Desert. <i>Microbial Ecology</i> , 2022, 83, 1036-1048.	1.4	5
3	Out of Thin Air? <i>Astrobiology and Atmospheric Chemotrophy</i> . <i>Astrobiology</i> , 2022, , .	1.5	5
4	The ecological assembly of bacterial communities in Antarctic wetlands varies across levels of phylogenetic resolution. <i>Environmental Microbiology</i> , 2022, , .	1.8	1
5	Polar soils exhibit distinct patterns in microbial diversity and dominant phylotypes. <i>Soil Biology and Biochemistry</i> , 2022, 166, 108550.	4.2	19
6	Microbial Biogeochemical Cycling of Nitrogen in Arid Ecosystems. <i>Microbiology and Molecular Biology Reviews</i> , 2022, 86, e0010921.	2.9	22
7	The lung microbiome in HIV-positive patients with active pulmonary tuberculosis. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
8	The plant rhizosphere "root niche is an edaphic "mini-oasis" in hyperarid deserts with enhanced microbial competition. <i>ISME Communications</i> , 2022, 2, .	1.7	18
9	Pollution shapes the microbial communities in river water and sediments from the Olifants River catchment, South Africa. <i>Archives of Microbiology</i> , 2021, 203, 295-303.	1.0	3
10	Foliar fungi of the enigmatic desert plant <i>Welwitschia mirabilis</i> show little adaptation to their unique host plant. <i>South African Journal of Science</i> , 2021, 117, .	0.3	2
11	Gone with the Wind: Microbial Communities Associated with Dust from Emissive Farmlands. <i>Microbial Ecology</i> , 2021, 82, 859-869.	1.4	9
12	Sublithic photosynthesis in hot desert habitats. <i>Environmental Microbiology</i> , 2021, 23, 3867-3880.	1.8	10
13	Shotgun metagenomics reveals distinct functional diversity and metabolic capabilities between 12,000-year-old permafrost and active layers on Muot da Barba Peider (Swiss Alps). <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
14	Diversity structure of the microbial communities in the guts of four neotropical termite species. <i>PeerJ</i> , 2021, 9, e10959.	0.9	14
15	Genomic characterization of a polyvalent hydrocarbonoclastic bacterium <i>Pseudomonas</i> sp. strain BUN14. <i>Scientific Reports</i> , 2021, 11, 8124.	1.6	9
16	Microbial anhydrobiosis. <i>Environmental Microbiology</i> , 2021, 23, 6377-6390.	1.8	19
17	The Rhizobial Microbiome from the Tropical Savannah Zones in Northern Côte d'Ivoire. <i>Microorganisms</i> , 2021, 9, 1842.	1.6	7
18	Microbial characterisation and Cold-Adapted Predicted Protein (CAPP) database construction from the active layer of Greenland's permafrost. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	2

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19	The soil microbiomics of intact, degraded and partially-restored semi-arid succulent thicket (Albany) Tj ETQq1 1 0.784314 rgBT /Overl	0.9	2
20	Multiple energy sources and metabolic strategies sustain microbial diversity in Antarctic desert soils. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	68
21	Editorial: Thematic issue on polar and alpine microbiology. FEMS Microbiology Ecology, 2020, 96, .	1.3	1
22	Microbial Nitrogen Cycling in Antarctic Soils. Microorganisms, 2020, 8, 1442.	1.6	25
23	Blind spots in global soil biodiversity and ecosystem function research. Nature Communications, 2020, 11, 3870.	5.8	192
24	Islands in the sand: are all hypolithic microbial communities the same?. FEMS Microbiology Ecology, 2020, 97, .	1.3	4
25	Genetic diversity of soil invertebrates corroborates timing estimates for past collapses of the West Antarctic Ice Sheet. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22293-22302.	3.3	29
26	Hydrogen-Oxidizing Bacteria Are Abundant in Desert Soils and Strongly Stimulated by Hydration. MSystems, 2020, 5, .	1.7	38
27	Multi-proxy analyses of a mid-15th century Middle Iron Age Bantu-speaker palaeo-faecal specimen elucidates the configuration of the "ancestral"™ sub-Saharan African intestinal microbiome. Microbiome, 2020, 8, 62.	4.9	14
28	Phages Actively Challenge Niche Communities in Antarctic Soils. MSystems, 2020, 5, .	1.7	17
29	Time-course Transcriptome of Parageobacillus thermoglucosidasius DSM 6285 Grown in the Presence of Carbon Monoxide and Air. International Journal of Molecular Sciences, 2020, 21, 3870.	1.8	6
30	Distinct assembly mechanisms underlie similar biogeographical patterns of rare and abundant bacteria in Tibetan Plateau grassland soils. Environmental Microbiology, 2020, 22, 2261-2272.	1.8	77
31	A clinically important, plasmid-borne antibiotic resistance gene (β -lactamase TEM-116) present in desert soils. Science of the Total Environment, 2020, 719, 137497.	3.9	14
32	Increased temperatures alter viable microbial biomass, ammonia oxidizing bacteria and extracellular enzymatic activities in Antarctic soils. FEMS Microbiology Ecology, 2020, 96, .	1.3	13
33	Energetic Basis of Microbial Growth and Persistence in Desert Ecosystems. MSystems, 2020, 5, .	1.7	66
34	The Functional Potential of the Rhizospheric Microbiome of an Invasive Tree Species, Acacia dealbata. Microbial Ecology, 2019, 77, 191-200.	1.4	46
35	Characterization and homology modelling of a novel multi-modular and multi-functional Paenibacillus mucilaginosus glycoside hydrolase. Extremophiles, 2019, 23, 681-686.	0.9	1
36	The genome of Alcaligenes aquatilis strain BU33N: Insights into hydrocarbon degradation capacity. PLoS ONE, 2019, 14, e0221574.	1.1	19

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37	Nutrient Acquisition, Rather Than Stress Response Over Diel Cycles, Drives Microbial Transcription in a Hyper-Arid Namib Desert Soil. <i>Frontiers in Microbiology</i> , 2019, 10, 1054.	1.5	37
38	Ancient landscapes of the Namib Desert harbor high levels of genetic variability and deeply divergent lineages for Collembola. <i>Ecology and Evolution</i> , 2019, 9, 4969-4979.	0.8	10
39	The Healthy Human Blood Microbiome: Fact or Fiction?. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 148.	1.8	221
40	Differences in Bacterial Diversity, Composition and Function due to Long-Term Agriculture in Soils in the Eastern Free State of South Africa. <i>Diversity</i> , 2019, 11, 61.	0.7	50
41	Airborne microbial transport limitation to isolated Antarctic soil habitats. <i>Nature Microbiology</i> , 2019, 4, 925-932.	5.9	114
42	Genomics of Alkaliphiles. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2019, 172, 135-155.	0.6	2
43	Biotic interactions are an unexpected yet critical control on the complexity of an abiotically driven polar ecosystem. <i>Communications Biology</i> , 2019, 2, 62.	2.0	42
44	5. Metagenomics of extreme environments: methods and applications. , 2019, , 93-126.		0
45	Reorganising the order Bacillales through phylogenomics. <i>Systematic and Applied Microbiology</i> , 2019, 42, 178-189.	1.2	11
46	Role of Cyanobacteria in the Ecology of Polar Environments. <i>Springer Polar Sciences</i> , 2019, , 3-23.	0.0	11
47	Trophic Selective Pressures Organize the Composition of Endolithic Microbial Communities From Global Deserts. <i>Frontiers in Microbiology</i> , 2019, 10, 2952.	1.5	26
48	Effects of different operating parameters on hydrogen production by <i>Parageobacillus thermoglucosidasius</i> DSM 6285. <i>AMB Express</i> , 2019, 9, 207.	1.4	12
49	From Antarctic DNA to stress tolerant crop plants “exploiting the why protein domain. <i>Access Microbiology</i> , 2019, 1, .	0.2	0
50	Structural Characterization and Directed Evolution of a Novel Acetyl Xylan Esterase Reveals Thermostability Determinants of the Carbohydrate Esterase 7 Family. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	18
51	Key microbial taxa in the rhizosphere of sorghum and sunflower grown in crop rotation. <i>Science of the Total Environment</i> , 2018, 624, 530-539.	3.9	69
52	Exploring Viral Diversity in a Unique South African Soil Habitat. <i>Scientific Reports</i> , 2018, 8, 111.	1.6	23
53	Namib Desert primary productivity is driven by cryptic microbial community N-fixation. <i>Scientific Reports</i> , 2018, 8, 6921.	1.6	33
54	Namib Desert Soil Microbial Community Diversity, Assembly, and Function Along a Natural Xeric Gradient. <i>Microbial Ecology</i> , 2018, 75, 193-203.	1.4	60

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73	Evidence of microbial rhodopsins in <scp>A</scp>antarctic <scp>D</scp>ry <scp>V</scp>alley edaphic systems. <i>Environmental Microbiology</i> , 2017, 19, 3755-3767.	1.8	17
74	4. Microbiology of Antarctic Edaphic and Lithic Habitats. , 2017, , 47-72.		2
75	Phylogenomic, Pan-genomic, Pathogenomic and Evolutionary Genomic Insights into the Agronomically Relevant Enterobacteria <i>Pantoea ananatis</i> and <i>Pantoea stewartii</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1755.	1.5	20
76	Advanced Photogrammetry to Assess Lichen Colonization in the Hyper-Arid Namib Desert. <i>Frontiers in Microbiology</i> , 2017, 8, 2083.	1.5	9
77	Cyanobacteria and Alphaproteobacteria May Facilitate Cooperative Interactions in Niche Communities. <i>Frontiers in Microbiology</i> , 2017, 8, 2099.	1.5	36
78	Environmental drivers of viral community composition in Antarctic soils identified by viromics. <i>Microbiome</i> , 2017, 5, 83.	4.9	94
79	Energy from thin air. <i>Nature</i> , 2017, 552, 336-337.	13.7	4
80	Metagenomic Analysis of Low-Temperature Environments. , 2017, , 389-421.		4
81	Metaviromics of Namib Desert Salt Pans: A Novel Lineage of Haloarchaeal Salterproviruses and a Rich Source of ssDNA Viruses. <i>Viruses</i> , 2016, 8, 14.	1.5	24
82	The <i>Geobacillus</i> Pan-Genome: Implications for the Evolution of the Genus. <i>Frontiers in Microbiology</i> , 2016, 7, 723.	1.5	20
83	Specific Microbial Communities Associate with the Rhizosphere of <i>Welwitschia mirabilis</i> , a Living Fossil. <i>PLoS ONE</i> , 2016, 11, e0153353.	1.1	41
84	Metagenomic analysis provides insights into functional capacity in a hyperarid desert soil niche community. <i>Environmental Microbiology</i> , 2016, 18, 1875-1888.	1.8	96
85	Comparative genomic analysis of the flagellin glycosylation island of the Gram-positive thermophile <i>Geobacillus</i> . <i>BMC Genomics</i> , 2016, 17, 913.	1.2	10
86	Unique Microbial Phylotypes in Namib Desert Dune and Gravel Plain Fairy Circle Soils. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4592-4601.	1.4	25
87	Plants of the fynbos biome harbour host species-specific bacterial communities. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw122.	0.7	16
88	Comparative Metagenomic Analysis Reveals Mechanisms for Stress Response in Hypoliths from Extreme Hyperarid Deserts. <i>Genome Biology and Evolution</i> , 2016, 8, 2737-2747.	1.1	61
89	Phylogenomic re-assessment of the thermophilic genus <i>Geobacillus</i> . <i>Systematic and Applied Microbiology</i> , 2016, 39, 527-533.	1.2	116
90	Phylogeny, classification and metagenomic bioprospecting of microbial acetyl xylan esterases. <i>Enzyme and Microbial Technology</i> , 2016, 93-94, 79-91.	1.6	54

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91	Genetic diversity among populations of Antarctic springtails (Collembola) within the Mackay Glacier ecotone. <i>Genome</i> , 2016, 59, 762-770.	0.9	13
92	Temporal dynamics of hot desert microbial communities reveal structural and functional responses to water input. <i>Scientific Reports</i> , 2016, 6, 34434.	1.6	74
93	Draft genome sequence of <i>Thermoactinomyces</i> sp. strain AS95 isolated from a Sebkhah in Thamelah, Algeria. <i>Standards in Genomic Sciences</i> , 2016, 11, 68.	1.5	4
94	Flashy flagella: flagellin modification is relatively common and highly versatile among the Enterobacteriaceae. <i>BMC Genomics</i> , 2016, 17, 377.	1.2	33
95	Habitat heterogeneity and connectivity shape microbial communities in South American peatlands. <i>Scientific Reports</i> , 2016, 6, 25712.	1.6	31
96	Diversity of <i>Frankia</i> in root nodules of six <i>Morella</i> sp. from the Cape flora of South Africa. <i>Plant and Soil</i> , 2016, 406, 375-388.	1.8	8
97	The genome of the Antarctic polyextremophile <i>Nesterenkonia</i> sp. AN1 reveals adaptive strategies for survival under multiple stress conditions. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw032.	1.3	32
98	Characterization of bacterial communities in lithobionts and soil niches from Victoria Valley, Antarctica. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw051.	1.3	69
99	Diversity and Ecology of Viruses in Hyperarid Desert Soils. <i>Applied and Environmental Microbiology</i> , 2016, 82, 770-777.	1.4	89
100	The Gut Microbiomes of Two <i>Pachysoma</i> MacLeay Desert Dung Beetle Species (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 T	1.1	53
101	Understanding diversity patterns in bacterioplankton communities from a subantarctic peatland. <i>Environmental Microbiology Reports</i> , 2015, 7, 547-553.	1.0	7
102	Draft Genome Sequence of Thermophilic <i>Geobacillus</i> sp. Strain Sah69, Isolated from Saharan Soil, Southeast Algeria. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
103	The influence of surface soil physicochemistry on the edaphic bacterial communities in contrasting terrain types of the Central Namib Desert. <i>Geobiology</i> , 2015, 13, 494-505.	1.1	23
104	Genomic analysis of six new <i>Geobacillus</i> strains reveals highly conserved carbohydrate degradation architectures and strategies. <i>Frontiers in Microbiology</i> , 2015, 6, 430.	1.5	24
105	Integrative conjugative elements of the ICEPan family play a potential role in <i>Pantoea ananatis</i> ecological diversification and antibiosis. <i>Frontiers in Microbiology</i> , 2015, 6, 576.	1.5	13
106	Namib Desert dune/interdune transects exhibit habitat-specific edaphic bacterial communities. <i>Frontiers in Microbiology</i> , 2015, 6, 845.	1.5	46
107	Metagenomics of extreme environments. <i>Current Opinion in Microbiology</i> , 2015, 25, 97-102.	2.3	117
108	Draft Genome Sequence of <i>Sphingomonas</i> sp. Strain Ant20, Isolated from Oil-Contaminated Soil on Ross Island, Antarctica. <i>Genome Announcements</i> , 2015, 3, .	0.8	6

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109	Genetic signatures indicate widespread antibiotic resistance and phage infection in microbial communities of the McMurdo Dry Valleys, East Antarctica. <i>Polar Biology</i> , 2015, 38, 919-925.	0.5	28
110	Microbial ecology of hot desert edaphic systems. <i>FEMS Microbiology Reviews</i> , 2015, 39, 203-221.	3.9	299
111	Metagenomic analysis of the viral community in Antarctic desert hypoliths. <i>Environmental Microbiology</i> , 2015, 17, 480-495.	1.8	83
112	Cyanobacteria drive community composition and functionality in rock-soil interface communities. <i>Molecular Ecology</i> , 2015, 24, 812-821.	2.0	63
113	Normalization of environmental metagenomic DNA enhances the discovery of under-represented microbial community members. <i>Letters in Applied Microbiology</i> , 2015, 60, 359-366.	1.0	7
114	Evidence of novel plant-specific ammonia oxidizing bacterial clades in acidic South African fynbos soils. <i>Journal of Basic Microbiology</i> , 2015, 55, 1040-1047.	1.8	8
115	Cold stress affects antioxidative response and accumulation of medicinally important withanolides in <i>Withania somnifera</i> (L.) Dunal. <i>Industrial Crops and Products</i> , 2015, 74, 1008-1016.	2.5	45
116	An unusual feruloyl esterase belonging to family VIII esterases and displaying a broad substrate range. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2015, 118, 79-88.	1.8	15
117	Water regime history drives responses of soil Namib Desert microbial communities to wetting events. <i>Scientific Reports</i> , 2015, 5, 12263.	1.6	52
118	A novel bacterial Water Hypersensitivity-like protein shows <i>in vivo</i> protection against cold and freeze damage. <i>FEMS Microbiology Letters</i> , 2015, 362, fmv110.	0.7	17
119	Protection of Antarctic microbial communities – out of sight, out of mind. <i>Frontiers in Microbiology</i> , 2015, 6, 151.	1.5	47
120	A roadmap for Antarctic and Southern Ocean science for the next two decades and beyond. <i>Antarctic Science</i> , 2015, 27, 3-18.	0.5	158
121	Ecology and biogeochemistry of cyanobacteria in soils, permafrost, aquatic and cryptic polar habitats. <i>Biodiversity and Conservation</i> , 2015, 24, 819-840.	1.2	66
122	Draft genomic DNA sequence of the multi-resistant <i>Sphingomonas</i> sp. strain Anth11 isolated from an Antarctic hypolith. <i>FEMS Microbiology Letters</i> , 2015, 362, fmv037.	0.7	9
123	Identification and characterization of a novel <i>Geobacillus thermoglucosidasius</i> bacteriophage, GVE3. <i>Archives of Virology</i> , 2015, 160, 2269-2282.	0.9	14
124	Recent Progress in Understanding the Mode of Action of Acetylxylan Esterases. <i>Journal of Applied Glycoscience</i> (1999), 2014, 61, 35-44.	0.3	21
125	Structure and functional characterization of pyruvate decarboxylase from <i>Gluconacetobacter diazotrophicus</i> . <i>BMC Structural Biology</i> , 2014, 14, 21.	2.3	18
126	Comparative analysis of the <i>Geobacillus</i> hemicellulose utilization locus reveals a highly variable target for improved hemicellulolysis. <i>BMC Genomics</i> , 2014, 15, 836.	1.2	36

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127	Draft Genome Sequences of the Onion Center Rot Pathogen <i>Pantoea ananatis</i> PA4 and Maize Brown Stalk Rot Pathogen <i>P. ananatis</i> BD442. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
128	Contrasting assembly processes in a bacterial metacommunity along a desiccation gradient. <i>Frontiers in Microbiology</i> , 2014, 5, 668.	1.5	34
129	Draft Genome Sequence of the Antarctic Polyextremophile <i>Nesterenkonia</i> sp. Strain AN1. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
130	Draft Genome Sequences of <i>Geobacillus</i> sp. Strains CAMR5420 and CAMR12739. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
131	Draft Genome Sequence of <i>Microbacterium</i> sp. Strain CH12i, Isolated from Shallow Groundwater in Cape Hallett, Antarctica. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
132	Selection of <i>Clostridium</i> spp. in biological sand filters neutralizing synthetic acid mine drainage. <i>FEMS Microbiology Ecology</i> , 2014, 87, 678-690.	1.3	8
133	Niche-dependent genetic diversity in Antarctic metaviromes. <i>Bacteriophage</i> , 2014, 4, e980125.	1.9	12
134	Draft Genome Sequence of the Aromatic Hydrocarbon-Degrading Bacterium <i>Sphingobium</i> sp. Strain Ant17, Isolated from Antarctic Soil. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
135	Engineering pyruvate decarboxylase-mediated ethanol production in the thermophilic host <i>Geobacillus thermoglucosidasius</i> . <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 1247-1259.	1.7	43
136	<i>Antarctic Terrestrial Microbiology</i> . , 2014, , .		19
137	Some like it cold: understanding the survival strategies of psychrophiles. <i>EMBO Reports</i> , 2014, 15, 508-517.	2.0	501
138	Enhanced production of withaferin-A in shoot cultures of <i>Withania somnifera</i> (L) Dunal. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2014, 23, 430-434.	0.9	13
139	Draft Genome Sequence of <i>Williamsia</i> sp. Strain D3, Isolated From the Darwin Mountains, Antarctica. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
140	A sequential co-extraction method for DNA, RNA and protein recovery from soil for future system-based approaches. <i>Journal of Microbiological Methods</i> , 2014, 103, 118-123.	0.7	22
141	Recombinant hyperthermophilic enzyme expression in plants: a novel approach for lignocellulose digestion. <i>Trends in Biotechnology</i> , 2014, 32, 281-289.	4.9	21
142	Minor differences in sand physicochemistry lead to major differences in bacterial community structure and function after exposure to synthetic acid mine drainage. <i>Biotechnology and Bioprocess Engineering</i> , 2014, 19, 211-220.	1.4	8
143	High-Level Diversity of Tailed Phages, Eukaryote-Associated Viruses, and Virophage-Like Elements in the Metaviromes of Antarctic Soils. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6888-6897.	1.4	121
144	The spatial structures of hypolithic communities in the Dry Valleys of East Antarctica. <i>Polar Biology</i> , 2014, 37, 1823-1833.	0.5	41

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145	Using Signature Genes as Tools To Assess Environmental Viral Ecology and Diversity. Applied and Environmental Microbiology, 2014, 80, 4470-4480.	1.4	141
146	Microbial ecology and biogeochemistry of continental Antarctic soils. Frontiers in Microbiology, 2014, 5, 154.	1.5	119
147	Lithobionts: Cryptic and Refuge Niches. , 2014, , 163-179.		8
148	First Report of a Potyvirus Infecting <i>Albuca rautanenii</i> in the Namib Desert. Plant Disease, 2014, 98, 1749-1749.	0.7	3
149	Niche-Partitioning of Edaphic Microbial Communities in the Namib Desert Gravel Plain Fairy Circles. PLoS ONE, 2014, 9, e109539.	1.1	19
150	Selection of Diazotrophic Bacterial Communities in Biological Sand Filter Mesocosms Used for the Treatment of Phenolic-Laden Wastewater. Microbial Ecology, 2013, 66, 563-570.	1.4	7
151	Assessment of temporal and spatial evolution of bacterial communities in a biological sand filter mesocosm treating winery wastewater. Journal of Applied Microbiology, 2013, 115, 91-101.	1.4	24
152	Dissimilatory sulphate reduction in hypersaline coastal pans: an integrated microbiological and geochemical study. Geobiology, 2013, 11, 224-233.	1.1	16
153	Balancing redox cofactor generation and ATP synthesis: Key microaerobic responses in thermophilic fermentations. Biotechnology and Bioengineering, 2013, 110, 1057-1065.	1.7	13
154	Evidence for successional development in Antarctic hypolithic bacterial communities. ISME Journal, 2013, 7, 2080-2090.	4.4	93
155	Evidence of variability in the structure and recruitment of rhizospheric and endophytic bacterial communities associated with arable sweet sorghum (<i>Sorghum bicolor</i> (L) Moench). Plant and Soil, 2013, 372, 265-278.	1.8	26
156	Hypolithic and soil microbial community assembly along an aridity gradient in the Namib Desert. Extremophiles, 2013, 17, 329-337.	0.9	104
157	Biodiversity: So much more than legs and leaves. South African Journal of Science, 2013, 109, 9.	0.3	11
158	South African research in the Southern Ocean: New opportunities but serious challenges. South African Journal of Science, 2013, 109, 4.	0.3	3
159	Evidence of species recruitment and development of hot desert hypolithic communities. Environmental Microbiology Reports, 2013, 5, 219-224.	1.0	88
160	The Mechanism of the Amidases. Journal of Biological Chemistry, 2013, 288, 28514-28523.	1.6	28
161	Meeting Report: 1st International Functional Metagenomics Workshop May 7-8, 2012, St. Jacobs, Ontario, Canada.. Standards in Genomic Sciences, 2013, 8, 106-111.	1.5	2
162	Physical ecology of hypolithic communities in the central Namib Desert: The role of fog, rain, rock habitat, and light. Journal of Geophysical Research G: Biogeosciences, 2013, 118, 1451-1460.	1.3	54

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163	Micro-Eukaryotic Diversity in Hypolithons from Miers Valley, Antarctica. <i>Biology</i> , 2013, 2, 331-340.	1.3	9
164	Subtractive Hybridization Magnetic Bead Capture: Molecular Technique for Recovery of Full-Length ORFs from Metagenomes. , 2013, , 1-7.		0
165	Comparative investigations on thermostable pyrimidine nucleoside phosphorylases from <i>Geobacillus thermoglucosidasius</i> and <i>Thermus thermophilus</i> . <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2012, 84, 27-34.	1.8	38
166	Challenges to the Future Conservation of the Antarctic. <i>Science</i> , 2012, 337, 158-159.	6.0	146
167	Microbial community structure stability, a key parameter in monitoring the development of constructed wetland mesocosms during start-up. <i>Research in Microbiology</i> , 2012, 163, 28-35.	1.0	41
168	Treatment of high ethanol concentration wastewater by biological sand filters: Enhanced COD removal and bacterial community dynamics. <i>Journal of Environmental Management</i> , 2012, 109, 54-60.	3.8	24
169	Phenolic removal processes in biological sand filters, sand columns and microcosms. <i>Bioresource Technology</i> , 2012, 119, 262-269.	4.8	27
170	Antarctic psychrophiles: models for understanding the molecular basis of survival at low temperature and responses to climate change. <i>Biodiversity</i> , 2012, 13, 249-256.	0.5	27
171	Rapid microbial response to the presence of an ancient relic in the Antarctic Dry Valleys. <i>Nature Communications</i> , 2012, 3, 660.	5.8	69
172	Understanding and protecting the world's biodiversity: The role and legacy of the SCAR programme "Evolution and Biodiversity in the Antarctic". <i>Marine Genomics</i> , 2012, 8, 3-8.	0.4	26
173	Genome sequence of temperate bacteriophage Psymv2 from Antarctic Dry Valley soil isolate <i>Psychrobacter</i> sp. MV2. <i>Extremophiles</i> , 2012, 16, 715-726.	0.9	30
174	Understanding physiological responses to pre-treatment inhibitors in ethanologenic fermentations. <i>Biotechnology Journal</i> , 2012, 7, 1169-1181.	1.8	44
175	Bacterial and archaeal diversity in two hot spring microbial mats from the geothermal region of Tengchong, China. <i>Extremophiles</i> , 2012, 16, 607-618.	0.9	49
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