Mark V Brown

List of Publications by Year
in descending order

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61
papers

6,606
citations

101543
36
h-index

118850
62
g-index

64
all docs

64
docs citations

64
times ranked

8737
citing authors

#	ARTICLE	IF	CITATIONS
1	Biogeography of Southern Ocean prokaryotes: a comparison of the Indian and Pacific sectors. Environmental Microbiology, 2022, 24, 2449-2466.	3.8	6
2	Diatom Biogeography, Temporal Dynamics, and Links to Bacterioplankton across Seven Oceanographic Time-Series Sites Spanning the Australian Continent. Microorganisms, 2022, 10, 338.	3.6	5
3	Biogeographical and seasonal dynamics of the marine Roseobacter community and ecological links to DMSP-producing phytoplankton. ISME Communications, 2022, 2, .	4.2	6
4	Temperate southern Australian coastal waters are characterised by surprisingly high rates of nitrogen fixation and diversity of diazotrophs. PeerJ, 2021, 9, e10809.	2.0	12
5	Metabolic pathways inferred from a bacterial marker gene illuminate ecological changes across South Pacific frontal boundaries. Nature Communications, 2021, 12, 2213.	12.8	25
6	Highly heterogeneous temporal dynamics in the abundance and diversity of the emerging pathogens Arcobacter at an urban beach. Water Research, 2020, 171, 115405.	11.3	11
7	Microbial tropicalization driven by a strengthening western ocean boundary current. Global Change Biology, 2020, 26, 5613-5629.	9.5	16
8	Investigating the Diversity of Marine Bacteriophage in Contrasting Water Masses Associated with the East Australian Current (EAC) System. Viruses, 2020, 12, 317.	3.3	3
9	Harnessing long-read amplicon sequencing to uncover NRPS and Type I PKS gene sequence diversity in polar desert soils. FEMS Microbiology Ecology, 2019, 95, .	2.7	25
10	A phylogenomic and ecological analysis of the globally abundant Marine Group II archaea (<i>Ca</i>.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	9.8	158
11	Wave 2 strains of atypical Vibrio cholerae El Tor caused the 2009â€"2011 cholera outbreak in Papua New Guinea. Microbial Genomics, 2019, 5, .	2.0	4
12	Alpha-diversity is strongly influenced by the composition of other samples when using multiplexed sequencing approaches. Soil Biology and Biochemistry, 2018, 127, 79-81.	8.8	4
13	Oceanographic boundaries constrain microbial diversity gradients in the South Pacific Ocean. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8266-E8275.	7.1	96
14	Unicellular Cyanobacteria Are Important Components of Phytoplankton Communities in Australiaâ€™s Northern Oceanic Ecoregions. Frontiers in Microbiology, 2018, 9, 3356.	3.5	12
15	Systematic, continental scale temporal monitoring of marine pelagic microbiota by the Australian Marine Microbial Biodiversity Initiative. Scientific Data, 2018, 5, 180130.	5.3	41
16	Circular linkages between soil biodiversity, fertility and plant productivity are limited to topsoil at the continental scale. New Phytologist, 2017, 215, 1186-1196.	7.3	103
17	Multiple stressors in sediments impact adjacent hard substrate habitats and across biological domains. Science of the Total Environment, 2017, 592, 295-305.	8.0	20
18	Diversity and Activity of Diazotrophs in Great Barrier Reef Surface Waters. Frontiers in Microbiology, 2017, 8, 967.	3.5	23

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19	Editorial: Anthropogenic Impacts on the Microbial Ecology and Function of Aquatic Environments. Frontiers in Microbiology, 2016, 7, 1044.	3.5	39
20	Geological connectivity drives microbial community structure and connectivity in polar, terrestrial ecosystems. Environmental Microbiology, 2016, 18, 1834-1849.	3.8	51
21	Introducing BASE: the Biomes of Australian Soil Environments soil microbial diversity database. GigaScience, 2016, 5, 21.	6.4	204
22	Spatial and temporal variability of aerobic anoxygenic photoheterotrophic bacteria along the east coast of Australia. Environmental Microbiology, 2016, 18, 4485-4500.	3.8	16
23	Elevated nutrients change bacterial community composition and connectivity: high throughput sequencing of young marine biofilms. Biofouling, 2016, 32, 57-69.	2.2	87
24	High levels of heterogeneity in diazotroph diversity and activity within a putative hotspot for marine nitrogen fixation. ISME Journal, 2016, 10, 1499-1513.	9.8	55
25	Microbial diversity at Mitchell Peninsula, Eastern Antarctica: a potential biodiversity â€œhotspotâ€. Polar Biology, 2016, 39, 237-249.	1.2	101
26	Nutrient uplift in a cyclonic eddy increases diversity, primary productivity and iron demand of microbial communities relative to a western boundary current. PeerJ, 2016, 4, e1973.	2.0	35
27	Soil-foraging animals alter the composition and co-occurrence of microbial communities in a desert shrubland. ISME Journal, 2015, 9, 2671-2681.	9.8	69
28	The marine mammal microbiome: current knowledge and future directions. Microbiology Australia, 2015, 36, 8.	0.4	71
29	The Common Oceanographer: Crowdsourcing the Collection of Oceanographic Data. PLoS Biology, 2014, 12, e1001947.	5.6	41
30	<i>Cob</i> gene pyrosequencing enables characterization of benthic dinoflagellate diversity and biogeography. Environmental Microbiology, 2014, 16, 467-485.	3.8	29
31	Faster, Higher and Stronger? The Pros and Cons of Molecular Faunal Data for Assessing Ecosystem Condition. Advances in Ecological Research, 2014, 51, 1-40.	2.7	30
32	Community fingerprinting in a sequencing world. FEMS Microbiology Ecology, 2014, 89, 316-330.	2.7	140
33	Soil fertility is associated with fungal and bacterial richness, whereas pH is associated with community composition in polar soil microbial communities. Soil Biology and Biochemistry, 2014, 78, 10-20.	8.8	243
34	Land-use and management practices affect soil ammonia oxidiser community structure, activity and connectedness. Soil Biology and Biochemistry, 2014, 78, 138-148.	8.8	24
35	A trait based perspective on the biogeography of common and abundant marine bacterioplankton clades. Marine Genomics, 2014, 15, 17-28.	1.1	69
36	Metagenomic insights into strategies of carbon conservation and unusual sulfur biogeochemistry in a hypersaline Antarctic lake. ISME Journal, 2013, 7, 1944-1961.	9.8	75

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37	Microbial diversity and diazotrophy associated with the freshwater non-heterocyst forming cyanobacterium Lyngbya robusta. Journal of Applied Phycology, 2013, 25, 1039-1045.	2.8	19
38	High level of intergenera gene exchange shapes the evolution of haloarchaea in an isolated Antarctic lake. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16939-16944.	7.1	105
39	Key microbial drivers in Antarctic aquatic environments. FEMS Microbiology Reviews, 2013, 37, 303-335.	8.6	144
40	Psychrophiles. Annual Review of Earth and Planetary Sciences, 2013, 41, 87-115.	11.0	121
41	Deep sequencing of non-ribosomal peptide synthetases and polyketide synthases from the microbiomes of Australian marine sponges. ISME Journal, 2013, 7, 1842-1851.	9.8	53
42	Biogeographic partitioning of <scp>S</scp>outhern <scp>O</scp>cean microorganisms revealed by metagenomics. Environmental Microbiology, 2013, 15, 1318-1333.	3.8	82
43	Core sediment bacteria drive community response to anthropogenic contamination over multiple environmental gradients. Environmental Microbiology, 2013, 15, 2517-2531.	3.8	206
44	Diet and phylogeny shape the gut microbiota of <scp>A</scp>ntarctic seals: a comparison of wild and captive animals. Environmental Microbiology, 2013, 15, 1132-1145.	3.8	199
45	The Gut Bacterial Community of Mammals from Marine and Terrestrial Habitats. PLoS ONE, 2013, 8, e83655.	2.5	88
46	Global biogeography of SAR11 marine bacteria. Molecular Systems Biology, 2012, 8, 595.	7.2	215
47	Temporal stability and species specificity in bacteria associated with the bottlenose dolphins respiratory system. Environmental Microbiology Reports, 2012, 4, 89-96.	2.4	45
48	Contrasting microbial assemblages in adjacent water masses associated with the <scp>E</scp>ast <scp>A</scp>ustralian <scp>C</scp>urrent. Environmental Microbiology Reports, 2012, 4, 548-555.	2.4	33
49	Bacterial communities are sensitive indicators of contaminant stress. Marine Pollution Bulletin, 2012, 64, 1029-1038.	5.0	174
50	An integrative study of a meromictic lake ecosystem in Antarctica. ISME Journal, 2011, 5, 879-895.	9.8	204
51	Virophage control of antarctic algal hostâ€“virus dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6163-6168.	7.1	252
52	The genomic basis of trophic strategy in marine bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15527-15533.	7.1	685
53	Microbial community structure in the North Pacific ocean. ISME Journal, 2009, 3, 1374-1386.	9.8	224
54	<i>Sympodiomycopsis lanaiensis</i>sp. nov., a basidiomycetous yeast (Ustilaginomycotina:<i>Microstromatales</i>) from marine driftwood in HawaiÃ¢Â€Â˜i. FEMS Yeast Research, 2008, 8, 1357-1363.	2.3	12

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55	A latitudinal diversity gradient in planktonic marine bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7774-7778.	7.1	599
56	Culture clash: challenging the dogma of microbial diversity. ISME Journal, 2007, 1, 97-99.	9.8	88
57	Annually reoccurring bacterial communities are predictable from ocean conditions. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13104-13109.	7.1	578
58	Coupling 16S-ITS rDNA clone libraries and automated ribosomal intergenic spacer analysis to show marine microbial diversity: development and application to a time series. Environmental Microbiology, 2005, 7, 1466-1479.	3.8	230
59	The Growing Contributions of Molecular Biology and Immunology to Protistan Ecology: Molecular Signatures as Ecological Tools1. Journal of Eukaryotic Microbiology, 2004, 51, 38-48.	1.7	68
60	A molecular phylogenetic survey of sea-ice microbial communities (SIMCO). FEMS Microbiology Ecology, 2001, 35, 267-275.	2.7	200
61	Biodiversity and ecophysiology of bacteria associated with Antarctic sea ice. Antarctic Science, 1997, 9, 134-142.	0.9	30