

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	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
2	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
3	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
4	Virophage control of antarctic algal host-virus dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6163-6168.	7.1	252
5	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
6	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
7	Microbial community structure in the North Pacific ocean. ISME Journal, 2009, 3, 1374-1386.	9.8	224
8	Global biogeography of SAR11 marine bacteria. Molecular Systems Biology, 2012, 8, 595.	7.2	215
9	Core sediment bacteria drive community response to anthropogenic contamination over multiple environmental gradients. Environmental Microbiology, 2013, 15, 2517-2531.	3.8	206
10	An integrative study of a meromictic lake ecosystem in Antarctica. ISME Journal, 2011, 5, 879-895.	9.8	204
11	Introducing BASE: the Biomes of Australian Soil Environments soil microbial diversity database. GigaScience, 2016, 5, 21.	6.4	204
12	A molecular phylogenetic survey of sea-ice microbial communities (SIMCO). FEMS Microbiology Ecology, 2001, 35, 267-275.	2.7	200
13	Diet and phylogeny shape the gut microbiota of antarctic seals: a comparison of wild and captive animals. Environmental Microbiology, 2013, 15, 1132-1145.	3.8	199
14	Bacterial communities are sensitive indicators of contaminant stress. Marine Pollution Bulletin, 2012, 64, 1029-1038.	5.0	174
15	A phylogenomic and ecological analysis of the globally abundant Marine Group II archaea (<i>Candidatus</i> Thaumarchaeum ETQq1). Environmental Microbiology, 2013, 15, 1132-1145.	9.8	158
16	Key microbial drivers in Antarctic aquatic environments. FEMS Microbiology Reviews, 2013, 37, 303-335.	8.6	144
17	Community fingerprinting in a sequencing world. FEMS Microbiology Ecology, 2014, 89, 316-330.	2.7	140
18	Psychrophiles. Annual Review of Earth and Planetary Sciences, 2013, 41, 87-115.	11.0	121

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19	High level of intergenera gene exchange shapes the evolution of haloarchaea in an isolated Antarctic lake. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16939-16944.	7.1	105
20	Circular linkages between soil biodiversity, fertility and plant productivity are limited to topsoil at the continental scale. <i>New Phytologist</i> , 2017, 215, 1186-1196.	7.3	103
21	Microbial diversity at Mitchell Peninsula, Eastern Antarctica: a potential biodiversity "hotspot". <i>Polar Biology</i> , 2016, 39, 237-249.	1.2	101
22	Oceanographic boundaries constrain microbial diversity gradients in the South Pacific Ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8266-E8275.	7.1	96
23	Culture clash: challenging the dogma of microbial diversity. <i>ISME Journal</i> , 2007, 1, 97-99.	9.8	88
24	The Gut Bacterial Community of Mammals from Marine and Terrestrial Habitats. <i>PLoS ONE</i> , 2013, 8, e83655.	2.5	88
25	Elevated nutrients change bacterial community composition and connectivity: high throughput sequencing of young marine biofilms. <i>Biofouling</i> , 2016, 32, 57-69.	2.2	87
26	Biogeographic partitioning of Southern Ocean microorganisms revealed by metagenomics. <i>Environmental Microbiology</i> , 2013, 15, 1318-1333.	3.8	82
27	Metagenomic insights into strategies of carbon conservation and unusual sulfur biogeochemistry in a hypersaline Antarctic lake. <i>ISME Journal</i> , 2013, 7, 1944-1961.	9.8	75
28	The marine mammal microbiome: current knowledge and future directions. <i>Microbiology Australia</i> , 2015, 36, 8.	0.4	71
29	A trait based perspective on the biogeography of common and abundant marine bacterioplankton clades. <i>Marine Genomics</i> , 2014, 15, 17-28.	1.1	69
30	Soil-foraging animals alter the composition and co-occurrence of microbial communities in a desert shrubland. <i>ISME Journal</i> , 2015, 9, 2671-2681.	9.8	69
31	The Growing Contributions of Molecular Biology and Immunology to Protistan Ecology: Molecular Signatures as Ecological Tools. <i>Journal of Eukaryotic Microbiology</i> , 2004, 51, 38-48.	1.7	68
32	High levels of heterogeneity in diazotroph diversity and activity within a putative hotspot for marine nitrogen fixation. <i>ISME Journal</i> , 2016, 10, 1499-1513.	9.8	55
33	Deep sequencing of non-ribosomal peptide synthetases and polyketide synthases from the microbiomes of Australian marine sponges. <i>ISME Journal</i> , 2013, 7, 1842-1851.	9.8	53
34	Geological connectivity drives microbial community structure and connectivity in polar, terrestrial ecosystems. <i>Environmental Microbiology</i> , 2016, 18, 1834-1849.	3.8	51
35	Temporal stability and species specificity in bacteria associated with the bottlenose dolphins respiratory system. <i>Environmental Microbiology Reports</i> , 2012, 4, 89-96.	2.4	45
36	The Common Oceanographer: Crowdsourcing the Collection of Oceanographic Data. <i>PLoS Biology</i> , 2014, 12, e1001947.	5.6	41

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37	Systematic, continental scale temporal monitoring of marine pelagic microbiota by the Australian Marine Microbial Biodiversity Initiative. <i>Scientific Data</i> , 2018, 5, 180130.	5.3	41
38	Editorial: Anthropogenic Impacts on the Microbial Ecology and Function of Aquatic Environments. <i>Frontiers in Microbiology</i> , 2016, 7, 1044.	3.5	39
39	Nutrient uplift in a cyclonic eddy increases diversity, primary productivity and iron demand of microbial communities relative to a western boundary current. <i>PeerJ</i> , 2016, 4, e1973.	2.0	35
40	Contrasting microbial assemblages in adjacent water masses associated with the East Australian Current. <i>Environmental Microbiology Reports</i> , 2012, 4, 548-555.	2.4	33
41	Biodiversity and ecophysiology of bacteria associated with Antarctic sea ice. <i>Antarctic Science</i> , 1997, 9, 134-142.	0.9	30
42	Faster, Higher and Stronger? The Pros and Cons of Molecular Faunal Data for Assessing Ecosystem Condition. <i>Advances in Ecological Research</i> , 2014, 51, 1-40.	2.7	30
43	<i>Cob</i> gene pyrosequencing enables characterization of benthic dinoflagellate diversity and biogeography. <i>Environmental Microbiology</i> , 2014, 16, 467-485.	3.8	29
44	Harnessing long-read amplicon sequencing to uncover NRPS and Type I PKS gene sequence diversity in polar desert soils. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	25
45	Metabolic pathways inferred from a bacterial marker gene illuminate ecological changes across South Pacific frontal boundaries. <i>Nature Communications</i> , 2021, 12, 2213.	12.8	25
46	Land-use and management practices affect soil ammonia oxidiser community structure, activity and connectedness. <i>Soil Biology and Biochemistry</i> , 2014, 78, 138-148.	8.8	24
47	Diversity and Activity of Diazotrophs in Great Barrier Reef Surface Waters. <i>Frontiers in Microbiology</i> , 2017, 8, 967.	3.5	23
48	Multiple stressors in sediments impact adjacent hard substrate habitats and across biological domains. <i>Science of the Total Environment</i> , 2017, 592, 295-305.	8.0	20
49	Microbial diversity and diazotrophy associated with the freshwater non-heterocyst forming cyanobacterium <i>Lyngbya robusta</i> . <i>Journal of Applied Phycology</i> , 2013, 25, 1039-1045.	2.8	19
50	Spatial and temporal variability of aerobic anoxygenic photoheterotrophic bacteria along the east coast of Australia. <i>Environmental Microbiology</i> , 2016, 18, 4485-4500.	3.8	16
51	Microbial tropicalization driven by a strengthening western ocean boundary current. <i>Global Change Biology</i> , 2020, 26, 5613-5629.	9.5	16
52	<i>Sympodiomyces lanaiensis</i> sp. nov., a basidiomycetous yeast (Ustilaginomycotina: Microstromatales) from marine driftwood in Hawaii. <i>FEMS Yeast Research</i> , 2008, 8, 1357-1363.	2.3	12
53	Unicellular Cyanobacteria Are Important Components of Phytoplankton Communities in Australia's Northern Oceanic Ecoregions. <i>Frontiers in Microbiology</i> , 2018, 9, 3356.	3.5	12
54	Temperate southern Australian coastal waters are characterised by surprisingly high rates of nitrogen fixation and diversity of diazotrophs. <i>PeerJ</i> , 2021, 9, e10809.	2.0	12

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55	Highly heterogeneous temporal dynamics in the abundance and diversity of the emerging pathogens <i>Arcobacter</i> at an urban beach. <i>Water Research</i> , 2020, 171, 115405.	11.3	11
56	Biogeography of Southern Ocean prokaryotes: a comparison of the Indian and Pacific sectors. <i>Environmental Microbiology</i> , 2022, 24, 2449-2466.	3.8	6
57	Biogeographical and seasonal dynamics of the marine <i>Roseobacter</i> community and ecological links to DMSP-producing phytoplankton. <i>ISME Communications</i> , 2022, 2, .	4.2	6
58	Diatom Biogeography, Temporal Dynamics, and Links to Bacterioplankton across Seven Oceanographic Time-Series Sites Spanning the Australian Continent. <i>Microorganisms</i> , 2022, 10, 338.	3.6	5
59	Alpha-diversity is strongly influenced by the composition of other samples when using multiplexed sequencing approaches. <i>Soil Biology and Biochemistry</i> , 2018, 127, 79-81.	8.8	4
60	Wave 2 strains of atypical <i>Vibrio cholerae</i> El Tor caused the 2009–2011 cholera outbreak in Papua New Guinea. <i>Microbial Genomics</i> , 2019, 5, .	2.0	4
61	Investigating the Diversity of Marine Bacteriophage in Contrasting Water Masses Associated with the East Australian Current (EAC) System. <i>Viruses</i> , 2020, 12, 317.	3.3	3