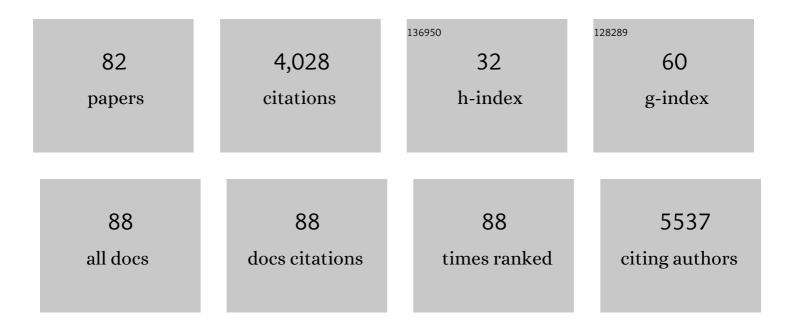
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Atmospheric trace gases support primary production in Antarctic desert surface soil. Nature, 2017, 552, 400-403.	27.8	290
2	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
3	Fluorescence staining and flow cytometry for monitoring microbial cells. Journal of Immunological Methods, 2000, 243, 191-210.	1.4	216
4	Microcolony Cultivation on a Soil Substrate Membrane System Selects for Previously Uncultured Soil Bacteria. Applied and Environmental Microbiology, 2005, 71, 8714-8720.	3.1	204
5	Introducing BASE: the Biomes of Australian Soil Environments soil microbial diversity database. GigaScience, 2016, 5, 21.	6.4	204
6	Legacy effects of soil moisture on microbial community structure and N2O emissions. Soil Biology and Biochemistry, 2016, 95, 40-50.	8.8	175
7	A fluorescent natural product for ultra sensitive detection of proteins in oneâ€dimensional and twoâ€dimensional gel electrophoresis. Proteomics, 2003, 3, 2273-2288.	2.2	146
8	Community fingerprinting in a sequencing world. FEMS Microbiology Ecology, 2014, 89, 316-330.	2.7	140
9	Iron uptake and toxin synthesis in the bloomâ€forming <i>Microcystis aeruginosa</i> under iron limitation. Environmental Microbiology, 2011, 13, 1064-1077.	3.8	123
10	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
11	Microbial diversity at Mitchell Peninsula, Eastern Antarctica: a potential biodiversity "hotspot― Polar Biology, 2016, 39, 237-249.	1.2	101
12	Molecular Epidemiology, Spatiotemporal Analysis, and Ecology of Sporadic Human Cryptosporidiosis in Australia. Applied and Environmental Microbiology, 2011, 77, 7757-7765.	3.1	87
13	Cultivating previously uncultured soil bacteria using a soil substrate membrane system. Nature Protocols, 2008, 3, 1261-1269.	12.0	85
14	Detection of Oxytetracycline Production by Streptomyces rimosus in Soil Microcosms by Combining Whole-Cell Biosensors and Flow Cytometry. Applied and Environmental Microbiology, 2001, 67, 239-244.	3.1	77
15	Ecological Advantages of Autolysis during the Development and Dispersal of Pseudoalteromonas tunicata Biofilms. Applied and Environmental Microbiology, 2006, 72, 5414-5420.	3.1	77
16	Distinct assembly mechanisms underlie similar biogeographical patterns of rare and abundant bacteria in Tibetan Plateau grassland soils. Environmental Microbiology, 2020, 22, 2261-2272.	3.8	77
17	Bacterial Targets as Potential Indicators of Diesel Fuel Toxicity in Subantarctic Soils. Applied and Environmental Microbiology, 2014, 80, 4021-4033.	3.1	73
18	Glycoprotein 60 diversity in C. hominis and C. parvum causing human cryptosporidiosis in NSW, Australia. Experimental Parasitology, 2009, 122, 124-127.	1.2	68

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19	Insights into the distribution and abundance of the ubiquitous Candidatus Saccharibacteria phylum following tag pyrosequencing. Scientific Reports, 2014, 4, 3957.	3.3	66
20	Microbial Diversity of Browning Peninsula, Eastern Antarctica Revealed Using Molecular and Cultivation Methods. Frontiers in Microbiology, 2017, 8, 591.	3.5	66
21	Molecular Epidemiology and Spatial Distribution of a Waterborne Cryptosporidiosis Outbreak in Australia. Applied and Environmental Microbiology, 2011, 77, 7766-7771.	3.1	62
22	Recovering Greater Fungal Diversity from Pristine and Diesel Fuel Contaminated Sub-Antarctic Soil Through Cultivation Using Both a High and a Low Nutrient Media Approach. Frontiers in Microbiology, 2011, 2, 217.	3.5	57
23	Comparative Protein Expression in Different Strains of the Bloom-forming Cyanobacterium Microcystis aeruginosa. Molecular and Cellular Proteomics, 2011, 10, M110.003749.	3.8	54
24	Capturing Greater 16S rRNA Gene Sequence Diversity within the Domain Bacteria. Applied and Environmental Microbiology, 2012, 78, 5938-5941.	3.1	51
25	Geological connectivity drives microbial community structure and connectivity in polar, terrestrial ecosystems. Environmental Microbiology, 2016, 18, 1834-1849.	3.8	51
26	Quantitative and qualitative comparisons of Cryptosporidium faecal purification procedures for the isolation of oocysts suitable for proteomic analysis. International Journal for Parasitology, 2006, 36, 811-819.	3.1	43
27	Catalyzed Reporter Deposition-Fluorescence In Situ Hybridization Allows for Enrichment-Independent Detection of Microcolony-Forming Soil Bacteria. Applied and Environmental Microbiology, 2006, 72, 918-922.	3.1	42
28	Applications of flow cytometry in environmental microbiology and biotechnology. Extremophiles, 2009, 13, 389-401.	2.3	41
29	Cultivation of Fastidious Bacteria by Viability Staining and Micromanipulation in a Soil Substrate Membrane System. Applied and Environmental Microbiology, 2009, 75, 3352-3354.	3.1	39
30	Discovery of an Abundance of Biosynthetic Gene Clusters in Shark Bay Microbial Mats. Frontiers in Microbiology, 2020, 11, 1950.	3.5	39
31	A novel two-color flow cytometric assay for the detection ofCryptosporidium in environmental water samples. Cytometry, 2000, 41, 216-222.	1.8	37
32	Quantum dots as alternatives to organic fluorophores forCryptosporidium detection using conventional flow cytometry and specific monoclonal antibodies: Lessons learned. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2007, 71A, 265-271.	1.5	36
33	<i>Candidatus</i> Eremiobacterota, a metabolically and phylogenetically diverse terrestrial phylum with acid-tolerant adaptations. ISME Journal, 2021, 15, 2692-2707.	9.8	36
34	Life without water: how do bacteria generate biomass in desert ecosystems?. Microbiology Australia, 2018, 39, 28.	0.4	36
35	Recovery of GFP-Labeled Bacteria for Culturing and Molecular Analysis after Cell Sorting Using a Benchtop Flow Cytometer. Microbial Ecology, 2004, 48, 239-245.	2.8	35
36	Time-gated flow cytometry: an ultra-high selectivity method to recover ultra-rare-event μ-targets in high-background biosamples. Journal of Biomedical Optics, 2009, 14, 024023.	2.6	33

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37	The ecological controls on the prevalence of candidate division TM7 in polar regions. Frontiers in Microbiology, 2014, 5, 345.	3.5	32
38	Novel Culturing Techniques Select for Heterotrophs and Hydrocarbon Degraders in a Subantarctic Soil. Scientific Reports, 2016, 6, 36724.	3.3	31
39	Microfluidic qPCR Enables High Throughput Quantification of Microbial Functional Genes but Requires Strict Curation of Primers. Frontiers in Environmental Science, 2018, 6, .	3.3	31
40	The ecological roles of microbial lipopeptides: Where are we going?. Computational and Structural Biotechnology Journal, 2021, 19, 1400-1413.	4.1	30
41	Comparison of Cryptosporidium-specific and Giardia-specific monoclonal antibodies for monitoring water samples. Water Research, 1999, 33, 1611-1617.	11.3	29
42	Why do cytotoxic T lymphocytes fail to eliminate hepatitis C virus? Lessons from studies using major histocompatibility complex class I peptide tetramers. Philosophical Transactions of the Royal Society B: Biological Sciences, 2000, 355, 1085-1092.	4.0	28
43	Potential Use of Quantum Dots in Flow Cytometry. International Journal of Molecular Sciences, 2008, 9, 2622-2638.	4.1	28
44	Global and local-scale variation in bacterial community structure of snow from the Swiss and Australian Alps. FEMS Microbiology Ecology, 2016, 92, fiw132.	2.7	28
45	Terminal Restriction Fragment Length Polymorphism for Identification of <i>Cryptosporidium</i> Species in Human Feces. Applied and Environmental Microbiology, 2009, 75, 108-112.	3.1	27
46	Specific global responses to N and Fe nutrition in toxic and nonâ€ŧoxic <i>Microcystis aeruginosa</i> . Environmental Microbiology, 2016, 18, 401-413.	3.8	27
47	An Immunoglobulin G1 Monoclonal Antibody Highly Specific to the Wall of Cryptosporidium Oocysts. Vaccine Journal, 2000, 7, 745-750.	2.6	25
48	A Naturally Occurring Novel Allele of Escherichia coli Outer Membrane Protein A Reduces Sensitivity to Bacteriophage. Applied and Environmental Microbiology, 2006, 72, 7930-7932.	3.1	25
49	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
50	In vitro effects of noradrenaline on Sydney rock oyster (Saccostrea glomerata) hemocytes. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2008, 151, 691-697.	1.8	22
51	Lifting the veil on arid-to-hyperarid Antarctic soil microbiomes: a tale of two oases. Microbiome, 2020, 8, 37.	11.1	22
52	Development of a Two-Color Fluorescence In Situ Hybridization Technique for Species-Level Identification of Human-Infectious <i>Cryptosporidium</i> spp. Applied and Environmental Microbiology, 2009, 75, 5996-5998.	3.1	20
53	Soil Microbiomes With the Genetic Capacity for Atmospheric Chemosynthesis Are Widespread Across the Poles and Are Associated With Moisture, Carbon, and Nitrogen Limitation. Frontiers in Microbiology, 2020, 11, 1936.	3.5	19
54	Polar soils exhibit distinct patterns in microbial diversity and dominant phylotypes. Soil Biology and Biochemistry, 2022, 166, 108550.	8.8	19

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55	Analysis-only detection ofGiardia by combining immunomagnetic separation and two-color flow cytometry. Cytometry, 2003, 51A, 79-86.	1.8	18
56	Closed-tube DNA extraction using a thermostable proteinase is highly sensitive, capable of single parasite detection. Biotechnology Letters, 2007, 29, 1831-1837.	2.2	18
57	Development of fluorescent in situ hybridisation for Cryptosporidium detection reveals zoonotic and anthroponotic transmission of sporadic cryptosporidiosis in Sydney. Journal of Microbiological Methods, 2008, 75, 535-539.	1.6	18
58	Antarctic desert soil bacteria exhibit high novel natural product potential, evaluated through longâ€read genome sequencing and comparative genomics. Environmental Microbiology, 2021, 23, 3646-3664.	3.8	18
59	Applying fluorescence based technology to the recovery and isolation of Cryptosporidium and Giardia from industrial wastewater streams. Water Research, 2006, 40, 541-548.	11.3	17
60	Exophiala macquariensis sp. nov., a cold adapted black yeast species recovered from a hydrocarbon contaminated sub-Antarctic soil. Fungal Biology, 2019, 123, 151-158.	2.5	15
61	Respiratory microbiota of humpback whales may be reduced in diversity and richness the longer they fast. Scientific Reports, 2020, 10, 12645.	3.3	15
62	Application of the novel fluorescent dye Beljian red to the differentiation of Giardia cysts. Journal of Microbiological Methods, 2003, 52, 133-135.	1.6	12
63	Communication within East Antarctic Soil Bacteria. Applied and Environmental Microbiology, 2019, 86,	3.1	11
64	Interannual comparison of core taxa and community composition of the blow microbiota from East Australian humpback whales. FEMS Microbiology Ecology, 2019, 95, .	2.7	10
65	Izhakiella australiensis sp. nov. isolated from an Australian desert soil. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4317-4322.	1.7	10
66	Flow Cytometry in Environmental Microbiology: A Rapid Approach for the Isolation of Single Cells for Advanced Molecular Biology Analysis. Methods in Molecular Biology, 2012, 881, 3-26.	0.9	9
67	Applying microbial indicators of hydrocarbon toxicity to contaminated sites undergoing bioremediation on subantarctic Macquarie Island. Environmental Pollution, 2020, 259, 113780.	7.5	9
68	A novel two-color flow cytometric assay for the detection of Cryptosporidium in environmental water samples. Cytometry, 2000, 41, 216-22.	1.8	8
69	New Insights into the Microbial Diversity of Polar Desert Soils: A Biotechnological Perspective. , 2017, , 169-183.		7
70	Characterization of polar metabolites and evaluation of their potential toxicity in hydrocarbon contaminated Antarctic soil elutriates. Science of the Total Environment, 2019, 689, 390-397.	8.0	7
71	Persistence and resistance: survival mechanisms of <i>Candidatus</i> Dormibacterota from nutrientâ€poor Antarctic soils. Environmental Microbiology, 2021, 23, 4276-4294.	3.8	7
72	Does sociality drive diversity and composition of airway microbiota in cetaceans?. Environmental Microbiology Reports, 2020, 12, 324-333.	2.4	5

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73	Highly abundant core taxa in the blow within and across captive bottlenose dolphins provide evidence for a temporally stable airway microbiota. BMC Microbiology, 2021, 21, 20.	3.3	5
74	Microbial community analysis of biopiles in Antarctica provides evidence of successful hydrocarbon biodegradation and initial soil ecosystem recovery. Environmental Pollution, 2021, 290, 117977.	7.5	5
75	Out of Thin Air? Astrobiology and Atmospheric Chemotrophy. Astrobiology, 2022, , .	3.0	5
76	Soil substrate culturing approaches recover diverse members of Actinomycetota from desert soils of Herring Island, East Antarctica. Extremophiles, 2022, 26, .	2.3	4
77	A novel real-world ecotoxicological dataset of pelagic microbial community responses to wastewater. Scientific Data, 2020, 7, 158.	5.3	3
78	Microbiology of Eutrophic (Ornithogenic and Hydrocarbon-Contaminated) Soil. , 2014, , 91-113.		3
79	UV LED excited time-gated luminescence flow cytometry: evaluation for rare-event particle counting. Proceedings of SPIE, 2008, , .	0.8	1
80	Detection of environmental microorganisms with a bead-based assay and quantum dots. International Journal of Biomedical Nanoscience and Nanotechnology, 2011, 2, 75.	0.1	0
81	Response to Letter to Editor regarding Pudasaini et al. (2019), Characterisation of polar metabolites and evaluation of their potential toxicity in hydrocarbon contaminated soil elutriates. Science of the Total Environment, v689, 390–397. Science of the Total Environment, 2020, 712, 135470.	8.0	0
82	Three-color Cytometry for the Simultaneous Detection of the Cryptosporidium Species Contributing to the Majority of Human Cryptosporidiosis. Public Health Frontier, 2013, 2, 103-108.	0.1	0