

Chris Greening

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

99
papers

2,755
citations

30
h-index

50
g-index

121
ext. papers

4,349
ext. citations

10.3
avg, IF

5.6
L-index

#	Paper	IF	Citations
99	Phylogenetically and functionally diverse microorganisms reside under the Ross Ice Shelf.. <i>Nature Communications</i> , 2022 , 13, 117	17.4	0
98	Simultaneous detection of multiple pathogens with the TaqMan Array Card.. <i>MethodsX</i> , 2022 , 9, 101707	1.9	0
97	Multiple energy sources and metabolic strategies sustain microbial diversity in Antarctic desert soils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	7
96	Genome-resolved metagenomics reveals how soil bacterial communities respond to elevated H ₂ availability. <i>Soil Biology and Biochemistry</i> , 2021 , 163, 108464	7.5	0
95	Bark-dwelling methanotrophic bacteria decrease methane emissions from trees. <i>Nature Communications</i> , 2021 , 12, 2127	17.4	18
94	Isotopic evidence for axial tree stem methane oxidation within subtropical lowland forests. <i>New Phytologist</i> , 2021 , 230, 2200-2212	9.8	9
93	Monitoring of diverse enteric pathogens across environmental and host reservoirs with TaqMan array cards and standard qPCR: a methodological comparison study. <i>Lancet Planetary Health</i> , 2021 , 5, e297-e308	9.8	5
92	Mycobacteria Tolerate Carbon Monoxide by Remodeling Their Respiratory Chain. <i>MSystems</i> , 2021 , 6,	7.6	1
91	Metabolic flexibility allows bacterial habitat generalists to become dominant in a frequently disturbed ecosystem. <i>ISME Journal</i> , 2021 , 15, 2986-3004	11.9	12
90	Chemosynthetic and photosynthetic bacteria contribute differentially to primary production across a steep desert aridity gradient. <i>ISME Journal</i> , 2021 , 15, 3339-3356	11.9	9
89	Freshwater Exhibit Metabolic Specialization among Cosmopolitan and Endemic Populations. <i>MSystems</i> , 2021 , 6,	7.6	4
88	An integrated gene catalog and over 10,000 metagenome-assembled genomes from the gastrointestinal microbiome of ruminants. <i>Microbiome</i> , 2021 , 9, 137	16.6	14
87	Acidobacteria are active and abundant members of diverse atmospheric H ₂ -oxidizing communities detected in temperate soils. <i>ISME Journal</i> , 2021 , 15, 363-376	11.9	9
86	Technical note: Inexpensive modification of Exetainers for the reliable storage of trace-level hydrogen and carbon monoxide gas samples. <i>Biogeosciences</i> , 2021 , 18, 729-737	4.6	1
85	Termite gas emissions select for hydrogenotrophic microbial communities in termite mounds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3
84	Large-scale protein level comparison of Deltaproteobacteria reveals cohesive metabolic groups. <i>ISME Journal</i> , 2021 ,	11.9	3
83	BonA from <i>Formosa</i> Forms a Divisome-Localized Decamer That Supports Outer Envelope Function. <i>MBio</i> , 2021 , e0148021	7.8	2

82	Hydrogen is a major lifeline for aerobic bacteria. <i>Trends in Microbiology</i> , 2021 ,	12.4	1
81	Understanding the transmission of <i>Mycobacterium ulcerans</i> : A step towards controlling Buruli ulcer. <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0009678	4.8	6
80	Hydrodynamic disturbance controls microbial community assembly and biogeochemical processes in coastal sediments. <i>ISME Journal</i> , 2021 ,	11.9	4
79	Effects of drift algae accumulation and nitrate loading on nitrogen cycling in a eutrophic coastal sediment. <i>Science of the Total Environment</i> , 2021 , 790, 147749	10.2	2
78	A planetary health model for reducing exposure to faecal contamination in urban informal settlements: Baseline findings from Makassar, Indonesia. <i>Environment International</i> , 2021 , 155, 106679	12.9	8
77	Study design, rationale and methods of the Revitalising Informal Settlements and their Environments (RISE) study: a cluster randomised controlled trial to evaluate environmental and human health impacts of a water-sensitive intervention in informal settlements in Indonesia and Fiji. <i>BMJ Open</i> , 2021 , 11, e02650	3	12
76	Trace gas oxidizers are widespread and active members of soil microbial communities. <i>Nature Microbiology</i> , 2021 , 6, 246-256	26.6	24
75	Hydrogen-Oxidizing Bacteria Are Abundant in Desert Soils and Strongly Stimulated by Hydration. <i>MSystems</i> , 2020 , 5,	7.6	16
74	Cellular and Structural Basis of Synthesis of the Unique Intermediate Dehydro-F-0 in <i>Mycobacteria</i> . <i>MSystems</i> , 2020 , 5,	7.6	4
73	Molecular Hydrogen Metabolism: a Widespread Trait of Pathogenic Bacteria and Protists. <i>Microbiology and Molecular Biology Reviews</i> , 2020 , 84,	13.2	28
72	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering. <i>PLoS Pathogens</i> , 2020 , 16, e1008287	7.6	18
71	Pore water conditions driving calcium carbonate dissolution in reef sands. <i>Geochimica Et Cosmochimica Acta</i> , 2020 , 279, 16-28	5.5	5
70	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering. <i>FASEB Journal</i> , 2020 , 34, 1-1	0.9	
69	A widely distributed hydrogenase oxidises atmospheric H during bacterial growth. <i>ISME Journal</i> , 2020 , 14, 2649-2658	11.9	15
68	Thermogenic hydrocarbon biodegradation by diverse depth-stratified microbial populations at a Scotian Basin cold seep. <i>Nature Communications</i> , 2020 , 11, 5825	17.4	14
67	Formation and function of bacterial organelles. <i>Nature Reviews Microbiology</i> , 2020 , 18, 677-689	22.2	40
66	Soil Bacterial Communities Exhibit Strong Biogeographic Patterns at Fine Taxonomic Resolution. <i>MSystems</i> , 2020 , 5,	7.6	18
65	Termite mounds contain soil-derived methanotroph communities kinetically adapted to elevated methane concentrations. <i>ISME Journal</i> , 2020 , 14, 2715-2731	11.9	15

64	Energetic Basis of Microbial Growth and Persistence in Desert Ecosystems. <i>MSystems</i> , 2020 , 5,	7.6	33
63	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering 2020 , 16, e1008287		
62	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering 2020 , 16, e1008287		
61	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering 2020 , 16, e1008287		
60	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering 2020 , 16, e1008287		
59	Hydrogen Oxidation Influences Glycogen Accumulation in a Verrucomicrobial Methanotroph. <i>Frontiers in Microbiology</i> , 2019 , 10, 1873	5.7	8
58	Plumage redness signals mitochondrial function in the house finch. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019 , 286, 20191354	4.4	27
57	Uncovering the Metabolic Strategies of the Dormant Microbial Majority: towards Integrative Approaches. <i>MSystems</i> , 2019 , 4,	7.6	14
56	Metabolic potential of uncultured bacteria and archaea associated with petroleum seepage in deep-sea sediments. <i>Nature Communications</i> , 2019 , 10, 1816	17.4	59
55	Two Chloroflexi classes independently evolved the ability to persist on atmospheric hydrogen and carbon monoxide. <i>ISME Journal</i> , 2019 , 13, 1801-1813	11.9	57
54	Bacterial fermentation and respiration processes are uncoupled in anoxic permeable sediments. <i>Nature Microbiology</i> , 2019 , 4, 1014-1023	26.6	34
53	Proposal of the reverse flow model for the origin of the eukaryotic cell based on comparative analyses of Asgard archaeal metabolism. <i>Nature Microbiology</i> , 2019 , 4, 1138-1148	26.6	87
52	A revised biosynthetic pathway for the cofactor F in prokaryotes. <i>Nature Communications</i> , 2019 , 10, 1558	7.4	35
51	Atmospheric carbon monoxide oxidation is a widespread mechanism supporting microbial survival. <i>ISME Journal</i> , 2019 , 13, 2868-2881	11.9	66
50	Diverse hydrogen production and consumption pathways influence methane production in ruminants. <i>ISME Journal</i> , 2019 , 13, 2617-2632	11.9	54
49	Two uptake hydrogenases differentially interact with the aerobic respiratory chain during mycobacterial growth and persistence. <i>Journal of Biological Chemistry</i> , 2019 , 294, 18980-18991	5.4	14
48	Protease-associated import systems are widespread in Gram-negative bacteria. <i>PLoS Genetics</i> , 2019 , 15, e1008435	6	7
47	Putative Iron-Sulfur Proteins Are Required for Hydrogen Consumption and Enhance Survival of Mycobacteria. <i>Frontiers in Microbiology</i> , 2019 , 10, 2749	5.7	4

46	Occurrence and expression of genes encoding methyl-compound production in rumen bacteria. <i>Animal Microbiome</i> , 2019 , 1, 15	4.1	13
45	Assessing the fitness consequences of mitonuclear interactions in natural populations. <i>Biological Reviews</i> , 2019 , 94, 1089-1104	13.5	55
44	FAD-sequestering proteins protect mycobacteria against hypoxic and oxidative stress. <i>Journal of Biological Chemistry</i> , 2019 , 294, 2903-2912	5.4	7
43	Climate-driven mitochondrial selection: A test in Australian songbirds. <i>Molecular Ecology</i> , 2018 , 27, 898-918	5.18	25
42	Coupling between Nitrogen Fixation and Tetrachlorobiphenyl Dechlorination in a Rhizobium-Legume Symbiosis. <i>Environmental Science & Technology</i> , 2018 , 52, 2217-2224	10.3	18
41	Concordant divergence of mitogenomes and a mitonuclear gene cluster in bird lineages inhabiting different climates. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1258-1267	12.3	45
40	Life without water: how do bacteria generate biomass in desert ecosystems?. <i>Microbiology Australia</i> , 2018 , 39, 28	0.8	20
39	Population mitogenomics provides insights into evolutionary history, source of invasions and diversifying selection in the House Crow (<i>Corvus splendens</i>). <i>Heredity</i> , 2018 , 120, 296-309	3.6	6
38	<i>Pyrinomonas</i> 2018 , 1-8		
37	Fermentative Spirochaetes mediate necromass recycling in anoxic hydrocarbon-contaminated habitats. <i>ISME Journal</i> , 2018 , 12, 2039-2050	11.9	37
36	Oxidative Phosphorylation as a Target Space for Tuberculosis: Success, Caution, and Future Directions. <i>Microbiology Spectrum</i> , 2017 , 5,	8.9	61
35	Mixotrophy drives niche expansion of verrucomicrobial methanotrophs. <i>ISME Journal</i> , 2017 , 11, 2599-2610	10.9	64
34	Atmospheric trace gases support primary production in Antarctic desert surface soil. <i>Nature</i> , 2017 , 552, 400-403	50.4	159
33	The methanogenic redox cofactor F is widely synthesized by aerobic soil bacteria. <i>ISME Journal</i> , 2017 , 11, 125-137	11.9	43
32	Metabolism in anoxic permeable sediments is dominated by eukaryotic dark fermentation. <i>Nature Geoscience</i> , 2017 , 10, 30-35	18.3	20
31	Oxidative Phosphorylation as a Target Space for Tuberculosis: Success, Caution, and Future Directions 2017 , 295-316		1
30	Integrative Approaches for Studying Mitochondrial and Nuclear Genome Co-evolution in Oxidative Phosphorylation. <i>Frontiers in Genetics</i> , 2017 , 8, 25	4.5	43
29	Mycobacterial FH-Dependent Reductases Promiscuously Reduce Diverse Compounds through a Common Mechanism. <i>Frontiers in Microbiology</i> , 2017 , 8, 1000	5.7	20

28	Cofactor Tail Length Modulates Catalysis of Bacterial F-Dependent Oxidoreductases. <i>Frontiers in Microbiology</i> , 2017 , 8, 1902	5.7	10
27	The Redox Cofactor F Protects Mycobacteria from Diverse Antimicrobial Compounds and Mediates a Reductive Detoxification System. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 6810-6818	4.8	23
26	Genomic and metagenomic surveys of hydrogenase distribution indicate H ₂ is a widely utilised energy source for microbial growth and survival. <i>ISME Journal</i> , 2016 , 10, 761-77	11.9	319
25	Atmospheric H ₂ fuels plant-microbe interactions. <i>Environmental Microbiology</i> , 2016 , 18, 2289-91	5.2	1
24	HydDB: A web tool for hydrogenase classification and analysis. <i>Scientific Reports</i> , 2016 , 6, 34212	4.9	198
23	Physiology, Biochemistry, and Applications of F ₄₂₀ - and F _o -Dependent Redox Reactions. <i>Microbiology and Molecular Biology Reviews</i> , 2016 , 80, 451-93	13.2	88
22	H ₂ metabolism is widespread and diverse among human colonic microbes. <i>Gut Microbes</i> , 2016 , 7, 235-458.8		65
21	Sequence-Structure-Function Classification of a Catalytically Diverse Oxidoreductase Superfamily in Mycobacteria. <i>Journal of Molecular Biology</i> , 2015 , 427, 3554-3571	6.5	47
20	Persistence of the dominant soil phylum Acidobacteria by trace gas scavenging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 10497-502	11.5	78
19	Atmospheric hydrogen scavenging: from enzymes to ecosystems. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 1190-9	4.8	65
18	A soil actinobacterium scavenges atmospheric H ₂ using two membrane-associated, oxygen-dependent [NiFe] hydrogenases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 4257-61	11.5	84
17	Integration of hydrogenase expression and hydrogen sensing in bacterial cell physiology. <i>Current Opinion in Microbiology</i> , 2014 , 18, 30-8	7.9	31
16	Energetics of pathogenic bacteria and opportunities for drug development. <i>Advances in Microbial Physiology</i> , 2014 , 65, 1-62	4.4	79
15	An obligately aerobic soil bacterium activates fermentative hydrogen production to survive reductive stress during hypoxia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 11479-84	11.5	74
14	Three different [NiFe] hydrogenases confer metabolic flexibility in the obligate aerobe <i>Mycobacterium smegmatis</i> . <i>Environmental Microbiology</i> , 2014 , 16, 318-30	5.2	42
13	The growth and survival of <i>Mycobacterium smegmatis</i> is enhanced by co-metabolism of atmospheric H ₂ . <i>PLoS ONE</i> , 2014 , 9, e103034	3.7	35
12	A widely distributed hydrogenase oxidises atmospheric H ₂ during bacterial growth		1
11	Mitochondrial-nuclear interactions maintain geographic separation of deeply diverged mitochondrial lineages in the face of nuclear gene flow		7

10	Metabolic flexibility allows generalist bacteria to become dominant in a frequently disturbed ecosystem	13
9	Cellular and structural basis of synthesis of the unique intermediate dehydro-F420-0 in mycobacteria	1
8	A genome compendium reveals diverse metabolic adaptations of Antarctic soil microorganisms	9
7	TaqMan Array Cards enable monitoring of diverse enteric pathogens across environmental and host reservoirs	2
6	Distinct hydrogenotrophic bacteria are stimulated by elevated H ₂ levels in upland and wetland soils	1
5	Metabolic potential of uncultured bacteria and archaea associated with petroleum seepage in deep-sea sediments	1
4	Two Chloroflexi classes independently evolved the ability to persist on atmospheric hydrogen and carbon monoxide	2
3	Alternative hydrogen uptake pathways suppress methane production in ruminants	2
2	Carbon monoxide dehydrogenases enhance bacterial survival by oxidising atmospheric CO	2
1	The evolution of nitroimidazole antibiotic resistance in <i>Mycobacterium tuberculosis</i>	2