Chris Greening

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1252368/publications.pdf

Version: 2024-02-01

76294 106281 5,469 93 40 65 citations h-index g-index papers 121 121 121 5091 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Genomic and metagenomic surveys of hydrogenase distribution indicate H2 is a widely utilised energy source for microbial growth and survival. ISME Journal, 2016, 10, 761-777.	4.4	503
2	HydDB: A web tool for hydrogenase classification and analysis. Scientific Reports, 2016, 6, 34212.	1.6	372
3	Atmospheric trace gases support primary production in Antarctic desert surface soil. Nature, 2017, 552, 400-403.	13.7	290
4	Proposal of the reverse flow model for the origin of the eukaryotic cell based on comparative analyses of Asgard archaeal metabolism. Nature Microbiology, 2019, 4, 1138-1148.	5.9	143
5	Physiology, Biochemistry, and Applications of F ₄₂₀ - and F _o -Dependent Redox Reactions. Microbiology and Molecular Biology Reviews, 2016, 80, 451-493.	2.9	136
6	Atmospheric carbon monoxide oxidation is a widespread mechanism supporting microbial survival. ISME Journal, $2019,13,2868-2881.$	4.4	133
7	Diverse hydrogen production and consumption pathways influence methane production in ruminants. ISME Journal, 2019, 13, 2617-2632.	4.4	132
8	Two Chloroflexi classes independently evolved the ability to persist on atmospheric hydrogen and carbon monoxide. ISME Journal, 2019, 13, 1801-1813.	4.4	129
9	Metabolic potential of uncultured bacteria and archaea associated with petroleum seepage in deep-sea sediments. Nature Communications, 2019, 10, 1816.	5.8	118
10	An obligately aerobic soil bacterium activates fermentative hydrogen production to survive reductive stress during hypoxia. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11479-11484.	3.3	117
11	Persistence of the dominant soil phylum <i>Acidobacteria</i> by trace gas scavenging. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10497-10502.	3.3	117
12	A soil actinobacterium scavenges atmospheric H ₂ using two membrane-associated, oxygen-dependent [NiFe] hydrogenases. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4257-4261.	3.3	116
13	Formation and function of bacterial organelles. Nature Reviews Microbiology, 2020, 18, 677-689.	13.6	112
14	An integrated gene catalog and over 10,000 metagenome-assembled genomes from the gastrointestinal microbiome of ruminants. Microbiome, 2021, 9, 137.	4.9	110
15	Mixotrophy drives niche expansion of verrucomicrobial methanotrophs. ISME Journal, 2017, 11, 2599-2610.	4.4	107
16	H ₂ metabolism is widespread and diverse among human colonic microbes. Gut Microbes, 2016, 7, 235-245.	4.3	105
17	Energetics of Pathogenic Bacteria and Opportunities for Drug Development. Advances in Microbial Physiology, 2014, 65, 1-62.	1.0	102
18	Trace gas oxidizers are widespread and active members of soil microbial communities. Nature Microbiology, 2021, 6, 246-256.	5.9	97

#	Article	IF	CITATIONS
19	Assessing the fitness consequences of mitonuclear interactions in natural populations. Biological Reviews, 2019, 94, 1089-1104.	4.7	90
20	Oxidative Phosphorylation as a Target Space for Tuberculosis: Success, Caution, and Future Directions. Microbiology Spectrum, 2017, 5, .	1.2	89
21	Metabolic flexibility allows bacterial habitat generalists to become dominant in a frequently disturbed ecosystem. ISME Journal, 2021, 15, 2986-3004.	4.4	89
22	Atmospheric Hydrogen Scavenging: from Enzymes to Ecosystems. Applied and Environmental Microbiology, 2015, 81, 1190-1199.	1.4	81
23	Bacterial fermentation and respiration processes are uncoupled in anoxic permeable sediments. Nature Microbiology, 2019, 4, 1014-1023.	5. 9	76
24	Fermentative Spirochaetes mediate necromass recycling in anoxic hydrocarbon-contaminated habitats. ISME Journal, 2018, 12, 2039-2050.	4.4	74
25	Thermogenic hydrocarbon biodegradation by diverse depth-stratified microbial populations at a Scotian Basin cold seep. Nature Communications, 2020, 11, 5825.	5.8	72
26	Large-scale protein level comparison of Deltaproteobacteria reveals cohesive metabolic groups. ISME Journal, 2022, 16, 307-320.	4.4	71
27	Molecular Hydrogen Metabolism: a Widespread Trait of Pathogenic Bacteria and Protists. Microbiology and Molecular Biology Reviews, 2020, 84, .	2.9	70
28	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
29	Sequence–Structure–Function Classification of a Catalytically Diverse Oxidoreductase Superfamily in Mycobacteria. Journal of Molecular Biology, 2015, 427, 3554-3571.	2.0	67
30	The methanogenic redox cofactor F420 is widely synthesized by aerobic soil bacteria. ISME Journal, 2017, 11, 125-137.	4.4	66
31	Energetic Basis of Microbial Growth and Persistence in Desert Ecosystems. MSystems, 2020, 5, .	1.7	66
32	Integrative Approaches for Studying Mitochondrial and Nuclear Genome Co-evolution in Oxidative Phosphorylation. Frontiers in Genetics, 2017, 8, 25.	1.1	65
33	Three different [<scp><scp>NiFe</scp> hydrogenases confer metabolic flexibility in the obligate aerobe <scp><i>M</i></scp><i>ycobacterium smegmatis</i>. Environmental Microbiology, 2014, 16, 318-330.</scp>	1.8	63
34	Concordant divergence of mitogenomes and a mitonuclear gene cluster in bird lineages inhabiting different climates. Nature Ecology and Evolution, 2018, 2, 1258-1267.	3.4	63
35	A revised biosynthetic pathway for the cofactor F420 in prokaryotes. Nature Communications, 2019, 10, 1558.	5.8	55
36	The Growth and Survival of Mycobacterium smegmatis Is Enhanced by Co-Metabolism of Atmospheric H2. PLoS ONE, 2014, 9, e103034.	1.1	55

#	Article	IF	CITATIONS
37	Plumage redness signals mitochondrial function in the house finch. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191354.	1.2	52
38	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering. PLoS Pathogens, 2020, 16, e1008287.	2.1	51
39	Bark-dwelling methanotrophic bacteria decrease methane emissions from trees. Nature Communications, 2021, 12, 2127.	5.8	51
40	Integration of hydrogenase expression and hydrogen sensing in bacterial cell physiology. Current Opinion in Microbiology, 2014, 18, 30-38.	2.3	49
41	Chemosynthetic and photosynthetic bacteria contribute differentially to primary production across a steep desert aridity gradient. ISME Journal, 2021, 15, 3339-3356.	4.4	48
42	Climateâ€driven mitochondrial selection: A test in Australian songbirds. Molecular Ecology, 2018, 27, 898-918.	2.0	43
43	A widely distributed hydrogenase oxidises atmospheric H2 during bacterial growth. ISME Journal, 2020, 14, 2649-2658.	4.4	41
44	Hydrogen-Oxidizing Bacteria Are Abundant in Desert Soils and Strongly Stimulated by Hydration. MSystems, 2020, 5, .	1.7	38
45	Hydrodynamic disturbance controls microbial community assembly and biogeochemical processes in coastal sediments. ISME Journal, 2022, 16, 750-763.	4.4	38
46	Life without water: how do bacteria generate biomass in desert ecosystems?. Microbiology Australia, 2018, 39, 28.	0.1	36
47	Microbial oxidation of atmospheric trace gases. Nature Reviews Microbiology, 2022, 20, 513-528.	13.6	36
48	The Redox Cofactor F 420 Protects Mycobacteria from Diverse Antimicrobial Compounds and Mediates a Reductive Detoxification System. Applied and Environmental Microbiology, 2016, 82, 6810-6818.	1.4	35
49	Soil Bacterial Communities Exhibit Strong Biogeographic Patterns at Fine Taxonomic Resolution. MSystems, 2020, 5, .	1.7	33
50	Metabolism in anoxic permeable sediments is dominated by eukaryotic dark fermentation. Nature Geoscience, 2017, 10, 30-35.	5.4	31
51	Coupling between Nitrogen Fixation and Tetrachlorobiphenyl Dechlorination in a Rhizobium–Legume Symbiosis. Environmental Science & Environmental Sc	4.6	30
52	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. BMJ Open, 2021, 11, e042850.	0.8	29
53	Two uptake hydrogenases differentially interact with the aerobic respiratory chain during mycobacterial growth and persistence. Journal of Biological Chemistry, 2019, 294, 18980-18991.	1.6	28
54	Mycobacterial F420H2-Dependent Reductases Promiscuously Reduce Diverse Compounds through a Common Mechanism. Frontiers in Microbiology, 2017, 8, 1000.	1.5	27

#	Article	IF	Citations
55	Occurrence and expression of genes encoding methyl-compound production in rumen bacteria. Animal Microbiome, 2019, 1, 15.	1.5	27
56	Isotopic evidence for axial tree stem methane oxidation within subtropical lowland forests. New Phytologist, 2021, 230, 2200-2212.	3.5	27
57	Understanding the transmission of Mycobacterium ulcerans: A step towards controlling Buruli ulcer. PLoS Neglected Tropical Diseases, 2021, 15, e0009678.	1.3	26
58	Hydrogen is a major lifeline for aerobic bacteria. Trends in Microbiology, 2022, 30, 330-337.	3.5	24
59	A planetary health model for reducing exposure to faecal contamination in urban informal settlements: Baseline findings from Makassar, Indonesia. Environment International, 2021, 155, 106679.	4.8	24
60	Acidobacteria are active and abundant members of diverse atmospheric H2-oxidizing communities detected in temperate soils. ISME Journal, 2021, 15, 363-376.	4.4	23
61	Global and seasonal variation of marine phosphonate metabolism. ISME Journal, 2022, 16, 2198-2212.	4.4	22
62	Termite mounds contain soil-derived methanotroph communities kinetically adapted to elevated methane concentrations. ISME Journal, 2020, 14, 2715-2731.	4.4	21
63	Monitoring of diverse enteric pathogens across environmental and host reservoirs with TaqMan array cards and standard qPCR: a methodological comparison study. Lancet Planetary Health, The, 2021, 5, e297-e308.	5.1	21
64	Uncovering the Metabolic Strategies of the Dormant Microbial Majority: towards Integrative Approaches. MSystems, 2019, 4, .	1.7	19
65	Cofactor F420: an expanded view of its distribution, biosynthesis and roles in bacteria and archaea. FEMS Microbiology Reviews, 2021, 45, .	3.9	17
66	Phylogenetically and functionally diverse microorganisms reside under the Ross Ice Shelf. Nature Communications, 2022, 13, 117.	5.8	17
67	A nitrite-oxidising bacterium constitutively consumes atmospheric hydrogen. ISME Journal, 2022, 16, 2213-2219.	4.4	17
68	Cofactor Tail Length Modulates Catalysis of Bacterial F420-Dependent Oxidoreductases. Frontiers in Microbiology, 2017, 8, 1902.	1.5	15
69	Protease-associated import systems are widespread in Gram-negative bacteria. PLoS Genetics, 2019, 15, e1008435.	1.5	15
70	Hydrogen Oxidation Influences Glycogen Accumulation in a Verrucomicrobial Methanotroph. Frontiers in Microbiology, 2019, 10, 1873.	1.5	15
71	Termite gas emissions select for hydrogenotrophic microbial communities in termite mounds. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	15
72	Putative Iron-Sulfur Proteins Are Required for Hydrogen Consumption and Enhance Survival of Mycobacteria. Frontiers in Microbiology, 2019, 10, 2749.	1.5	14

#	Article	IF	CITATIONS
73	FAD-sequestering proteins protect mycobacteria against hypoxic and oxidative stress. Journal of Biological Chemistry, 2019, 294, 2903-5814.	1.6	14
74	Effects of drift algae accumulation and nitrate loading on nitrogen cycling in a eutrophic coastal sediment. Science of the Total Environment, 2021, 790, 147749.	3.9	14
75	Genome-resolved metagenomics reveals how soil bacterial communities respond to elevated H2 availability. Soil Biology and Biochemistry, 2021, 163, 108464.	4.2	12
76	Pore water conditions driving calcium carbonate dissolution in reef sands. Geochimica Et Cosmochimica Acta, 2020, 279, 16-28.	1.6	11
77	Cellular and Structural Basis of Synthesis of the Unique Intermediate Dehydro-F ₄₂₀ -0 in Mycobacteria. MSystems, 2020, 5, .	1.7	9
78	Editorial: Microbial Hydrogen Metabolism. Frontiers in Microbiology, 2020, 11, 56.	1.5	8
79	Freshwater <i>Chlorobia</i> Exhibit Metabolic Specialization among Cosmopolitan and Endemic Populations. MSystems, 2021, 6, .	1.7	8
80	Mycobacteria Tolerate Carbon Monoxide by Remodeling Their Respiratory Chain. MSystems, 2021, 6, .	1.7	7
81	Population mitogenomics provides insights into evolutionary history, source of invasions and diversifying selection in the House Crow (Corvus splendens). Heredity, 2018, 120, 296-309.	1.2	6
82	Simultaneous detection of multiple pathogens with the TaqMan Array Card. MethodsX, 2022, 9, 101707.	0.7	6
83	Technical note: Inexpensive modification of Exetainers for the reliable storage of trace-level hydrogen and carbon monoxide gas samples. Biogeosciences, 2021, 18, 729-737.	1.3	5
84	BonA from <i>Acinetobacter baumannii</i> Forms a Divisome-Localized Decamer That Supports Outer Envelope Function. MBio, 2021, 12, e0148021.	1.8	5
85	Oxidative Phosphorylation as a Target Space for Tuberculosis: Success, Caution, and Future Directions., 0,, 295-316.		4
86	Termite-engineered microbial communities of termite nest structures: a new dimension to the extended phenotype. FEMS Microbiology Reviews, 2022, 46, .	3.9	3
87	Atmospheric <scp>H</scp> fuels plant–microbe interactions. Environmental Microbiology, 2016, 18, 2289-2291.	1.8	2
88	Implementing baseline ecological and human health field assessments in the Revitalizing Informal Settlements and their Environments (RISE) programme in Makassar, Indonesia: an interdisciplinary study. Lancet Planetary Health, The, 2019, 3, S8.	5.1	0
89	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering. FASEB Journal, 2020, 34, 1-1.	0.2	0
90	Title is missing!. , 2020, 16, e1008287.		0

#	Article	IF	CITATIONS
91	Title is missing!. , 2020, 16, e1008287.		O
92	Title is missing!. , 2020, 16, e1008287.		0
93	Title is missing!. , 2020, 16, e1008287.		O