

Craig W Herbold

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

7,675
citations

70961

41
h-index

60497

81
g-index

102
all docs

102
docs citations

102
times ranked

8087
citing authors

#	ARTICLE	IF	CITATIONS
1	Ammonia-oxidizing archaea possess a wide range of cellular ammonia affinities. <i>ISME Journal</i> , 2022, 16, 272-283.	4.4	96
2	Ecological Processes Shaping Microbiomes of Extremely Low Birthweight Infants. <i>Frontiers in Microbiology</i> , 2022, 13, 812136.	1.5	5
3	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.	4.4	23
4	Anaerobic bacterial degradation of protein and lipid macromolecules in subarctic marine sediment. <i>ISME Journal</i> , 2021, 15, 833-847.	4.4	38
5	Genomic and kinetic analysis of novel Nitrospinae enriched by cell sorting. <i>ISME Journal</i> , 2021, 15, 732-745.	4.4	23
6	Sulfoquinovose is a select nutrient of prominent bacteria and a source of hydrogen sulfide in the human gut. <i>ISME Journal</i> , 2021, 15, 2779-2791.	4.4	30
7	Survival strategies of ammonia-oxidizing archaea (AOA) in a full-scale WWTP treating mixed landfill leachate containing copper ions and operating at low-intensity of aeration. <i>Water Research</i> , 2021, 191, 116798.	5.3	39
8	An Economical and Flexible Dual Barcoding, Two-Step PCR Approach for Highly Multiplexed Amplicon Sequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 669776.	1.5	48
9	Novel taxa of Acidobacteriota implicated in seafloor sulfur cycling. <i>ISME Journal</i> , 2021, 15, 3159-3180.	4.4	54
10	Genomic insights into diverse bacterial taxa that degrade extracellular DNA in marine sediments. <i>Nature Microbiology</i> , 2021, 6, 885-898.	5.9	29
11	Novel <i>Alcaligenes ammonioxydans</i> sp. nov. from wastewater treatment sludge oxidizes ammonia to N_2 with a previously unknown pathway. <i>Environmental Microbiology</i> , 2021, 23, 6965-6980.	1.8	33
12	Ecological memory of recurrent drought modifies soil processes via changes in soil microbial community. <i>Nature Communications</i> , 2021, 12, 5308.	5.8	108
13	Gilbert's Syndrome and the Gut Microbiota – Insights From the Case-Control BILIHEALTH Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 701109.	1.8	4
14	Activities and metabolic versatility of distinct anammox bacteria in a full-scale wastewater treatment system. <i>Water Research</i> , 2021, 206, 117763.	5.3	42
15	Increased microbial expression of organic nitrogen cycling genes in long-term warmed grassland soils. <i>ISME Communications</i> , 2021, 1, .	1.7	14
16	Rational design of a microbial consortium of mucosal sugar utilizers reduces <i>Clostridiodes difficile</i> colonization. <i>Nature Communications</i> , 2020, 11, 5104.	5.8	177
17	Conversion of Rutin, a Prevalent Dietary Flavonol, by the Human Gut Microbiota. <i>Frontiers in Microbiology</i> , 2020, 11, 585428.	1.5	47
18	Composition and activity of nitrifier communities in soil are unresponsive to elevated temperature and CO ₂ , but strongly affected by drought. <i>ISME Journal</i> , 2020, 14, 3038-3053.	4.4	43

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19	Exploring the upper pH limits of nitrite oxidation: diversity, ecophysiology, and adaptive traits of haloalkalitolerant <i>Nitrospira</i> . ISME Journal, 2020, 14, 2967-2979.	4.4	52
20	Abiotic factors influence patterns of bacterial diversity and community composition in the Dry Valleys of Antarctica. FEMS Microbiology Ecology, 2020, 96, .	1.3	23
21	Activity and Metabolic Versatility of Complete Ammonia Oxidizers in Full-Scale Wastewater Treatment Systems. MBio, 2020, 11, .	1.8	65
22	Single cell analyses reveal contrasting life strategies of the two main nitrifiers in the ocean. Nature Communications, 2020, 11, 767.	5.8	67
23	Membrane Lipid Composition of the Moderately Thermophilic Ammonia-Oxidizing Archaeon <i>Candidatus Nitrosotenuis uzonensis</i> at Different Growth Temperatures. Applied and Environmental Microbiology, 2019, 85, .	1.4	31
24	Draft Genome Sequence of <i>Desulfosporosinus</i> sp. Strain Sb-LF, Isolated from an Acidic Peatland in Germany. Microbiology Resource Announcements, 2019, 8, .	0.3	8
25	Characterization of a thaumarchaeal symbiont that drives incomplete nitrification in the tropical sponge <i>Lanthella basta</i> . Environmental Microbiology, 2019, 21, 3831-3854.	1.8	50
26	Diversity decoupled from sulfur isotope fractionation in a sulfate-reducing microbial community. Geobiology, 2019, 17, 660-675.	1.1	7
27	A Bioinformatics Guide to Plant Microbiome Analysis. Frontiers in Plant Science, 2019, 10, 1313.	1.7	54
28	Expansion of <i>Thaumarchaeota</i> habitat range is correlated with horizontal transfer of ATPase operons. ISME Journal, 2019, 13, 3067-3079.	4.4	59
29	Draft Genome Sequence of <i>Desulfosporosinus fructosivorans</i> Strain 63.6F T , Isolated from Marine Sediment in the Baltic Sea. Microbiology Resource Announcements, 2019, 8, .	0.3	1
30	A fiber-deprived diet disturbs the fine-scale spatial architecture of the murine colon microbiome. Nature Communications, 2019, 10, 4366.	5.8	82
31	Indications for enzymatic denitrification to N ₂ O at low pH in an ammonia-oxidizing archaeon. ISME Journal, 2019, 13, 2633-2638.	4.4	35
32	Soil multifunctionality is affected by the soil environment and by microbial community composition and diversity. Soil Biology and Biochemistry, 2019, 136, 107521.	4.2	217
33	The cooling tower water microbiota: Seasonal dynamics and co-occurrence of bacterial and protist phylotypes. Water Research, 2019, 159, 464-479.	5.3	51
34	Low yield and abiotic origin of N ₂ O formed by the complete nitrifier <i>Nitrospira inopinata</i> . Nature Communications, 2019, 10, 1836.	5.8	123
35	Widespread soil bacterium that oxidizes atmospheric methane. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8515-8524.	3.3	149
36	Glacial Runoff Promotes Deep Burial of Sulfur Cycling-Associated Microorganisms in Marine Sediments. Frontiers in Microbiology, 2019, 10, 2558.	1.5	16

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37	Hair eruption initiates and commensal skin microbiota aggravate adverse events of anti-EGFR therapy. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	23
38	Cyanate and urea are substrates for nitrification by Thaumarchaeota in the marine environment. <i>Nature Microbiology</i> , 2019, 4, 234-243.	5.9	103
39	Peatland <i>Acidobacteria</i> with a dissimilatory sulfur metabolism. <i>ISME Journal</i> , 2018, 12, 1729-1742.	4.4	168
40	Draft Genome Sequence of <i>Telmatospirillum siberiense</i> 26-4b1, an Acidotolerant Peatland Alphaproteobacterium Potentially Involved in Sulfur Cycling. <i>Genome Announcements</i> , 2018, 6, .	0.8	13
41	Genomic insights into the <i>Acidobacteria</i> reveal strategies for their success in terrestrial environments. <i>Environmental Microbiology</i> , 2018, 20, 1041-1063.	1.8	228
42	Application of stable isotope labelling techniques for the detection of active diazotrophs. <i>Environmental Microbiology</i> , 2018, 20, 44-61.	1.8	44
43	Microbial temperature sensitivity and biomass change explain soil carbon loss with warming. <i>Nature Climate Change</i> , 2018, 8, 885-889.	8.1	230
44	Genomic Insights Into the Acid Adaptation of Novel Methanotrophs Enriched From Acidic Forest Soils. <i>Frontiers in Microbiology</i> , 2018, 9, 1982.	1.5	23
45	Cultivation and Genomic Analysis of <i>Candidatus Nitrosocaldus islandicus</i> , an Obligately Thermophilic, Ammonia-Oxidizing Thaumarchaeon from a Hot Spring Biofilm in Graendalur Valley, Iceland. <i>Frontiers in Microbiology</i> , 2018, 9, 193.	1.5	76
46	Evaluation of Primers Targeting the Diazotroph Functional Gene and Development of NifMAP – A Bioinformatics Pipeline for Analyzing nifH Amplicon Data. <i>Frontiers in Microbiology</i> , 2018, 9, 703.	1.5	50
47	Distinct Microbial Assemblage Structure and Archaeal Diversity in Sediments of Arctic Thermokarst Lakes Differing in Methane Sources. <i>Frontiers in Microbiology</i> , 2018, 9, 1192.	1.5	25
48	Characterization of the First <i>Candidatus Nitrotoga</i> Isolate Reveals Metabolic Versatility and Separate Evolution of Widespread Nitrite-Oxidizing Bacteria. <i>MBio</i> , 2018, 9, .	1.8	112
49	Ammonia-oxidising archaea living at low pH: Insights from comparative genomics. <i>Environmental Microbiology</i> , 2017, 19, 4939-4952.	1.8	107
50	Chemosynthetic symbionts of marine invertebrate animals are capable of nitrogen fixation. <i>Nature Microbiology</i> , 2017, 2, 16195.	5.9	151
51	AmoA-Targeted Polymerase Chain Reaction Primers for the Specific Detection and Quantification of Comammox <i>Nitrospira</i> in the Environment. <i>Frontiers in Microbiology</i> , 2017, 8, 1508.	1.5	313
52	Bottled aqua incognita: microbiota assembly and dissolved organic matter diversity in natural mineral waters. <i>Microbiome</i> , 2017, 5, 126.	4.9	26
53	Diversity analysis of sulfite- and sulfate-reducing microorganisms by multiplex <i>dsrA</i> and <i>dsrB</i> amplicon sequencing using new primers and mock community-optimized bioinformatics. <i>Environmental Microbiology</i> , 2016, 18, 2994-3009.	1.8	98
54	Insights into the metabolism of the high temperature microbial community of Tramway Ridge, Mount Erebus, Antarctica. <i>Antarctic Science</i> , 2016, 28, 241-249.	0.5	4

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55	Biotransformation of Two Pharmaceuticals by the Ammonia-Oxidizing Archaeon <i>Nitrososphaera gargensis</i> . <i>Environmental Science & Technology</i> , 2016, 50, 4682-4692.	4.6	68
56	Temporal, regional and geochemical drivers of microbial community variation in the melt ponds of the Ross Sea region, Antarctica. <i>Polar Biology</i> , 2016, 39, 267-282.	0.5	6
57	Benthic microbial communities of coastal terrestrial and ice shelf Antarctic meltwater ponds. <i>Frontiers in Microbiology</i> , 2015, 6, 485.	1.5	28
58	A flexible and economical barcoding approach for highly multiplexed amplicon sequencing of diverse target genes. <i>Frontiers in Microbiology</i> , 2015, 6, 731.	1.5	164
59	Cyanate as an energy source for nitrifiers. <i>Nature</i> , 2015, 524, 105-108.	13.7	231
60	Complete nitrification by <i>Nitrospira</i> bacteria. <i>Nature</i> , 2015, 528, 504-509.	13.7	1,878
61	Expanded metabolic versatility of ubiquitous nitrite-oxidizing bacteria from the genus <i>Nitrospira</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11371-11376.	3.3	439
62	Evidence of global-scale aeolian dispersal and endemism in isolated geothermal microbial communities of Antarctica. <i>Nature Communications</i> , 2014, 5, 3875.	5.8	76
63	Influence of soil properties on archaeal diversity and distribution in the McMurdo Dry Valleys, Antarctica. <i>FEMS Microbiology Ecology</i> , 2014, 89, 347-359.	1.3	44
64	Characterisation of bacterioplankton communities in the meltwater ponds of Bratina Island, Victoria Land, Antarctica. <i>FEMS Microbiology Ecology</i> , 2014, 89, 451-464.	1.3	20
65	Microbial Ecology of Geothermal Habitats in Antarctica. , 2014, , 181-215.		22
66	Local and regional influences over soil microbial metacommunities in the Transantarctic Mountains. <i>Ecosphere</i> , 2013, 4, 1-24.	1.0	45
67	Phylogenetic Delineation of the Novel Phylum Armatimonadetes (Former Candidate Division OP10) and Definition of Two Novel Candidate Divisions. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2484-2487.	1.4	21
68	<i>Bacillus simplex</i> —A Little Known PGPB with Anti-Fungal Activity—Alters Pea Legume Root Architecture and Nodule Morphology When Coinoculated with <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> . <i>Agronomy</i> , 2013, 3, 595-620.	1.3	97
69	Groundtruthing Next-Gen Sequencing for Microbial Ecology—Biases and Errors in Community Structure Estimates from PCR Amplicon Pyrosequencing. <i>PLoS ONE</i> , 2012, 7, e44224.	1.1	145
70	An automated dye-dilution based seepage meter for the time-series measurement of submarine groundwater discharge. <i>Limnology and Oceanography: Methods</i> , 2011, 1, 16-28.	1.0	24
71	Genome beginnings: rooting the tree of life. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2009, 364, 2177-2185.	1.8	69
72	Evidence for a New Root of the Tree of Life. <i>Systematic Biology</i> , 2008, 57, 835-843.	2.7	31

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73	Evidence for a Gram-positive, Eubacterial Root of the Tree of Life. <i>Molecular Biology and Evolution</i> , 2007, 24, 1761-1768.	3.5	46
74	Rooting the Tree of Life Using Nonubiquitous Genes. <i>Molecular Biology and Evolution</i> , 2007, 24, 130-136.	3.5	39
75	Evidence Excluding the Root of the Tree of Life from the Actinobacteria. <i>Molecular Biology and Evolution</i> , 2007, 25, 1-4.	3.5	69
76	Evidence that the Root of the Tree of Life Is Not within the Archaea. <i>Molecular Biology and Evolution</i> , 2006, 23, 1648-1651.	3.5	25
77	Decoding the genomic tree of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 6608-6613.	3.3	70
78	Salt marsh submarine groundwater discharge as traced by radium isotopes. <i>Marine Chemistry</i> , 2003, 84, 113-121.	0.9	89
79	An automated dye dilution based seepage meter for the time series measurement of submarine groundwater discharge. <i>Limnology and Oceanography: Methods</i> , 2003, 1, 16-28.	1.0	54
80	Dissolved Iron Cycling in the Subterranean Estuary of a Coastal Bay: Waquoit Bay, Massachusetts. <i>Biological Bulletin</i> , 2002, 203, 255-256.	0.7	51
81	Cytochrome c unfolding on an anionic surface. <i>Journal of Chromatography A</i> , 1999, 863, 137-146.	1.8	26