

David M Ward

List of Publications by Year in descending order

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95
papers

10,765
citations

30070

54
h-index

46799

89
g-index

97
all docs

97
docs citations

97
times ranked

7037
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Allochrochromatium tepidum</i> , sp. nov., a hot spring species of purple sulfur bacteria. <i>Archives of Microbiology</i> , 2022, 204, 115.	2.2	9
2	Relationship between Microorganisms Inhabiting Alkaline Siliceous Hot Spring Mat Communities and Overflowing Water. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	1
3	Biogeography of American Northwest Hot Spring A/B ϵ ² -Lineage <i>Synechococcus</i> Populations. <i>Frontiers in Microbiology</i> , 2020, 11, 77.	3.5	24
4	Short-Term Stable Isotope Probing of Proteins Reveals Taxa Incorporating Inorganic Carbon in a Hot Spring Microbial Mat. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	7
5	<i>Candidatus Thermonerobacter thiotrophicus</i> , a Non-phototrophic Member of the Bacteroidetes/Chlorobi With Dissimilatory Sulfur Metabolism in Hot Spring Mat Communities. <i>Frontiers in Microbiology</i> , 2018, 9, 3159.	3.5	57
6	A Panoply of Phototrophs: An Overview of the Thermophilic Chlorophototrophs of the Microbial Mats of Alkaline Siliceous Hot Springs in Yellowstone National Park, WY, USA. , 2017, , 87-137.		62
7	The Dark Side of the Mushroom Spring Microbial Mat: Life in the Shadow of Chlorophototrophs. II. Metabolic Functions of Abundant Community Members Predicted from Metagenomic Analyses. <i>Frontiers in Microbiology</i> , 2017, 8, 943.	3.5	100
8	The Dark Side of the Mushroom Spring Microbial Mat: Life in the Shadow of Chlorophototrophs. I. Microbial Diversity Based on 16S rRNA Gene Amplicons and Metagenomic Sequencing. <i>Frontiers in Microbiology</i> , 2016, 7, 919.	3.5	123
9	<i>In Situ</i> Hydrogen Dynamics in a Hot Spring Microbial Mat during a Diel Cycle. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4209-4217.	3.1	20
10	The molecular dimension of microbial species: 1. Ecological distinctions among, and homogeneity within, putative ecotypes of <i>Synechococcus</i> inhabiting the cyanobacterial mat of Mushroom Spring, Yellowstone National Park. <i>Frontiers in Microbiology</i> , 2015, 6, 590.	3.5	49
11	The molecular dimension of microbial species: 3. Comparative genomics of <i>Synechococcus</i> strains with different light responses and <i>in situ</i> diel transcription patterns of associated putative ecotypes in the Mushroom Spring microbial mat. <i>Frontiers in Microbiology</i> , 2015, 6, 604.	3.5	67
12	The molecular dimension of microbial species: 2. <i>Synechococcus</i> strains representative of putative ecotypes inhabiting different depths in the Mushroom Spring microbial mat exhibit different adaptive and acclimative responses to light. <i>Frontiers in Microbiology</i> , 2015, 6, 626.	3.5	56
13	Diel metabolomics analysis of a hot spring chlorophototrophic microbial mat leads to new hypotheses of community member metabolisms. <i>Frontiers in Microbiology</i> , 2015, 6, 209.	3.5	104
14	Draft Genome Sequence of the Deinococcus-Thermus Bacterium <i>Meiothermus ruber</i> Strain A. <i>Genome Announcements</i> , 2015, 3, .	0.8	8
15	Recombination Does Not Hinder Formation or Detection of Ecological Species of <i>Synechococcus</i> Inhabiting a Hot Spring Cyanobacterial Mat. <i>Frontiers in Microbiology</i> , 2015, 6, 1540.	3.5	16
16	Draft Genome Sequence of a Sulfide-Oxidizing, Autotrophic Filamentous Anoxygenic Phototrophic Bacterium, <i>Chloroflexus</i> sp. Strain MS-G (<i>Chloroflexi</i>). <i>Genome Announcements</i> , 2014, 2, .	0.8	18
17	Automated Data Extraction from <i>In Situ</i> Protein-Stable Isotope Probing Studies. <i>Journal of Proteome Research</i> , 2014, 13, 1200-1210.	3.7	20
18	Temporal metatranscriptomic patterning in phototrophic <i>Chloroflexi</i> inhabiting a microbial mat in a geothermal spring. <i>ISME Journal</i> , 2013, 7, 1775-1789.	9.8	168

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19	Effects of petroleum mixture types on soil bacterial population dynamics associated with the biodegradation of hydrocarbons in soil environments. <i>FEMS Microbiology Ecology</i> , 2013, 85, 168-178.	2.7	47
20	Community Structure and Function of High-Temperature Chlorophototrophic Microbial Mats Inhabiting Diverse Geothermal Environments. <i>Frontiers in Microbiology</i> , 2013, 4, 106.	3.5	112
21	Identification and Distribution of High-Abundance Proteins in the Octopus Spring Microbial Mat Community. <i>Applied and Environmental Microbiology</i> , 2012, 78, 8481-8484.	3.1	13
22	Functional Genomics in an Ecological and Evolutionary Context: Maximizing the Value of Genomes in Systems Biology. <i>Advances in Photosynthesis and Respiration</i> , 2012, , 1-16.	1.0	7
23	â€ˆ<i>Candidatus</i> <i>Thermochlorobacter aerophilum</i> :â€™ an aerobic chlorophotoheterotrophic member of the phylum <i>Chlorobi</i> defined by metagenomics and metatranscriptomics. <i>ISME Journal</i> , 2012, 6, 1869-1882.	9.8	108
24	Cyanobacteria in Geothermal Habitats. , 2012, , 39-63.		77
25	Comparative and Functional Genomics of Anoxygenic Green Bacteria from the Taxa <i>Chlorobi</i> , <i>Chloroflexi</i> , and <i>Acidobacteria</i> . <i>Advances in Photosynthesis and Respiration</i> , 2012, , 47-102.	1.0	145
26	Complete genome of <i>Candidatus</i> <i>Chloracidobacterium thermophilum</i> , a chlorophyllâ€¢based photoheterotroph belonging to the phylum <i>Acidobacteria</i>. <i>Environmental Microbiology</i> , 2012, 14, 177-190.	3.8	79
27	Fine-Scale Distribution Patterns of <i>Synechococcus</i> Ecological Diversity in Microbial Mats of Mushroom Spring, Yellowstone National Park. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7689-7697.	3.1	72
28	Community ecology of hot spring cyanobacterial mats: predominant populations and their functional potential. <i>ISME Journal</i> , 2011, 5, 1262-1278.	9.8	206
29	Influence of Molecular Resolution on Sequence-Based Discovery of Ecological Diversity among <i>Synechococcus</i> Populations in an Alkaline Siliceous Hot Spring Microbial Mat. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1359-1367.	3.1	44
30	Metatranscriptomic analyses of chlorophototrophs of a hot-spring microbial mat. <i>ISME Journal</i> , 2011, 5, 1279-1290.	9.8	101
31	Cultivation and Genomic, Nutritional, and Lipid Biomarker Characterization of <i>Roseiflexus</i> Strains Closely Related to Predominant <i>In Situ</i> Populations Inhabiting Yellowstone Hot Spring Microbial Mats. <i>Journal of Bacteriology</i> , 2010, 192, 3033-3042.	2.2	100
32	In silico approaches to study mass and energy flows in microbial consortia: a syntrophic case study. <i>BMC Systems Biology</i> , 2009, 3, 114.	3.0	96
33	Regulation of <i>nif</i> gene expression and the energetics of N ₂ fixation over the diel cycle in a hot spring microbial mat. <i>ISME Journal</i> , 2008, 2, 364-378.	9.8	133
34	Assessing Soil Microbial Populations Responding to Crude-Oil Amendment at Different Temperatures Using Phylogenetic, Functional Gene (<i>alkB</i>) and Physiological Analyses. <i>Environmental Science & Technology</i> , 2008, 42, 7580-7586.	10.0	50
35	Identifying the fundamental units of bacterial diversity: A paradigm shift to incorporate ecology into bacterial systematics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 2504-2509.	7.1	286
36	Archaeal and Bacterial Glycerol Dialkyl Glycerol Tetraether Lipids in Hot Springs of Yellowstone National Park. <i>Applied and Environmental Microbiology</i> , 2007, 73, 6181-6191.	3.1	150

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37	Competitive Fitness of Isolates Enriched on Phenanthrene Sorbed to Model Phases. Applied and Environmental Microbiology, 2007, 73, 4074-4077.	3.1	2
38	<i>Candidatus</i> Chloracidobacterium thermophilum: An Aerobic Phototrophic Acidobacterium. Science, 2007, 317, 523-526.	12.6	384
39	Population level functional diversity in a microbial community revealed by comparative genomic and metagenomic analyses. ISME Journal, 2007, 1, 703-713.	9.8	216
40	Impact of carbon metabolism on ^{13}C signatures of cyanobacteria and green non-sulfur-like bacteria inhabiting a microbial mat from an alkaline siliceous hot spring in Yellowstone National Park (USA). Environmental Microbiology, 2007, 9, 482-491.	3.8	54
41	Comparative genomics provides evidence for the 3-hydroxypropionate autotrophic pathway in filamentous anoxygenic phototrophic bacteria and in hot spring microbial mats. Environmental Microbiology, 2007, 9, 2067-2078.	3.8	131
42	Effect of Temperature and Light on Growth of and Photosynthesis by Synechococcus Isolates Typical of Those Predominating in the Octopus Spring Microbial Mat Community of Yellowstone National Park. Applied and Environmental Microbiology, 2006, 72, 544-550.	3.1	176
43	Microbial diversity in natural environments: focusing on fundamental questions. Antonie Van Leeuwenhoek, 2006, 90, 309-324.	1.7	33
44	Cyanobacterial ecotypes in the microbial mat community of Mushroom Spring (Yellowstone National) function. Philosophical Transactions of the Royal Society B: Biological Sciences, 2006, 361, 1997-2008.	4.0	183
45	Microbial Population Dynamics Associated with Crude-Oil Biodegradation in Diverse Soils. Applied and Environmental Microbiology, 2006, 72, 6316-6324.	3.1	196
46	In situ analysis of nitrogen fixation and metabolic switching in unicellular thermophilic cyanobacteria inhabiting hot spring microbial mats. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2398-2403.	7.1	239
47	A Macrobiological Perspective on Microbial Species. Microbe Magazine, 2006, 1, 269-278.	0.4	25
48	Diversity and Functional Analysis of Bacterial Communities Associated with Natural Hydrocarbon Seeps in Acidic Soils at Rainbow Springs, Yellowstone National Park. Applied and Environmental Microbiology, 2005, 71, 5943-5950.	3.1	82
49	Diel Variations in Carbon Metabolism by Green Nonsulfur-Like Bacteria in Alkaline Siliceous Hot Spring Microbial Mats from Yellowstone National Park. Applied and Environmental Microbiology, 2005, 71, 3978-3986.	3.1	130
50	The importance of physical isolation to microbial diversification. FEMS Microbiology Ecology, 2004, 48, 293-303.	2.7	170
51	Geographical isolation in hot spring cyanobacteria. Environmental Microbiology, 2003, 5, 650-659.	3.8	446
52	Compound-Specific Isotopic Fractionation Patterns Suggest Different Carbon Metabolisms among Chloroflexus-Like Bacteria in Hot-Spring Microbial Mats. Applied and Environmental Microbiology, 2003, 69, 6000-6006.	3.1	57
53	Cyanobacterial Ecotypes in Different Optical Microenvironments of a 68°C Hot Spring Mat Community Revealed by 16S-23S rRNA Internal Transcribed Spacer Region Variation. Applied and Environmental Microbiology, 2003, 69, 2893-2898.	3.1	96
54	Microscopic Examination of Distribution and Phenotypic Properties of Phylogenetically Diverse Chloroflexaceae-Related Bacteria in Hot Spring Microbial Mats. Applied and Environmental Microbiology, 2002, 68, 4593-4603.	3.1	101

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55	Alkane-1,2-diol-based glycosides and fatty glycosides and wax esters in <i>Roseiflexus castenholzii</i> and hot spring microbial mats. <i>Archives of Microbiology</i> , 2002, 178, 229-237.	2.2	37
56	Diversity and Distribution in Hypersaline Microbial Mats of Bacteria Related to <i>Chloroflexus</i> spp. <i>Applied and Environmental Microbiology</i> , 2001, 67, 4365-4371.	3.1	89
57	Biosynthetic Controls on the ¹³ C Contents of Organic Components in the Photoautotrophic Bacterium <i>Chloroflexus aurantiacus</i> . <i>Journal of Biological Chemistry</i> , 2001, 276, 10971-10976.	3.4	77
58	Use of 16S rRNA, Lipid, and Naturally Preserved Components of Hot Spring Mats and Microorganisms to Help Interpret the Record of Microbial Evolution. , 2001, , 167-181.		2
59	Autotrophy of green non-sulphur bacteria in hot spring microbial mats: biological explanations for isotopically heavy organic carbon in the geological record. <i>Environmental Microbiology</i> , 2000, 2, 428-435.	3.8	100
60	Highly Ordered Vertical Structure of <i>Synechococcus</i> Populations within the One-Millimeter-Thick Photic Zone of a Hot Spring Cyanobacterial Mat. <i>Applied and Environmental Microbiology</i> , 2000, 66, 1038-1049.	3.1	138
61	Effect of Model Sorptive Phases on Phenanthrene Biodegradation: Different Enrichment Conditions Influence Bioavailability and Selection of Phenanthrene-Degrading Isolates. <i>Applied and Environmental Microbiology</i> , 2000, 66, 2695-2702.	3.1	71
62	Molecular Analysis of Surfactant-Driven Microbial Population Shifts in Hydrocarbon-Contaminated Soil. <i>Applied and Environmental Microbiology</i> , 2000, 66, 2959-2964.	3.1	93
63	Cyanobacteria in Geothermal Habitats. , 2000, , 37-59.		13
64	All-cis hentriaconta-9,15,22-triene in microbial mats formed by the phototrophic prokaryote <i>Chloroflexus</i> . <i>Organic Geochemistry</i> , 1999, 30, 1585-1587.	1.8	21
65	A natural species concept for prokaryotes. <i>Current Opinion in Microbiology</i> , 1998, 1, 271-277.	5.1	168
66	A Natural View of Microbial Biodiversity within Hot Spring Cyanobacterial Mat Communities. <i>Microbiology and Molecular Biology Reviews</i> , 1998, 62, 1353-1370.	6.6	531
67	Biodiversity within hot spring microbial mat communities: molecular monitoring of enrichment cultures. <i>Antonie Van Leeuwenhoek</i> , 1997, 71, 143-150.	1.7	86
68	Diverse <i>Thermolus</i> Species Inhabit a Single Hot Spring Microbial Mat. <i>Systematic and Applied Microbiology</i> , 1995, 18, 274-278.	2.8	43
69	Methods for extracting RNA or ribosomes from microbial mats and cultivated microorganisms. , 1995, , 31-44.		3
70	Species diversity in hot spring microbial mats as revealed by both molecular and enrichment culture approaches â€” relationship between biodiversity and community structure. , 1994, , 33-44.		36
71	Biogeochemistry of hot spring environments. <i>Chemical Geology</i> , 1992, 95, 327-345.	3.3	57
72	Biogeochemistry of hot spring environments. <i>Chemical Geology</i> , 1992, 95, 347-360.	3.3	53

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73	Ribosomal RNA Analysis of Microorganisms as They Occur in Nature. <i>Advances in Microbial Ecology</i> , 1992, , 219-286.	0.1	379
74	Comparative analysis of extractable lipids in hot spring microbial mats and their component photosynthetic bacteria. <i>Organic Geochemistry</i> , 1991, 17, 309-319.	1.8	100
75	16S rRNA sequences reveal uncultured inhabitants of a well-studied thermal community. <i>FEMS Microbiology Letters</i> , 1990, 75, 105-115.	1.8	112
76	16S rRNA sequences reveal numerous uncultured microorganisms in a natural community. <i>Nature</i> , 1990, 345, 63-65.	27.8	1,329
77	Comparative Analysis of 16S Ribosomal RNA Sequences of <i>Thermus</i> Species. <i>Systematic and Applied Microbiology</i> , 1990, 13, 8-13.	2.8	23
78	Mid-chain branched mono- and dimethyl alkanes in hot spring cyanobacterial mats: A direct biogenic source for branched alkanes in ancient sediments?. <i>Organic Geochemistry</i> , 1990, 15, 223-231.	1.8	217
79	16S rRNA sequences reveal uncultured inhabitants of a well-studied thermal community. <i>FEMS Microbiology Letters</i> , 1990, 75, 105-115.	1.8	1
80	Comparative Analysis of 16S Ribosomal RNA Sequences of Thermophilic Fermentative Bacteria Isolated from Hot Spring Cyanobacterial Mats. <i>Systematic and Applied Microbiology</i> , 1989, 12, 1-7.	2.8	37
81	Selective Recovery of 16S rRNA Sequences from Natural Microbial Communities in the Form of cDNA. <i>Applied and Environmental Microbiology</i> , 1989, 55, 1818-1822.	3.1	105
82	Distinctive hydrocarbon biomarkers from fossiliferous sediment of the Late Proterozoic Walcott Member, Chuar Group, Grand Canyon, Arizona. <i>Geochimica Et Cosmochimica Acta</i> , 1988, 52, 2625-2637.	3.9	193
83	Photoexcretion and Fate of Glycolate in a Hot Spring Cyanobacterial Mat. <i>Applied and Environmental Microbiology</i> , 1988, 54, 1738-1743.	3.1	157
84	Formation and Fate of Fermentation Products in Hot Spring Cyanobacterial Mats. <i>Applied and Environmental Microbiology</i> , 1987, 53, 2343-2352.	3.1	124
85	Use of <i>Chloroflexus</i> -Specific Antiserum To Evaluate Filamentous Bacteria of a Hot Spring Microbial Mat. <i>Applied and Environmental Microbiology</i> , 1987, 53, 1962-1964.	3.1	12
86	Microelectrode Studies of Interstitial Water Chemistry and Photosynthetic Activity in a Hot Spring Microbial Mat. <i>Applied and Environmental Microbiology</i> , 1984, 48, 270-275.	3.1	123
87	Substrates for Sulfate Reduction and Methane Production in Intertidal Sediments. <i>Applied and Environmental Microbiology</i> , 1983, 45, 193-199.	3.1	183
88	Oxygen Microelectrode That Is Insensitive to Medium Chemical Composition: Use in an Acid Microbial Mat Dominated by <i>Cyanidium caldarium</i> . <i>Applied and Environmental Microbiology</i> , 1983, 45, 755-759.	3.1	189
89	Impact of crude oil on sulphate reduction and methane production in sediments impacted by the Amoco Cadiz oil spill. <i>Marine Environmental Research</i> , 1982, 7, 175-194.	2.5	4
90	Temperature Adaptations in the Terminal Processes of Anaerobic Decomposition of Yellowstone National Park and Icelandic Hot Spring Microbial Mats. <i>Applied and Environmental Microbiology</i> , 1982, 44, 844-851.	3.1	39

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91	Vertical distribution of sulfate reduction, methane production, and bacteria in marine sediments. Geomicrobiology Journal, 1981, 2, 341-362.	2.0	23
92	Fate of Immediate Methane Precursors in Low-Sulfate, Hot-Spring Algal-Bacterial Mats. Applied and Environmental Microbiology, 1981, 41, 775-782.	3.1	62
93	Terminal Processes in the Anaerobic Degradation of an Algal-Bacterial Mat in a High-Sulfate Hot Spring. Applied and Environmental Microbiology, 1980, 40, 67-74.	3.1	49
94	Anaerobic metabolism of hexadecane in sediments. Geomicrobiology Journal, 1978, 1, 1-9.	2.0	44
95	Hydrocarbon Biodegradation in Hypersaline Environments. Applied and Environmental Microbiology, 1978, 35, 353-359.	3.1	183