

# David M Ward

## List of Publications by Year in descending order

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95  
papers

10,765  
citations

29994

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48187

88  
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97  
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97  
docs citations

97  
times ranked

7037  
citing authors

#	ARTICLE	IF	CITATIONS
1	16S rRNA sequences reveal numerous uncultured microorganisms in a natural community. <i>Nature</i> , 1990, 345, 63-65.	13.7	1,329
2	A Natural View of Microbial Biodiversity within Hot Spring Cyanobacterial Mat Communities. <i>Microbiology and Molecular Biology Reviews</i> , 1998, 62, 1353-1370.	2.9	531
3	Geographical isolation in hot spring cyanobacteria. <i>Environmental Microbiology</i> , 2003, 5, 650-659.	1.8	446
4	<i>Candidatus</i> Chloracidobacterium thermophilum: An Aerobic Phototrophic Acidobacterium. <i>Science</i> , 2007, 317, 523-526.	6.0	384
5	Ribosomal RNA Analysis of Microorganisms as They Occur in Nature. <i>Advances in Microbial Ecology</i> , 1992, , 219-286.	0.1	379
6	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.	3.3	286
7	In situ analysis of nitrogen fixation and metabolic switching in unicellular thermophilic cyanobacteria inhabiting hot spring microbial mats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2398-2403.	3.3	239
8	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.	0.9	217
9	Population level functional diversity in a microbial community revealed by comparative genomic and metagenomic analyses. <i>ISME Journal</i> , 2007, 1, 703-713.	4.4	216
10	Community ecology of hot spring cyanobacterial mats: predominant populations and their functional potential. <i>ISME Journal</i> , 2011, 5, 1262-1278.	4.4	206
11	Microbial Population Dynamics Associated with Crude-Oil Biodegradation in Diverse Soils. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6316-6324.	1.4	196
12	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.	1.6	193
13	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.	1.4	189
14	Cyanobacterial ecotypes in the microbial mat community of Mushroom Spring (Yellowstone National) function. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 1997-2008.	1.8	183
15	Hydrocarbon Biodegradation in Hypersaline Environments. <i>Applied and Environmental Microbiology</i> , 1978, 35, 353-359.	1.4	183
16	Substrates for Sulfate Reduction and Methane Production in Intertidal Sediments. <i>Applied and Environmental Microbiology</i> , 1983, 45, 193-199.	1.4	183
17	Effect of Temperature and Light on Growth of and Photosynthesis by <i>Synechococcus</i> Isolates Typical of Those Predominating in the Octopus Spring Microbial Mat Community of Yellowstone National Park. <i>Applied and Environmental Microbiology</i> , 2006, 72, 544-550.	1.4	176
18	The importance of physical isolation to microbial diversification. <i>FEMS Microbiology Ecology</i> , 2004, 48, 293-303.	1.3	170

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19	A natural species concept for prokaryotes. <i>Current Opinion in Microbiology</i> , 1998, 1, 271-277.	2.3	168
20	Temporal metatranscriptomic patterning in phototrophic Chloroflexi inhabiting a microbial mat in a geothermal spring. <i>ISME Journal</i> , 2013, 7, 1775-1789.	4.4	168
21	Photoexcretion and Fate of Glycolate in a Hot Spring Cyanobacterial Mat. <i>Applied and Environmental Microbiology</i> , 1988, 54, 1738-1743.	1.4	157
22	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.	1.4	150
23	Comparative and Functional Genomics of Anoxygenic Green Bacteria from the Taxa Chlorobi, Chloroflexi, and Acidobacteria. <i>Advances in Photosynthesis and Respiration</i> , 2012, , 47-102.	1.0	145
24	Highly Ordered Vertical Structure of Synechococcus Populations within the One-Millimeter-Thick Photic Zone of a Hot Spring Cyanobacterial Mat. <i>Applied and Environmental Microbiology</i> , 2000, 66, 1038-1049.	1.4	138
25	Regulation of <i>nif</i> gene expression and the energetics of N <sub>2</sub> fixation over the diel cycle in a hot spring microbial mat. <i>ISME Journal</i> , 2008, 2, 364-378.	4.4	133
26	Comparative genomics provides evidence for the 3-hydroxypropionate autotrophic pathway in filamentous anoxygenic phototrophic bacteria and in hot spring microbial mats. <i>Environmental Microbiology</i> , 2007, 9, 2067-2078.	1.8	131
27	Diel Variations in Carbon Metabolism by Green Nonsulfur-Like Bacteria in Alkaline Siliceous Hot Spring Microbial Mats from Yellowstone National Park. <i>Applied and Environmental Microbiology</i> , 2005, 71, 3978-3986.	1.4	130
28	Formation and Fate of Fermentation Products in Hot Spring Cyanobacterial Mats. <i>Applied and Environmental Microbiology</i> , 1987, 53, 2343-2352.	1.4	124
29	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.	1.5	123
30	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.	1.4	123
31	16S rRNA sequences reveal uncultured inhabitants of a well-studied thermal community. <i>FEMS Microbiology Letters</i> , 1990, 75, 105-115.	0.7	112
32	Community Structure and Function of High-Temperature Chlorophototrophic Microbial Mats Inhabiting Diverse Geothermal Environments. <i>Frontiers in Microbiology</i> , 2013, 4, 106.	1.5	112
33	<i>Candidatus</i> <i>Thermochlorobacter aerophilum</i> : an aerobic chlorophotoheterotrophic member of the phylum Chlorobi defined by metagenomics and metatranscriptomics. <i>ISME Journal</i> , 2012, 6, 1869-1882.	4.4	108
34	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.	1.4	105
35	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.	1.5	104
36	Microscopic Examination of Distribution and Phenotypic Properties of Phylogenetically Diverse Chloroflexaceae-Related Bacteria in Hot Spring Microbial Mats. <i>Applied and Environmental Microbiology</i> , 2002, 68, 4593-4603.	1.4	101

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37	Metatranscriptomic analyses of chlorophototrophs of a hot-spring microbial mat. ISME Journal, 2011, 5, 1279-1290.	4.4	101
38	Comparative analysis of extractable lipids in hot spring microbial mats and their component photosynthetic bacteria. Organic Geochemistry, 1991, 17, 309-319.	0.9	100
39	Autotrophy of green non-sulphur bacteria in hot spring microbial mats: biological explanations for isotopically heavy organic carbon in the geological record. Environmental Microbiology, 2000, 2, 428-435.	1.8	100
40	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. Journal of Bacteriology, 2010, 192, 3033-3042.	1.0	100
41	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. Frontiers in Microbiology, 2017, 8, 943.	1.5	100
42	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.	1.4	96
43	In silico approaches to study mass and energy flows in microbial consortia: a syntrophic case study. BMC Systems Biology, 2009, 3, 114.	3.0	96
44	Molecular Analysis of Surfactant-Driven Microbial Population Shifts in Hydrocarbon-Contaminated Soil. Applied and Environmental Microbiology, 2000, 66, 2959-2964.	1.4	93
45	Diversity and Distribution in Hypersaline Microbial Mats of Bacteria Related to Chloroflexus spp. Applied and Environmental Microbiology, 2001, 67, 4365-4371.	1.4	89
46	Biodiversity within hot spring microbial mat communities: molecular monitoring of enrichment cultures. Antonie Van Leeuwenhoek, 1997, 71, 143-150.	0.7	86
47	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.	1.4	82
48	Complete genome of <i>Candidatus</i> Chloracidobacterium thermophilum, a chlorophyll <i>a</i> -based photoheterotroph belonging to the phylum <i>Acidobacteria</i> . Environmental Microbiology, 2012, 14, 177-190.	1.8	79
49	Biosynthetic Controls on the <sup>13</sup> C Contents of Organic Components in the Photoautotrophic Bacterium Chloroflexus aurantiacus. Journal of Biological Chemistry, 2001, 276, 10971-10976.	1.6	77
50	Cyanobacteria in Geothermal Habitats. , 2012, , 39-63.		77
51	Fine-Scale Distribution Patterns of Synechococcus Ecological Diversity in Microbial Mats of Mushroom Spring, Yellowstone National Park. Applied and Environmental Microbiology, 2011, 77, 7689-7697.	1.4	72
52	Effect of Model Sorptive Phases on Phenanthrene Biodegradation: Different Enrichment Conditions Influence Bioavailability and Selection of Phenanthrene-Degrading Isolates. Applied and Environmental Microbiology, 2000, 66, 2695-2702.	1.4	71
53	The molecular dimension of microbial species: 3. Comparative genomics of Synechococcus strains with different light responses and in situ diel transcription patterns of associated putative ecotypes in the Mushroom Spring microbial mat. Frontiers in Microbiology, 2015, 6, 604.	1.5	67
54	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

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55	Fate of Immediate Methane Precursors in Low-Sulfate, Hot-Spring Algal-Bacterial Mats. Applied and Environmental Microbiology, 1981, 41, 775-782.	1.4	62
56	Biogeochemistry of hot spring environments. Chemical Geology, 1992, 95, 327-345.	1.4	57
57	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.	1.4	57
58	â€œCandidatus Thermomonobacter thiotrophicus,â€•A Non-phototrophic Member of the Bacteroidetes/Chlorobi With Dissimilatory Sulfur Metabolism in Hot Spring Mat Communities. Frontiers in Microbiology, 2018, 9, 3159.	1.5	57
59	The molecular dimension of microbial species: 2. Synechococcus strains representative of putative ecotypes inhabiting different depths in the Mushroom Spring microbial mat exhibit different adaptive and acclimative responses to light. Frontiers in Microbiology, 2015, 6, 626.	1.5	56
60	Impact of carbon metabolism on <sup>13</sup> 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.	1.8	54
61	Biogeochemistry of hot spring environments. Chemical Geology, 1992, 95, 347-360.	1.4	53
62	Assessing Soil Microbial Populations Responding to Crude-Oil Amendment at Different Temperatures Using Phylogenetic, Functional Gene (<i>alkB</i>) and Physiological Analyses. Environmental Science & Technology, 2008, 42, 7580-7586.	4.6	50
63	The molecular dimension of microbial species: 1. Ecological distinctions among, and homogeneity within, putative ecotypes of Synechococcus inhabiting the cyanobacterial mat of Mushroom Spring, Yellowstone National Park. Frontiers in Microbiology, 2015, 6, 590.	1.5	49
64	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.	1.4	49
65	Effects of petroleum mixture types on soil bacterial population dynamics associated with the biodegradation of hydrocarbons in soil environments. FEMS Microbiology Ecology, 2013, 85, 168-178.	1.3	47
66	Anaerobic metabolism of hexadecane in sediments. Geomicrobiology Journal, 1978, 1, 1-9.	1.0	44
67	Influence of Molecular Resolution on Sequence-Based Discovery of Ecological Diversity among <i>Synechococcus</i> Populations in an Alkaline Siliceous Hot Spring Microbial Mat. Applied and Environmental Microbiology, 2011, 77, 1359-1367.	1.4	44
68	Diverse Thermophilic Species Inhabit a Single Hot Spring Microbial Mat. Systematic and Applied Microbiology, 1995, 18, 274-278.	1.2	43
69	Temperature Adaptations in the Terminal Processes of Anaerobic Decomposition of Yellowstone National Park and Icelandic Hot Spring Microbial Mats. Applied and Environmental Microbiology, 1982, 44, 844-851.	1.4	39
70	Comparative Analysis of 16S Ribosomal RNA Sequences of Thermophilic Fermentative Bacteria Isolated from Hot Spring Cyanobacterial Mats. Systematic and Applied Microbiology, 1989, 12, 1-7.	1.2	37
71	Alkane-1,2-diol-based glycosides and fatty glycosides and wax esters in Roseiflexus castenholzii and hot spring microbial mats. Archives of Microbiology, 2002, 178, 229-237.	1.0	37
72	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

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73	Microbial diversity in natural environments: focusing on fundamental questions. Antonie Van Leeuwenhoek, 2006, 90, 309-324.	0.7	33
74	A Macrobiological Perspective on Microbial Species. Microbe Magazine, 2006, 1, 269-278.	0.4	25
75	Biogeography of American Northwest Hot Spring A/B <sup>2</sup> -Lineage Synechococcus Populations. Frontiers in Microbiology, 2020, 11, 77.	1.5	24
76	Vertical distribution of sulfate reduction, methane production, and bacteria in marine sediments. Geomicrobiology Journal, 1981, 2, 341-362.	1.0	23
77	Comparative Analysis of 16S Ribosomal RNA Sequences of Thermus Species. Systematic and Applied Microbiology, 1990, 13, 8-13.	1.2	23
78	All-cis hentriaconta-9,15,22-triene in microbial mats formed by the phototrophic prokaryote Chloroflexus. Organic Geochemistry, 1999, 30, 1585-1587.	0.9	21
79	Automated Data Extraction from <i>In Situ</i> Protein-Stable Isotope Probing Studies. Journal of Proteome Research, 2014, 13, 1200-1210.	1.8	20
80	<i>In Situ</i> Hydrogen Dynamics in a Hot Spring Microbial Mat during a Diel Cycle. Applied and Environmental Microbiology, 2016, 82, 4209-4217.	1.4	20
81	Draft Genome Sequence of a Sulfide-Oxidizing, Autotrophic Filamentous Anoxygenic Phototrophic Bacterium, <i>Chloroflexus</i> sp. Strain MS-G ( <i>Chloroflexi</i> ). Genome Announcements, 2014, 2, .	0.8	18
82	Recombination Does Not Hinder Formation or Detection of Ecological Species of Synechococcus Inhabiting a Hot Spring Cyanobacterial Mat. Frontiers in Microbiology, 2015, 6, 1540.	1.5	16
83	Cyanobacteria in Geothermal Habitats. , 2000, , 37-59.		13
84	Identification and Distribution of High-Abundance Proteins in the Octopus Spring Microbial Mat Community. Applied and Environmental Microbiology, 2012, 78, 8481-8484.	1.4	13
85	Use of <i>Chloroflexus</i> -Specific Antiserum To Evaluate Filamentous Bacteria of a Hot Spring Microbial Mat. Applied and Environmental Microbiology, 1987, 53, 1962-1964.	1.4	12
86	Allochromatium tepidum, sp. nov., a hot spring species of purple sulfur bacteria. Archives of Microbiology, 2022, 204, 115.	1.0	9
87	Draft Genome Sequence of the Deinococcus-Thermus Bacterium Meiothermus ruber Strain A. Genome Announcements, 2015, 3, .	0.8	8
88	Functional Genomics in an Ecological and Evolutionary Context: Maximizing the Value of Genomes in Systems Biology. Advances in Photosynthesis and Respiration, 2012, , 1-16.	1.0	7
89	Short-Term Stable Isotope Probing of Proteins Reveals Taxa Incorporating Inorganic Carbon in a Hot Spring Microbial Mat. Applied and Environmental Microbiology, 2020, 86, .	1.4	7
90	Impact of crude oil on sulphate reduction and methane production in sediments impacted by the Amoco Cadiz oil spill. Marine Environmental Research, 1982, 7, 175-194.	1.1	4

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91	Methods for extracting RNA or ribosomes from microbial mats and cultivated microorganisms. , 1995, , 31-44.		3
92	Competitive Fitness of Isolates Enriched on Phenanthrene Sorbed to Model Phases. Applied and Environmental Microbiology, 2007, 73, 4074-4077.	1.4	2
93	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
94	Relationship between Microorganisms Inhabiting Alkaline Siliceous Hot Spring Mat Communities and Overflowing Water. Applied and Environmental Microbiology, 2020, 86, .	1.4	1
95	16S rRNA sequences reveal uncultured inhabitants of a well-studied thermal community. , 0, .		1