

David M Ward

List of Publications by Year in descending order

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papers

10,765
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30070

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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. | 27.8 | 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. | 6.6 | 531 |
| 3 | Geographical isolation in hot spring cyanobacteria. <i>Environmental Microbiology</i> , 2003, 5, 650-659. | 3.8 | 446 |
| 4 | <i>Candidatus</i> Chloracidobacterium thermophilum: An Aerobic Phototrophic Acidobacterium. <i>Science</i> , 2007, 317, 523-526. | 12.6 | 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. | 7.1 | 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. | 7.1 | 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. | 1.8 | 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. | 9.8 | 216 |
| 10 | Community ecology of hot spring cyanobacterial mats: predominant populations and their functional potential. <i>ISME Journal</i> , 2011, 5, 1262-1278. | 9.8 | 206 |
| 11 | Microbial Population Dynamics Associated with Crude-Oil Biodegradation in Diverse Soils. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6316-6324. | 3.1 | 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. | 3.9 | 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. | 3.1 | 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. | 4.0 | 183 |
| 15 | Hydrocarbon Biodegradation in Hypersaline Environments. <i>Applied and Environmental Microbiology</i> , 1978, 35, 353-359. | 3.1 | 183 |
| 16 | Substrates for Sulfate Reduction and Methane Production in Intertidal Sediments. <i>Applied and Environmental Microbiology</i> , 1983, 45, 193-199. | 3.1 | 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. | 3.1 | 176 |
| 18 | The importance of physical isolation to microbial diversification. <i>FEMS Microbiology Ecology</i> , 2004, 48, 293-303. | 2.7 | 170 |

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|----|---|-----|-----------|
| 19 | A natural species concept for prokaryotes. <i>Current Opinion in Microbiology</i> , 1998, 1, 271-277. | 5.1 | 168 |
| 20 | Temporal metatranscriptomic patterning in phototrophic Chloroflexi inhabiting a microbial mat in a geothermal spring. <i>ISME Journal</i> , 2013, 7, 1775-1789. | 9.8 | 168 |
| 21 | Photoexcretion and Fate of Glycolate in a Hot Spring Cyanobacterial Mat. <i>Applied and Environmental Microbiology</i> , 1988, 54, 1738-1743. | 3.1 | 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. | 3.1 | 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. | 3.1 | 138 |
| 25 | 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 |
| 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. | 3.8 | 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. | 3.1 | 130 |
| 28 | Formation and Fate of Fermentation Products in Hot Spring Cyanobacterial Mats. <i>Applied and Environmental Microbiology</i> , 1987, 53, 2343-2352. | 3.1 | 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. | 3.5 | 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. | 3.1 | 123 |
| 31 | 16S rRNA sequences reveal uncultured inhabitants of a well-studied thermal community. <i>FEMS Microbiology Letters</i> , 1990, 75, 105-115. | 1.8 | 112 |
| 32 | 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 |
| 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. | 9.8 | 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. | 3.1 | 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. | 3.5 | 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. | 3.1 | 101 |

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|----|---|-----|-----------|
| 37 | Metatranscriptomic analyses of chlorophototrophs of a hot-spring microbial mat. ISME Journal, 2011, 5, 1279-1290. | 9.8 | 101 |
| 38 | Comparative analysis of extractable lipids in hot spring microbial mats and their component photosynthetic bacteria. Organic Geochemistry, 1991, 17, 309-319. | 1.8 | 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. | 3.8 | 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. | 2.2 | 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. | 3.5 | 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. | 3.1 | 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. | 3.1 | 93 |
| 45 | Diversity and Distribution in Hypersaline Microbial Mats of Bacteria Related to <i>Chloroflexus</i> spp. Applied and Environmental Microbiology, 2001, 67, 4365-4371. | 3.1 | 89 |
| 46 | Biodiversity within hot spring microbial mat communities: molecular monitoring of enrichment cultures. Antonie Van Leeuwenhoek, 1997, 71, 143-150. | 1.7 | 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. | 3.1 | 82 |
| 48 | Complete genome of <i>Candidatus Chloracidobacterium thermophilum</i> , a chlorophyll <i>a</i> -based photoheterotroph belonging to the phylum <i>Acidobacteria</i> . Environmental Microbiology, 2012, 14, 177-190. | 3.8 | 79 |
| 49 | Biosynthetic Controls on the ¹³ C Contents of Organic Components in the Photoautotrophic Bacterium <i>Chloroflexus aurantiacus</i> . Journal of Biological Chemistry, 2001, 276, 10971-10976. | 3.4 | 77 |
| 50 | Cyanobacteria in Geothermal Habitats. , 2012, , 39-63. | | 77 |
| 51 | Fine-Scale Distribution Patterns of <i>Synechococcus</i> Ecological Diversity in Microbial Mats of Mushroom Spring, Yellowstone National Park. Applied and Environmental Microbiology, 2011, 77, 7689-7697. | 3.1 | 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. | 3.1 | 71 |
| 53 | The molecular dimension of microbial species: 3. Comparative genomics of <i>Synechococcus</i> 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. | 3.5 | 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. | 3.1 | 62 |
| 56 | Biogeochemistry of hot spring environments. Chemical Geology, 1992, 95, 327-345. | 3.3 | 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. | 3.1 | 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. | 3.5 | 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. | 3.5 | 56 |
| 60 | 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 |
| 61 | Biogeochemistry of hot spring environments. Chemical Geology, 1992, 95, 347-360. | 3.3 | 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. | 10.0 | 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. | 3.5 | 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. | 3.1 | 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. | 2.7 | 47 |
| 66 | Anaerobic metabolism of hexadecane in sediments. Geomicrobiology Journal, 1978, 1, 1-9. | 2.0 | 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. | 3.1 | 44 |
| 68 | Diverse Thermophilic Species Inhabit a Single Hot Spring Microbial Mat. Systematic and Applied Microbiology, 1995, 18, 274-278. | 2.8 | 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. | 3.1 | 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. | 2.8 | 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. | 2.2 | 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. | 1.7 | 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 ² -Lineage Synechococcus Populations. Frontiers in Microbiology, 2020, 11, 77. | 3.5 | 24 |
| 76 | Vertical distribution of sulfate reduction, methane production, and bacteria in marine sediments. Geomicrobiology Journal, 1981, 2, 341-362. | 2.0 | 23 |
| 77 | Comparative Analysis of 16S Ribosomal RNA Sequences of Thermus Species. Systematic and Applied Microbiology, 1990, 13, 8-13. | 2.8 | 23 |
| 78 | All-cis hentriaconta-9,15,22-triene in microbial mats formed by the phototrophic prokaryote Chloroflexus. Organic Geochemistry, 1999, 30, 1585-1587. | 1.8 | 21 |
| 79 | Automated Data Extraction from <i>In Situ</i> Protein-Stable Isotope Probing Studies. Journal of Proteome Research, 2014, 13, 1200-1210. | 3.7 | 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. | 3.1 | 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. | 3.5 | 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. | 3.1 | 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. | 3.1 | 12 |
| 86 | Allochromatium tepidum, sp. nov., a hot spring species of purple sulfur bacteria. Archives of Microbiology, 2022, 204, 115. | 2.2 | 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, . | 3.1 | 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. | 2.5 | 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. | 3.1 | 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, . | 3.1 | 1 |
| 95 | 16S rRNA sequences reveal uncultured inhabitants of a well-studied thermal community. FEMS Microbiology Letters, 1990, 75, 105-115. | 1.8 | 1 |