

Edward F DeLong

List of Publications by Year in descending order

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Version: 2024-02-01

129
papers

27,270
citations

12330

69
h-index

15266

126
g-index

139
all docs

139
docs citations

139
times ranked

17941
citing authors

#	ARTICLE	IF	CITATIONS
1	Biogeochemical Dynamics in Adjacent Mesoscale Eddies of Opposite Polarity. <i>Global Biogeochemical Cycles</i> , 2022, 36, .	4.9	13
2	Complex marine microbial communities partition metabolism of scarce resources over the diel cycle. <i>Nature Ecology and Evolution</i> , 2022, 6, 218-229.	7.8	21
3	Diversity and origins of bacterial and archaeal viruses on sinking particles reaching the abyssal ocean. <i>ISME Journal</i> , 2022, 16, 1627-1635.	9.8	18
4	Microbial Sources of Exocellular DNA in the Ocean. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0209321.	3.1	6
5	Evidence of Genomic Diversification in a Natural Symbiotic Population Within Its Host. <i>Frontiers in Microbiology</i> , 2022, 13, 854355.	3.5	3
6	Diverse Genomic Traits Differentiate Sinking-Particle-Associated versus Free-Living Microbes throughout the Oligotrophic Open Ocean Water Column. <i>MBio</i> , 2022, 13, .	4.1	21
7	Planet Microbe: a platform for marine microbiology to discover and analyze interconnected omics and environmental data. <i>Nucleic Acids Research</i> , 2021, 49, D792-D802.	14.5	14
8	Combined pigment and metatranscriptomic analysis reveals highly synchronized diel patterns of phenotypic light response across domains in the open oligotrophic ocean. <i>ISME Journal</i> , 2021, 15, 520-533.	9.8	28
9	A method for characterizing dissolved <scp>DNA</scp> and its application to the North Pacific Subtropical Gyre. <i>Limnology and Oceanography: Methods</i> , 2021, 19, 210-221.	2.0	9
10	Microbial dynamics of elevated carbon flux in the open ocean's abyss. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	65
11	A system of coordinated autonomous robots for Lagrangian studies of microbes in the oceanic deep chlorophyll maximum. <i>Science Robotics</i> , 2021, 6, .	17.6	32
12	Genome-enabled exploration of microbial ecology and evolution in the sea: a rising tide lifts all boats. <i>Environmental Microbiology</i> , 2021, 23, 1301-1321.	3.8	1
13	Come rain or shine: Depth not season shapes the active protistan community at station ALOHA in the North Pacific Subtropical Gyre. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2021, 170, 103494.	1.4	26
14	Particulate Metabolites and Transcripts Reflect Diel Oscillations of Microbial Activity in the Surface Ocean. <i>MSystems</i> , 2021, 6, .	3.8	29
15	Metapangenomics reveals depth-dependent shifts in metabolic potential for the ubiquitous marine bacterial SAR324 lineage. <i>Microbiome</i> , 2021, 9, 172.	11.1	25
16	Planktonic Archaeal Ether Lipid Origins in Surface Waters of the North Pacific Subtropical Gyre. <i>Frontiers in Microbiology</i> , 2021, 12, 610675.	3.5	5
17	Iron Depletion in the Deep Chlorophyll Maximum: Mesoscale Eddies as Natural Iron Fertilization Experiments. <i>Global Biogeochemical Cycles</i> , 2021, 35, e2021GB007112.	4.9	20
18	Ontology-Enriched Specifications Enabling Findable, Accessible, Interoperable, and Reusable Marine Metagenomic Datasets in Cyberinfrastructure Systems. <i>Frontiers in Microbiology</i> , 2021, 12, 765268.	3.5	3

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19	Autonomous Tracking and Sampling of the Deep Chlorophyll Maximum Layer in an Open-Ocean Eddy by a Long-Range Autonomous Underwater Vehicle. <i>IEEE Journal of Oceanic Engineering</i> , 2020, 45, 1308-1321.	3.8	22
20	Diel cycling of the cosmopolitan abundant Pelagibacter virus 37â€¢6: one of the most abundant viruses on earth. <i>Environmental Microbiology Reports</i> , 2020, 12, 214-219.	2.4	8
21	Alternative strategies of nutrient acquisition and energy conservation map to the biogeography of marine ammonia-oxidizing archaea. <i>ISME Journal</i> , 2020, 14, 2595-2609.	9.8	62
22	Double-stranded DNA viroplankton dynamics and reproductive strategies in the oligotrophic open ocean water column. <i>ISME Journal</i> , 2020, 14, 1304-1315.	9.8	65
23	Assembly-free single-molecule sequencing recovers complete virus genomes from natural microbial communities. <i>Genome Research</i> , 2020, 30, 437-446.	5.5	80
24	Exploring Marine Planktonic Archaea: Then and Now. <i>Frontiers in Microbiology</i> , 2020, 11, 616086.	3.5	11
25	K�lauea lava fuels phytoplankton bloom in the North Pacific Ocean. <i>Science</i> , 2019, 365, 1040-1044.	12.6	35
26	Diel Oscillation of Microbial Gene Transcripts Declines With Depth in Oligotrophic Ocean Waters. <i>Frontiers in Microbiology</i> , 2019, 10, 2191.	3.5	19
27	A distinct lineage of giant viruses brings a rhodopsin photosystem to unicellular marine predators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20574-20583.	7.1	120
28	Persistent Core Populations Shape the Microbiome Throughout the Water Column in the North Pacific Subtropical Gyre. <i>Frontiers in Microbiology</i> , 2019, 10, 2273.	3.5	17
29	Biological composition and microbial dynamics of sinking particulate organic matter at abyssal depths in the oligotrophic open ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11824-11832.	7.1	150
30	Phosphate�limited ocean regions select for bacterial populations enriched in the carbon�phosphorus lyase pathway for phosphonate degradation. <i>Environmental Microbiology</i> , 2019, 21, 2402-2414.	3.8	73
31	Proteorhodopsin variability and distribution in the North Pacific Subtropical Gyre. <i>ISME Journal</i> , 2018, 12, 1047-1060.	9.8	45
32	Solar-panel and parasol strategies shape the proteorhodopsin distribution pattern in marine Flavobacteria. <i>ISME Journal</i> , 2018, 12, 1329-1343.	9.8	18
33	Towards a microbial universal theory of all (nearly) totality: MUTANT. <i>Environmental Microbiology</i> , 2018, 20, 1962-1963.	3.8	0
34	Thank You Ken, Joan and Dave, for 20 years of Environmental Microbiology!. <i>Environmental Microbiology</i> , 2018, 20, 1964-1965.	3.8	0
35	Diel cycling and long-term persistence of viruses in the ocean�s euphotic zone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11446-11451.	7.1	116
36	Environmental drivers of a microbial genomic transition zone in the ocean�s interior. <i>Nature Microbiology</i> , 2017, 2, 1367-1373.	13.3	177

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37	Coordinated regulation of growth, activity and transcription in natural populations of the unicellular nitrogen-fixing cyanobacterium <i>Crocospaera</i> . <i>Nature Microbiology</i> , 2017, 2, 17118.	13.3	122
38	Bacteriophage Distributions and Temporal Variability in the Ocean's Interior. <i>MBio</i> , 2017, 8, .	4.1	76
39	Isolation and Characterization of Bacteria That Degrade Phosphonates in Marine Dissolved Organic Matter. <i>Frontiers in Microbiology</i> , 2017, 8, 1786.	3.5	49
40	Bacterial Succession on Sinking Particles in the Ocean's Interior. <i>Frontiers in Microbiology</i> , 2017, 8, 2269.	3.5	59
41	Improved Environmental Genomes via Integration of Metagenomic and Single-Cell Assemblies. <i>Frontiers in Microbiology</i> , 2016, 7, 143.	3.5	24
42	Structural Mechanism for Light-driven Transport by a New Type of Chloride Ion Pump, Nonlabens marinus Rhodopsin-3. <i>Journal of Biological Chemistry</i> , 2016, 291, 17488-17495.	3.4	34
43	Diversity and Activity of Communities Inhabiting Plastic Debris in the North Pacific Gyre. <i>MSystems</i> , 2016, 1, .	3.8	330
44	Siderophore-based microbial adaptations to iron scarcity across the eastern Pacific Ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14237-14242.	7.1	179
45	Quantitative Transcriptomics Reveals the Growth- and Nutrient-Dependent Response of a Streamlined Marine Methylotroph to Methanol and Naturally Occurring Dissolved Organic Matter. <i>MBio</i> , 2016, 7, .	4.1	33
46	Marine Bacterial and Archaeal Ion-Pumping Rhodopsins: Genetic Diversity, Physiology, and Ecology. <i>Microbiology and Molecular Biology Reviews</i> , 2016, 80, 929-954.	6.6	173
47	Marine methane paradox explained by bacterial degradation of dissolved organic matter. <i>Nature Geoscience</i> , 2016, 9, 884-887.	12.9	231
48	Wind and sunlight shape microbial diversity in surface waters of the North Pacific Subtropical Gyre. <i>ISME Journal</i> , 2016, 10, 1308-1322.	9.8	73
49	Genetic Diversity Affects the Daily Transcriptional Oscillations of Marine Microbial Populations. <i>PLoS ONE</i> , 2016, 11, e0146706.	2.5	6
50	Microbial community structure and function on sinking particles in the North Pacific Subtropical Gyre. <i>Frontiers in Microbiology</i> , 2015, 6, 469.	3.5	148
51	High molecular weight dissolved organic matter enrichment selects for methylotrophs in dilution to extinction cultures. <i>ISME Journal</i> , 2015, 9, 2725-2739.	9.8	58
52	Genomic potential for nitrogen assimilation in uncultivated members of <i>Prochlorococcus</i> from an anoxic marine zone. <i>ISME Journal</i> , 2015, 9, 1264-1267.	9.8	11
53	Microbial community transcriptional networks are conserved in three domains at ocean basin scales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5443-5448.	7.1	225
54	Metagenomic analysis of size-fractionated picoplankton in a marine oxygen minimum zone. <i>ISME Journal</i> , 2014, 8, 187-211.	9.8	281

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55	Oxygen at Nanomolar Levels Reversibly Suppresses Process Rates and Gene Expression in Anammox and Denitrification in the Oxygen Minimum Zone off Northern Chile. <i>MBio</i> , 2014, 5, e01966.	4.1	216
56	Microbial eukaryote diversity in the marine oxygen minimum zone off northern Chile. <i>Frontiers in Microbiology</i> , 2014, 5, 543.	3.5	47
57	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	5.6	190
58	Planktonic Euryarchaeota are a significant source of archaeal tetraether lipids in the ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9858-9863.	7.1	134
59	Functional characterization of flavobacteria rhodopsins reveals a unique class of light-driven chloride pump in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6732-6737.	7.1	140
60	Single-cell enabled comparative genomics of a deep ocean SAR11 bathytype. <i>ISME Journal</i> , 2014, 8, 1440-1451.	9.8	119
61	Reply to Schouten et al.: Marine Group II planktonic Euryarchaeota are significant contributors to tetraether lipids in the ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4286.	7.1	20
62	Alien Invasions and Gut Biogeography. <i>Cell</i> , 2014, 159, 233-235.	28.9	20
63	Multispecies diel transcriptional oscillations in open ocean heterotrophic bacterial assemblages. <i>Science</i> , 2014, 345, 207-212.	12.6	245
64	Closely related phytoplankton species produce similar suites of dissolved organic matter. <i>Frontiers in Microbiology</i> , 2014, 5, 111.	3.5	124
65	Meeting report: Ocean omics science, technology and cyberinfrastructure: current challenges and future requirements (August 20-23, 2013). <i>Standards in Genomic Sciences</i> , 2014, 9, 1252-1258.	1.5	7
66	Draft genome sequence of marine alphaproteobacterial strain HIMB11, the first cultivated representative of a unique lineage within the Roseobacter clade possessing an unusually small genome. <i>Standards in Genomic Sciences</i> , 2014, 9, 632-645.	1.5	40
67	Pattern and synchrony of gene expression among sympatric marine microbial populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E488-97.	7.1	164
68	Prokaryotic Super Program Advisory Committee DOE Joint Genome Institute, Walnut Creek, CA, March 27, 2013. <i>Standards in Genomic Sciences</i> , 2013, 8, 561-570.	1.5	5
69	Metatranscriptomic and functional metagenomic analysis of methylphosphonate utilization by marine bacteria. <i>Frontiers in Microbiology</i> , 2013, 4, 340.	3.5	63
70	Microbial oceanography of anoxic oxygen minimum zones. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15996-16003.	7.1	365
71	Microbial community phylogenetic and trait diversity declines with depth in a marine oxygen minimum zone. <i>Ecology</i> , 2012, 93, 1659-1673.	3.2	129
72	Experimental Incubations Elicit Profound Changes in Community Transcription in OMZ Bacterioplankton. <i>PLoS ONE</i> , 2012, 7, e37118.	2.5	79

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73	Microbial Evolution in the Wild. <i>Science</i> , 2012, 336, 422-424.	12.6	12
74	PhnY and PhnZ Comprise a New Oxidative Pathway for Enzymatic Cleavage of a Carbon-Phosphorus Bond. <i>Journal of the American Chemical Society</i> , 2012, 134, 8364-8367.	13.7	70
75	Microbial metatranscriptomics in a permanent marine oxygen minimum zone. <i>Environmental Microbiology</i> , 2012, 14, 23-40.	3.8	318
76	Phosphite utilization by the marine picocyanobacterium <i>Prochlorococcus</i> MIT9301. <i>Environmental Microbiology</i> , 2012, 14, 1363-1377.	3.8	78
77	Potential for Chemolithoautotrophy Among Ubiquitous Bacteria Lineages in the Dark Ocean. <i>Science</i> , 2011, 333, 1296-1300.	12.6	510
78	Time-series analyses of Monterey Bay coastal microbial picoplankton using a genome proxy microarray. <i>Environmental Microbiology</i> , 2011, 13, 116-134.	3.8	31
79	Integrated metatranscriptomic and metagenomic analyses of stratified microbial assemblages in the open ocean. <i>ISME Journal</i> , 2011, 5, 999-1013.	9.8	230
80	Metatranscriptomic analysis of autonomously collected and preserved marine bacterioplankton. <i>ISME Journal</i> , 2011, 5, 1881-1895.	9.8	141
81	Development and quantitative analyses of a universal rRNA-subtraction protocol for microbial metatranscriptomics. <i>ISME Journal</i> , 2010, 4, 896-907.	9.8	222
82	Widespread known and novel phosphonate utilization pathways in marine bacteria revealed by functional screening and metagenomic analyses. <i>Environmental Microbiology</i> , 2010, 12, 222-238.	3.8	166
83	Abundances of crenarchaeal <i>amoA</i> genes and transcripts in the Pacific Ocean. <i>Environmental Microbiology</i> , 2010, 12, 679-688.	3.8	209
84	The Light-Driven Proton Pump Proteorhodopsin Enhances Bacterial Survival during Tough Times. <i>PLoS Biology</i> , 2010, 8, e1000359.	5.6	124
85	A Cryptic Sulfur Cycle in Oxygen-Minimum Zone Waters off the Chilean Coast. <i>Science</i> , 2010, 330, 1375-1378.	12.6	545
86	Comparative Metagenomic Analysis of a Microbial Community Residing at a Depth of 4,000 Meters at Station ALOHA in the North Pacific Subtropical Gyre. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5345-5355.	3.1	203
87	Metatranscriptomics reveals unique microbial small RNAs in the ocean's water column. <i>Nature</i> , 2009, 459, 266-269.	27.8	249
88	The microbial ocean from genomes to biomes. <i>Nature</i> , 2009, 459, 200-206.	27.8	193
89	Aerobic production of methane in the sea. <i>Nature Geoscience</i> , 2008, 1, 473-478.	12.9	450
90	Phylogenetic analyses of ribosomal DNA-containing bacterioplankton genome fragments from a 4000m vertical profile in the North Pacific Subtropical Gyre. <i>Environmental Microbiology</i> , 2008, 10, 2313-2330.	3.8	104

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91	The Microbial Engines That Drive Earth's Biogeochemical Cycles. <i>Science</i> , 2008, 320, 1034-1039.	12.6	2,449
92	Microbial community gene expression in ocean surface waters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3805-3810.	7.1	699
93	Low genomic diversity in tropical oceanic N ₂ -fixing cyanobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17807-17812.	7.1	70
94	Sea change for metagenomics?. <i>Nature Reviews Microbiology</i> , 2007, 5, 326-326.	28.6	3
95	Proteorhodopsin photosystem gene clusters exhibit co-evolutionary trends and shared ancestry among diverse marine microbial phyla. <i>Environmental Microbiology</i> , 2007, 9, 846-858.	3.8	87
96	Archaeal mysteries of the deep revealed. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6417-6418.	7.1	41
97	Community Genomics Among Stratified Microbial Assemblages in the Ocean's Interior. <i>Science</i> , 2006, 311, 496-503.	12.6	1,261
98	Genomic Islands and the Ecology and Evolution of <i>Prochlorococcus</i> . <i>Science</i> , 2006, 311, 1768-1770.	12.6	437
99	Proteorhodopsin lateral gene transfer between marine planktonic Bacteria and Archaea. <i>Nature</i> , 2006, 439, 847-850.	27.8	278
100	Genomic analysis of the uncultivated marine crenarchaeote <i>Cenarchaeum symbiosum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18296-18301.	7.1	420
101	Pathways of Carbon Assimilation and Ammonia Oxidation Suggested by Environmental Genomic Analyses of Marine Crenarchaeota. <i>PLoS Biology</i> , 2006, 4, e95.	5.6	554
102	Microbial community genomics in the ocean. <i>Nature Reviews Microbiology</i> , 2005, 3, 459-469.	28.6	273
103	Genomic perspectives in microbial oceanography. <i>Nature</i> , 2005, 437, 336-342.	27.8	241
104	Microbial population genomics and ecology: the road ahead. <i>Environmental Microbiology</i> , 2004, 6, 875-878.	3.8	67
105	Different SAR86 subgroups harbour divergent proteorhodopsins. <i>Environmental Microbiology</i> , 2004, 6, 903-910.	3.8	106
106	MICROBIOLOGY: Microbial Life Breathes Deep. <i>Science</i> , 2004, 306, 2198-2200.	12.6	38
107	Reverse Methanogenesis: Testing the Hypothesis with Environmental Genomics. <i>Science</i> , 2004, 305, 1457-1462.	12.6	624
108	Growth and Methane Oxidation Rates of Anaerobic Methanotrophic Archaea in a Continuous-Flow Bioreactor. <i>Applied and Environmental Microbiology</i> , 2003, 69, 5472-5482.	3.1	133

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109	Identification of Methyl Coenzyme M Reductase A (<i>mcrA</i>) Genes Associated with Methane-Oxidizing Archaea. Applied and Environmental Microbiology, 2003, 69, 5483-5491.	3.1	353
110	Comparative Genomic Analysis of Archaeal Genotypic Variants in a Single Population and in Two Different Oceanic Provinces. Applied and Environmental Microbiology, 2002, 68, 335-345.	3.1	164
111	Towards microbial systems science: integrating microbial perspective, from genomes to biomes. Environmental Microbiology, 2002, 4, 9-10.	3.8	12
112	Multiple archaeal groups mediate methane oxidation in anoxic cold seep sediments. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7663-7668.	7.1	604
113	Microbial population genomics and ecology. Current Opinion in Microbiology, 2002, 5, 520-524.	5.1	105
114	Unsuspected diversity among marine aerobic anoxygenic phototrophs. Nature, 2002, 415, 630-633.	27.8	380
115	Archaeal dominance in the mesopelagic zone of the Pacific Ocean. Nature, 2001, 409, 507-510.	27.8	1,373
116	Proteorhodopsin phototrophy in the ocean. Nature, 2001, 411, 786-789.	27.8	740
117	Environmental Diversity of Bacteria and Archaea. Systematic Biology, 2001, 50, 470-478.	5.6	329
118	Methane-Consuming Archaea Revealed by Directly Coupled Isotopic and Phylogenetic Analysis. Science, 2001, 293, 484-487.	12.6	957
119	Construction and analysis of bacterial artificial chromosome libraries from a marine microbial assemblage. Environmental Microbiology, 2000, 2, 516-529.	3.8	313
120	Resolving a methane mystery. Nature, 2000, 407, 577-579.	27.8	68
121	Bacterial Rhodopsin: Evidence for a New Type of Phototrophy in the Sea. Science, 2000, 289, 1902-1906.	12.6	1,357
122	Methane-consuming archaeobacteria in marine sediments. Nature, 1999, 398, 802-805.	27.8	1,135
123	<i>Nitrospira</i> -Like Bacteria Associated with Nitrite Oxidation in Freshwater Aquaria. Applied and Environmental Microbiology, 1998, 64, 258-264.	3.1	197
124	Genomic Analysis Reveals Chromosomal Variation in Natural Populations of the Uncultured Psychrophilic Archaeon <i>Cenarchaeum symbiosum</i> . Journal of Bacteriology, 1998, 180, 5003-5009.	2.2	137
125	High abundance of Archaea in Antarctic marine picoplankton. Nature, 1994, 371, 695-697.	27.8	539
126	Phylogenetic diversity of aggregate-attached vs. free-living marine bacterial assemblages. Limnology and Oceanography, 1993, 38, 924-934.	3.1	917

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127	Biochemical Function and Ecological Significance of Novel Bacterial Lipids in Deep-Sea Procaryotes. Applied and Environmental Microbiology, 1986, 51, 730-737.	3.1	300
128	Evolutionary relationships of superoxide dismutases and glutamine synthetases from marine species of Alteromonas, Oceanospirillum, Pseudomonas and Deleya. Archives of Microbiology, 1984, 138, 170-178.	2.2	19
129	Novel Integrative Elements and Genomic Plasticity in Ocean Ecosystems. SSRN Electronic Journal, 0, , .	0.4	2