

Edward F DeLong

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3874370/publications.pdf>

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	The Microbial Engines That Drive Earth's Biogeochemical Cycles. <i>Science</i> , 2008, 320, 1034-1039.	12.6	2,449
2	Archaeal dominance in the mesopelagic zone of the Pacific Ocean. <i>Nature</i> , 2001, 409, 507-510.	27.8	1,373
3	Bacterial Rhodopsin: Evidence for a New Type of Phototrophy in the Sea. <i>Science</i> , 2000, 289, 1902-1906.	12.6	1,357
4	Community Genomics Among Stratified Microbial Assemblages in the Ocean's Interior. <i>Science</i> , 2006, 311, 496-503.	12.6	1,261
5	Methane-consuming archaeobacteria in marine sediments. <i>Nature</i> , 1999, 398, 802-805.	27.8	1,135
6	Methane-Consuming Archaea Revealed by Directly Coupled Isotopic and Phylogenetic Analysis. <i>Science</i> , 2001, 293, 484-487.	12.6	957
7	Phylogenetic diversity of aggregate-attached vs. free-living marine bacterial assemblages. <i>Limnology and Oceanography</i> , 1993, 38, 924-934.	3.1	917
8	Proteorhodopsin phototrophy in the ocean. <i>Nature</i> , 2001, 411, 786-789.	27.8	740
9	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
10	Reverse Methanogenesis: Testing the Hypothesis with Environmental Genomics. <i>Science</i> , 2004, 305, 1457-1462.	12.6	624
11	Multiple archaeal groups mediate methane oxidation in anoxic cold seep sediments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 7663-7668.	7.1	604
12	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
13	A Cryptic Sulfur Cycle in Oxygen-Minimum Zone Waters off the Chilean Coast. <i>Science</i> , 2010, 330, 1375-1378.	12.6	545
14	High abundance of Archaea in Antarctic marine picoplankton. <i>Nature</i> , 1994, 371, 695-697.	27.8	539
15	Potential for Chemolithoautotrophy Among Ubiquitous Bacteria Lineages in the Dark Ocean. <i>Science</i> , 2011, 333, 1296-1300.	12.6	510
16	Aerobic production of methane in the sea. <i>Nature Geoscience</i> , 2008, 1, 473-478.	12.9	450
17	Genomic Islands and the Ecology and Evolution of <i>Prochlorococcus</i> . <i>Science</i> , 2006, 311, 1768-1770.	12.6	437
18	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

#	ARTICLE	IF	CITATIONS
19	Unsuspected diversity among marine aerobic anoxygenic phototrophs. <i>Nature</i> , 2002, 415, 630-633.	27.8	380
20	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
21	Identification of Methyl Coenzyme M Reductase A (mcrA) Genes Associated with Methane-Oxidizing Archaea. <i>Applied and Environmental Microbiology</i> , 2003, 69, 5483-5491.	3.1	353
22	Diversity and Activity of Communities Inhabiting Plastic Debris in the North Pacific Gyre. <i>MSystems</i> , 2016, 1, .	3.8	330
23	Environmental Diversity of Bacteria and Archaea. <i>Systematic Biology</i> , 2001, 50, 470-478.	5.6	329
24	Microbial metatranscriptomics in a permanent marine oxygen minimum zone. <i>Environmental Microbiology</i> , 2012, 14, 23-40.	3.8	318
25	Construction and analysis of bacterial artificial chromosome libraries from a marine microbial assemblage. <i>Environmental Microbiology</i> , 2000, 2, 516-529.	3.8	313
26	Biochemical Function and Ecological Significance of Novel Bacterial Lipids in Deep-Sea Prokaryotes. <i>Applied and Environmental Microbiology</i> , 1986, 51, 730-737.	3.1	300
27	Metagenomic analysis of size-fractionated picoplankton in a marine oxygen minimum zone. <i>ISME Journal</i> , 2014, 8, 187-211.	9.8	281
28	Proteorhodopsin lateral gene transfer between marine planktonic Bacteria and Archaea. <i>Nature</i> , 2006, 439, 847-850.	27.8	278
29	Microbial community genomics in the ocean. <i>Nature Reviews Microbiology</i> , 2005, 3, 459-469.	28.6	273
30	Metatranscriptomics reveals unique microbial small RNAs in the ocean's water column. <i>Nature</i> , 2009, 459, 266-269.	27.8	249
31	Multispecies diel transcriptional oscillations in open ocean heterotrophic bacterial assemblages. <i>Science</i> , 2014, 345, 207-212.	12.6	245
32	Genomic perspectives in microbial oceanography. <i>Nature</i> , 2005, 437, 336-342.	27.8	241
33	Marine methane paradox explained by bacterial degradation of dissolved organic matter. <i>Nature Geoscience</i> , 2016, 9, 884-887.	12.9	231
34	Integrated metatranscriptomic and metagenomic analyses of stratified microbial assemblages in the open ocean. <i>ISME Journal</i> , 2011, 5, 999-1013.	9.8	230
35	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
36	Development and quantitative analyses of a universal rRNA-subtraction protocol for microbial metatranscriptomics. <i>ISME Journal</i> , 2010, 4, 896-907.	9.8	222

#	ARTICLE	IF	CITATIONS
37	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
38	Abundances of crenarchaeal <i>amoA</i> genes and transcripts in the Pacific Ocean. <i>Environmental Microbiology</i> , 2010, 12, 679-688.	3.8	209
39	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
40	<i>Nitrospira</i> -Like Bacteria Associated with Nitrite Oxidation in Freshwater Aquaria. <i>Applied and Environmental Microbiology</i> , 1998, 64, 258-264.	3.1	197
41	The microbial ocean from genomes to biomes. <i>Nature</i> , 2009, 459, 200-206.	27.8	193
42	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	5.6	190
43	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
44	Environmental drivers of a microbial genomic transition zone in the ocean's interior. <i>Nature Microbiology</i> , 2017, 2, 1367-1373.	13.3	177
45	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
46	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
47	Comparative Genomic Analysis of Archaeal Genotypic Variants in a Single Population and in Two Different Oceanic Provinces. <i>Applied and Environmental Microbiology</i> , 2002, 68, 335-345.	3.1	164
48	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
49	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
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	Metatranscriptomic analysis of autonomously collected and preserved marine bacterioplankton. <i>ISME Journal</i> , 2011, 5, 1881-1895.	9.8	141
52	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
53	Genomic Analysis Reveals Chromosomal Variation in Natural Populations of the Uncultured Psychrophilic Archaeon <i>Cenarchaeum symbiosum</i> . <i>Journal of Bacteriology</i> , 1998, 180, 5003-5009.	2.2	137
54	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

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	The Light-Driven Proton Pump Proteorhodopsin Enhances Bacterial Survival during Tough Times. <i>PLoS Biology</i> , 2010, 8, e1000359.	5.6	124
58	Closely related phytoplankton species produce similar suites of dissolved organic matter. <i>Frontiers in Microbiology</i> , 2014, 5, 111.	3.5	124
59	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
60	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
61	Single-cell enabled comparative genomics of a deep ocean SAR11 bathytype. <i>ISME Journal</i> , 2014, 8, 1440-1451.	9.8	119
62	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
63	Different SAR86 subgroups harbour divergent proteorhodopsins. <i>Environmental Microbiology</i> , 2004, 6, 903-910.	3.8	106
64	Microbial population genomics and ecology. <i>Current Opinion in Microbiology</i> , 2002, 5, 520-524.	5.1	105
65	Phylogenetic analyses of ribosomal DNA-containing bacterioplankton genome fragments from a 4000-m vertical profile in the North Pacific Subtropical Gyre. <i>Environmental Microbiology</i> , 2008, 10, 2313-2330.	3.8	104
66	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
67	Assembly-free single-molecule sequencing recovers complete virus genomes from natural microbial communities. <i>Genome Research</i> , 2020, 30, 437-446.	5.5	80
68	Experimental Incubations Elicit Profound Changes in Community Transcription in OMZ Bacterioplankton. <i>PLoS ONE</i> , 2012, 7, e37118.	2.5	79
69	Phosphite utilization by the marine picocyanobacterium <i>Prochlorococcus</i> MIT9301. <i>Environmental Microbiology</i> , 2012, 14, 1363-1377.	3.8	78
70	Bacteriophage Distributions and Temporal Variability in the Ocean's Interior. <i>MBio</i> , 2017, 8, .	4.1	76
71	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
72	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

#	ARTICLE	IF	CITATIONS
73	Low genomic diversity in tropical oceanic N ₂ -fixing cyanobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17807-17812.	7.1	70
74	PhnY and PhnZ Comprise a New Oxidative Pathway for Enzymatic Cleavage of a Carbon-Phosphorus Bond. Journal of the American Chemical Society, 2012, 134, 8364-8367.	13.7	70
75	Resolving a methane mystery. Nature, 2000, 407, 577-579.	27.8	68
76	Microbial population genomics and ecology: the road ahead. Environmental Microbiology, 2004, 6, 875-878.	3.8	67
77	Double-stranded DNA viroplankton dynamics and reproductive strategies in the oligotrophic open ocean water column. ISME Journal, 2020, 14, 1304-1315.	9.8	65
78	Microbial dynamics of elevated carbon flux in the open ocean's abyss. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	65
79	Metatranscriptomic and functional metagenomic analysis of methylphosphonate utilization by marine bacteria. Frontiers in Microbiology, 2013, 4, 340.	3.5	63
80	Alternative strategies of nutrient acquisition and energy conservation map to the biogeography of marine ammonia-oxidizing archaea. ISME Journal, 2020, 14, 2595-2609.	9.8	62
81	Bacterial Succession on Sinking Particles in the Ocean's Interior. Frontiers in Microbiology, 2017, 8, 2269.	3.5	59
82	High molecular weight dissolved organic matter enrichment selects for methylotrophs in dilution to extinction cultures. ISME Journal, 2015, 9, 2725-2739.	9.8	58
83	Isolation and Characterization of Bacteria That Degrade Phosphonates in Marine Dissolved Organic Matter. Frontiers in Microbiology, 2017, 8, 1786.	3.5	49
84	Microbial eukaryote diversity in the marine oxygen minimum zone off northern Chile. Frontiers in Microbiology, 2014, 5, 543.	3.5	47
85	Proteorhodopsin variability and distribution in the North Pacific Subtropical Gyre. ISME Journal, 2018, 12, 1047-1060.	9.8	45
86	Archaeal mysteries of the deep revealed. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6417-6418.	7.1	41
87	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. Standards in Genomic Sciences, 2014, 9, 632-645.	1.5	40
88	MICROBIOLOGY: Microbial Life Breathes Deep. Science, 2004, 306, 2198-2200.	12.6	38
89	Klauea lava fuels phytoplankton bloom in the North Pacific Ocean. Science, 2019, 365, 1040-1044.	12.6	35
90	Structural Mechanism for Light-driven Transport by a New Type of Chloride Ion Pump, Nonlabens marinus Rhodopsin-3. Journal of Biological Chemistry, 2016, 291, 17488-17495.	3.4	34

#	ARTICLE	IF	CITATIONS
91	Quantitative Transcriptomics Reveals the Growth- and Nutrient-Dependent Response of a Streamlined Marine Methylophile to Methanol and Naturally Occurring Dissolved Organic Matter. <i>MBio</i> , 2016, 7, .	4.1	33
92	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
93	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
94	Particulate Metabolites and Transcripts Reflect Diel Oscillations of Microbial Activity in the Surface Ocean. <i>MSystems</i> , 2021, 6, .	3.8	29
95	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
96	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
97	Metapangenomics reveals depth-dependent shifts in metabolic potential for the ubiquitous marine bacterial SAR324 lineage. <i>Microbiome</i> , 2021, 9, 172.	11.1	25
98	Improved Environmental Genomes via Integration of Metagenomic and Single-Cell Assemblies. <i>Frontiers in Microbiology</i> , 2016, 7, 143.	3.5	24
99	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
100	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
101	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
102	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
103	Alien Invasions and Gut "Island Biogeography". <i>Cell</i> , 2014, 159, 233-235.	28.9	20
104	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
105	Evolutionary relationships of superoxide dismutases and glutamine synthetases from marine species of <i>Alteromonas</i> , <i>Oceanospirillum</i> , <i>Pseudomonas</i> and <i>Deleya</i> . <i>Archives of Microbiology</i> , 1984, 138, 170-178.	2.2	19
106	Diel Oscillation of Microbial Gene Transcripts Declines With Depth in Oligotrophic Ocean Waters. <i>Frontiers in Microbiology</i> , 2019, 10, 2191.	3.5	19
107	Solar-panel and parasol strategies shape the proteorhodopsin distribution pattern in marine Flavobacteriia. <i>ISME Journal</i> , 2018, 12, 1329-1343.	9.8	18
108	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

#	ARTICLE	IF	CITATIONS
109	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
110	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
111	Biogeochemical Dynamics in Adjacent Mesoscale Eddies of Opposite Polarity. <i>Global Biogeochemical Cycles</i> , 2022, 36, .	4.9	13
112	Towards microbial systems science: integrating microbial perspective, from genomes to biomes. <i>Environmental Microbiology</i> , 2002, 4, 9-10.	3.8	12
113	Microbial Evolution in the Wild. <i>Science</i> , 2012, 336, 422-424.	12.6	12
114	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
115	Exploring Marine Planktonic Archaea: Then and Now. <i>Frontiers in Microbiology</i> , 2020, 11, 616086.	3.5	11
116	A method for characterizing dissolved <i>scp</i> DNA and its application to the North Pacific Subtropical Gyre. <i>Limnology and Oceanography: Methods</i> , 2021, 19, 210-221.	2.0	9
117	Diel cycling of the cosmopolitan abundant Pelagibacter virus 37F6: one of the most abundant viruses on earth. <i>Environmental Microbiology Reports</i> , 2020, 12, 214-219.	2.4	8
118	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
119	Genetic Diversity Affects the Daily Transcriptional Oscillations of Marine Microbial Populations. <i>PLoS ONE</i> , 2016, 11, e0146706.	2.5	6
120	Microbial Sources of Exocellular DNA in the Ocean. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0209321.	3.1	6
121	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
122	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
123	Sea change for metagenomics?. <i>Nature Reviews Microbiology</i> , 2007, 5, 326-326.	28.6	3
124	Evidence of Genomic Diversification in a Natural Symbiotic Population Within Its Host. <i>Frontiers in Microbiology</i> , 2022, 13, 854355.	3.5	3
125	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
126	Novel Integrative Elements and Genomic Plasticity in Ocean Ecosystems. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2

#	ARTICLE	IF	CITATIONS
127	Genome-enabled exploration of microbial ecology and evolution in the sea: a rising tide lifts all boats. Environmental Microbiology, 2021, 23, 1301-1321.	3.8	1
128	Towards a microbial universal theory of all (nearly) totality: MUTANT. Environmental Microbiology, 2018, 20, 1962-1963.	3.8	0
129	Thank You Ken, Joan and Dave, for 20 years of Environmental Microbiology!. Environmental Microbiology, 2018, 20, 1964-1965.	3.8	0