

Mary A Moran

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2731314/publications.pdf>

Version: 2024-02-01

179
papers

21,878
citations

9264

74
h-index

9861

141
g-index

196
all docs

196
docs citations

196
times ranked

16276
citing authors

#	ARTICLE	IF	CITATIONS
1	The Ocean's labile <sc>DOC</sc> supply chain. <i>Limnology and Oceanography</i> , 2022, 67, 1007-1021.	3.1	39
2	Growth-stage-related shifts in diatom endometabolome composition set the stage for bacterial heterotrophy. <i>ISME Communications</i> , 2022, 2, .	4.2	6
3	Microbial metabolites in the marine carbon cycle. <i>Nature Microbiology</i> , 2022, 7, 508-523.	13.3	71
4	Diel investments in metabolite production and consumption in a model microbial system. <i>ISME Journal</i> , 2022, 16, 1306-1317.	9.8	13
5	Resource partitioning of phytoplankton metabolites that support bacterial heterotrophy. <i>ISME Journal</i> , 2021, 15, 762-773.	9.8	77
6	Niche dimensions of a marine bacterium are identified using invasion studies in coastal seawater. <i>Nature Microbiology</i> , 2021, 6, 524-532.	13.3	18
7	Transcriptional activity differentiates families of Marine Group II <i>Euryarchaeota</i> in the coastal ocean. <i>ISME Communications</i> , 2021, 1, .	4.2	2
8	Quantification of Amine- and Alcohol-Containing Metabolites in Saline Samples Using Pre-extraction Benzoyl Chloride Derivatization and Ultrahigh Performance Liquid Chromatography Tandem Mass Spectrometry (UHPLC MS/MS). <i>Analytical Chemistry</i> , 2021, 93, 4809-4817.	6.5	17
9	Bacterial responses to background organic pollutants in the northeast subarctic Pacific Ocean. <i>Environmental Microbiology</i> , 2021, 23, 4532-4546.	3.8	11
10	Assessing the Contribution of Seasonality, Tides, and Microbial Processing to Dissolved Organic Matter Composition Variability in a Southeastern U.S. Estuary. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	3
11	Genome Sequences and Metagenome-Assembled Genome Sequences of Microbial Communities Enriched on Phytoplankton Exometabolites. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	5
12	Ecological drivers of bacterial community assembly in synthetic phycospheres. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 3656-3662.	7.1	82
13	Microbial metagenomes and metatranscriptomes during a coastal phytoplankton bloom. <i>Scientific Data</i> , 2019, 6, 129.	5.3	36
14	Towards Integrating Evolution, Metabolism, and Climate Change Studies of Marine Ecosystems. <i>Trends in Ecology and Evolution</i> , 2019, 34, 1022-1033.	8.7	28
15	Unprecedented DMSP Concentrations in a Massive Dinoflagellate Bloom in Monterey Bay, CA. <i>Geophysical Research Letters</i> , 2019, 46, 12279-12288.	4.0	26
16	Sulfur metabolites in the pelagic ocean. <i>Nature Reviews Microbiology</i> , 2019, 17, 665-678.	28.6	104
17	Scientistsâ€™ warning to humanity: microorganisms and climate change. <i>Nature Reviews Microbiology</i> , 2019, 17, 569-586.	28.6	1,138
18	Sulfur metabolites that facilitate oceanic phytoplanktonâ€™s bacteria carbon flux. <i>ISME Journal</i> , 2019, 13, 2536-2550.	9.8	70

#	ARTICLE	IF	CITATIONS
19	Microdiversity and temporal dynamics of marine bacterial dimethylsulfoniopropionate genes. <i>Environmental Microbiology</i> , 2019, 21, 1687-1701.	3.8	38
20	Coastal Ocean Metagenomes and Curated Metagenome-Assembled Genomes from Marsh Landing, Sapelo Island (Georgia, USA). <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
21	Mosaic patterns of B vitamin synthesis and utilization in a natural marine microbial community. <i>Environmental Microbiology</i> , 2018, 20, 2809-2823.	3.8	59
22	Identifying labile DOM components in a coastal ocean through depleted bacterial transcripts and chemical signals. <i>Environmental Microbiology</i> , 2018, 20, 3012-3030.	3.8	56
23	Expression patterns of elemental cycling genes in the Amazon River Plume. <i>ISME Journal</i> , 2017, 11, 1852-1864.	9.8	54
24	Spontaneous mutations of a model heterotrophic marine bacterium. <i>ISME Journal</i> , 2017, 11, 1713-1718.	9.8	22
25	Bacterial transcriptome remodeling during sequential co-culture with a marine dinoflagellate and diatom. <i>ISME Journal</i> , 2017, 11, 2677-2690.	9.8	96
26	Ocean biogeochemistry modeled with emergent trait-based genomics. <i>Science</i> , 2017, 358, 1149-1154.	12.6	122
27	Recognition cascade and metabolite transfer in a marine bacteria-phytoplankton model system. <i>Environmental Microbiology</i> , 2017, 19, 3500-3513.	3.8	111
28	Microbially-Mediated Transformations of Estuarine Dissolved Organic Matter. <i>Frontiers in Marine Science</i> , 2017, 4, .	2.5	36
29	Patterns of Bacterial and Archaeal Gene Expression through the Lower Amazon River. <i>Frontiers in Marine Science</i> , 2017, 4, .	2.5	14
30	Bacterial Biogeography across the Amazon River-Ocean Continuum. <i>Frontiers in Microbiology</i> , 2017, 8, 882.	3.5	75
31	The Ocean Microbiome: Metabolic Engine of the Marine Carbon Cycle. <i>Microbe Magazine</i> , 2016, 11, 262-267.	0.4	1
32	Experimental Identification of Small Non-Coding RNAs in the Model Marine Bacterium <i>Ruegeria pomeroyi</i> DSS-3. <i>Frontiers in Microbiology</i> , 2016, 7, 380.	3.5	14
33	Low genome content diversity of marine planktonic Thaumarchaeota. <i>Environmental Microbiology Reports</i> , 2016, 8, 501-507.	2.4	6
34	Small RNAs expressed during dimethylsulfoniopropionate degradation by a model marine bacterium. <i>Environmental Microbiology Reports</i> , 2016, 8, 763-773.	2.4	1
35	Deciphering ocean carbon in a changing world. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3143-3151.	7.1	253
36	Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. <i>ISME Journal</i> , 2016, 10, 1589-1601.	9.8	226

#	ARTICLE	IF	CITATIONS
37	Drought-induced variability in dissolved organic matter composition in a marsh-dominated estuary. <i>Geophysical Research Letters</i> , 2015, 42, 6446-6453.	4.0	24
38	How do divergent ecological strategies emerge among marine bacterioplankton lineages?. <i>Trends in Microbiology</i> , 2015, 23, 577-584.	7.7	65
39	Interaction and signalling between a cosmopolitan phytoplankton and associated bacteria. <i>Nature</i> , 2015, 522, 98-101.	27.8	875
40	The global ocean microbiome. <i>Science</i> , 2015, 350, aac8455.	12.6	167
41	Cryptic carbon and sulfur cycling between surface ocean plankton. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 453-457.	7.1	348
42	Single-taxon field measurements of bacterial gene regulation controlling DMSP fate. <i>ISME Journal</i> , 2015, 9, 1677-1686.	9.8	37
43	Metagenomic and metatranscriptomic inventories of the lower Amazon River, May 2011. <i>Microbiome</i> , 2015, 3, 39.	11.1	47
44	Microbial life in Bourlyashchy, the hottest thermal pool of Uzon Caldera, Kamchatka. <i>Extremophiles</i> , 2015, 19, 1157-1171.	2.3	29
45	Phenotypic plasticity in heterotrophic marine microbial communities in continuous cultures. <i>ISME Journal</i> , 2015, 9, 1141-1151.	9.8	20
46	The transcriptional response of prokaryotes to phytoplankton-derived dissolved organic matter in seawater. <i>Environmental Microbiology</i> , 2015, 17, 3466-3480.	3.8	55
47	Linking activity and function to ecosystem dynamics in a coastal bacterioplankton community. <i>Frontiers in Microbiology</i> , 2014, 5, 185.	3.5	55
48	Evolutionary Ecology of the Marine Roseobacter Clade. <i>Microbiology and Molecular Biology Reviews</i> , 2014, 78, 573-587.	6.6	279
49	The Marine Microbial Eukaryote Transcriptome Sequencing Project (MMETSP): Illuminating the Functional Diversity of Eukaryotic Life in the Oceans through Transcriptome Sequencing. <i>PLoS Biology</i> , 2014, 12, e1001889.	5.6	885
50	Quantitative Microbial Metatranscriptomics. <i>Methods in Molecular Biology</i> , 2014, 1096, 213-229.	0.9	10
51	Regulatory and Functional Diversity of Methylmercaptopropionate Coenzyme A Ligases from the Dimethylsulfoniopropionate Demethylation Pathway in <i>Ruegeria pomeroyi</i> DSS-3 and Other Proteobacteria. <i>Journal of Bacteriology</i> , 2014, 196, 1275-1285.	2.2	27
52	Comparing effective population sizes of dominant marine alphaproteobacteria lineages. <i>Environmental Microbiology Reports</i> , 2014, 6, 167-172.	2.4	27
53	Microbial controls on DMSP degradation and DMS formation in the Sargasso Sea. <i>Biogeochemistry</i> , 2014, 120, 295-305.	3.5	18
54	Microspatial gene expression patterns in the Amazon River Plume. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11085-11090.	7.1	128

#	ARTICLE	IF	CITATIONS
55	The Amazon continuum dataset: quantitative metagenomic and metatranscriptomic inventories of the Amazon River plume, June 2010. <i>Microbiome</i> , 2014, 2, 17.	11.1	54
56	Evolutionary analysis of a streamlined lineage of surface ocean Roseobacters. <i>ISME Journal</i> , 2014, 8, 1428-1439.	9.8	55
57	Seasonal variation in the metatranscriptomes of a Thaumarchaeota population from SE USA coastal waters. <i>ISME Journal</i> , 2014, 8, 685-698.	9.8	58
58	Single-cell genomics shedding light on marine Thaumarchaeota diversification. <i>ISME Journal</i> , 2014, 8, 732-736.	9.8	98
59	An Updated genome annotation for the model marine bacterium <i>Ruegeria pomeroyi</i> DSS-3. <i>Standards in Genomic Sciences</i> , 2014, 9, 11.	1.5	20
60	Use of Internal Standards for Quantitative Metatranscriptome and Metagenome Analysis. <i>Methods in Enzymology</i> , 2013, 531, 237-250.	1.0	112
61	Assembly-free metagenomic analysis reveals new metabolic capabilities in surface ocean bacterioplankton. <i>Environmental Microbiology Reports</i> , 2013, 5, 686-696.	2.4	8
62	Transcriptional response of bathypelagic marine bacterioplankton to the Deepwater Horizon oil spill. <i>ISME Journal</i> , 2013, 7, 2315-2329.	9.8	172
63	Expression patterns reveal niche diversification in a marine microbial assemblage. <i>ISME Journal</i> , 2013, 7, 281-298.	9.8	175
64	Sizing up metatranscriptomics. <i>ISME Journal</i> , 2013, 7, 237-243.	9.8	298
65	Metabolism of dimethylsulphoniopropionate by <i>Ruegeria pomeroyi</i> DSS-3. <i>Molecular Microbiology</i> , 2013, 89, 774-791.	2.5	46
66	Bacterial and archaeal community structure in the surface microlayer of high mountain lakes examined under two atmospheric aerosol loading scenarios. <i>FEMS Microbiology Ecology</i> , 2013, 84, 387-397.	2.7	36
67	Diel gene expression profiles of a phosphorus limited mountain lake using metatranscriptomics. <i>Environmental Microbiology</i> , 2013, 15, 1190-1203.	3.8	41
68	Evolution of Divergent Life History Strategies in Marine Alphaproteobacteria. <i>MBio</i> , 2013, 4, .	4.1	103
69	Prevalent genome streamlining and latitudinal divergence of planktonic bacteria in the surface ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11463-11468.	7.1	328
70	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
71	Bacterial Dimethylsulfoniopropionate Degradation Genes in the Oligotrophic North Pacific Subtropical Gyre. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2775-2782.	3.1	39
72	Genomic Insights into Bacterial DMSP Transformations. <i>Annual Review of Marine Science</i> , 2012, 4, 523-542.	11.6	165

#	ARTICLE	IF	CITATIONS
73	Transcriptional Changes Underlying Elemental Stoichiometry Shifts in a Marine Heterotrophic Bacterium. <i>Frontiers in Microbiology</i> , 2012, 3, 159.	3.5	21
74	Structures of dimethylsulfoniopropionate-dependent demethylase from the marine organism <i>Pelagabacter ubique</i> . <i>Protein Science</i> , 2012, 21, 289-298.	7.6	24
75	Omics for understanding microbial functional dynamics. <i>Environmental Microbiology</i> , 2012, 14, 1-3.	3.8	71
76	Genome content of uncultivated marine <i>Roseobacters</i> in the surface ocean. <i>Environmental Microbiology</i> , 2012, 14, 41-51.	3.8	42
77	Bacterial community transcription patterns during a marine phytoplankton bloom. <i>Environmental Microbiology</i> , 2012, 14, 228-239.	3.8	95
78	Environmental, biochemical and genetic drivers of DMSP degradation and DMS production in the Sargasso Sea. <i>Environmental Microbiology</i> , 2012, 14, 1210-1223.	3.8	54
79	Community analysis of high and low nucleic acid-containing bacteria in NW Mediterranean coastal waters using 16S rDNA pyrosequencing. <i>Environmental Microbiology</i> , 2012, 14, 1390-1402.	3.8	106
80	Metatranscriptomic signature of exogenous polyamine utilization by coastal bacterioplankton. <i>Environmental Microbiology Reports</i> , 2011, 3, 798-806.	2.4	47
81	Bacterial Catabolism of Dimethylsulfoniopropionate (DMSP). <i>Frontiers in Microbiology</i> , 2011, 2, 172.	3.5	171
82	Bromodeoxyuridine (BrdU) Labeling and Subsequent Fluorescence Activated Cell Sorting for Culture-independent Identification of Dissolved Organic Carbon-degrading Bacterioplankton. <i>Journal of Visualized Experiments</i> , 2011, . .	0.3	2
83	Analysis of sulfur-related transcription by <i>Roseobacter</i> communities using a taxon-specific functional gene microarray. <i>Environmental Microbiology</i> , 2011, 13, 453-467.	3.8	22
84	Quantitative analysis of a deeply sequenced marine microbial metatranscriptome. <i>ISME Journal</i> , 2011, 5, 461-472.	9.8	195
85	Metatranscriptomic analysis of ammonia-oxidizing organisms in an estuarine bacterioplankton assemblage. <i>ISME Journal</i> , 2011, 5, 866-878.	9.8	108
86	Novel pathway for assimilation of dimethylsulphoniopropionate widespread in marine bacteria. <i>Nature</i> , 2011, 473, 208-211.	27.8	126
87	Changes in Dimethylsulfoniopropionate Demethylase Gene Assemblages in Response to an Induced Phytoplankton Bloom. <i>Applied and Environmental Microbiology</i> , 2011, 77, 524-531.	3.1	45
88	Genome characteristics of a generalist marine bacterial lineage. <i>ISME Journal</i> , 2010, 4, 784-798.	9.8	358
89	Transcriptomic analysis of a marine bacterial community enriched with dimethylsulfoniopropionate. <i>ISME Journal</i> , 2010, 4, 1410-1420.	9.8	61
90	Transporter genes expressed by coastal bacterioplankton in response to dissolved organic carbon. <i>Environmental Microbiology</i> , 2010, 12, 616-627.	3.8	225

#	ARTICLE	IF	CITATIONS
91	Deep Sequencing of a Dimethylsulfoniopropionate-Degrading Gene (<i>dmdA</i>) by Using PCR Primer Pairs Designed on the Basis of Marine Metagenomic Data. <i>Applied and Environmental Microbiology</i> , 2010, 76, 609-617.	3.1	68
92	Analyzing Gene Expression from Marine Microbial Communities using Environmental Transcriptomics. <i>Journal of Visualized Experiments</i> , 2009, , .	0.3	47
93	The Diverse Bacterial Community in Intertidal, Anaerobic Sediments at Sapelo Island, Georgia. <i>Microbial Ecology</i> , 2009, 58, 244-261.	2.8	37
94	Microbial Community Response to Seawater Amendment in Low-Salinity Tidal Sediments. <i>Microbial Ecology</i> , 2009, 58, 558-568.	2.8	70
95	<i>In situ</i> transcriptomic analysis of the globally important keystone N ₂ -fixing taxon <i>Crocospaera watsonii</i> . <i>ISME Journal</i> , 2009, 3, 618-631.	9.8	67
96	Comparative day/night metatranscriptomic analysis of microbial communities in the North Pacific subtropical gyre. <i>Environmental Microbiology</i> , 2009, 11, 1358-1375.	3.8	285
97	Metatranscriptomics: Eavesdropping on Complex Microbial Communities. <i>Microbe Magazine</i> , 2009, 4, 329-335.	0.4	86
98	Bacterial carbon processing by generalist species in the coastal ocean. <i>Nature</i> , 2008, 451, 708-711.	27.8	284
99	Functional metagenomic profiling of nine biomes. <i>Nature</i> , 2008, 452, 629-632.	27.8	842
100	Abundant and diverse bacteria involved in DMSP degradation in marine surface waters. <i>Environmental Microbiology</i> , 2008, 10, 2397-2410.	3.8	149
101	Dimethylsulfoniopropionate-Dependent Demethylase (DmdA) from <i>Pelagibacter ubique</i> and <i>Silicibacter pomeroyi</i> . <i>Journal of Bacteriology</i> , 2008, 190, 8018-8024.	2.2	111
102	Occurrence and Expression of Gene Transfer Agent Genes in Marine Bacterioplankton. <i>Applied and Environmental Microbiology</i> , 2008, 74, 2933-2939.	3.1	88
103	Variation in Prokaryotic Community Composition as a Function of Resource Availability in Tidal Creek Sediments. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1836-1844.	3.1	15
104	Using DNA Technology To Explore Marine Bacterial Diversity in a Coastal Georgia Salt Marsh. <i>American Biology Teacher</i> , 2008, 70, 279-283.	0.2	3
105	Toward a Standards-Compliant Genomic and Metagenomic Publication Record. <i>OMICS A Journal of Integrative Biology</i> , 2008, 12, 157-160.	2.0	33
106	Section 8 Update - Environmental transcriptomics: a method to access expressed genes in complex microbial communities. , 2008, , 1892-1904.		3
107	Section 3 update: In situ PCR methodologies for visualization of microscale genetic and taxonomic diversities of prokaryotic communities. , 2008, , 2591-2612.		0
108	Ecological Genomics of Marine Roseobacters. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4559-4569.	3.1	327

#	ARTICLE	IF	CITATIONS
109	Genomes of Sea Microbes. <i>Oceanography</i> , 2007, 20, 47-55.	1.0	4
110	The role of nitrogen in chromophoric and fluorescent dissolved organic matter formation. <i>Marine Chemistry</i> , 2007, 103, 46-60.	2.3	62
111	Resourceful heterotrophs make the most of light in the coastal ocean. <i>Nature Reviews Microbiology</i> , 2007, 5, 792-800.	28.6	185
112	Comparison of chitinolytic enzymes from an alkaline, hypersaline lake and an estuary. <i>Environmental Microbiology</i> , 2007, 9, 197-205.	3.8	52
113	Bacterioplankton assemblages transforming dissolved organic compounds in coastal seawater. <i>Environmental Microbiology</i> , 2007, 9, 2025-2037.	3.8	57
114	Transcriptional response of <i>Silicibacter pomeroyi</i> to dimethylsulfoniopropionate (DMS). <i>Environmental Microbiology</i> , 2007, 9, 2742-2755.	3.8	54
115	Bacterial Taxa That Limit Sulfur Flux from the Ocean. <i>Science</i> , 2006, 314, 649-652.	12.6	296
116	Screening for bacterial-fungal associations in a south-eastern US salt marsh using pre-established fungal monocultures. <i>FEMS Microbiology Ecology</i> , 2005, 54, 179-187.	2.7	5
117	Variations in the spectral properties of freshwater and estuarine CDOM caused by partitioning onto river and estuarine sediments. <i>Estuarine, Coastal and Shelf Science</i> , 2005, 65, 289-301.	2.1	44
118	Sources, bioavailability, and photoreactivity of dissolved organic carbon in the Sacramento-San Joaquin River Delta. <i>Biogeochemistry</i> , 2005, 74, 131-149.	3.5	40
119	Flow-Cytometric Cell Sorting and Subsequent Molecular Analyses for Culture-Independent Identification of Bacterioplankton Involved in Dimethylsulfoniopropionate Transformations. <i>Applied and Environmental Microbiology</i> , 2005, 71, 1405-1416.	3.1	33
120	Overview of the Marine Roseobacter Lineage. <i>Applied and Environmental Microbiology</i> , 2005, 71, 5665-5677.	3.1	753
121	Analysis of Microbial Gene Transcripts in Environmental Samples. <i>Applied and Environmental Microbiology</i> , 2005, 71, 4121-4126.	3.1	211
122	Dimethylsulfoniopropionate Turnover Is Linked to the Composition and Dynamics of the Bacterioplankton Assemblage during a Microcosm Phytoplankton Bloom. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7650-7660.	3.1	69
123	Use of Microautoradiography Combined with Fluorescence In Situ Hybridization To Determine Dimethylsulfoniopropionate Incorporation by Marine Bacterioplankton Taxa. <i>Applied and Environmental Microbiology</i> , 2004, 70, 4648-4657.	3.1	86
124	Diverse Organization of Genes of the Î²-Ketoadipate Pathway in Members of the Marine Roseobacter Lineage. <i>Applied and Environmental Microbiology</i> , 2004, 70, 1658-1668.	3.1	52
125	Genome sequence of <i>Silicibacter pomeroyi</i> reveals adaptations to the marine environment. <i>Nature</i> , 2004, 432, 910-913.	27.8	415
126	Dissolved organic fluorophores in southeastern US coastal waters: correction method for eliminating Rayleigh and Raman scattering peaks in excitation-emission matrices. <i>Marine Chemistry</i> , 2004, 89, 15-36.	2.3	378

#	ARTICLE	IF	CITATIONS
127	Chromophoric dissolved organic matter (CDOM) source characterization in the Louisiana Bight. <i>Marine Chemistry</i> , 2004, 89, 257-272.	2.3	83
128	Temporal dynamics of three culturable $\delta^{13}\text{C}$ -Proteobacteria taxa in salt marsh sediments. <i>Aquatic Ecology</i> , 2003, 37, 55-64.	1.5	7
129	Diversity of Ascomycete Laccase Gene Sequences in a Southeastern US Salt Marsh. <i>Microbial Ecology</i> , 2003, 45, 270-281.	2.8	79
130	Linking a Bacterial Taxon to Sulfur Cycling in the Sea: Studies of the Marine Roseobacter Group. <i>Geomicrobiology Journal</i> , 2003, 20, 375-388.	2.0	133
131	<i>Silicibacter pomeroyi</i> sp. nov. and <i>Roseovarius nubinhibens</i> sp. nov., dimethylsulfoniopropionate-demethylating bacteria from marine environments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 1261-1269.	1.7	231
132	Dynamics of Bacterial and Fungal Communities on Decaying Salt Marsh Grass. <i>Applied and Environmental Microbiology</i> , 2003, 69, 6676-6687.	3.1	105
133	Oxidation of organic and inorganic sulfur compounds by aerobic heterotrophic marine bacteria. <i>Progress in Industrial Microbiology</i> , 2002, 36, 291-310.	0.0	2
134	Determination of apparent quantum yield spectra for the formation of biologically labile photoproducts. <i>Limnology and Oceanography</i> , 2002, 47, 343-352.	3.1	136
135	Analysis of Internal Transcribed Spacer (ITS) Regions of rRNA Genes in Fungal Communities in a Southeastern U.S. Salt Marsh. <i>Microbial Ecology</i> , 2002, 43, 329-340.	2.8	114
136	Diversity of the Ring-Cleaving Dioxygenase Gene <i>pcaH</i> in a Salt Marsh Bacterial Community. <i>Applied and Environmental Microbiology</i> , 2001, 67, 5801-5809.	3.1	58
137	Identification and characterization of humic substances-degrading bacterial isolates from an estuarine environment. <i>FEMS Microbiology Ecology</i> , 2000, 34, 103-111.	2.7	35
138	Carbon loss and optical property changes during long-term photochemical and biological degradation of estuarine dissolved organic matter. <i>Limnology and Oceanography</i> , 2000, 45, 1254-1264.	3.1	624
139	Key Aromatic-Ring-Cleaving Enzyme, Protocatechuate 3,4-Dioxygenase, in the Ecologically Important Marine Roseobacter Lineage. <i>Applied and Environmental Microbiology</i> , 2000, 66, 4662-4672.	3.1	132
140	Bacterial Community Structure Associated with a Dimethylsulfoniopropionate-Producing North Atlantic Algal Bloom. <i>Applied and Environmental Microbiology</i> , 2000, 66, 4237-4246.	3.1	402
141	Dimethylsulfoniopropionate and Methanethiol Are Important Precursors of Methionine and Protein-Sulfur in Marine Bacterioplankton. <i>Applied and Environmental Microbiology</i> , 1999, 65, 4549-4558.	3.1	229
142	Biodegradation of Riverine Dissolved Organic Carbon in Five Estuaries of the Southeastern United States. <i>Estuaries and Coasts</i> , 1999, 22, 55.	1.7	162
143	Oxygen and carbon dioxide mass balance for the estuarine-intertidal marsh complex of five rivers in the southeastern U.S.. <i>Limnology and Oceanography</i> , 1999, 44, 639-649.	3.1	139
144	Transformation of Sulfur Compounds by an Abundant Lineage of Marine Bacteria in the $\delta^{13}\text{C}$ -Subclass of the Class <i>Proteobacteria</i> . <i>Applied and Environmental Microbiology</i> , 1999, 65, 3810-3819.	3.1	327

#	ARTICLE	IF	CITATIONS
145	Bacterial populations in replicate marine enrichment cultures: assessing variability in abundance using 16S rRNA-based probes. , 1999, , 69-75.		3
146	Title is missing!. Biogeochemistry, 1998, 43, 211-234.	3.5	174
147	Sagittula stellata gen. nov., sp. nov., a Lignin-Transforming Bacterium from a Coastal Environment. International Journal of Systematic Bacteriology, 1997, 47, 773-780.	2.8	150
148	Role of photoreactions in the formation of biologically labile compounds from dissolved organic matter. Limnology and Oceanography, 1997, 42, 1307-1316.	3.1	733
149	Interaction of photochemical and microbial processes in the degradation of refractory dissolved organic matter from a coastal marine environment. Limnology and Oceanography, 1997, 42, 1317-1324.	3.1	282
150	Numerical dominance of a group of marine bacteria in the alpha-subclass of the class Proteobacteria in coastal seawater. Applied and Environmental Microbiology, 1997, 63, 4237-4242.	3.1	347
151	In situ reverse transcription, an approach to characterize genetic diversity and activities of prokaryotes. Applied and Environmental Microbiology, 1997, 63, 4907-4913.	3.1	47
152	Photochemical release of biologically available nitrogen from aquatic dissolved organic matter. Nature, 1996, 381, 404-407.	27.8	387
153	Impact of a genetically engineered bacterium with enhanced alkaline phosphatase activity on marine phytoplankton communities. Applied and Environmental Microbiology, 1996, 62, 6-12.	3.1	33
154	Identifying numerically abundant culturable bacteria from complex communities: an example from a lignin enrichment culture. Applied and Environmental Microbiology, 1996, 62, 4433-4440.	3.1	89
155	Productivities of microbial decomposers during early stages of decomposition of leaves of a freshwater sedge. Freshwater Biology, 1995, 34, 135-148.	2.4	86
156	Evidence for indigenous Streptomyces populations in a marine environment determined with a 16S rRNA probe. Applied and Environmental Microbiology, 1995, 61, 3695-3700.	3.1	98
157	In situ PCR for visualization of microscale distribution of specific genes and gene products in prokaryotic communities. Applied and Environmental Microbiology, 1995, 61, 4074-4082.	3.1	178
158	Preface. Microbial Ecology, 1994, 28, 111-112.	2.8	0
159	Dissolved humic substances of vascular plant origin in a coastal marine environment. Limnology and Oceanography, 1994, 39, 762-771.	3.1	103
160	Direct extraction and purification of rRNA for ecological studies. Applied and Environmental Microbiology, 1993, 59, 915-918.	3.1	119
161	Decomposition of lignocellulose from a freshwater macrophyte by aero-aquatic fungi. Microbial Ecology, 1992, 23, 159-167.	2.8	12
162	Contributions of three subsystems of a freshwater marsh to total bacterial secondary productivity. Microbial Ecology, 1992, 24, 161-70.	2.8	18

#	ARTICLE	IF	CITATIONS
163	Adaptation of model genetically engineered microorganisms to lake water: growth rate enhancements and plasmid loss. <i>Applied and Environmental Microbiology</i> , 1992, 58, 3630-3637.	3.1	33
164	Distribution of terrestrially derived dissolved organic matter on the southeastern U.S. continental shelf. <i>Limnology and Oceanography</i> , 1991, 36, 1134-1149.	3.1	120
165	Carbohydrate Signatures of Aquatic Macrophytes and Their Dissolved Degradation Products as Determined by a Sensitive High-Performance Ion Chromatography Method. <i>Applied and Environmental Microbiology</i> , 1991, 57, 3135-3143.	3.1	60
166	Bacterial production on humic and nonhumic components of dissolved organic carbon. <i>Limnology and Oceanography</i> , 1990, 35, 1744-1756.	3.1	238
167	Formation and bacterial utilization of dissolved organic carbon derived from detrital lignocellulose. <i>Limnology and Oceanography</i> , 1989, 34, 1034-1047.	3.1	83
168	Kinetics of microbial degradation of vascular plant material in two wetland ecosystems. <i>Oecologia</i> , 1989, 79, 158-167.	2.0	38
169	Bacterial secondary production on vascular plant detritus: relationships to detritus composition and degradation rate. <i>Applied and Environmental Microbiology</i> , 1989, 55, 2178-2189.	3.1	73
170	Horizontal Gene Transfer Among Bacteria in Aquatic Systems: Effects of Nutrient Concentrations. , 1989, , 131-138.		0
171	Carbon Flow From Lignocellulose: A Simulation Analysis of a Detritus-Based Ecosystem. <i>Ecology</i> , 1988, 69, 1525-1536.	3.2	32
172	Dynamics of microbial biomass and activity in five habitats of the Okefenokee Swamp ecosystem. <i>Microbial Ecology</i> , 1987, 14, 203-217.	2.8	7
173	Modeling the Persistence of Lignocellulosic Detritus in Wetland Ecosystems. , 1987, , 357-374.		0
174	Biogeochemical cycling of lignocellulosic carbon in marine and freshwater ecosystems: Relative contributions of procaryotes and eucaryotes ¹ . <i>Limnology and Oceanography</i> , 1986, 31, 89-100.	3.1	173
175	The Hudson River Ecosystem. <i>Springer Series on Environmental Management</i> , 1986, , 6-39.	0.3	3
176	Effects of pH and plant source on lignocellulose biodegradation rates in two wetland ecosystems, the Okefenokee Swamp and a Georgia salt marsh ^{1,2,3} . <i>Limnology and Oceanography</i> , 1985, 30, 489-499.	3.1	94
177	Influence of adjacent land use on understory vegetation of New York forests. <i>Urban Ecology</i> , 1984, 8, 329-340.	0.1	51
178	On Estimators Obtained From a Sample Augmented by Multiple Regression. <i>Water Resources Research</i> , 1974, 10, 81-85.	4.2	18
179	A saltmarsh decomposition system and its ascomycetous laccase genes. , 0, , 371-378.		0