

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

9234

74
h-index

9839

141
g-index

196
all docs

196
docs citations

196
times ranked

16276
citing authors

#	ARTICLE	IF	CITATIONS
1	Scientistsâ€™ warning to humanity: microorganisms and climate change. <i>Nature Reviews Microbiology</i> , 2019, 17, 569-586.	13.6	1,138
2	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.	2.6	885
3	Interaction and signalling between a cosmopolitan phytoplankton and associated bacteria. <i>Nature</i> , 2015, 522, 98-101.	13.7	875
4	Functional metagenomic profiling of nine biomes. <i>Nature</i> , 2008, 452, 629-632.	13.7	842
5	Overview of the Marine Roseobacter Lineage. <i>Applied and Environmental Microbiology</i> , 2005, 71, 5665-5677.	1.4	753
6	Role of photoreactions in the formation of biologically labile compounds from dissolved organic matter. <i>Limnology and Oceanography</i> , 1997, 42, 1307-1316.	1.6	733
7	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.	1.6	624
8	Genome sequence of <i>Silicibacter pomeroyi</i> reveals adaptations to the marine environment. <i>Nature</i> , 2004, 432, 910-913.	13.7	415
9	Bacterial Community Structure Associated with a Dimethylsulfoniopropionate-Producing North Atlantic Algal Bloom. <i>Applied and Environmental Microbiology</i> , 2000, 66, 4237-4246.	1.4	402
10	Photochemical release of biologically available nitrogen from aquatic dissolved organic matter. <i>Nature</i> , 1996, 381, 404-407.	13.7	387
11	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.	0.9	378
12	Genome characteristics of a generalist marine bacterial lineage. <i>ISME Journal</i> , 2010, 4, 784-798.	4.4	358
13	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.	3.3	348
14	Numerical dominance of a group of marine bacteria in the alpha-subclass of the class Proteobacteria in coastal seawater. <i>Applied and Environmental Microbiology</i> , 1997, 63, 4237-4242.	1.4	347
15	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.	3.3	328
16	Ecological Genomics of Marine Roseobacters. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4559-4569.	1.4	327
17	Transformation of Sulfur Compounds by an Abundant Lineage of Marine Bacteria in the Î±-Subclass of the Class <i>Proteobacteria</i> . <i>Applied and Environmental Microbiology</i> , 1999, 65, 3810-3819.	1.4	327
18	Sizing up metatranscriptomics. <i>ISME Journal</i> , 2013, 7, 237-243.	4.4	298

#	ARTICLE	IF	CITATIONS
19	Bacterial Taxa That Limit Sulfur Flux from the Ocean. <i>Science</i> , 2006, 314, 649-652.	6.0	296
20	Comparative day/night metatranscriptomic analysis of microbial communities in the North Pacific subtropical gyre. <i>Environmental Microbiology</i> , 2009, 11, 1358-1375.	1.8	285
21	Bacterial carbon processing by generalist species in the coastal ocean. <i>Nature</i> , 2008, 451, 708-711.	13.7	284
22	Interaction of photochemical and microbial processes in the degradation of refractory dissolved organic matter from a coastal marine environment. <i>Limnology and Oceanography</i> , 1997, 42, 1317-1324.	1.6	282
23	Evolutionary Ecology of the Marine Roseobacter Clade. <i>Microbiology and Molecular Biology Reviews</i> , 2014, 78, 573-587.	2.9	279
24	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.	3.3	253
25	Bacterial production on humic and nonhumic components of dissolved organic carbon. <i>Limnology and Oceanography</i> , 1990, 35, 1744-1756.	1.6	238
26	<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.	0.8	231
27	Dimethylsulfoniopropionate and Methanethiol Are Important Precursors of Methionine and Protein-Sulfur in Marine Bacterioplankton. <i>Applied and Environmental Microbiology</i> , 1999, 65, 4549-4558.	1.4	229
28	Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. <i>ISME Journal</i> , 2016, 10, 1589-1601.	4.4	226
29	Transporter genes expressed by coastal bacterioplankton in response to dissolved organic carbon. <i>Environmental Microbiology</i> , 2010, 12, 616-627.	1.8	225
30	Analysis of Microbial Gene Transcripts in Environmental Samples. <i>Applied and Environmental Microbiology</i> , 2005, 71, 4121-4126.	1.4	211
31	Quantitative analysis of a deeply sequenced marine microbial metatranscriptome. <i>ISME Journal</i> , 2011, 5, 461-472.	4.4	195
32	Resourceful heterotrophs make the most of light in the coastal ocean. <i>Nature Reviews Microbiology</i> , 2007, 5, 792-800.	13.6	185
33	In situ PCR for visualization of microscale distribution of specific genes and gene products in prokaryotic communities. <i>Applied and Environmental Microbiology</i> , 1995, 61, 4074-4082.	1.4	178
34	Expression patterns reveal niche diversification in a marine microbial assemblage. <i>ISME Journal</i> , 2013, 7, 281-298.	4.4	175
35	Title is missing!. <i>Biogeochemistry</i> , 1998, 43, 211-234.	1.7	174
36	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.	1.6	173

#	ARTICLE	IF	CITATIONS
37	Transcriptional response of bathypelagic marine bacterioplankton to the Deepwater Horizon oil spill. ISME Journal, 2013, 7, 2315-2329.	4.4	172
38	Bacterial Catabolism of Dimethylsulfoniopropionate (DMSP). Frontiers in Microbiology, 2011, 2, 172.	1.5	171
39	The global ocean microbiome. Science, 2015, 350, aac8455.	6.0	167
40	Genomic Insights into Bacterial DMSP Transformations. Annual Review of Marine Science, 2012, 4, 523-542.	5.1	165
41	Biodegradation of Riverine Dissolved Organic Carbon in Five Estuaries of the Southeastern United States. Estuaries and Coasts, 1999, 22, 55.	1.7	162
42	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
43	Abundant and diverse bacteria involved in DMSP degradation in marine surface waters. Environmental Microbiology, 2008, 10, 2397-2410.	1.8	149
44	Oxygen and carbon dioxide mass balance for the estuarine-intertidal marsh complex of five rivers in the southeastern U.S.. Limnology and Oceanography, 1999, 44, 639-649.	1.6	139
45	Determination of apparent quantum yield spectra for the formation of biologically labile photoproducts. Limnology and Oceanography, 2002, 47, 343-352.	1.6	136
46	Linking a Bacterial Taxon to Sulfur Cycling in the Sea: Studies of the Marine Roseobacter Group. Geomicrobiology Journal, 2003, 20, 375-388.	1.0	133
47	Key Aromatic-Ring-Cleaving Enzyme, Protocatechuate 3,4-Dioxygenase, in the Ecologically Important Marine Roseobacter Lineage. Applied and Environmental Microbiology, 2000, 66, 4662-4672.	1.4	132
48	Microspatial gene expression patterns in the Amazon River Plume. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11085-11090.	3.3	128
49	Novel pathway for assimilation of dimethylsulphonioipropionate widespread in marine bacteria. Nature, 2011, 473, 208-211.	13.7	126
50	Ocean biogeochemistry modeled with emergent trait-based genomics. Science, 2017, 358, 1149-1154.	6.0	122
51	Distribution of terrestrially derived dissolved organic matter on the southeastern U.S. continental shelf. Limnology and Oceanography, 1991, 36, 1134-1149.	1.6	120
52	Direct extraction and purification of rRNA for ecological studies. Applied and Environmental Microbiology, 1993, 59, 915-918.	1.4	119
53	Analysis of Internal Transcribed Spacer (ITS) Regions of rRNA Genes in Fungal Communities in a Southeastern U.S. Salt Marsh. Microbial Ecology, 2002, 43, 329-340.	1.4	114
54	Use of Internal Standards for Quantitative Metatranscriptome and Metagenome Analysis. Methods in Enzymology, 2013, 531, 237-250.	0.4	112

#	ARTICLE	IF	CITATIONS
55	Dimethylsulfoniopropionate-Dependent Demethylase (DmdA) from <i>Pelagibacter ubique</i> and <i>Silicibacter pomeroyi</i> . <i>Journal of Bacteriology</i> , 2008, 190, 8018-8024.	1.0	111
56	Recognition cascade and metabolite transfer in a marine bacteria-phytoplankton model system. <i>Environmental Microbiology</i> , 2017, 19, 3500-3513.	1.8	111
57	Metatranscriptomic analysis of ammonia-oxidizing organisms in an estuarine bacterioplankton assemblage. <i>ISME Journal</i> , 2011, 5, 866-878.	4.4	108
58	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.	1.8	106
59	Dynamics of Bacterial and Fungal Communities on Decaying Salt Marsh Grass. <i>Applied and Environmental Microbiology</i> , 2003, 69, 6676-6687.	1.4	105
60	Sulfur metabolites in the pelagic ocean. <i>Nature Reviews Microbiology</i> , 2019, 17, 665-678.	13.6	104
61	Dissolved humic substances of vascular plant origin in a coastal marine environment. <i>Limnology and Oceanography</i> , 1994, 39, 762-771.	1.6	103
62	Evolution of Divergent Life History Strategies in Marine Alphaproteobacteria. <i>MBio</i> , 2013, 4, .	1.8	103
63	Single-cell genomics shedding light on marine Thaumarchaeota diversification. <i>ISME Journal</i> , 2014, 8, 732-736.	4.4	98
64	Evidence for indigenous <i>Streptomyces</i> populations in a marine environment determined with a 16S rRNA probe. <i>Applied and Environmental Microbiology</i> , 1995, 61, 3695-3700.	1.4	98
65	Bacterial transcriptome remodeling during sequential co-culture with a marine dinoflagellate and diatom. <i>ISME Journal</i> , 2017, 11, 2677-2690.	4.4	96
66	Bacterial community transcription patterns during a marine phytoplankton bloom. <i>Environmental Microbiology</i> , 2012, 14, 228-239.	1.8	95
67	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.	1.6	94
68	Identifying numerically abundant culturable bacteria from complex communities: an example from a lignin enrichment culture. <i>Applied and Environmental Microbiology</i> , 1996, 62, 4433-4440.	1.4	89
69	Occurrence and Expression of Gene Transfer Agent Genes in Marine Bacterioplankton. <i>Applied and Environmental Microbiology</i> , 2008, 74, 2933-2939.	1.4	88
70	Productivities of microbial decomposers during early stages of decomposition of leaves of a freshwater sedge. <i>Freshwater Biology</i> , 1995, 34, 135-148.	1.2	86
71	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.	1.4	86
72	Metatranscriptomics: Eavesdropping on Complex Microbial Communities. <i>Microbe Magazine</i> , 2009, 4, 329-335.	0.4	86

#	ARTICLE	IF	CITATIONS
73	Formation and bacterial utilization of dissolved organic carbon derived from detrital lignocellulose. <i>Limnology and Oceanography</i> , 1989, 34, 1034-1047.	1.6	83
74	Chromophoric dissolved organic matter (CDOM) source characterization in the Louisiana Bight. <i>Marine Chemistry</i> , 2004, 89, 257-272.	0.9	83
75	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.	3.3	82
76	Diversity of Ascomycete Laccase Gene Sequences in a Southeastern US Salt Marsh. <i>Microbial Ecology</i> , 2003, 45, 270-281.	1.4	79
77	Resource partitioning of phytoplankton metabolites that support bacterial heterotrophy. <i>ISME Journal</i> , 2021, 15, 762-773.	4.4	77
78	Bacterial Biogeography across the Amazon River-Ocean Continuum. <i>Frontiers in Microbiology</i> , 2017, 8, 882.	1.5	75
79	Bacterial secondary production on vascular plant detritus: relationships to detritus composition and degradation rate. <i>Applied and Environmental Microbiology</i> , 1989, 55, 2178-2189.	1.4	73
80	Omics for understanding microbial functional dynamics. <i>Environmental Microbiology</i> , 2012, 14, 1-3.	1.8	71
81	Microbial metabolites in the marine carbon cycle. <i>Nature Microbiology</i> , 2022, 7, 508-523.	5.9	71
82	Microbial Community Response to Seawater Amendment in Low-Salinity Tidal Sediments. <i>Microbial Ecology</i> , 2009, 58, 558-568.	1.4	70
83	Sulfur metabolites that facilitate oceanic phytoplankton bacteria carbon flux. <i>ISME Journal</i> , 2019, 13, 2536-2550.	4.4	70
84	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.	1.4	69
85	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.	1.4	68
86	<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.	4.4	67
87	How do divergent ecological strategies emerge among marine bacterioplankton lineages?. <i>Trends in Microbiology</i> , 2015, 23, 577-584.	3.5	65
88	The role of nitrogen in chromophoric and fluorescent dissolved organic matter formation. <i>Marine Chemistry</i> , 2007, 103, 46-60.	0.9	62
89	Transcriptomic analysis of a marine bacterial community enriched with dimethylsulfoniopropionate. <i>ISME Journal</i> , 2010, 4, 1410-1420.	4.4	61
90	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.	1.4	60

#	ARTICLE	IF	CITATIONS
91	Mosaic patterns of B-vitamin synthesis and utilization in a natural marine microbial community. <i>Environmental Microbiology</i> , 2018, 20, 2809-2823.	1.8	59
92	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.	1.4	58
93	Seasonal variation in the metatranscriptomes of a Thaumarchaeota population from SE USA coastal waters. <i>ISME Journal</i> , 2014, 8, 685-698.	4.4	58
94	Bacterioplankton assemblages transforming dissolved organic compounds in coastal seawater. <i>Environmental Microbiology</i> , 2007, 9, 2025-2037.	1.8	57
95	Identifying labile DOM components in a coastal ocean through depleted bacterial transcripts and chemical signals. <i>Environmental Microbiology</i> , 2018, 20, 3012-3030.	1.8	56
96	Linking activity and function to ecosystem dynamics in a coastal bacterioplankton community. <i>Frontiers in Microbiology</i> , 2014, 5, 185.	1.5	55
97	Evolutionary analysis of a streamlined lineage of surface ocean Roseobacters. <i>ISME Journal</i> , 2014, 8, 1428-1439.	4.4	55
98	The transcriptional response of prokaryotes to phytoplankton-derived dissolved organic matter in seawater. <i>Environmental Microbiology</i> , 2015, 17, 3466-3480.	1.8	55
99	Transcriptional response of <i>Silicibacter pomeroyi</i> DSS-3 to dimethylsulfoniopropionate (DMSP). <i>Environmental Microbiology</i> , 2007, 9, 2742-2755.	1.8	54
100	Environmental, biochemical and genetic drivers of DMSP degradation and DMS production in the Sargasso Sea. <i>Environmental Microbiology</i> , 2012, 14, 1210-1223.	1.8	54
101	The Amazon continuum dataset: quantitative metagenomic and metatranscriptomic inventories of the Amazon River plume, June 2010. <i>Microbiome</i> , 2014, 2, 17.	4.9	54
102	Expression patterns of elemental cycling genes in the Amazon River Plume. <i>ISME Journal</i> , 2017, 11, 1852-1864.	4.4	54
103	Diverse Organization of Genes of the Î ² -Ketoacid Pathway in Members of the Marine Roseobacter Lineage. <i>Applied and Environmental Microbiology</i> , 2004, 70, 1658-1668.	1.4	52
104	Comparison of chitinolytic enzymes from an alkaline, hypersaline lake and an estuary. <i>Environmental Microbiology</i> , 2007, 9, 197-205.	1.8	52
105	Influence of adjacent land use on understory vegetation of New York forests. <i>Urban Ecology</i> , 1984, 8, 329-340.	0.1	51
106	Analyzing Gene Expression from Marine Microbial Communities using Environmental Transcriptomics. <i>Journal of Visualized Experiments</i> , 2009, , .	0.2	47
107	Metatranscriptomic signature of exogenous polyamine utilization by coastal bacterioplankton. <i>Environmental Microbiology Reports</i> , 2011, 3, 798-806.	1.0	47
108	Metagenomic and metatranscriptomic inventories of the lower Amazon River, May 2011. <i>Microbiome</i> , 2015, 3, 39.	4.9	47

#	ARTICLE	IF	CITATIONS
109	In situ reverse transcription, an approach to characterize genetic diversity and activities of prokaryotes. Applied and Environmental Microbiology, 1997, 63, 4907-4913.	1.4	47
110	Metabolism of dimethylsulphoniopropionate by <i>Ruegeria pomeroyi</i> DSS-3. Molecular Microbiology, 2013, 89, 774-791.	1.2	46
111	Changes in Dimethylsulfonylpropionate Demethylase Gene Assemblages in Response to an Induced Phytoplankton Bloom. Applied and Environmental Microbiology, 2011, 77, 524-531.	1.4	45
112	Variations in the spectral properties of freshwater and estuarine CDOM caused by partitioning onto river and estuarine sediments. Estuarine, Coastal and Shelf Science, 2005, 65, 289-301.	0.9	44
113	Genome content of uncultivated marine <i>Roseobacters</i> in the surface ocean. Environmental Microbiology, 2012, 14, 41-51.	1.8	42
114	Diel gene expression profiles of a phosphorus limited mountain lake using metatranscriptomics. Environmental Microbiology, 2013, 15, 1190-1203.	1.8	41
115	Sources, bioavailability, and photoreactivity of dissolved organic carbon in the Sacramento-San Joaquin River Delta. Biogeochemistry, 2005, 74, 131-149.	1.7	40
116	Bacterial Dimethylsulfonylpropionate Degradation Genes in the Oligotrophic North Pacific Subtropical Gyre. Applied and Environmental Microbiology, 2012, 78, 2775-2782.	1.4	39
117	The Ocean's labile DOC supply chain. Limnology and Oceanography, 2022, 67, 1007-1021.	1.6	39
118	Kinetics of microbial degradation of vascular plant material in two wetland ecosystems. Oecologia, 1989, 79, 158-167.	0.9	38
119	Microdiversity and temporal dynamics of marine bacterial dimethylsulfonylpropionate genes. Environmental Microbiology, 2019, 21, 1687-1701.	1.8	38
120	The Diverse Bacterial Community in Intertidal, Anaerobic Sediments at Sapelo Island, Georgia. Microbial Ecology, 2009, 58, 244-261.	1.4	37
121	Single-taxon field measurements of bacterial gene regulation controlling DMSP fate. ISME Journal, 2015, 9, 1677-1686.	4.4	37
122	Bacterial and archaeal community structure in the surface microlayer of high mountain lakes examined under two atmospheric aerosol loading scenarios. FEMS Microbiology Ecology, 2013, 84, 387-397.	1.3	36
123	Microbially-Mediated Transformations of Estuarine Dissolved Organic Matter. Frontiers in Marine Science, 2017, 4, .	1.2	36
124	Microbial metagenomes and metatranscriptomes during a coastal phytoplankton bloom. Scientific Data, 2019, 6, 129.	2.4	36
125	Identification and characterization of humic substances-degrading bacterial isolates from an estuarine environment. FEMS Microbiology Ecology, 2000, 34, 103-111.	1.3	35
126	Flow-Cytometric Cell Sorting and Subsequent Molecular Analyses for Culture-Independent Identification of Bacterioplankton Involved in Dimethylsulfonylpropionate Transformations. Applied and Environmental Microbiology, 2005, 71, 1405-1416.	1.4	33

#	ARTICLE	IF	CITATIONS
127	Toward a Standards-Compliant Genomic and Metagenomic Publication Record. <i>OMICS A Journal of Integrative Biology</i> , 2008, 12, 157-160.	1.0	33
128	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.	1.4	33
129	Impact of a genetically engineered bacterium with enhanced alkaline phosphatase activity on marine phytoplankton communities. <i>Applied and Environmental Microbiology</i> , 1996, 62, 6-12.	1.4	33
130	Carbon Flow From Lignocellulose: A Simulation Analysis of a Detritus-Based Ecosystem. <i>Ecology</i> , 1988, 69, 1525-1536.	1.5	32
131	Microbial life in Bourlyashchy, the hottest thermal pool of Uzon Caldera, Kamchatka. <i>Extremophiles</i> , 2015, 19, 1157-1171.	0.9	29
132	Towards Integrating Evolution, Metabolism, and Climate Change Studies of Marine Ecosystems. <i>Trends in Ecology and Evolution</i> , 2019, 34, 1022-1033.	4.2	28
133	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.	1.0	27
134	Comparing effective population sizes of dominant marine alphaproteobacteria lineages. <i>Environmental Microbiology Reports</i> , 2014, 6, 167-172.	1.0	27
135	Unprecedented DMSP Concentrations in a Massive Dinoflagellate Bloom in Monterey Bay, CA. <i>Geophysical Research Letters</i> , 2019, 46, 12279-12288.	1.5	26
136	Structures of dimethylsulfoniopropionate-dependent demethylase from the marine organism <i>Pelagabacter ubique</i> . <i>Protein Science</i> , 2012, 21, 289-298.	3.1	24
137	Drought-induced variability in dissolved organic matter composition in a marsh-dominated estuary. <i>Geophysical Research Letters</i> , 2015, 42, 6446-6453.	1.5	24
138	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.	1.8	22
139	Spontaneous mutations of a model heterotrophic marine bacterium. <i>ISME Journal</i> , 2017, 11, 1713-1718.	4.4	22
140	Transcriptional Changes Underlying Elemental Stoichiometry Shifts in a Marine Heterotrophic Bacterium. <i>Frontiers in Microbiology</i> , 2012, 3, 159.	1.5	21
141	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
142	Phenotypic plasticity in heterotrophic marine microbial communities in continuous cultures. <i>ISME Journal</i> , 2015, 9, 1141-1151.	4.4	20
143	On Estimators Obtained From a Sample Augmented by Multiple Regression. <i>Water Resources Research</i> , 1974, 10, 81-85.	1.7	18
144	Contributions of three subsystems of a freshwater marsh to total bacterial secondary productivity. <i>Microbial Ecology</i> , 1992, 24, 161-70.	1.4	18

#	ARTICLE	IF	CITATIONS
145	Microbial controls on DMSP degradation and DMS formation in the Sargasso Sea. <i>Biogeochemistry</i> , 2014, 120, 295-305.	1.7	18
146	Niche dimensions of a marine bacterium are identified using invasion studies in coastal seawater. <i>Nature Microbiology</i> , 2021, 6, 524-532.	5.9	18
147	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.	3.2	17
148	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.	1.4	15
149	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.	1.5	14
150	Patterns of Bacterial and Archaeal Gene Expression through the Lower Amazon River. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	14
151	Diel investments in metabolite production and consumption in a model microbial system. <i>ISME Journal</i> , 2022, 16, 1306-1317.	4.4	13
152	Decomposition of lignocellulose from a freshwater macrophyte by aero-aquatic fungi. <i>Microbial Ecology</i> , 1992, 23, 159-167.	1.4	12
153	Bacterial responses to background organic pollutants in the northeast subarctic Pacific Ocean. <i>Environmental Microbiology</i> , 2021, 23, 4532-4546.	1.8	11
154	Quantitative Microbial Metatranscriptomics. <i>Methods in Molecular Biology</i> , 2014, 1096, 213-229.	0.4	10
155	Assembly-free metagenomic analysis reveals new metabolic capabilities in surface ocean bacterioplankton. <i>Environmental Microbiology Reports</i> , 2013, 5, 686-696.	1.0	8
156	Dynamics of microbial biomass and activity in five habitats of the Okefenokee Swamp ecosystem. <i>Microbial Ecology</i> , 1987, 14, 203-217.	1.4	7
157	Temporal dynamics of three culturable $\hat{1}^3$ -Proteobacteria taxa in salt marsh sediments. <i>Aquatic Ecology</i> , 2003, 37, 55-64.	0.7	7
158	Low genome content diversity of marine planktonic Thaumarchaeota. <i>Environmental Microbiology Reports</i> , 2016, 8, 501-507.	1.0	6
159	Growth-stage-related shifts in diatom endometabolome composition set the stage for bacterial heterotrophy. <i>ISME Communications</i> , 2022, 2, .	1.7	6
160	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.	1.3	5
161	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
162	Genome Sequences and Metagenome-Assembled Genome Sequences of Microbial Communities Enriched on Phytoplankton Exometabolites. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	5

#	ARTICLE	IF	CITATIONS
163	Genomes of Sea Microbes. <i>Oceanography</i> , 2007, 20, 47-55.	0.5	4
164	Coastal Ocean Metagenomes and Curated Metagenome-Assembled Genomes from Marsh Landing, Sapelo Island (Georgia, USA). <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
165	Using DNA Technology To Explore Marine Bacterial Diversity in a Coastal Georgia Salt Marsh. <i>American Biology Teacher</i> , 2008, 70, 279-283.	0.1	3
166	Section 8 Update - Environmental transcriptomics: a method to access expressed genes in complex microbial communities. , 2008, , 1892-1904.		3
167	The Hudson River Ecosystem. <i>Springer Series on Environmental Management</i> , 1986, , 6-39.	0.3	3
168	Bacterial populations in replicate marine enrichment cultures: assessing variability in abundance using 16S rRNA-based probes. , 1999, , 69-75.		3
169	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, .	1.2	3
170	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
171	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, , .	0.2	2
172	Transcriptional activity differentiates families of Marine Group II <i>Euryarchaeota</i> in the coastal ocean. <i>ISME Communications</i> , 2021, 1, .	1.7	2
173	The Ocean Microbiome: Metabolic Engine of the Marine Carbon Cycle. <i>Microbe Magazine</i> , 2016, 11, 262-267.	0.4	1
174	Small RNAs expressed during dimethylsulfoniopropionate degradation by a model marine bacterium. <i>Environmental Microbiology Reports</i> , 2016, 8, 763-773.	1.0	1
175	Preface. <i>Microbial Ecology</i> , 1994, 28, 111-112.	1.4	0
176	A saltmarsh decomposition system and its ascomycetous laccase genes. , 0, , 371-378.		0
177	Section 3 update: In situ PCR methodologies for visualization of microscale genetic and taxonomic diversities of prokaryotic communities. , 2008, , 2591-2612.		0
178	Modeling the Persistence of Lignocellulosic Detritus in Wetland Ecosystems. , 1987, , 357-374.		0
179	Horizontal Gene Transfer Among Bacteria in Aquatic Systems: Effects of Nutrient Concentrations. , 1989, , 131-138.		0