

Andreas Teske

List of Publications by Year in descending order

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Version: 2024-02-01

127
papers

12,975
citations

34016

52
h-index

24915

109
g-index

131
all docs

131
docs citations

131
times ranked

9237
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogenetic relationships of <i>Thiomicrospira</i> species and their identification in deep-sea hydrothermal vent samples by denaturing gradient gel electrophoresis of 16S rDNA fragments. <i>Archives of Microbiology</i> , 1995, 164, 165-172.	1.0	1,031
2	Late Proterozoic rise in atmospheric oxygen concentration inferred from phylogenetic and sulphur-isotope studies. <i>Nature</i> , 1996, 382, 127-132.	13.7	790
3	Distributions of Microbial Activities in Deep Subseafloor Sediments. <i>Science</i> , 2004, 306, 2216-2221.	6.0	681
4	Heterotrophic Archaea dominate sedimentary subsurface ecosystems off Peru. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 3846-3851.	3.3	654
5	Biogeographical distribution and diversity of microbes in methane hydrate-bearing deep marine sediments on the Pacific Ocean Margin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2815-2820.	3.3	644
6	Microbial Diversity of Hydrothermal Sediments in the Guaymas Basin: Evidence for Anaerobic Methanotrophic Communities. <i>Applied and Environmental Microbiology</i> , 2002, 68, 1994-2007.	1.4	632
7	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
8	Uncultured archaea in deep marine subsurface sediments: have we caught them all?. <i>ISME Journal</i> , 2008, 2, 3-18.	4.4	413
9	Benthic eukaryotic diversity in the Guaymas Basin hydrothermal vent environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 7658-7662.	3.3	343
10	Archaea of the Miscellaneous Crenarchaeotal Group are abundant, diverse and widespread in marine sediments. <i>ISME Journal</i> , 2012, 6, 1949-1965.	4.4	281
11	Hydrocarbon-degrading bacteria enriched by the <i>Deepwater Horizon</i> oil spill identified by cultivation and DNA-SIP. <i>ISME Journal</i> , 2013, 7, 2091-2104.	4.4	278
12	Molecular Characterization of Sulfate-Reducing Bacteria in the Guaymas Basin. <i>Applied and Environmental Microbiology</i> , 2003, 69, 2765-2772.	1.4	277
13	Nitrogen, Carbon, and Sulfur Metabolism in Natural <i>Thioploca</i> Samples. <i>Applied and Environmental Microbiology</i> , 1999, 65, 3148-3157.	1.4	223
14	Evidence for Microbial Carbon and Sulfur Cycling in Deeply Buried Ridge Flank Basalt. <i>Science</i> , 2013, 339, 1305-1308.	6.0	210
15	An Anaerobic Methane-Oxidizing Community of ANME-1b Archaea in Hypersaline Gulf of Mexico Sediments. <i>Applied and Environmental Microbiology</i> , 2006, 72, 7218-7230.	1.4	206
16	Sulfate-Reducing Bacteria and Their Activities in Cyanobacterial Mats of Solar Lake (Sinai, Egypt). <i>Applied and Environmental Microbiology</i> , 1998, 64, 2943-2951.	1.4	204
17	Marine subsurface eukaryotes: the fungal majority. <i>Environmental Microbiology</i> , 2011, 13, 172-183.	1.8	200
18	Stratified Communities of Active Archaea in Deep Marine Subsurface Sediments. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4596-4603.	1.4	196

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19	Thermophilic anaerobic oxidation of methane by marine microbial consortia. ISME Journal, 2011, 5, 1946-1956.	4.4	185
20	Composition and enzymatic function of particle-associated and free-living bacteria: a coastal/offshore comparison. ISME Journal, 2014, 8, 2167-2179.	4.4	159
21	Methanogen Diversity Evidenced by Molecular Characterization of Methyl Coenzyme M Reductase A () Tj ETQq1 1 0.784314 rgBT /Ove Microbiology, 2005, 71, 4592-4601.	1.4	152
22	Anaerobic oxidation of methane at different temperature regimes in Guaymas Basin hydrothermal sediments. ISME Journal, 2012, 6, 1018-1031.	4.4	149
23	Microbial diversity and stratification of South Pacific abyssal marine sediments. Environmental Microbiology, 2011, 13, 3219-3234.	1.8	148
24	Environmental evidence for net methane production and oxidation in putative ANaerobic MEthanotrophic (ANME) archaea. Environmental Microbiology, 2011, 13, 2548-2564.	1.8	146
25	Influence of water column dynamics on sulfide oxidation and other major biogeochemical processes in the chemocline of Mariager Fjord (Denmark). Marine Chemistry, 2001, 74, 29-51.	0.9	142
26	Role of Bacterial Exopolysaccharides (EPS) in the Fate of the Oil Released during the Deepwater Horizon Oil Spill. PLoS ONE, 2013, 8, e67717.	1.1	135
27	Expanding frontiers in deep subsurface microbiology. Palaeogeography, Palaeoclimatology, Palaeoecology, 2005, 219, 131-155.	1.0	134
28	Microbial Activities and Dissolved Organic Matter Dynamics in Oil-Contaminated Surface Seawater from the Deepwater Horizon Oil Spill Site. PLoS ONE, 2012, 7, e34816.	1.1	132
29	Molecular analysis of deep subsurface microbial communities in Nankai Trough sediments (ODP Leg) Tj ETQq1 1 0.784314 rgBT /Ove 1.3 125	1.3	125
30	Phylogenetic characterization of epibiotic bacteria in the accessory nidamental gland and egg capsules of the squid <i>Loligo pealei</i> (Cephalopoda: Loliginidae). Environmental Microbiology, 2001, 3, 151-167.	1.8	123
31	Bacterial and archaeal phylotypes associated with distinct mineralogical layers of a white smoker spire from a deep-sea hydrothermal vent site (9oN, East Pacific Rise). Environmental Microbiology, 2006, 8, 909-920.	1.8	121
32	Trends in Basalt and Sediment Core Contamination During IODP Expedition 301. Geomicrobiology Journal, 2006, 23, 517-530.	1.0	119
33	Spatial Structure and Activity of Sedimentary Microbial Communities Underlying a <i>Beggiatoa</i> spp. Mat in a Gulf of Mexico Hydrocarbon Seep. PLoS ONE, 2010, 5, e8738.	1.1	117
34	Pulsed blooms and persistent oil-degrading bacterial populations in the water column during and after the Deepwater Horizon blowout. Deep-Sea Research Part II: Topical Studies in Oceanography, 2016, 129, 282-291.	0.6	111
35	Molecular characterization of sulfate-reducing bacteria in a New England salt marsh. Environmental Microbiology, 2005, 7, 1175-1185.	1.8	109
36	Archaea in Organic-Lean and Organic-Rich Marine Subsurface Sediments: An Environmental Gradient Reflected in Distinct Phylogenetic Lineages. Frontiers in Microbiology, 2012, 3, 168.	1.5	101

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37	Desulforhopalus vacuolatus gen. nov., sp. nov., a new moderately psychrophilic sulfate-reducing bacterium with gas vacuoles isolated from a temperate estuary. Archives of Microbiology, 1996, 166, 160-168.	1.0	90
38	Acetogenesis in Deep Subseafloor Sediments of The Juan de Fuca Ridge Flank: A Synthesis of Geochemical, Thermodynamic, and Gene-based Evidence. Geomicrobiology Journal, 2010, 27, 183-211.	1.0	89
39	Strategies of sulfate-reducing bacteria to escape oxygen stress in a cyanobacterial mat. FEMS Microbiology Ecology, 1998, 25, 89-96.	1.3	85
40	The Guaymas Basin Hiking Guide to Hydrothermal Mounds, Chimneys, and Microbial Mats: Complex Seafloor Expressions of Subsurface Hydrothermal Circulation. Frontiers in Microbiology, 2016, 7, 75.	1.5	82
41	Thermal and geochemical influences on microbial biogeography in the hydrothermal sediments of Guaymas Basin, California. Environmental Microbiology Reports, 2016, 8, 150-161.	1.0	79
42	Sediment-associated microdiversity within the Marine Group I Crenarchaeota. Environmental Microbiology Reports, 2010, 2, 693-703.	1.0	77
43	Phylogeny of Thioploca and Related Filamentous Sulfide-Oxidizing Bacteria. Systematic and Applied Microbiology, 1995, 18, 517-526.	1.2	74
44	Biosphere frontiers of subsurface life in the sedimented hydrothermal system of Guaymas Basin. Frontiers in Microbiology, 2014, 5, 362.	1.5	74
45	Multiple evidence for methylotrophic methanogenesis as the dominant methanogenic pathway in hypersaline sediments from the Orca Basin, Gulf of Mexico. Geochimica Et Cosmochimica Acta, 2016, 187, 1-20.	1.6	73
46	Microbial Communities in Methane- and Short Chain Alkane-Rich Hydrothermal Sediments of Guaymas Basin. Frontiers in Microbiology, 2016, 7, 17.	1.5	72
47	Anaerobic oxidation of thiosulfate to tetrathionate by obligately heterotrophic bacteria, belonging to the Pseudomonas stutzeri group. FEMS Microbiology Ecology, 1999, 30, 113-123.	1.3	71
48	Sulfate Reduction and Possible Aerobic Metabolism of the Sulfate-Reducing Bacterium Desulfovibrio oxyclinae in a Chemostat Coculture with Marinobacter sp. Strain MB under Exposure to Increasing Oxygen Concentrations. Applied and Environmental Microbiology, 2000, 66, 5013-5018.	1.4	68
49	Domain Evolution and Functional Diversification of Sulfite Reductases. Astrobiology, 2005, 5, 18-29.	1.5	67
50	Thermophilic Genus of Archaea Mediating the Anaerobic Oxidation of Ethane. MBio, 2020, 11, .	1.8	66
51	The Genera Beggiatoa and Thioploca. , 2006, , 784-810.		64
52	Quantitative PCR methods for RNA and DNA in marine sediments: maximizing yield while overcoming inhibition. FEMS Microbiology Ecology, 2010, 72, 143-151.	1.3	62
53	Oil-derived marine aggregates "hot spots" of polysaccharide degradation by specialized bacterial communities. Deep-Sea Research Part II: Topical Studies in Oceanography, 2016, 129, 179-186.	0.6	59
54	Phylogenetic and morphologic complexity of giant sulphur bacteria. Antonie Van Leeuwenhoek, 2013, 104, 169-186.	0.7	58

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55	Sulfide Ameliorates Metal Toxicity for Deep-Sea Hydrothermal Vent Archaea. <i>Applied and Environmental Microbiology</i> , 2004, 70, 2551-2555.	1.4	56
56	Genomic Markers of Ancient Anaerobic Microbial Pathways: Sulfate Reduction, Methanogenesis, and Methane Oxidation. <i>Biological Bulletin</i> , 2003, 204, 186-191.	0.7	52
57	Distinct Bacterial Communities in Surficial Seafloor Sediments Following the 2010 Deepwater Horizon Blowout. <i>Frontiers in Microbiology</i> , 2016, 7, 1384.	1.5	52
58	Riverine Bacterial Communities Reveal Environmental Disturbance Signatures within the Betaproteobacteria and Verrucomicrobia. <i>Frontiers in Microbiology</i> , 2016, 7, 1441.	1.5	52
59	Metabolic strategies of marine subseafloor Chloroflexi inferred from genome reconstructions. <i>Environmental Microbiology</i> , 2020, 22, 3188-3204.	1.8	49
60	Endosymbionts of <i>Siboglinum fiordicum</i> and the Phylogeny of Bacterial Endosymbionts in Siboglinidae (Annelida). <i>Biological Bulletin</i> , 2008, 214, 135-144.	0.7	44
61	Microbial Communities and Chemosynthesis in Yellowstone Lake Sublacustrine Hydrothermal Vent Waters. <i>Frontiers in Microbiology</i> , 2011, 2, 130.	1.5	40
62	Community structural differences shape microbial responses to high molecular weight organic matter. <i>Environmental Microbiology</i> , 2019, 21, 557-571.	1.8	40
63	Ethane- and propane-producing potential and molecular characterization of an ethanogenic enrichment in an anoxic estuarine sediment. <i>Organic Geochemistry</i> , 2013, 59, 37-48.	0.9	39
64	The archaeal lipidome in estuarine sediment dominated by members of the <i>Miscellaneous Crenarchaeotal Group</i> . <i>Environmental Microbiology</i> , 2015, 17, 2441-2458.	1.8	38
65	Morphological and Phylogenetic Characterizations of Freshwater <i>Thioploca</i> Species from Lake Biwa, Japan, and Lake Constance, Germany. <i>Applied and Environmental Microbiology</i> , 2003, 69, 390-398.	1.4	36
66	Why Orange Guaymas Basin <i>Beggiatoa</i> spp. Are Orange: Single-Filament-Genome-Enabled Identification of an Abundant Octaheme Cytochrome with Hydroxylamine Oxidase, Hydrazine Oxidase, and Nitrite Reductase Activities. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1183-1190.	1.4	36
67	Near-surface Heating of Young Rift Sediment Causes Mass Production and Discharge of Reactive Dissolved Organic Matter. <i>Scientific Reports</i> , 2017, 7, 44864.	1.6	36
68	Mobile Elements in a Single-Filament Orange Guaymas Basin <i>Beggiatoa</i> (‘‘Candidate Maribeggiatoa’’) sp. Draft Genome: Evidence for Genetic Exchange with Cyanobacteria. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3974-3985.	1.4	33
69	Characteristics and Evolution of sill-driven off-axis hydrothermalism in Guaymas Basin ‘‘the Ringvent site. <i>Scientific Reports</i> , 2019, 9, 13847.	1.6	33
70	A molecular and physiological survey of a diverse collection of hydrothermal vent <i>Thermococcus</i> and <i>Pyrococcus</i> isolates. <i>Extremophiles</i> , 2009, 13, 905-915.	0.9	32
71	Sulfide oxidation, nitrate respiration, carbon acquisition, and electron transport pathways suggested by the draft genome of a single orange Guaymas Basin <i>Beggiatoa</i> (Cand. <i>Maribeggiatoa</i>) sp. filament. <i>Marine Genomics</i> , 2013, 11, 53-65.	0.4	32
72	Phylogeography, Salinity Adaptations and Metabolic Potential of the Candidate Division KB1 Bacteria Based on a Partial Single Cell Genome. <i>Frontiers in Microbiology</i> , 2016, 7, 1266.	1.5	32

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73	Possible roles of uncultured archaea in carbon cycling in methane-seep sediments. <i>Geochimica Et Cosmochimica Acta</i> , 2015, 164, 35-52.	1.6	31
74	Structure and function of high Arctic pelagic, particle-associated and benthic bacterial communities. <i>Environmental Microbiology</i> , 2018, 20, 2941-2954.	1.8	31
75	Filamentous Giant Beggiatoaceae from the Guaymas Basin Are Capable of both Denitrification and Dissimilatory Nitrate Reduction to Ammonium. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	30
76	Effects of Dissolved Sulfide, pH, and Temperature on Growth and Survival of Marine Hyperthermophilic Archaea. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6383-6387.	1.4	29
77	Filamentous bacteria inhabiting the sheaths of marine <i>Thioploca</i> spp. on the Chilean continental shelf. <i>FEMS Microbiology Ecology</i> , 2009, 68, 164-172.	1.3	29
78	Cultivation-dependent and cultivation-independent characterization of hydrocarbon-degrading bacteria in Guaymas Basin sediments. <i>Frontiers in Microbiology</i> , 2015, 6, 695.	1.5	29
79	Calcite-accumulating large sulfur bacteria of the genus <i>Achromatium</i> in Sippewissett Salt Marsh. <i>ISME Journal</i> , 2015, 9, 2503-2514.	4.4	29
80	Hydrocarbon-degradation and MOS-formation capabilities of the dominant bacteria enriched in sea surface oil slicks during the Deepwater Horizon oil spill. <i>Marine Pollution Bulletin</i> , 2018, 135, 205-215.	2.3	29
81	Phylogenetic Relationships of a Large Marine Beggiatoa. <i>Systematic and Applied Microbiology</i> , 1999, 22, 39-44.	1.2	28
82	Microbial habitat connectivity across spatial scales and hydrothermal temperature gradients at Guaymas Basin. <i>Frontiers in Microbiology</i> , 2013, 4, 207.	1.5	28
83	Microbial Communities Under Distinct Thermal and Geochemical Regimes in Axial and Off-Axis Sediments of Guaymas Basin. <i>Frontiers in Microbiology</i> , 2021, 12, 633649.	1.5	28
84	<i>Tritonibacter horizontis</i> gen. nov., sp. nov., a member of the Rhodobacteraceae, isolated from the Deepwater Horizon oil spill. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 736-744.	0.8	25
85	Enrichment of Fusobacteria in Sea Surface Oil Slicks from the Deepwater Horizon Oil Spill. <i>Microorganisms</i> , 2016, 4, 24.	1.6	23
86	Phylogenetic Characterization of Marine Benthic Archaea in Organic-Poor Sediments of the Eastern Equatorial Pacific Ocean (ODP Site 1225). <i>Microorganisms</i> , 2016, 4, 32.	1.6	22
87	Generation and Utilization of Volatile Fatty Acids and Alcohols in Hydrothermally Altered Sediments in the Guaymas Basin, Gulf of California. <i>Geophysical Research Letters</i> , 2019, 46, 2637-2646.	1.5	22
88	Microbial communities at the borehole observatory on the Costa Rica Rift flank (Ocean Drilling) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 14	1.5	20
89	Effect of Storage Conditions on Archaeal and Bacterial Communities in Subsurface Marine Sediments. <i>Geomicrobiology Journal</i> , 2010, 27, 261-272.	1.0	19
90	Survival and growth of two heterotrophic hydrothermal vent archaea, <i>Pyrococcus</i> strain GB-D and <i>Thermococcus fumicolans</i> , under low pH and high sulfide concentrations in combination with high temperature and pressure regimes. <i>Extremophiles</i> , 2007, 11, 329-342.	0.9	17

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91	Editorial: Microbial Exopolymers: Sources, Chemico-Physiological Properties, and Ecosystem Effects in the Marine Environment. <i>Frontiers in Microbiology</i> , 2018, 9, 1822.	1.5	17
92	Sharp contrasts between freshwater and marine microbial enzymatic capabilities, community composition, and DOM pools in a NE Greenland fjord. <i>Limnology and Oceanography</i> , 2020, 65, 77-95.	1.6	17
93	How Clonal Is Clonal? Genome Plasticity across Multicellular Segments of a <i>Candidatus Marithrix</i> sp. Filament from Sulfidic, Briny Seafloor Sediments in the Gulf of Mexico. <i>Frontiers in Microbiology</i> , 2016, 7, 1173.	1.5	15
94	Microbial community structure and methane-cycling activity of subsurface sediments at Mississippi Canyon 118 before the Deepwater Horizon disaster. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2016, 129, 148-156.	0.6	15
95	Identification, Expression and Activity of Candidate Nitrite Reductases From Orange Beggiatoaceae, Guaymas Basin. <i>Frontiers in Microbiology</i> , 2019, 10, 644.	1.5	15
96	The Family Beggiatoaceae. , 2014, , 93-134.		15
97	Cryptic Links in the Ocean. <i>Science</i> , 2010, 330, 1326-1327.	6.0	14
98	Microbial ecology and biogeochemistry of hypersaline sediments in Orca Basin. <i>PLoS ONE</i> , 2020, 15, e0231676.	1.1	14
99	Insights into the single cell draft genome of <i>Candidatus Achromatium palustre</i> . <i>Standards in Genomic Sciences</i> , 2016, 11, 28.	1.5	13
100	Cable bacteria, living electrical conduits in the microbial world. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18759-18761.	3.3	13
101	Marine Deep Sediment Microbial Communities. , 2013, , 123-138.		12
102	Expanding frontiers in deep subsurface microbiology. , 2005, , 131-155.		11
103	Draft genome sequence of the marine Rhodobacteraceae strain O3.65, cultivated from oil-polluted seawater of the Deepwater Horizon oil spill. <i>Standards in Genomic Sciences</i> , 2016, 11, 81.	1.5	11
104	Microbial Communities of Hydrothermal Guaymas Basin Surficial Sediment Profiled at 2 Millimeter-Scale Resolution. <i>Frontiers in Microbiology</i> , 2021, 12, 710881.	1.5	11
105	Deep-sea hydrothermal vent sediments reveal diverse fungi with antibacterial activities. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	11
106	The Limits of Life and the Biosphere in Earth's Interior. <i>Oceanography</i> , 2019, 32, 208-211.	0.5	10
107	Interactions between temperature and energy supply drive microbial communities in hydrothermal sediment. <i>Communications Biology</i> , 2021, 4, 1006.	2.0	10
108	Deep subsurface microbiology: a guide to the research topic papers. <i>Frontiers in Microbiology</i> , 2013, 4, 122.	1.5	10

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109	Microbial epibiotic community of the deep-sea galatheid squat lobster <i>Munidopsis alvisca</i> . <i>Scientific Reports</i> , 2022, 12, 2675.	1.6	9
110	Genetic Evidence of Subseafloor Microbial Communities. <i>Developments in Marine Geology</i> , 2014, 7, 85-125.	0.4	8
111	Intracellular calcite and sulfur dynamics of <i>Achromatium</i> cells observed in a lab-based enrichment and aerobic incubation experiment. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 263-274.	0.7	8
112	Enrichment and Isolation. , 0, , 215-269.		7
113	Analysis of Deep Subsurface Microbial Communities by Functional Genes and Genomics. <i>Modern Approaches in Solid Earth Sciences</i> , 2008, , 159-176.	0.1	6
114	Hydrocarbon-Degrading Microbial Communities in Natural Oil Seeps. , 2019, , 1-31.		6
115	Editorial: Hydrothermal microbial ecosystems. <i>Frontiers in Microbiology</i> , 2015, 6, 884.	1.5	5
116	Hydrocarbon-Degrading Microbial Communities in Natural Oil Seeps. , 2019, , 81-111.		5
117	Guaymas Basin, a Hydrothermal Hydrocarbon Seep Ecosystem. <i>Springer Oceanography</i> , 2020, , 43-68.	0.2	4
118	Grand Challenges in Extreme Microbiology. <i>Frontiers in Microbiology</i> , 2010, 1, 111.	1.5	3
119	Aerobic Archaea in iron-rich springs. <i>Nature Microbiology</i> , 2018, 3, 646-647.	5.9	3
120	10 Years of Extreme Microbiology: An Interim Reflection and Future Prospects. <i>Frontiers in Microbiology</i> , 2020, 11, 131.	1.5	3
121	7. Archaea in deep marine subsurface sediments. , 2014, , 143-160.		2
122	Enigmatic Archaeal and Eukaryotic Life at Hydrothermal Vents and in Marine Subsurface Sediments. <i>Cellular Origin and Life in Extreme Habitats</i> , 2007, , 519-533.	0.3	2
123	Hydrocarbon-Degrading Microbial Communities in Natural Oil Seeps. , 2019, , 1-31.		1
124	Editorial: Archaea in the Environment: Views on Archaeal Distribution, Activity, and Biogeography. <i>Frontiers in Microbiology</i> , 2021, 12, 667596.	1.5	1
125	The Gulf of Mexico: An Introductory Survey of a Seep-Dominated Seafloor Landscape. <i>Springer Oceanography</i> , 2020, , 69-100.	0.2	1
126	Large Sulfur-Oxidizing Bacteria at Gulf of Mexico Hydrocarbon Seeps. <i>Springer Oceanography</i> , 2020, , 149-171.	0.2	0

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127	Growth Patterns of Giant Deep Sea Beggiatoaceae from a Guaymas Basin Vent Site. Springer Oceanography, 2020, , 173-181.	0.2	0