

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	Microbial epibiotic community of the deep-sea galatheid squat lobster <i>Munidopsis alvisca</i> . <i>Scientific Reports</i> , 2022, 12, 2675.	1.6	9
2	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
3	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
4	Editorial: Archaea in the Environment: Views on Archaeal Distribution, Activity, and Biogeography. <i>Frontiers in Microbiology</i> , 2021, 12, 667596.	1.5	1
5	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
6	Deep-sea hydrothermal vent sediments reveal diverse fungi with antibacterial activities. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	11
7	Interactions between temperature and energy supply drive microbial communities in hydrothermal sediment. <i>Communications Biology</i> , 2021, 4, 1006.	2.0	10
8	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
9	Metabolic strategies of marine subsurface Chloroflexi inferred from genome reconstructions. <i>Environmental Microbiology</i> , 2020, 22, 3188-3204.	1.8	49
10	10 Years of Extreme Microbiology: An Interim Reflection and Future Prospects. <i>Frontiers in Microbiology</i> , 2020, 11, 131.	1.5	3
11	â€œ <i>Candidatus</i> <i>Ethanoperedens</i> ,â€•a Thermophilic Genus of <i>Archaea</i> Mediating the Anaerobic Oxidation of Ethane. <i>MBio</i> , 2020, 11, .	1.8	66
12	Microbial ecology and biogeochemistry of hypersaline sediments in Orca Basin. <i>PLoS ONE</i> , 2020, 15, e0231676.	1.1	14
13	The Gulf of Mexico: An Introductory Survey of a Seep-Dominated Seafloor Landscape. <i>Springer Oceanography</i> , 2020, , 69-100.	0.2	1
14	Guaymas Basin, a Hydrothermal Hydrocarbon Seep Ecosystem. <i>Springer Oceanography</i> , 2020, , 43-68.	0.2	4
15	Large Sulfur-Oxidizing Bacteria at Gulf of Mexico Hydrocarbon Seeps. <i>Springer Oceanography</i> , 2020, , 149-171.	0.2	0
16	Growth Patterns of Giant Deep Sea Beggiatoaceae from a Guaymas Basin Vent Site. <i>Springer Oceanography</i> , 2020, , 173-181.	0.2	0
17	Hydrocarbon-Degrading Microbial Communities in Natural Oil Seeps. , 2019, , 81-111.		5
18	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

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19	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
20	The Limits of Life and the Biosphere in Earth’s Interior. <i>Oceanography</i> , 2019, 32, 208-211.	0.5	10
21	Identification, Expression and Activity of Candidate Nitrite Reductases From Orange Beggiatoaceae, Guaymas Basin. <i>Frontiers in Microbiology</i> , 2019, 10, 644.	1.5	15
22	Hydrocarbon-Degrading Microbial Communities in Natural Oil Seeps. , 2019, , 1-31.		6
23	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
24	Community structural differences shape microbial responses to high molecular weight organic matter. <i>Environmental Microbiology</i> , 2019, 21, 557-571.	1.8	40
25	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
26	Hydrocarbon-Degrading Microbial Communities in Natural Oil Seeps. , 2019, , 1-31.		1
27	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
28	Aerobic Archaea in iron-rich springs. <i>Nature Microbiology</i> , 2018, 3, 646-647.	5.9	3
29	Structure and function of high Arctic pelagic, particle-associated and benthic bacterial communities. <i>Environmental Microbiology</i> , 2018, 20, 2941-2954.	1.8	31
30	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
31	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
32	<i>Tritonibacter horizontalis</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
33	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
34	Pulsed blooms and persistent oil-degrading bacterial populations in the water column during and after the Deepwater Horizon blowout. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2016, 129, 282-291.	0.6	111
35	Enrichment of <i>Fusobacteria</i> in Sea Surface Oil Slicks from the Deepwater Horizon Oil Spill. <i>Microorganisms</i> , 2016, 4, 24.	1.6	23
36	Microbial Communities in Methane- and Short Chain Alkane-Rich Hydrothermal Sediments of Guaymas Basin. <i>Frontiers in Microbiology</i> , 2016, 7, 17.	1.5	72

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37	The Guaymas Basin Hiking Guide to Hydrothermal Mounds, Chimneys, and Microbial Mats: Complex Seafloor Expressions of Subsurface Hydrothermal Circulation. <i>Frontiers in Microbiology</i> , 2016, 7, 75.	1.5	82
38	How Clonal Is Clonal? Genome Plasticity across Multicellular Segments of a <i>Candidatus Maritrix</i> sp. Filament from Sulfidic, Briny Seafloor Sediments in the Gulf of Mexico. <i>Frontiers in Microbiology</i> , 2016, 7, 1173.	1.5	15
39	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
40	Distinct Bacterial Communities in Surficial Seafloor Sediments Following the 2010 Deepwater Horizon Blowout. <i>Frontiers in Microbiology</i> , 2016, 7, 1384.	1.5	52
41	Riverine Bacterial Communities Reveal Environmental Disturbance Signatures within the Betaproteobacteria and Verrucomicrobia. <i>Frontiers in Microbiology</i> , 2016, 7, 1441.	1.5	52
42	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
43	Thermal and geochemical influences on microbial biogeography in the hydrothermal sediments of Guaymas Basin, Gulf of California. <i>Environmental Microbiology Reports</i> , 2016, 8, 150-161.	1.0	79
44	Multiple evidence for methylotrophic methanogenesis as the dominant methanogenic pathway in hypersaline sediments from the Orca Basin, Gulf of Mexico. <i>Geochimica Et Cosmochimica Acta</i> , 2016, 187, 1-20.	1.6	73
45	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
46	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
47	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
48	Oil-derived marine aggregates as hot spots of polysaccharide degradation by specialized bacterial communities. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2016, 129, 179-186.	0.6	59
49	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
50	Editorial: Hydrothermal microbial ecosystems. <i>Frontiers in Microbiology</i> , 2015, 6, 884.	1.5	5
51	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
52	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
53	The archaeal lipidome in estuarine sediment dominated by members of the Miscellaneous Crenarchaeotal Group. <i>Environmental Microbiology</i> , 2015, 17, 2441-2458.	1.8	38
54	Biosphere frontiers of subsurface life in the sedimented hydrothermal system of Guaymas Basin. <i>Frontiers in Microbiology</i> , 2014, 5, 362.	1.5	74

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55	7. Archaea in deep marine subsurface sediments. , 2014, , 143-160.		2
56	Genetic Evidence of Subseafloor Microbial Communities. <i>Developments in Marine Geology</i> , 2014, 7, 85-125.	0.4	8
57	Composition and enzymatic function of particle-associated and free-living bacteria: a coastal/offshore comparison. <i>ISME Journal</i> , 2014, 8, 2167-2179.	4.4	159
58	The Family Beggiatoaceae. , 2014, , 93-134.		15
59	Phylogenetic and morphologic complexity of giant sulphur bacteria. <i>Antonie Van Leeuwenhoek</i> , 2013, 104, 169-186.	0.7	58
60	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
61	Sulfide oxidation, nitrate respiration, carbon acquisition, and electron transport pathways suggested by the draft genome of a single orange Guaymas Basin Beggiatoa (<i>Cand. Maribeggiatoa</i>) sp. filament. <i>Marine Genomics</i> , 2013, 11, 53-65.	0.4	32
62	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
63	Evidence for Microbial Carbon and Sulfur Cycling in Deeply Buried Ridge Flank Basalt. <i>Science</i> , 2013, 339, 1305-1308.	6.0	210
64	Marine Deep Sediment Microbial Communities. , 2013, , 123-138.		12
65	Mobile Elements in a Single-Filament Orange Guaymas Basin Beggiatoa (â€œCandidatus Maribeggiatoaâ€) sp. Draft Genome: Evidence for Genetic Exchange with Cyanobacteria. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3974-3985.	1.4	33
66	Why Orange Guaymas Basin Beggiatoa 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	Microbial habitat connectivity across spatial scales and hydrothermal temperature gradients at Guaymas Basin. <i>Frontiers in Microbiology</i> , 2013, 4, 207.	1.5	28
68	Role of Bacterial Exopolysaccharides (EPS) in the Fate of the Oil Released during the Deepwater Horizon Oil Spill. <i>PLoS ONE</i> , 2013, 8, e67717.	1.1	135
69	Deep subsurface microbiology: a guide to the research topic papers. <i>Frontiers in Microbiology</i> , 2013, 4, 122.	1.5	10
70	Anaerobic oxidation of methane at different temperature regimes in Guaymas Basin hydrothermal sediments. <i>ISME Journal</i> , 2012, 6, 1018-1031.	4.4	149
71	Microbial Activities and Dissolved Organic Matter Dynamics in Oil-Contaminated Surface Seawater from the Deepwater Horizon Oil Spill Site. <i>PLoS ONE</i> , 2012, 7, e34816.	1.1	132
72	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

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73	Archaea in Organic-Lean and Organic-Rich Marine Subsurface Sediments: An Environmental Gradient Reflected in Distinct Phylogenetic Lineages. <i>Frontiers in Microbiology</i> , 2012, 3, 168.	1.5	101
74	Microbial communities at the borehole observatory on the Costa Rica Rift flank (Ocean Drilling) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 70	1.5	20
75	Microbial Communities and Chemosynthesis in Yellowstone Lake Sublacustrine Hydrothermal Vent Waters. <i>Frontiers in Microbiology</i> , 2011, 2, 130.	1.5	40
76	Marine subsurface eukaryotes: the fungal majority. <i>Environmental Microbiology</i> , 2011, 13, 172-183.	1.8	200
77	Environmental evidence for net methane production and oxidation in putative ANaerobic MEthanotrophic (ANME) archaea. <i>Environmental Microbiology</i> , 2011, 13, 2548-2564.	1.8	146
78	Microbial diversity and stratification of South Pacific abyssal marine sediments. <i>Environmental Microbiology</i> , 2011, 13, 3219-3234.	1.8	148
79	Thermophilic anaerobic oxidation of methane by marine microbial consortia. <i>ISME Journal</i> , 2011, 5, 1946-1956.	4.4	185
80	Quantitative PCR methods for RNA and DNA in marine sediments: maximizing yield while overcoming inhibition. <i>FEMS Microbiology Ecology</i> , 2010, 72, 143-151.	1.3	62
81	Grand Challenges in Extreme Microbiology. <i>Frontiers in Microbiology</i> , 2010, 1, 111.	1.5	3
82	Cryptic Links in the Ocean. <i>Science</i> , 2010, 330, 1326-1327.	6.0	14
83	Sediment-associated microdiversity within the Marine Group I Crenarchaeota. <i>Environmental Microbiology Reports</i> , 2010, 2, 693-703.	1.0	77
84	Effect of Storage Conditions on Archaeal and Bacterial Communities in Subsurface Marine Sediments. <i>Geomicrobiology Journal</i> , 2010, 27, 261-272.	1.0	19
85	Acetogenesis in Deep Subseafloor Sediments of The Juan de Fuca Ridge Flank: A Synthesis of Geochemical, Thermodynamic, and Gene-based Evidence. <i>Geomicrobiology Journal</i> , 2010, 27, 183-211.	1.0	89
86	Spatial Structure and Activity of Sedimentary Microbial Communities Underlying a <i>Beggiatoa</i> spp. Mat in a Gulf of Mexico Hydrocarbon Seep. <i>PLoS ONE</i> , 2010, 5, e8738.	1.1	117
87	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
88	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
89	Uncultured archaea in deep marine subsurface sediments: have we caught them all?. <i>ISME Journal</i> , 2008, 2, 3-18.	4.4	413
90	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

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91	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
92	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
93	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
94	The Genera <i>Beggiatoa</i> and <i>Thioploca</i> . , 2006, , 784-810.		64
95	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
96	Stratified Communities of Active Archaea in Deep Marine Subsurface Sediments. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4596-4603.	1.4	196
97	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
98	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). <i>Environmental Microbiology</i> , 2006, 8, 909-920.	1.8	121
99	Trends in Basalt and Sediment Core Contamination During IODP Expedition 301. <i>Geomicrobiology Journal</i> , 2006, 23, 517-530.	1.0	119
100	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
101	Molecular characterization of sulfate-reducing bacteria in a New England salt marsh. <i>Environmental Microbiology</i> , 2005, 7, 1175-1185.	1.8	109
102	Expanding frontiers in deep subsurface microbiology. , 2005, , 131-155.		11
103	Methanogen Diversity Evidenced by Molecular Characterization of Methyl Coenzyme M Reductase A () Tj ETQq1 1 0.784314 rgBT /Ov <i>Microbiology</i> , 2005, 71, 4592-4601.	1.4	152
104	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
105	Expanding frontiers in deep subsurface microbiology. <i>Palaeogeography, Palaeoclimatology, Palaeoecology</i> , 2005, 219, 131-155.	1.0	134
106	Domain Evolution and Functional Diversification of Sulfite Reductases. <i>Astrobiology</i> , 2005, 5, 18-29.	1.5	67
107	Sulfide Ameliorates Metal Toxicity for Deep-Sea Hydrothermal Vent Archaea. <i>Applied and Environmental Microbiology</i> , 2004, 70, 2551-2555.	1.4	56
108	Distributions of Microbial Activities in Deep Subseafloor Sediments. <i>Science</i> , 2004, 306, 2216-2221.	6.0	681

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109	Molecular analysis of deep subsurface microbial communities in Nankai Trough sediments (ODP Leg) Tj ETQq1 1 0.784314 rgBT/Ov	1.3	125
110	Genomic Markers of Ancient Anaerobic Microbial Pathways: Sulfate Reduction, Methanogenesis, and Methane Oxidation. Biological Bulletin, 2003, 204, 186-191.	0.7	52
111	Morphological and Phylogenetic Characterizations of Freshwater Thioploca Species from Lake Biwa, Japan, and Lake Constance, Germany. Applied and Environmental Microbiology, 2003, 69, 390-398.	1.4	36
112	Molecular Characterization of Sulfate-Reducing Bacteria in the Guaymas Basin. Applied and Environmental Microbiology, 2003, 69, 2765-2772.	1.4	277
113	Benthic eukaryotic diversity in the Guaymas Basin hydrothermal vent environment. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7658-7662.	3.3	343
114	Microbial Diversity of Hydrothermal Sediments in the Guaymas Basin: Evidence for Anaerobic Methanotrophic Communities. Applied and Environmental Microbiology, 2002, 68, 1994-2007.	1.4	632
115	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
116	Phylogenetic characterization of epibiotic bacteria in the accessory nidamental gland and egg capsules of the squid Loligo pealei (Cephalopoda: Loliginidae). Environmental Microbiology, 2001, 3, 151-167.	1.8	123
117	Sulfate Reduction and Possible Aerobic Metabolism of the Sulfate-Reducing Bacterium Desulfovibrio oxycliniae 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
118	Nitrogen, Carbon, and Sulfur Metabolism in Natural <i>Thioploca</i> Samples. Applied and Environmental Microbiology, 1999, 65, 3148-3157.	1.4	223
119	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
120	Phylogenetic Relationships of a Large Marine Beggiatoa. Systematic and Applied Microbiology, 1999, 22, 39-44.	1.2	28
121	Strategies of sulfate-reducing bacteria to escape oxygen stress in a cyanobacterial mat. FEMS Microbiology Ecology, 1998, 25, 89-96.	1.3	85
122	Sulfate-Reducing Bacteria and Their Activities in Cyanobacterial Mats of Solar Lake (Sinai, Egypt). Applied and Environmental Microbiology, 1998, 64, 2943-2951.	1.4	204
123	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
124	Late Proterozoic rise in atmospheric oxygen concentration inferred from phylogenetic and sulphur-isotope studies. Nature, 1996, 382, 127-132.	13.7	790
125	Phylogeny of Thioploca and Related Filamentous Sulfide-Oxidizing Bacteria. Systematic and Applied Microbiology, 1995, 18, 517-526.	1.2	74
126	Phylogenetic relationships of Thiomicrospira species and their identification in deep-sea hydrothermal vent samples by denaturing gradient gel electrophoresis of 16S rDNA fragments. Archives of Microbiology, 1995, 164, 165-172.	1.0	1,031

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127	Enrichment and Isolation. , 0, , 215-269.		7