

Victoria Orphan

List of Publications by Year in descending order

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144
papers

14,385
citations

26567

56
h-index

22102

113
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162
all docs

162
docs citations

162
times ranked

12183
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	Methane-Consuming Archaea Revealed by Directly Coupled Isotopic and Phylogenetic Analysis. <i>Science</i> , 2001, 293, 484-487.	6.0	957
3	Manganese- and Iron-Dependent Marine Methane Oxidation. <i>Science</i> , 2009, 325, 184-187.	6.0	873
4	Methane metabolism in the archaeal phylum Bathyarchaeota revealed by genome-centric metagenomics. <i>Science</i> , 2015, 350, 434-438.	6.0	677
5	Multiple archaeal groups mediate methane oxidation in anoxic cold seep sediments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 7663-7668.	3.3	604
6	Comparative Analysis of Methane-Oxidizing Archaea and Sulfate-Reducing Bacteria in Anoxic Marine Sediments. <i>Applied and Environmental Microbiology</i> , 2001, 67, 1922-1934.	1.4	594
7	Single cell activity reveals direct electron transfer in methanotrophic consortia. <i>Nature</i> , 2015, 526, 531-535.	13.7	529
8	Culture-Dependent and Culture-Independent Characterization of Microbial Assemblages Associated with High-Temperature Petroleum Reservoirs. <i>Applied and Environmental Microbiology</i> , 2000, 66, 700-711.	1.4	441
9	Artificial electron acceptors decouple archaeal methane oxidation from sulfate reduction. <i>Science</i> , 2016, 351, 703-707.	6.0	346
10	Molecular and isotopic analysis of anaerobic methane-oxidizing communities in marine sediments. <i>Organic Geochemistry</i> , 2000, 31, 1685-1701.	0.9	321
11	Deep-Sea Archaea Fix and Share Nitrogen in Methane-Consuming Microbial Consortia. <i>Science</i> , 2009, 326, 422-426.	6.0	295
12	Trace Metal Requirements for Microbial Enzymes Involved in the Production and Consumption of Methane and Nitrous Oxide. <i>Frontiers in Microbiology</i> , 2012, 3, 61.	1.5	291
13	Diverse syntrophic partnerships from deep-sea methane vents revealed by direct cell capture and metagenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7052-7057.	3.3	261
14	Authigenic carbonate formation at hydrocarbon seeps in continental margin sediments: A comparative study. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2007, 54, 1268-1291.	0.6	229
15	Anaerobic methane oxidation coupled to manganese reduction by members of the <i>Methanoperedenaceae</i> . <i>ISME Journal</i> , 2020, 14, 1030-1041.	4.4	203
16	<i>In situ</i> visualization of newly synthesized proteins in environmental microbes using amino acid tagging and click chemistry. <i>Environmental Microbiology</i> , 2014, 16, 2568-2590.	1.8	190
17	Visualizing in situ translational activity for identifying and sorting slow-growing archaeal~bacterial consortia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4069-78.	3.3	180
18	Consumption of Methane and CO ₂ by Methanotrophic Microbial Mats from Gas Seeps of the Anoxic Black Sea. <i>Applied and Environmental Microbiology</i> , 2007, 73, 2271-2283.	1.4	157

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19	Evolutionary innovation: a bone-eating marine symbiosis. <i>Environmental Microbiology</i> , 2005, 7, 1369-1378.	1.8	154
20	Novel Forms of Structural Integration between Microbes and a Hydrothermal Vent Gastropod from the Indian Ocean. <i>Applied and Environmental Microbiology</i> , 2004, 70, 3082-3090.	1.4	150
21	A novel family of functional operons encoding methane/ammonia monooxygenase-related proteins in gammaproteobacterial methanotrophs. <i>Environmental Microbiology Reports</i> , 2011, 3, 91-100.	1.0	149
22	Micron-scale mapping of sulfur cycling across the oxycline of a cyanobacterial mat: a paired nanoSIMS and CARD-FISH approach. <i>ISME Journal</i> , 2008, 2, 749-759.	4.4	146
23	Variations in Archaeal and Bacterial Diversity Associated with the Sulfate-Methane Transition Zone in Continental Margin Sediments (Santa Barbara Basin, California). <i>Applied and Environmental Microbiology</i> , 2009, 75, 1487-1499.	1.4	145
24	Growth and Methane Oxidation Rates of Anaerobic Methanotrophic Archaea in a Continuous-Flow Bioreactor. <i>Applied and Environmental Microbiology</i> , 2003, 69, 5472-5482.	1.4	133
25	The rise and fall of methanotrophy following a deepwater oil-well blowout. <i>Nature Geoscience</i> , 2014, 7, 423-427.	5.4	121
26	Geological, geochemical, and microbiological heterogeneity of the seafloor around methane vents in the Eel River Basin, offshore California. <i>Chemical Geology</i> , 2004, 205, 265-289.	1.4	120
27	Methyl sulfides as intermediates in the anaerobic oxidation of methane. <i>Environmental Microbiology</i> , 2008, 10, 162-173.	1.8	118
28	Iron oxides stimulate sulfate-driven anaerobic methane oxidation in seeps. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4139-47.	3.3	112
29	Microscale sulfur cycling in the phototrophic pink berry consortia of the <i>Sippewissett</i> <i>Mars</i> . <i>Environmental Microbiology</i> , 2014, 16, 3398-3415.	1.8	106
30	Trace incorporation of heavy water reveals slow and heterogeneous pathogen growth rates in cystic fibrosis sputum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E110-6.	3.3	104
31	Age Mosaicism across Multiple Scales in Adult Tissues. <i>Cell Metabolism</i> , 2019, 30, 343-351.e3.	7.2	96
32	Heavy water and ¹⁵ N labelling with <i>NanoSIMS</i> analysis reveals growth rate-dependent metabolic heterogeneity in chemostats. <i>Environmental Microbiology</i> , 2015, 17, 2542-2556.	1.8	94
33	Methyl-compound use and slow growth characterize microbial life in 2-km-deep subseafloor coal and shale beds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9206-E9215.	3.3	94
34	Bacterial community shifts in taxa and diversity in response to localized organic loading in the deep sea. <i>Environmental Microbiology</i> , 2010, 12, 344-363.	1.8	90
35	Phylogenomic analysis of <i>Candidatus</i> <i>zimaplasma</i> ™ species: free-living representatives from a <i>Tenericutes</i> clade found in methane seeps. <i>ISME Journal</i> , 2016, 10, 2679-2692.	4.4	88
36	Planktonic and Sediment-Associated Aerobic Methanotrophs in Two Seep Systems along the North American Margin. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3985-3995.	1.4	85

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37	Patterns of ¹⁵ N assimilation and growth of methanotrophic ANME-2 archaea and sulfate-reducing bacteria within structured syntrophic consortia revealed by FISH-NanoSIMS. <i>Environmental Microbiology</i> , 2009, 11, 1777-1791.	1.8	85
38	NanoSIMS imaging reveals metabolic stratification within current-producing biofilms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20716-20724.	3.3	83
39	A hydrothermal seep on the Costa Rica margin: middle ground in a continuum of reducing ecosystems. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 2580-2588.	1.2	81
40	Characterization and spatial distribution of methanogens and methanogenic biosignatures in hypersaline microbial mats of Baja California. <i>Geobiology</i> , 2008, 6, 376-393.	1.1	80
41	Deep-biosphere methane production stimulated by geofluids in the Nankai accretionary complex. <i>Science Advances</i> , 2018, 4, eaao4631.	4.7	79
42	Filamentous sulfur bacteria preserved in modern and ancient phosphatic sediments: implications for the role of oxygen and bacteria in phosphogenesis. <i>Geobiology</i> , 2013, 11, 397-405.	1.1	78
43	Distributions of putative aerobic methanotrophs in diverse pelagic marine environments. <i>ISME Journal</i> , 2010, 4, 700-710.	4.4	77
44	Divergent methyl-coenzyme M reductase genes in a deep-subseafloor <i>Archaeoglobi</i> . <i>ISME Journal</i> , 2019, 13, 1269-1279.	4.4	76
45	Global Molecular Analyses of Methane Metabolism in Methanotrophic <i>Alphaproteobacterium</i> , <i>Methylosinus trichosporium</i> OB3b. Part II. Metabolomics and ¹³ C-Labeling Study. <i>Frontiers in Microbiology</i> , 2013, 4, 70.	1.5	75
46	Carbonate-hosted methanotrophy represents an unrecognized methane sink in the deep sea. <i>Nature Communications</i> , 2014, 5, 5094.	5.8	75
47	Peptidoglycan Production by an Insect-Bacterial Mosaic. <i>Cell</i> , 2019, 179, 703-712.e7.	13.5	75
48	Temporal evolution of methane cycling and phylogenetic diversity of archaea in sediments from a deep-sea whale-fall in Monterey Canyon, California. <i>ISME Journal</i> , 2008, 2, 204-220.	4.4	74
49	Methane Seep Carbonates Host Distinct, Diverse, and Dynamic Microbial Assemblages. <i>MBio</i> , 2015, 6, e01348-15.	1.8	74
50	<i>Methyloprofundus sedimenti</i> gen. nov., sp. nov., an obligate methanotroph from ocean sediment belonging to the "deep-sea-1" clade of marine methanotrophs. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 251-259.	0.8	74
51	Autotrophic and heterotrophic acquisition of carbon and nitrogen by a mixotrophic chrysophyte established through stable isotope analysis. <i>ISME Journal</i> , 2017, 11, 2022-2034.	4.4	74
52	Subnanogram proteomics: Impact of LC column selection, MS instrumentation and data analysis strategy on proteome coverage for trace samples. <i>International Journal of Mass Spectrometry</i> , 2018, 427, 4-10.	0.7	67
53	Methods for unveiling cryptic microbial partnerships in nature. <i>Current Opinion in Microbiology</i> , 2009, 12, 231-237.	2.3	66
54	Activity and interactions of methane seep microorganisms assessed by parallel transcription and FISH-NanoSIMS analyses. <i>ISME Journal</i> , 2016, 10, 678-692.	4.4	66

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55	Geobiological investigations using secondary ion mass spectrometry: microanalysis of extant and paleo-microbial processes. <i>Geobiology</i> , 2009, 7, 360-372.	1.1	64
56	The gut of the finch: uniqueness of the gut microbiome of the Galápagos vampire finch. <i>Microbiome</i> , 2018, 6, 167.	4.9	63
57	Geochemical Influence on Diversity and Microbial Processes in High Temperature Oil Reservoirs. <i>Geomicrobiology Journal</i> , 2003, 20, 295-311.	1.0	62
58	Lipid biomarker and phylogenetic analyses to reveal archaeal biodiversity and distribution in hypersaline microbial mat and underlying sediment. <i>Geobiology</i> , 2008, 6, 394-410.	1.1	62
59	Classifying the metal dependence of uncharacterized nitrogenases. <i>Frontiers in Microbiology</i> , 2012, 3, 419.	1.5	62
60	Methane-Fueled Syntrophy through Extracellular Electron Transfer: Uncovering the Genomic Traits Conserved within Diverse Bacterial Partners of Anaerobic Methanotrophic Archaea. <i>MBio</i> , 2017, 8, .	1.8	62
61	Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. <i>PLoS Biology</i> , 2022, 20, e3001508.	2.6	62
62	Chemotrophic Microbial Mats and Their Potential for Preservation in the Rock Record. <i>Astrobiology</i> , 2009, 9, 843-859.	1.5	60
63	Spatial distribution of nitrogen fixation in methane seep sediment and the role of the <i>ANME</i> archaea. <i>Environmental Microbiology</i> , 2014, 16, 3012-3029.	1.8	60
64	Nitrate-based niche differentiation by distinct sulfate-reducing bacteria involved in the anaerobic oxidation of methane. <i>ISME Journal</i> , 2014, 8, 150-163.	4.4	53
65	Interrogating marine virus-host interactions and elemental transfer with BONCAT and nanoSIMS-based methods. <i>Environmental Microbiology</i> , 2018, 20, 671-692.	1.8	53
66	Extensive carbon isotopic heterogeneity among methane seep microbiota. <i>Environmental Microbiology</i> , 2009, 11, 2207-2215.	1.8	51
67	Identification of Diazotrophic Microorganisms in Marine Sediment via Fluorescence In Situ Hybridization Coupled to Nanoscale Secondary Ion Mass Spectrometry (FISH-NanoSIMS). <i>Methods in Enzymology</i> , 2011, 486, 281-305.	0.4	51
68	Lateral Gene Transfer Drives Metabolic Flexibility in the Anaerobic Methane-Oxidizing Archaeal Family <i>Methanoperedenaceae</i> . <i>MBio</i> , 2020, 11, .	1.8	51
69	The effect of sulfate concentration on (sub)millimeter-scale sulfide $\delta^{34}\text{S}$ in hypersaline cyanobacterial mats over the diurnal cycle. <i>Geochimica Et Cosmochimica Acta</i> , 2009, 73, 6187-6204.	1.6	50
70	Methane on Mars and Habitability: Challenges and Responses. <i>Astrobiology</i> , 2018, 18, 1221-1242.	1.5	50
71	Archaea in metazoan diets: implications for food webs and biogeochemical cycling. <i>ISME Journal</i> , 2012, 6, 1602-1612.	4.4	49
72	Metabolic strategies of marine seafloor Chloroflexi inferred from genome reconstructions. <i>Environmental Microbiology</i> , 2020, 22, 3188-3204.	1.8	49

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73	Polyphosphate Storage during Sporulation in the Gram-Negative Bacterium <i>Acetoneema longum</i> . <i>Journal of Bacteriology</i> , 2013, 195, 3940-3946.	1.0	48
74	Autonomous Application of Quantitative PCR in the Deep Sea: In Situ Surveys of Aerobic Methanotrophs Using the Deep-Sea Environmental Sample Processor. <i>Environmental Science & Technology</i> , 2013, 47, 9339-9346.	4.6	47
75	Geochemical, metagenomic and metaproteomic insights into trace metal utilization by methane-oxidizing microbial consortia in sulphidic marine sediments. <i>Environmental Microbiology</i> , 2014, 16, 1592-1611.	1.8	47
76	Characterization of microbial associations with methanotrophic archaea and sulfate-reducing bacteria through statistical comparison of nested Magneto-FISH enrichments. <i>PeerJ</i> , 2016, 4, e1913.	0.9	43
77	Abundance and distribution of diverse membrane-bound monooxygenase (<i>CMMO</i>) genes within the <i>Costa Rica</i> oxygen minimum zone. <i>Environmental Microbiology Reports</i> , 2013, 5, 414-423.	1.0	42
78	Comparison of Archaeal and Bacterial Diversity in Methane Seep Carbonate Nodules and Host Sediments, Eel River Basin and Hydrate Ridge, USA. <i>Microbial Ecology</i> , 2015, 70, 766-784.	1.4	40
79	Microbial eukaryotic distributions and diversity patterns in a deep-sea methane seep ecosystem. <i>Environmental Microbiology</i> , 2016, 18, 3022-3043.	1.8	40
80	Starvation and recovery in the deep-sea methanotroph <i>Methyloprofundus</i> sedimenti. <i>Molecular Microbiology</i> , 2017, 103, 242-252.	1.2	40
81	Microsporidia-nematode associations in methane seeps reveal basal fungal parasitism in the deep sea. <i>Frontiers in Microbiology</i> , 2014, 5, 43.	1.5	39
82	Widespread nitrogen fixation in sediments from diverse deep-sea sites of elevated carbon loading. <i>Environmental Microbiology</i> , 2018, 20, 4281-4296.	1.8	39
83	The next frontier for planetary and human exploration. <i>Nature Astronomy</i> , 2019, 3, 116-120.	4.2	39
84	Methanotrophic bacterial symbionts fuel dense populations of deep-sea feather duster worms (Sabellida, Annelida) and extend the spatial influence of methane seepage. <i>Science Advances</i> , 2020, 6, eaay8562.	4.7	39
85	Multicellular photo-magnetotactic bacteria. <i>Environmental Microbiology Reports</i> , 2011, 3, 233-238.	1.0	38
86	A novel sister clade to the enterobacteria microviruses (family) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Td (<i>Methyloprofundus</i>). <i>Environmental Microbiology</i> , 2015, 17, 3708-3721.	1.8	37
87	Genomic Reconstruction of an Uncultured Hydrothermal Vent Gammaproteobacterial Methanotroph (Family Methylothermaceae) Indicates Multiple Adaptations to Oxygen Limitation. <i>Frontiers in Microbiology</i> , 2015, 6, 1425.	1.5	36
88	Pseudofossils in relict methane seep carbonates resemble endemic microbial consortia. <i>Palaeogeography, Palaeoclimatology, Palaeoecology</i> , 2010, 285, 131-142.	1.0	34
89	Proteomic Stable Isotope Probing Reveals Biosynthesis Dynamics of Slow Growing Methane Based Microbial Communities. <i>Frontiers in Microbiology</i> , 2016, 7, 563.	1.5	34
90	Metabolic marker gene mining provides insight in global <i>mcrA</i> diversity and, coupled with targeted genome reconstruction, sheds further light on metabolic potential of the <i>Methanomassiliicoccales</i> . <i>PeerJ</i> , 2018, 6, e5614.	0.9	34

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91	Microbial abundance and diversity patterns associated with sediments and carbonates from the methane seep environments of Hydrate Ridge, OR. <i>Frontiers in Marine Science</i> , 2014, 1, .	1.2	33
92	Comparative Genomics and Proteomic Analysis of Assimilatory Sulfate Reduction Pathways in Anaerobic Methanotrophic Archaea. <i>Frontiers in Microbiology</i> , 2018, 9, 2917.	1.5	33
93	Convergent evolution of unusual complex I homologs with increased proton pumping capacity: energetic and ecological implications. <i>ISME Journal</i> , 2018, 12, 2668-2680.	4.4	33
94	Role of APS reductase in biogeochemical sulfur isotope fractionation. <i>Nature Communications</i> , 2019, 10, 44.	5.8	33
95	Autoendoliths: a distinct type of rock-hosted microbial life. <i>Geobiology</i> , 2015, 13, 303-307.	1.1	32
96	Metabolic associations with archaea drive shifts in hydrogen isotope fractionation in sulfate-reducing bacterial lipids in cocultures and methane seeps. <i>Geobiology</i> , 2015, 13, 462-477.	1.1	31
97	Measurement of rare isotopologues of nitrous oxide by high-resolution multi-collector mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2016, 30, 1923-1940.	0.7	31
98	Experimentally-validated correlation analysis reveals new anaerobic methane oxidation partnerships with consortium-level heterogeneity in diazotrophy. <i>ISME Journal</i> , 2021, 15, 377-396.	4.4	31
99	Methoxyl stable isotopic constraints on the origins and limits of coal-bed methane. <i>Science</i> , 2021, 374, 894-897.	6.0	31
100	Unique mobile elements and scalable gene flow at the prokaryote-eukaryote boundary revealed by circularized Asgard archaea genomes. <i>Nature Microbiology</i> , 2022, 7, 200-212.	5.9	29
101	Spatial variability in photosynthetic and heterotrophic activity drives localized $\delta^{13}\text{C}_{\text{org}}$ fluctuations and carbonate precipitation in hypersaline microbial mats. <i>Geobiology</i> , 2014, 12, 557-574.	1.1	28
102	Detection of Protein-Synthesizing Microorganisms in the Environment via Bioorthogonal Noncanonical Amino Acid Tagging (BONCAT). <i>Springer Protocols</i> , 2015, , 145-157.	0.1	27
103	Quantification and isotopic analysis of intracellular sulfur metabolites in the dissimilatory sulfate reduction pathway. <i>Geochimica Et Cosmochimica Acta</i> , 2017, 206, 57-72.	1.6	27
104	Dimorphism in methane seep-dwelling ecotypes of the largest known bacteria. <i>ISME Journal</i> , 2011, 5, 1926-1935.	4.4	25
105	Subgroup Characteristics of Marine Methane-Oxidizing ANME-2 Archaea and Their Syntrophic Partners as Revealed by Integrated Multimodal Analytical Microscopy. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	25
106	The Cell and the Sum of Its Parts: Patterns of Complexity in Biosignatures as Revealed by Deep UV Raman Spectroscopy. <i>Frontiers in Microbiology</i> , 2019, 10, 679.	1.5	24
107	Sulfate differentially stimulates but is not respired by diverse anaerobic methanotrophic archaea. <i>ISME Journal</i> , 2022, 16, 168-177.	4.4	21
108	Active sulfur cycling by diverse mesophilic and thermophilic microorganisms in terrestrial mud volcanoes of Azerbaijan. <i>Environmental Microbiology</i> , 2012, 14, 3271-3286.	1.8	20

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109	Stable Isotope Phenotyping via Cluster Analysis of NanoSIMS Data As a Method for Characterizing Distinct Microbial Ecophysiology and Sulfur-Cycling in the Environment. <i>Frontiers in Microbiology</i> , 2016, 7, 774.	1.5	20
110	Spatially resolved capture of hydrogen sulfide from the water column and sedimentary pore waters for abundance and stable isotopic analysis. <i>Marine Chemistry</i> , 2017, 197, 26-37.	0.9	20
111	The Potential for Biologically Catalyzed Anaerobic Methane Oxidation on Ancient Mars. <i>Astrobiology</i> , 2014, 14, 292-307.	1.5	19
112	Microbial interactions in the anaerobic oxidation of methane: model simulations constrained by process rates and activity patterns. <i>Environmental Microbiology</i> , 2019, 21, 631-647.	1.8	19
113	Aerobic and Anaerobic Methanotrophic Communities Associated with Methane Hydrates Exposed on the Seafloor: A High-Pressure Sampling and Stable Isotope-Incubation Experiment. <i>Frontiers in Microbiology</i> , 2017, 8, 2569.	1.5	18
114	Colonial Tube-Dwelling Ciliates Influence Methane Cycling and Microbial Diversity within Methane Seep Ecosystems. <i>Frontiers in Marine Science</i> , 2017, 3, .	1.2	17
115	Microbial communities of Auka hydrothermal sediments shed light on vent biogeography and the evolutionary history of thermophily. <i>ISME Journal</i> , 2022, 16, 1750-1764.	4.4	16
116	Microbial succession and dynamics in meromictic Mono Lake, California. <i>Geobiology</i> , 2021, 19, 376-393.	1.1	15
117	The Apparent Involvement of ANMEs in Mineral Dependent Methane Oxidation, as an Analog for Possible Martian Methanotrophy. <i>Life</i> , 2011, 1, 19-33.	1.1	14
118	Precise determination of equilibrium sulfur isotope effects during volatilization and deprotonation of dissolved H ₂ S. <i>Geochimica Et Cosmochimica Acta</i> , 2019, 248, 242-251.	1.6	14
119	Bacterial growth in multicellular aggregates leads to the emergence of complex life cycles. <i>Current Biology</i> , 2022, 32, 3059-3069.e7.	1.8	14
120	Characterization of Chemosynthetic Microbial Mats Associated with Intertidal Hydrothermal Sulfur Vents in White Point, San Pedro, CA, USA. <i>Frontiers in Microbiology</i> , 2016, 7, 1163.	1.5	13
121	Trace Metal Imaging of Sulfate-Reducing Bacteria and Methanogenic Archaea at Single-Cell Resolution by Synchrotron X-Ray Fluorescence Imaging. <i>Geomicrobiology Journal</i> , 2018, 35, 81-89.	1.0	13
122	Evidence of a Streamlined Extracellular Electron Transfer Pathway from Biofilm Structure, Metabolic Stratification, and Long-Range Electron Transfer Parameters. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0070621.	1.4	13
123	Rapid quantification and isotopic analysis of dissolved sulfur species. <i>Rapid Communications in Mass Spectrometry</i> , 2017, 31, 791-803.	0.7	11
124	A chemosynthetic ecotone in the sediments surrounding deep-sea methane seeps. <i>Limnology and Oceanography</i> , 2021, 66, 1687-1702.	1.6	11
125	Whole Cell Immunomagnetic Enrichment of Environmental Microbial Consortia Using rRNA-Targeted Magneto-FISH. <i>Methods in Enzymology</i> , 2013, 531, 21-44.	0.4	10
126	Controls on Interspecies Electron Transport and Size Limitation of Anaerobically Methane-Oxidizing Microbial Consortia. <i>MBio</i> , 2021, 12, .	1.8	9

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127	Carbonate-hosted microbial communities are prolific and pervasive methane oxidizers at geologically diverse marine methane seep sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	8
128	Community Structure and Microbial Associations in Sediment-Free Methanotrophic Enrichment Cultures from a Marine Methane Seep. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	8
129	Exploration of Subseafloor Life and the Biosphere Through IODP (2003â€“2013). <i>Developments in Marine Geology</i> , 2014, 7, 39-63.	0.4	7
130	Monodeuterated Methane, an Isotopic Tool To Assess Biological Methane Metabolism Rates. <i>MSphere</i> , 2017, 2, .	1.3	7
131	Patterns of in situ Mineral Colonization by Microorganisms in a ~60Â°C Deep Continental Subsurface Aquifer. <i>Frontiers in Microbiology</i> , 2020, 11, 536535.	1.5	7
132	Spatially Resolved Electron Transport through Anodeâ€Respiring <i>Geobacter sulfurreducens</i> Biofilms: Controls and Constraints. <i>ChemElectroChem</i> , 2021, 8, 1747-1758.	1.7	7
133	Early impacts of climate change on a coastal marine microbial mat ecosystem. <i>Science Advances</i> , 2022, 8, .	4.7	7
134	Method for Assessing Mineral Composition-Dependent Patterns in Microbial Diversity Using Magnetic and Density Separation. <i>Geomicrobiology Journal</i> , 2012, 29, 435-449.	1.0	6
135	Hydrogen for dinner. <i>Nature</i> , 2011, 476, 154-155.	13.7	5
136	Members of the methanotrophic genus <i>Methylomarinum</i> inhabit inland mud pots. <i>PeerJ</i> , 2016, 4, e2116.	0.9	5
137	Carbon isotopic heterogeneity of coenzyme F430 and membrane lipids in methaneâ€oxidizing archaea. <i>Geobiology</i> , 2019, 17, 611-627.	1.1	3
138	Sulfur isotope fractionations constrain the biological cycling of dimethylsulfoniopropionate in the upper ocean. <i>Limnology and Oceanography</i> , 2021, 66, 3607-3618.	1.6	3
139	A Reduced F ₄₂₀ -Dependent Nitrite Reductase in an Anaerobic Methanotrophic Archaeon. <i>Journal of Bacteriology</i> , 2022, 204, .	1.0	3
140	Spatially Resolved Electron Transport through Anodeâ€Respiring <i>Geobacter sulfurreducens</i> Biofilms: Controls and Constraints. <i>ChemElectroChem</i> , 2021, 8, 1697-1697.	1.7	1
141	Environmental Microbiology: evolution of your premier journal. <i>Environmental Microbiology</i> , 2012, 14, 2617-2619.	1.8	0
142	Resolving micron-scale heterogeneity in porewater ³⁴ S/H ₂ S by combining films for in-situ sulfide capture and secondary ion mass spectrometry. <i>Marine Chemistry</i> , 2020, 223, 103810.	0.9	0
143	Physiological, genomic, and sulfur isotopic characterization of methanol metabolism by <i>Desulfovibrio carbinolicus</i> . <i>PLoS ONE</i> , 2021, 16, e0245069.	1.1	0
144	Exploring Space via Astromycology: A Report on the CIFAR Programs <i>Earth 4D</i> and <i>Fungal Kingdom</i> Inaugural Joint Meeting. <i>Astrobiology</i> , 2022, , .	1.5	0