

Eric Allen

List of Publications by Year in descending order

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56
papers

3,996
citations

172457

29
h-index

149698

56
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62
all docs

62
docs citations

62
times ranked

5656
citing authors

#	ARTICLE	IF	CITATIONS
1	The Marine Microbial Eukaryote Transcriptome Sequencing Project (MMETSP): Illuminating the Functional Diversity of Eukaryotic Life in the Oceans through Transcriptome Sequencing. PLoS Biology, 2014, 12, e1001889.	5.6	885
2	Biosynthesis of polybrominated aromatic organic compounds by marine bacteria. Nature Chemical Biology, 2014, 10, 640-647.	8.0	246
3	Monounsaturated but Not Polyunsaturated Fatty Acids Are Required for Growth of the Deep-Sea Bacterium <i>Photobacterium profundum</i> SS9 at High Pressure and Low Temperature. Applied and Environmental Microbiology, 1999, 65, 1710-1720.	3.1	221
4	Defining and quantifying the core microbiome: Challenges and prospects. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	191
5	Characterization of Cyanobacterial Hydrocarbon Composition and Distribution of Biosynthetic Pathways. PLoS ONE, 2014, 9, e85140.	2.5	190
6	Structure and regulation of the omega-3 polyunsaturated fatty acid synthase genes from the deep-sea bacterium <i>Photobacterium profundum</i> strain SS9 The GenBank accession numbers for the sequences reported in this paper are AF409100 and AF467805.. Microbiology (United Kingdom), 2002, 148, 1903-1913.	1.8	151
7	Metagenomic discovery of polybrominated diphenyl ether biosynthesis by marine sponges. Nature Chemical Biology, 2017, 13, 537-543.	8.0	141
8	KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples. MSystems, 2018, 3, .	3.8	123
9	Influence of nutrients and currents on the genomic composition of microbes across an upwelling mosaic. ISME Journal, 2012, 6, 1403-1414.	9.8	120
10	Assembly-Driven Community Genomics of a Hypersaline Microbial Ecosystem. PLoS ONE, 2013, 8, e61692.	2.5	101
11	Visualizing $\hat{\Delta}$ omic feature rankings and log-ratios using Qurro. NAR Genomics and Bioinformatics, 2020, 2, lqaa023.	3.2	97
12	Going Deeper: Metagenome of a Hadopelagic Microbial Community. PLoS ONE, 2011, 6, e20388.	2.5	95
13	Seasonal fluctuations in ionic concentrations drive microbial succession in a hypersaline lake community. ISME Journal, 2014, 8, 979-990.	9.8	91
14	Genome and methylome of the oleaginous diatom <i>Cyclotella cryptica</i> reveal genetic flexibility toward a high lipid phenotype. Biotechnology for Biofuels, 2016, 9, 258.	6.2	87
15	Comparative genomics uncovers the prolific and distinctive metabolic potential of the cyanobacterial genus <i>Moorea</i> . Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3198-3203.	7.1	77
16	Widespread Occurrence of Secondary Lipid Biosynthesis Potential in Microbial Lineages. PLoS ONE, 2011, 6, e20146.	2.5	74
17	Microbial Ecology of Atlantic Salmon (<i>Salmo salar</i>) Hatcheries: Impacts of the Built Environment on Fish Mucosal Microbiota. Applied and Environmental Microbiology, 2020, 86, .	3.1	71
18	Use of plankton-derived vitamin B1 precursors, especially thiazole-related precursor, by key marine picoeukaryotic phytoplankton. ISME Journal, 2017, 11, 753-765.	9.8	69

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19	Pangenomic comparison of globally distributed Poribacteria associated with sponge hosts and marine particles. <i>ISME Journal</i> , 2019, 13, 468-481.	9.8	63
20	Vertically distinct microbial communities in the Mariana and Kermadec trenches. <i>PLoS ONE</i> , 2018, 13, e0195102.	2.5	62
21	Diel transcriptional response of a California Current plankton microbiome to light, low iron, and enduring viral infection. <i>ISME Journal</i> , 2019, 13, 2817-2833.	9.8	61
22	FabF Is Required for Piezoregulation of cis-Vaccenic Acid Levels and Piezophilic Growth of the Deep-Sea Bacterium <i>Photobacterium profundum</i> Strain SS9. <i>Journal of Bacteriology</i> , 2000, 182, 1264-1271.	2.2	60
23	Microbial Community Diversity Within Sediments from Two Geographically Separated Hadal Trenches. <i>Frontiers in Microbiology</i> , 2019, 10, 347.	3.5	59
24	High-Throughput Miniaturized 16S rRNA Amplicon Library Preparation Reduces Costs while Preserving Microbiome Integrity. <i>MSystems</i> , 2018, 3, .	3.8	58
25	Temporal, Environmental, and Biological Drivers of the Mucosal Microbiome in a Wild Marine Fish, <i>Scomber japonicus</i> . <i>MSphere</i> , 2020, 5, .	2.9	49
26	Fatty Acid Biosynthesis Pathways in <i>Methylobacterium buryatense</i> 5G(B1). <i>Frontiers in Microbiology</i> , 2016, 7, 2167.	3.5	38
27	A genomic view of trophic and metabolic diversity in clade-specific <i>Lamellodysidea</i> sponge microbiomes. <i>Microbiome</i> , 2020, 8, 97.	11.1	38
28	Diversity and distribution of microbial long-chain fatty acid biosynthetic genes in the marine environment. <i>Environmental Microbiology</i> , 2011, 13, 684-695.	3.8	37
29	Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. <i>ISME Journal</i> , 2015, 9, 2697-2711.	9.8	35
30	Non-targeted tandem mass spectrometry enables the visualization of organic matter chemotype shifts in coastal seawater. <i>Chemosphere</i> , 2021, 271, 129450.	8.2	33
31	Comparative Genomics of Cyanobacterial Symbionts Reveals Distinct, Specialized Metabolism in Tropical <i>Dysideidae</i> Sponges. <i>MBio</i> , 2019, 10, .	4.1	31
32	De Novo Sequences of <i>Haloquadratum walsbyi</i> from Lake Tyrrell, Australia, Reveal a Variable Genomic Landscape. <i>Archaea</i> , 2015, 2015, 1-12.	2.3	26
33	Copiotrophic marine bacteria are associated with strong iron-binding ligand production during phytoplankton blooms. <i>Limnology and Oceanography Letters</i> , 2016, 1, 36-43.	3.9	25
34	Microbial effects of livestock manure fertilization on freshwater aquaculture ponds rearing tilapia (<i>Oreochromis shiranus</i>) and North African catfish (<i>Clarias gariepinus</i>). <i>MicrobiologyOpen</i> , 2018, 7, e00716.	3.0	23
35	Adaptive laboratory evolution of <i>Escherichia coli</i> K-12 MG1655 for growth at high hydrostatic pressure. <i>Frontiers in Microbiology</i> , 2014, 5, 749.	3.5	22
36	Multi-Omic Profiling of <i>Melophlus</i> Sponges Reveals Diverse Metabolomic and Microbiome Architectures that Are Non-overlapping with Ecological Neighbors. <i>Marine Drugs</i> , 2020, 18, 124.	4.6	21

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37	Metabolic potential and <i>in situ</i> transcriptomic profiles of previously uncharacterized key microbial groups involved in coupled carbon, nitrogen and sulfur cycling in anoxic marine zones. <i>Environmental Microbiology</i> , 2018, 20, 2727-2742.	3.8	18
38	Characterization and Application of Marine Microbial Omega-3 Polyunsaturated Fatty Acid Synthesis. <i>Methods in Enzymology</i> , 2018, 605, 3-32.	1.0	18
39	Diversity and composition of intertidal gastropod microbiomes across a major marine biogeographic boundary. <i>Environmental Microbiology Reports</i> , 2019, 11, 434-447.	2.4	16
40	Decade-scale stability and change in a marine bivalve microbiome. <i>Molecular Ecology</i> , 2021, 30, 1237-1250.	3.9	15
41	Distinctive Archaeal Composition of an Artisanal Crystallizer Pond and Functional Insights Into Salt-Saturated Hypersaline Environment Adaptation. <i>Frontiers in Microbiology</i> , 2018, 9, 1800.	3.5	14
42	Linkage of Marine Bacterial Polyunsaturated Fatty Acid and Long-Chain Hydrocarbon Biosynthesis. <i>Frontiers in Microbiology</i> , 2019, 10, 702.	3.5	14
43	Sierra Nevada mountain lake microbial communities are structured by temperature, resources and geographic location. <i>Molecular Ecology</i> , 2020, 29, 2080-2093.	3.9	14
44	Feasibility of using alternative swabs and storage solutions for paired SARS-CoV-2 detection and microbiome analysis in the hospital environment. <i>Microbiome</i> , 2021, 9, 25.	11.1	13
45	Impacts of the Marine Hatchery Built Environment, Water and Feed on Mucosal Microbiome Colonization Across Ontogeny in Yellowtail Kingfish, <i>Seriola lalandi</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	13
46	The Southern Bluefin Tuna Mucosal Microbiome Is Influenced by Husbandry Method, Net Pen Location, and Anti-parasite Treatment. <i>Frontiers in Microbiology</i> , 2020, 11, 2015.	3.5	12
47	Diploid genomic architecture of <i>Nitzschia inconspicua</i> , an elite biomass production diatom. <i>Scientific Reports</i> , 2021, 11, 15592.	3.3	12
48	Fine scale transitions of the microbiota and metabolome along the gastrointestinal tract of herbivorous fishes. <i>Animal Microbiome</i> , 2022, 4, .	3.8	11
49	Bacterioplankton drawdown of coral mass-spawned organic matter. <i>ISME Journal</i> , 2018, 12, 2238-2251.	9.8	8
50	Meeting report: Ocean omics science, technology and cyberinfrastructure: current challenges and future requirements (August 20-23, 2013). <i>Standards in Genomic Sciences</i> , 2014, 9, 1252-1258.	1.5	7
51	Do host-associated microbes show a contrarian latitudinal diversity gradient? Insights from <i>Mytilus californianus</i> , an intertidal foundation host. <i>Journal of Biogeography</i> , 2021, 48, 2839-2852.	3.0	6
52	Genetic Regulation of the Bacterial Omega-3 Polyunsaturated Fatty Acid Biosynthesis Pathway. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	5
53	Variation in Survival and Gut Microbiome Composition of Hatchery-Grown Native Oysters at Various Locations within the Puget Sound. <i>Microbiology Spectrum</i> , 2022, 10, e0198221.	3.0	4
54	Complete Genome Sequence of a Cylindrospermopsin-Producing Cyanobacterium, <i>Cylindrospermopsis raciborskii</i> CS505, Containing a Circular Chromosome and a Single Extrachromosomal Element. <i>Genome Announcements</i> , 2016, 4, .	0.8	2

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55	Microbiomes of Hadal Fishes across Trench Habitats Contain Similar Taxa and Known Piezophiles. <i>MSphere</i> , 2022, 7, e0003222.	2.9	2
56	Genetic Suppression of Lethal Mutations in Fatty Acid Biosynthesis Mediated by a Secondary Lipid Synthase. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0003521.	3.1	1