

Eric Allen

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

57
papers

2,527
citations

24
h-index

50
g-index

62
ext. papers

3,425
ext. citations

6.8
avg, IF

4.93
L-index

#	Paper	IF	Citations
57	Microbiomes of Hadal Fishes across Trench Habitats Contain Similar Taxa and Known Piezophiles.. <i>MSphere</i> , 2022 , e0003222	5	
56	Variation in Survival and Gut Microbiome Composition of Hatchery-Grown Native Oysters at Various Locations within the Puget Sound.. <i>Microbiology Spectrum</i> , 2022 , e0198221	8.9	0
55	Defining and quantifying the core microbiome: Challenges and prospects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	21
54	Non-targeted tandem mass spectrometry enables the visualization of organic matter chemotype shifts in coastal seawater. <i>Chemosphere</i> , 2021 , 271, 129450	8.4	14
53	Genetic Suppression of Lethal Mutations in Fatty Acid Biosynthesis Mediated by a Secondary Lipid Synthase. <i>Applied and Environmental Microbiology</i> , 2021 , 87, e0003521	4.8	1
52	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	16.6	7
51	Decade-scale stability and change in a marine bivalve microbiome. <i>Molecular Ecology</i> , 2021 , 30, 1237-1250	5.7	4
50	Diploid genomic architecture of <i>Nitzschia inconspicua</i> , an elite biomass production diatom. <i>Scientific Reports</i> , 2021 , 11, 15592	4.9	4
49	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	4.1	1
48	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	5.7	1
47	Visualizing Omic feature rankings and log-ratios using Qurro. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa023	3.7	48
46	Temporal, Environmental, and Biological Drivers of the Mucosal Microbiome in a Wild Marine Fish, <i>Scomber japonicus</i> . <i>MSphere</i> , 2020 , 5,	5	11
45	Genetic regulation of the bacterial omega-3 polyunsaturated fatty acid biosynthesis pathway. <i>Journal of Bacteriology</i> , 2020 ,	3.5	3
44	Multi-Omic Profiling of Sponges Reveals Diverse Metabolomic and Microbiome Architectures that Are Non-overlapping with Ecological Neighbors. <i>Marine Drugs</i> , 2020 , 18,	6	12
43	Sierra Nevada mountain lake microbial communities are structured by temperature, resources and geographic location. <i>Molecular Ecology</i> , 2020 , 29, 2080-2093	5.7	5
42	A genomic view of trophic and metabolic diversity in clade-specific Lamellodysidea sponge microbiomes. <i>Microbiome</i> , 2020 , 8, 97	16.6	6
41	Microbial Ecology of Atlantic Salmon (<i>Salmo salar</i>) Hatcheries: Impacts of the Built Environment on Fish Mucosal Microbiota. <i>Applied and Environmental Microbiology</i> , 2020 , 86,	4.8	25

40	Feasibility of using alternative swabs and storage solutions for paired SARS-CoV-2 detection and microbiome analysis in the hospital environment 2020 ,		3
39	Comparative Genomics of Cyanobacterial Symbionts Reveals Distinct, Specialized Metabolism in Tropical Sponges. <i>MBio</i> , 2019 , 10,	7.8	16
38	Linkage of Marine Bacterial Polyunsaturated Fatty Acid and Long-Chain Hydrocarbon Biosynthesis. <i>Frontiers in Microbiology</i> , 2019 , 10, 702	5.7	10
37	Diversity and composition of intertidal gastropod microbiomes across a major marine biogeographic boundary. <i>Environmental Microbiology Reports</i> , 2019 , 11, 434-447	3.7	10
36	Microbial Community Diversity Within Sediments from Two Geographically Separated Hadal Trenches. <i>Frontiers in Microbiology</i> , 2019 , 10, 347	5.7	34
35	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	11.9	30
34	Pangenomic comparison of globally distributed Poribacteria associated with sponge hosts and marine particles. <i>ISME Journal</i> , 2019 , 13, 468-481	11.9	22
33	Metabolic potential and in situ 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	5.2	13
32	KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples. <i>MSystems</i> , 2018 , 3,	7.6	74
31	Bacterioplankton drawdown of coral mass-spawned organic matter. <i>ISME Journal</i> , 2018 , 12, 2238-2251	11.9	4
30	Characterization and Application of Marine Microbial Omega-3 Polyunsaturated Fatty Acid Synthesis. <i>Methods in Enzymology</i> , 2018 , 605, 3-32	1.7	11
29	High-Throughput Miniaturized 16S rRNA Amplicon Library Preparation Reduces Costs while Preserving Microbiome Integrity. <i>MSystems</i> , 2018 , 3,	7.6	33
28	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	3.4	13
27	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	5.7	11
26	Vertically distinct microbial communities in the Mariana and Kermadec trenches. <i>PLoS ONE</i> , 2018 , 13, e0195102	3.7	39
25	Comparative genomics uncovers the prolific and distinctive metabolic potential of the cyanobacterial genus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 3198-3203	11.5	47
24	Metagenomic discovery of polybrominated diphenyl ether biosynthesis by marine sponges. <i>Nature Chemical Biology</i> , 2017 , 13, 537-543	11.7	95
23	Use of plankton-derived vitamin B1 precursors, especially thiazole-related precursor, by key marine picoeukaryotic phytoplankton. <i>ISME Journal</i> , 2017 , 11, 753-765	11.9	38

22	Fatty Acid Biosynthesis Pathways in. <i>Frontiers in Microbiology</i> , 2016 , 7, 2167	5.7	30
21	Complete Genome Sequence of a Cyindrospermopsis-Producing Cyanobacterium, <i>Cyindrospermopsis raciborskii</i> CS505, Containing a Circular Chromosome and a Single Extrachromosomal Element. <i>Genome Announcements</i> , 2016 , 4,		1
20	Copiotrophic marine bacteria are associated with strong iron-binding ligand production during phytoplankton blooms. <i>Limnology and Oceanography Letters</i> , 2016 , 1, 36-43	7.9	19
19	Genome and methylome of the oleaginous diatom reveal genetic flexibility toward a high lipid phenotype. <i>Biotechnology for Biofuels</i> , 2016 , 9, 258	7.8	61
18	Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. <i>ISME Journal</i> , 2015 , 9, 2697-711	11.9	24
17	De novo sequences of <i>Haloquadratum walsbyi</i> from Lake Tyrrell, Australia, reveal a variable genomic landscape. <i>Archaea</i> , 2015 , 2015, 875784	2	9
16	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	5.7	17
15	Biosynthesis of polybrominated aromatic organic compounds by marine bacteria. <i>Nature Chemical Biology</i> , 2014 , 10, 640-7	11.7	188
14	Seasonal fluctuations in ionic concentrations drive microbial succession in a hypersaline lake community. <i>ISME Journal</i> , 2014 , 8, 979-90	11.9	58
13	Meeting report: Ocean genomics science, technology and cyberinfrastructure: current challenges and future requirements (August 20-23, 2013). <i>Standards in Genomic Sciences</i> , 2014 , 9, 1252-8		7
12	Characterization of cyanobacterial hydrocarbon composition and distribution of biosynthetic pathways. <i>PLoS ONE</i> , 2014 , 9, e85140	3.7	114
11	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	9.7	617
10	Assembly-driven community genomics of a hypersaline microbial ecosystem. <i>PLoS ONE</i> , 2013 , 8, e61692	3.7	71
9	Influence of nutrients and currents on the genomic composition of microbes across an upwelling mosaic. <i>ISME Journal</i> , 2012 , 6, 1403-14	11.9	87
8	Widespread occurrence of secondary lipid biosynthesis potential in microbial lineages. <i>PLoS ONE</i> , 2011 , 6, e20146	3.7	65
7	Going deeper: metagenome of a hadopelagic microbial community. <i>PLoS ONE</i> , 2011 , 6, e20388	3.7	74
6	Diversity and distribution of microbial long-chain fatty acid biosynthetic genes in the marine environment. <i>Environmental Microbiology</i> , 2011 , 13, 684-95	5.2	30
5	Structure and regulation of the omega-3 polyunsaturated fatty acid synthase genes from the deep-sea bacterium <i>Photobacterium profundum</i> strain SS9. <i>Microbiology (United Kingdom)</i> , 2002 , 148, 1903-1913	2.9	133

4	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, 1264-71	3.5	54
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. <i>Applied and Environmental Microbiology</i> , 1999 , 65, 1710-20	4.8	195
2	Temporal, environmental, and biological drivers of the mucosal microbiome in a wild marine fish, <i>Scomber japonicus</i>		5
1	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> , 8,	4.5	2