

Eric E 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.

62

papers

5,860

citations

32

h-index

66

g-index

66

ext. papers

7,085

ext. citations

8.9

avg, IF

5.33

L-index

#	Paper	IF	Citations
62	Microbiomes of Hadal Fishes across Trench Habitats Contain Similar Taxa and Known Piezophiles.. <i>MSphere</i> , 2022 , e0003222	5	
61	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
60	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
59	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
58	Decade-scale stability and change in a marine bivalve microbiome. <i>Molecular Ecology</i> , 2021 , 30, 1237-1250	5.7	4
57	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
56	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
55	Visualizing Tomic feature rankings and log-ratios using Qurro. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa023	3.7	48
54	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
53	Genetic regulation of the bacterial omega-3 polyunsaturated fatty acid biosynthesis pathway. <i>Journal of Bacteriology</i> , 2020 ,	3.5	3
52	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
51	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
50	A genomic view of trophic and metabolic diversity in clade-specific Lamellodysidea sponge microbiomes. <i>Microbiome</i> , 2020 , 8, 97	16.6	6
49	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
48	Feasibility of using alternative swabs and storage solutions for paired SARS-CoV-2 detection and microbiome analysis in the hospital environment 2020 ,		3
47	Comparative Genomics of Cyanobacterial Symbionts Reveals Distinct, Specialized Metabolism in Tropical Sponges. <i>MBio</i> , 2019 , 10,	7.8	16
46	Linkage of Marine Bacterial Polyunsaturated Fatty Acid and Long-Chain Hydrocarbon Biosynthesis. <i>Frontiers in Microbiology</i> , 2019 , 10, 702	5.7	10

45	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
44	Microbial Community Diversity Within Sediments from Two Geographically Separated Hadal Trenches. <i>Frontiers in Microbiology</i> , 2019 , 10, 347	5.7	34
43	Pangenomic comparison of globally distributed Poribacteria associated with sponge hosts and marine particles. <i>ISME Journal</i> , 2019 , 13, 468-481	11.9	22
42	KatharoSeq Enables High-Throughput Microbiome Analysis From Low-Biomass Samples. <i>MSystems</i> , 2018 , 3,	7.6	74
41	Characterization and Application of Marine Microbial Omega-3 Polyunsaturated Fatty Acid Synthesis. <i>Methods in Enzymology</i> , 2018 , 605, 3-32	1.7	11
40	High-Throughput Miniaturized 16S rRNA Amplicon Library Preparation Reduces Costs while Preserving Microbiome Integrity. <i>MSystems</i> , 2018 , 3,	7.6	33
39	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}	3.4	13
38	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
37	Vertically distinct microbial communities in the Mariana and Kermadec trenches. <i>PLoS ONE</i> , 2018 , 13, e0195102	3.7	39
36	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
35	Metagenomic discovery of polybrominated diphenyl ether biosynthesis by marine sponges. <i>Nature Chemical Biology</i> , 2017 , 13, 537-543	11.7	95
34	Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. <i>ISME Journal</i> , 2015 , 9, 2697-711	11.9	24
33	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
32	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
31	Biosynthesis of polybrominated aromatic organic compounds by marine bacteria. <i>Nature Chemical Biology</i> , 2014 , 10, 640-7	11.7	188
30	Seasonal fluctuations in ionic concentrations drive microbial succession in a hypersaline lake community. <i>ISME Journal</i> , 2014 , 8, 979-90	11.9	58
29	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
28	Metagenome sequencing of the microbial community of a solar saltern crystallizer pond at cBuil lagoon, Chile. <i>Genome Announcements</i> , 2014 , 2,		9

27	Draft Genome Sequence of "Candidatus Halobonum tyrrellensis" Strain G22, Isolated from the Hypersaline Waters of Lake Tyrrell, Australia. <i>Genome Announcements</i> , 2013 , 1,		4
26	Assembly-driven community genomics of a hypersaline microbial ecosystem. <i>PLoS ONE</i> , 2013 , 8, e61692	3.7	71
25	Microbial life in a fjord: metagenomic analysis of a microbial mat in Chilean patagonia. <i>PLoS ONE</i> , 2013 , 8, e71952	3.7	15
24	Virus-host and CRISPR dynamics in Archaea-dominated hypersaline Lake Tyrrell, Victoria, Australia. <i>Archaea</i> , 2013 , 2013, 370871	2	57
23	De novo metagenomic assembly reveals abundant novel major lineage of Archaea in hypersaline microbial communities. <i>ISME Journal</i> , 2012 , 6, 81-93	11.9	254
22	Dynamic viral populations in hypersaline systems as revealed by metagenomic assembly. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 6309-20	4.8	63
21	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
20	Compositional differences in particle-associated and free-living microbial assemblages from an extreme deep-ocean environment. <i>Environmental Microbiology Reports</i> , 2011 , 3, 449-58	3.7	122
19	Widespread occurrence of secondary lipid biosynthesis potential in microbial lineages. <i>PLoS ONE</i> , 2011 , 6, e20146	3.7	65
18	Going deeper: metagenome of a hadopelagic microbial community. <i>PLoS ONE</i> , 2011 , 6, e20388	3.7	74
17	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
16	Xenorhodopsins, an enigmatic new class of microbial rhodopsins horizontally transferred between archaea and bacteria. <i>Biology Direct</i> , 2011 , 6, 52	7.2	42
15	Genomic insights into the physiology and ecology of the marine filamentous cyanobacterium <i>Lyngbya majuscula</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 8815-20	11.5	90
14	Community cyberinfrastructure for Advanced Microbial Ecology Research and Analysis: the CAMERA resource. <i>Nucleic Acids Research</i> , 2011 , 39, D546-51	20.1	249
13	Genomic islands link secondary metabolism to functional adaptation in marine Actinobacteria. <i>ISME Journal</i> , 2009 , 3, 1193-203	11.9	153
12	A database of phylogenetically atypical genes in archaeal and bacterial genomes, identified using the DarkHorse algorithm. <i>BMC Bioinformatics</i> , 2008 , 9, 419	3.6	33
11	Strain-resolved community proteomics reveals recombining genomes of acidophilic bacteria. <i>Nature</i> , 2007 , 446, 537-41	50.4	193
10	Genome dynamics in a natural archaeal population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 1883-8	11.5	115

9	Lineages of acidophilic archaea revealed by community genomic analysis. <i>Science</i> , 2006 , 314, 1933-5	33.3	190
8	Community genomics in microbial ecology and evolution. <i>Nature Reviews Microbiology</i> , 2005 , 3, 489-98	22.2	182
7	Genome-directed isolation of the key nitrogen fixer <i>Leptospirillum ferrodiazotrophum</i> sp. nov. from an acidophilic microbial community. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 6319-24	4.8	195
6	Community structure and metabolism through reconstruction of microbial genomes from the environment. <i>Nature</i> , 2004 , 428, 37-43	50.4	1710
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	Microbiome divergence of marine gastropod species separated by the Isthmus of Panama		1