

# Eric E Allen

## List of Publications by Year in descending order

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59  
papers

7,843  
citations

101543

36  
h-index

133252

59  
g-index

66  
all docs

66  
docs citations

66  
times ranked

9315  
citing authors

#	ARTICLE	IF	CITATIONS
1	Microbiomes of Hadal Fishes across Trench Habitats Contain Similar Taxa and Known Piezophiles. <i>MSphere</i> , 2022, 7, e0003222.	2.9	2
2	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
3	Decade-scale stability and change in a marine bivalve microbiome. <i>Molecular Ecology</i> , 2021, 30, 1237-1250.	3.9	15
4	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
5	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
6	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, .	7.1	191
7	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
8	Visualizing omic feature rankings and log-ratios using Qurro. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa023.	3.2	97
9	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
10	Genetic Regulation of the Bacterial Omega-3 Polyunsaturated Fatty Acid Biosynthesis Pathway. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	5
11	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
12	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
13	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
14	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, .	3.1	71
15	Comparative Genomics of Cyanobacterial Symbionts Reveals Distinct, Specialized Metabolism in Tropical <i>Dysideidae</i> Sponges. <i>MBio</i> , 2019, 10, .	4.1	31
16	Linkage of Marine Bacterial Polyunsaturated Fatty Acid and Long-Chain Hydrocarbon Biosynthesis. <i>Frontiers in Microbiology</i> , 2019, 10, 702.	3.5	14
17	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
18	Microbial Community Diversity Within Sediments from Two Geographically Separated Hadal Trenches. <i>Frontiers in Microbiology</i> , 2019, 10, 347.	3.5	59

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19	Pangenomic comparison of globally distributed Poribacteria associated with sponge hosts and marine particles. ISME Journal, 2019, 13, 468-481.	9.8	63
20	KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples. MSystems, 2018, 3, .	3.8	123
21	High-Throughput Miniaturized 16S rRNA Amplicon Library Preparation Reduces Costs while Preserving Microbiome Integrity. MSystems, 2018, 3, .	3.8	58
22	Microbial effects of livestock manure fertilization on freshwater aquaculture ponds rearing tilapia ( <i>Oreochromis shiranus</i> ) and North African catfish ( <i>Clarias gariepinus</i> ). MicrobiologyOpen, 2018, 7, e00716.	3.0	23
23	Distinctive Archaeal Composition of an Artisanal Crystallizer Pond and Functional Insights Into Salt-Saturated Hypersaline Environment Adaptation. Frontiers in Microbiology, 2018, 9, 1800.	3.5	14
24	Vertically distinct microbial communities in the Mariana and Kermadec trenches. PLoS ONE, 2018, 13, e0195102.	2.5	62
25	Characterization and Application of Marine Microbial Omega-3 Polyunsaturated Fatty Acid Synthesis. Methods in Enzymology, 2018, 605, 3-32.	1.0	18
26	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
27	Metagenomic discovery of polybrominated diphenyl ether biosynthesis by marine sponges. Nature Chemical Biology, 2017, 13, 537-543.	8.0	141
28	<i>De Novo</i> Sequences of <i>Haloquadratum walsbyi</i> from Lake Tyrrell, Australia, Reveal a Variable Genomic Landscape. Archaea, 2015, 2015, 1-12.	2.3	26
29	Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. ISME Journal, 2015, 9, 2697-2711.	9.8	35
30	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
31	Metagenome Sequencing of the Microbial Community of a Solar Saltern Crystallizer Pond at Chuil Lagoon, Chile. Genome Announcements, 2014, 2, .	0.8	18
32	Biosynthesis of polybrominated aromatic organic compounds by marine bacteria. Nature Chemical Biology, 2014, 10, 640-647.	8.0	246
33	Seasonal fluctuations in ionic concentrations drive microbial succession in a hypersaline lake community. ISME Journal, 2014, 8, 979-990.	9.8	91
34	Adaptive laboratory evolution of <i>Escherichia coli</i> K-12 MG1655 for growth at high hydrostatic pressure. Frontiers in Microbiology, 2014, 5, 749.	3.5	22
35	Draft Genome Sequence of <i>Candidatus</i> <i>Halobnum tyrrellensis</i> Strain G22, Isolated from the Hypersaline Waters of Lake Tyrrell, Australia. Genome Announcements, 2013, 1, .	0.8	13
36	Assembly-Driven Community Genomics of a Hypersaline Microbial Ecosystem. PLoS ONE, 2013, 8, e61692.	2.5	101

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37	Microbial Life in a Fjord: Metagenomic Analysis of a Microbial Mat in Chilean Patagonia. PLoS ONE, 2013, 8, e71952.	2.5	15
38	Virus-Host and CRISPR Dynamics in Archaea-Dominated Hypersaline Lake Tyrrell, Victoria, Australia. Archaea, 2013, 2013, 1-12.	2.3	82
39	Dynamic Viral Populations in Hypersaline Systems as Revealed by Metagenomic Assembly. Applied and Environmental Microbiology, 2012, 78, 6309-6320.	3.1	83
40	Influence of nutrients and currents on the genomic composition of microbes across an upwelling mosaic. ISME Journal, 2012, 6, 1403-1414.	9.8	120
41	<i>De novo</i> metagenomic assembly reveals abundant novel major lineage of Archaea in hypersaline microbial communities. ISME Journal, 2012, 6, 81-93.	9.8	347
42	Compositional differences in particle-associated and free-living microbial assemblages from an extreme deep-ocean environment. Environmental Microbiology Reports, 2011, 3, 449-458.	2.4	189
43	Widespread Occurrence of Secondary Lipid Biosynthesis Potential in Microbial Lineages. PLoS ONE, 2011, 6, e20146.	2.5	74
44	Going Deeper: Metagenome of a Hadopelagic Microbial Community. PLoS ONE, 2011, 6, e20388.	2.5	95
45	Diversity and distribution of microbial long-chain fatty acid biosynthetic genes in the marine environment. Environmental Microbiology, 2011, 13, 684-695.	3.8	37
46	Xenorhodopsins, an enigmatic new class of microbial rhodopsins horizontally transferred between archaea and bacteria. Biology Direct, 2011, 6, 52.	4.6	50
47	Genomic insights into the physiology and ecology of the marine filamentous cyanobacterium <i>Lyngbya majuscula</i> . Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 8815-8820.	7.1	99
48	Community cyberinfrastructure for Advanced Microbial Ecology Research and Analysis: the CAMERA resource. Nucleic Acids Research, 2011, 39, D546-D551.	14.5	291
49	Genomic islands link secondary metabolism to functional adaptation in marine Actinobacteria. ISME Journal, 2009, 3, 1193-1203.	9.8	175
50	A database of phylogenetically atypical genes in archaeal and bacterial genomes, identified using the DarkHorse algorithm. BMC Bioinformatics, 2008, 9, 419.	2.6	40
51	Genome dynamics in a natural archaeal population. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1883-1888.	7.1	123
52	Strain-resolved community proteomics reveals recombining genomes of acidophilic bacteria. Nature, 2007, 446, 537-541.	27.8	205
53	Lineages of Acidophilic Archaea Revealed by Community Genomic Analysis. Science, 2006, 314, 1933-1935.	12.6	217
54	Community genomics in microbial ecology and evolution. Nature Reviews Microbiology, 2005, 3, 489-498.	28.6	218

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55	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, 6319-6324.	3.1	225
56	Community structure and metabolism through reconstruction of microbial genomes from the environment. <i>Nature</i> , 2004, 428, 37-43.	27.8	2,045
57	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.. <i>Microbiology (United Kingdom)</i> , 2002, 148, 1903-1913.	1.8	151
58	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
59	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, 1710-1720.	3.1	221