

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	Community structure and metabolism through reconstruction of microbial genomes from the environment. <i>Nature</i> , 2004, 428, 37-43.	27.8	2,045
2	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.	5.6	885
3	<i>De novo</i> metagenomic assembly reveals abundant novel major lineage of Archaea in hypersaline microbial communities. <i>ISME Journal</i> , 2012, 6, 81-93.	9.8	347
4	Community cyberinfrastructure for Advanced Microbial Ecology Research and Analysis: the CAMERA resource. <i>Nucleic Acids Research</i> , 2011, 39, D546-D551.	14.5	291
5	Biosynthesis of polybrominated aromatic organic compounds by marine bacteria. <i>Nature Chemical Biology</i> , 2014, 10, 640-647.	8.0	246
6	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
7	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
8	Community genomics in microbial ecology and evolution. <i>Nature Reviews Microbiology</i> , 2005, 3, 489-498.	28.6	218
9	Lineages of Acidophilic Archaea Revealed by Community Genomic Analysis. <i>Science</i> , 2006, 314, 1933-1935.	12.6	217
10	Strain-resolved community proteomics reveals recombining genomes of acidophilic bacteria. <i>Nature</i> , 2007, 446, 537-541.	27.8	205
11	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
12	Compositional differences in particle-associated and free-living microbial assemblages from an extreme deep-ocean environment. <i>Environmental Microbiology Reports</i> , 2011, 3, 449-458.	2.4	189
13	Genomic islands link secondary metabolism to functional adaptation in marine Actinobacteria. <i>ISME Journal</i> , 2009, 3, 1193-1203.	9.8	175
14	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
15	Metagenomic discovery of polybrominated diphenyl ether biosynthesis by marine sponges. <i>Nature Chemical Biology</i> , 2017, 13, 537-543.	8.0	141
16	Genome dynamics in a natural archaeal population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1883-1888.	7.1	123
17	KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples. <i>MSystems</i> , 2018, 3, .	3.8	123
18	Influence of nutrients and currents on the genomic composition of microbes across an upwelling mosaic. <i>ISME Journal</i> , 2012, 6, 1403-1414.	9.8	120

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19	Assembly-Driven Community Genomics of a Hypersaline Microbial Ecosystem. <i>PLoS ONE</i> , 2013, 8, e61692.	2.5	101
20	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, 8815-8820.	7.1	99
21	Visualizing TM omic feature rankings and log-ratios using Qurro. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa023.	3.2	97
22	Going Deeper: Metagenome of a Hadopelagic Microbial Community. <i>PLoS ONE</i> , 2011, 6, e20388.	2.5	95
23	Seasonal fluctuations in ionic concentrations drive microbial succession in a hypersaline lake community. <i>ISME Journal</i> , 2014, 8, 979-990.	9.8	91
24	Dynamic Viral Populations in Hypersaline Systems as Revealed by Metagenomic Assembly. <i>Applied and Environmental Microbiology</i> , 2012, 78, 6309-6320.	3.1	83
25	Virus-Host and CRISPR Dynamics in Archaea-Dominated Hypersaline Lake Tyrrell, Victoria, Australia. <i>Archaea</i> , 2013, 2013, 1-12.	2.3	82
26	Comparative genomics uncovers the prolific and distinctive metabolic potential of the cyanobacterial genus <i>Moorea</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3198-3203.	7.1	77
27	Widespread Occurrence of Secondary Lipid Biosynthesis Potential in Microbial Lineages. <i>PLoS ONE</i> , 2011, 6, e20146.	2.5	74
28	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
29	Pangenomic comparison of globally distributed Poribacteria associated with sponge hosts and marine particles. <i>ISME Journal</i> , 2019, 13, 468-481.	9.8	63
30	Vertically distinct microbial communities in the Mariana and Kermadec trenches. <i>PLoS ONE</i> , 2018, 13, e0195102.	2.5	62
31	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
32	Microbial Community Diversity Within Sediments from Two Geographically Separated Hadal Trenches. <i>Frontiers in Microbiology</i> , 2019, 10, 347.	3.5	59
33	High-Throughput Miniaturized 16S rRNA Amplicon Library Preparation Reduces Costs while Preserving Microbiome Integrity. <i>MSystems</i> , 2018, 3, .	3.8	58
34	Xenorhodopsins, an enigmatic new class of microbial rhodopsins horizontally transferred between archaea and bacteria. <i>Biology Direct</i> , 2011, 6, 52.	4.6	50
35	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
36	A database of phylogenetically atypical genes in archaeal and bacterial genomes, identified using the DarkHorse algorithm. <i>BMC Bioinformatics</i> , 2008, 9, 419.	2.6	40

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37	A genomic view of trophic and metabolic diversity in clade-specific Lamellodysidea sponge microbiomes. <i>Microbiome</i> , 2020, 8, 97.	11.1	38
38	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
39	Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. <i>ISME Journal</i> , 2015, 9, 2697-2711.	9.8	35
40	Comparative Genomics of Cyanobacterial Symbionts Reveals Distinct, Specialized Metabolism in Tropical <i>Dysideidae</i> Sponges. <i>MBio</i> , 2019, 10, .	4.1	31
41	<i>De Novo</i> 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
42	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
43	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
44	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
45	Metagenome Sequencing of the Microbial Community of a Solar Saltern Crystallizer Pond at Chuil Lagoon, Chile. <i>Genome Announcements</i> , 2014, 2, .	0.8	18
46	Characterization and Application of Marine Microbial Omega-3 Polyunsaturated Fatty Acid Synthesis. <i>Methods in Enzymology</i> , 2018, 605, 3-32.	1.0	18
47	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
48	Microbial Life in a Fjord: Metagenomic Analysis of a Microbial Mat in Chilean Patagonia. <i>PLoS ONE</i> , 2013, 8, e71952.	2.5	15
49	Decade-scale stability and change in a marine bivalve microbiome. <i>Molecular Ecology</i> , 2021, 30, 1237-1250.	3.9	15
50	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
51	Linkage of Marine Bacterial Polyunsaturated Fatty Acid and Long-Chain Hydrocarbon Biosynthesis. <i>Frontiers in Microbiology</i> , 2019, 10, 702.	3.5	14
52	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
53	Draft Genome Sequence of <i>Candidatus</i> <i>Halobnum tyrrellensis</i> Strain G22, Isolated from the Hypersaline Waters of Lake Tyrrell, Australia. <i>Genome Announcements</i> , 2013, 1, .	0.8	13
54	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

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55	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
56	Genetic Regulation of the Bacterial Omega-3 Polyunsaturated Fatty Acid Biosynthesis Pathway. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	5
57	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
58	Microbiomes of Hadal Fishes across Trench Habitats Contain Similar Taxa and Known Piezophiles. <i>MSphere</i> , 2022, 7, e0003222.	2.9	2
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.	3.1	1