

Frank O Aylward

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

3,393
citations

236833

25
h-index

206029

48
g-index

97
all docs

97
docs citations

97
times ranked

4055
citing authors

#	ARTICLE	IF	CITATIONS
1	Complex marine microbial communities partition metabolism of scarce resources over the diel cycle. <i>Nature Ecology and Evolution</i> , 2022, 6, 218-229.	3.4	21
2	Infection strategy and biogeography distinguish cosmopolitan groups of marine jumbo bacteriophages. <i>ISME Journal</i> , 2022, 16, 1657-1667.	4.4	27
3	Genome size distributions in bacteria and archaea are strongly linked to evolutionary history at broad phylogenetic scales. <i>PLoS Genetics</i> , 2022, 18, e1010220.	1.5	20
4	The coevolutionary history of the microbial planet. <i>Environmental Microbiology Reports</i> , 2021, 13, 12-14.	1.0	0
5	ViralRecall—A Flexible Command-Line Tool for the Detection of Giant Virus Signatures in -Omic Data. <i>Viruses</i> , 2021, 13, 150.	1.5	45
6	Comparative Genomics and Environmental Distribution of Large dsDNA Viruses in the Family Asfarviridae. <i>Frontiers in Microbiology</i> , 2021, 12, 657471.	1.5	19
7	Particulate Metabolites and Transcripts Reflect Diel Oscillations of Microbial Activity in the Surface Ocean. <i>MSystems</i> , 2021, 6, .	1.7	29
8	Phylogenetic Signal, Congruence, and Uncertainty across Bacteria and Archaea. <i>Molecular Biology and Evolution</i> , 2021, 38, 5514-5527.	3.5	42
9	Historical forest disturbance mediates soil microbial community responses to drought. <i>Environmental Microbiology</i> , 2021, 23, 6405-6419.	1.8	10
10	High Transcriptional Activity and Diverse Functional Repertoires of Hundreds of Giant Viruses in a Coastal Marine System. <i>MSystems</i> , 2021, 6, e0029321.	1.7	30
11	Historical land use has long-term effects on microbial community assembly processes in forest soils. <i>ISME Communications</i> , 2021, 1, .	1.7	25
12	Identifying Virus-Like Regions in Microbial Genomes Using Hidden Markov Models. , 2021, , 263-270.		0
13	Emergent properties of microbial communities drive accelerated biogeochemical cycling in disturbed temperate forests. <i>Ecology</i> , 2021, 102, e03553.	1.5	12
14	A phylogenomic framework for charting the diversity and evolution of giant viruses. <i>PLoS Biology</i> , 2021, 19, e3001430.	2.6	72
15	Time-series metatranscriptomes reveal conserved patterns between phototrophic and heterotrophic microbes in diverse freshwater systems. <i>Limnology and Oceanography</i> , 2020, 65, S101.	1.6	18
16	Widespread endogenization of giant viruses shapes genomes of green algae. <i>Nature</i> , 2020, 588, 141-145.	13.7	96
17	A distinct lineage of Caudovirales that encodes a deeply branching multi-subunit RNA polymerase. <i>Nature Communications</i> , 2020, 11, 4506.	5.8	12
18	Heterotrophic Thaumarchaea with Small Genomes Are Widespread in the Dark Ocean. <i>MSystems</i> , 2020, 5, .	1.7	50

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19	Dynamic genome evolution and complex virocell metabolism of globally-distributed giant viruses. <i>Nature Communications</i> , 2020, 11, 1710.	5.8	144
20	Periodic and coordinated gene expression between a diazotroph and its diatom host. <i>ISME Journal</i> , 2019, 13, 118-131.	4.4	29
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.	4.4	61
22	Strong Purifying Selection Is Associated with Genome Streamlining in Epipelagic Marinimicrobia. <i>Genome Biology and Evolution</i> , 2019, 11, 2887-2894.	1.1	30
23	Soil Bacterial and Fungal Communities Exhibit Distinct Long-Term Responses to Disturbance in Temperate Forests. <i>Frontiers in Microbiology</i> , 2019, 10, 2872.	1.5	37
24	Parallel Evolution of Genome Streamlining and Cellular Bioenergetics across the Marine Radiation of a Bacterial Phylum. <i>MBio</i> , 2018, 9, .	1.8	27
25	FastViromeExplorer: a pipeline for virus and phage identification and abundance profiling in metagenomics data. <i>PeerJ</i> , 2018, 6, e4227.	0.9	70
26	Diel cycling and long-term persistence of viruses in the ocean's euphotic zone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11446-11451.	3.3	116
27	Environmental drivers of a microbial genomic transition zone in the ocean's interior. <i>Nature Microbiology</i> , 2017, 2, 1367-1373.	5.9	177
28	Coordinated regulation of growth, activity and transcription in natural populations of the unicellular nitrogen-fixing cyanobacterium <i>Crocospaera</i> . <i>Nature Microbiology</i> , 2017, 2, 17118.	5.9	122
29	Bacteriophage Distributions and Temporal Variability in the Ocean's Interior. <i>MBio</i> , 2017, 8, .	1.8	76
30	Major changes in microbial diversity and community composition across gut sections of a juvenile <i>Panclora</i> cockroach. <i>PLoS ONE</i> , 2017, 12, e0177189.	1.1	20
31	Improved Environmental Genomes via Integration of Metagenomic and Single-Cell Assemblies. <i>Frontiers in Microbiology</i> , 2016, 7, 143.	1.5	24
32	Wind and sunlight shape microbial diversity in surface waters of the North Pacific Subtropical Gyre. <i>ISME Journal</i> , 2016, 10, 1308-1322.	4.4	73
33	Microbial community transcriptional networks are conserved in three domains at ocean basin scales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5443-5448.	3.3	225
34	Phylogenomic Analysis and Predicted Physiological Role of the Proton-Translocating NADH:Quinone Oxidoreductase (Complex I) Across Bacteria. <i>MBio</i> , 2015, 6, .	1.8	44
35	Enrichment and Broad Representation of Plant Biomass-Degrading Enzymes in the Specialized Hyphal Swellings of <i>Leucoagaricus gongylophorus</i> , the Fungal Symbiont of Leaf-Cutter Ants. <i>PLoS ONE</i> , 2015, 10, e0134752.	1.1	28
36	Convergent Bacterial Microbiotas in the Fungal Agricultural Systems of Insects. <i>MBio</i> , 2014, 5, e02077.	1.8	96

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37	The fungus gardens of leaf-cutter ants undergo a distinct physiological transition during biomass degradation. <i>Environmental Microbiology Reports</i> , 2014, 6, 389-395.	1.0	21
38	<i>Leucoagaricus gongylophorus</i> Produces Diverse Enzymes for the Degradation of Recalcitrant Plant Polymers in Leaf-Cutter Ant Fungus Gardens. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3770-3778.	1.4	98
39	Complete Genome of <i>Serratia</i> sp. Strain FGI 94, a Strain Associated with Leaf-Cutter Ant Fungus Gardens. <i>Genome Announcements</i> , 2013, 1, e0023912.	0.8	15
40	Comparison of 26 Sphingomonad Genomes Reveals Diverse Environmental Adaptations and Biodegradative Capabilities. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3724-3733.	1.4	151
41	Mountain Pine Beetles Colonizing Historical and Naïve Host Trees Are Associated with a Bacterial Community Highly Enriched in Genes Contributing to Terpene Metabolism. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3468-3475.	1.4	236
42	Complete Genome of <i>Enterobacteriaceae</i> Bacterium Strain FGI 57, a Strain Associated with Leaf-Cutter Ant Fungus Gardens. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
43	The Genome Sequences of <i>Cellulomonas fimi</i> and <i>Cellvibrio gilvus</i> Reveal the Cellulolytic Strategies of Two Facultative Anaerobes, Transfer of <i>Cellvibrio gilvus</i> to the Genus <i>Cellulomonas</i> , and Proposal of <i>Cellulomonas gilvus</i> sp. nov. <i>PLoS ONE</i> , 2013, 8, e53954.	1.1	56
44	The Evolutionary Innovation of Nutritional Symbioses in Leaf-Cutter Ants. <i>Insects</i> , 2012, 3, 41-61.	1.0	51
45	Metagenomic and metaproteomic insights into bacterial communities in leaf-cutter ant fungus gardens. <i>ISME Journal</i> , 2012, 6, 1688-1701.	4.4	126
46	The Complete Genome Sequence of <i>Fibrobacter succinogenes</i> S85 Reveals a Cellulolytic and Metabolic Specialist. <i>PLoS ONE</i> , 2011, 6, e18814.	1.1	199
47	An Insect Herbivore Microbiome with High Plant Biomass-Degrading Capacity. <i>PLoS Genetics</i> , 2010, 6, e1001129.	1.5	213
48	Triassic origin and early radiation of multicellular volvocine algae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3254-3258.	3.3	224
49	From Genetics to Genomics. , 0, , 255-266.		0