

# Emiley A Eloe-Fadrosch

## List of Publications by Year in descending order

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75  
papers

9,407  
citations

117453

34  
h-index

64668

79  
g-index

97  
all docs

97  
docs citations

97  
times ranked

10502  
citing authors

#	ARTICLE	IF	CITATIONS
1	Challenges in Bioinformatics Workflows for Processing Microbiome Omics Data at Scale. <i>Frontiers in Bioinformatics</i> , 2022, 1, .	1.0	6
2	Diverse events have transferred genes for edible seaweed digestion from marine to human gut bacteria. <i>Cell Host and Microbe</i> , 2022, 30, 314-328.e11.	5.1	25
3	Mechanistic insights into consumption of the food additive xanthan gum by the human gut microbiota. <i>Nature Microbiology</i> , 2022, 7, 556-569.	5.9	21
4	Dissecting the dominant hot spring microbial populations based on community-wide sampling at single-cell genomic resolution. <i>ISME Journal</i> , 2022, 16, 1337-1347.	4.4	15
5	Microbes and Climate Change: a Research Prospectus for the Future. <i>MBio</i> , 2022, 13, e0080022.	1.8	53
6	Metagenome-assembled genomes of phytoplankton microbiomes from the Arctic and Atlantic Oceans. <i>Microbiome</i> , 2022, 10, 67.	4.9	17
7	The role of zinc in the adaptive evolution of polar phytoplankton. <i>Nature Ecology and Evolution</i> , 2022, 6, 965-978.	3.4	14
8	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
9	In-depth Spatiotemporal Characterization of Planktonic Archaeal and Bacterial Communities in North and South San Francisco Bay. <i>Microbial Ecology</i> , 2021, 81, 601-616.	1.4	11
10	The IMG/M data management and analysis system v.6.0: new tools and advanced capabilities. <i>Nucleic Acids Research</i> , 2021, 49, D751-D763.	6.5	332
11	IMG/VR v3: an integrated ecological and evolutionary framework for interrogating genomes of uncultivated viruses. <i>Nucleic Acids Research</i> , 2021, 49, D764-D775.	6.5	240
12	CheckV assesses the quality and completeness of metagenome-assembled viral genomes. <i>Nature Biotechnology</i> , 2021, 39, 578-585.	9.4	569
13	Host population diversity as a driver of viral infection cycle in wild populations of green sulfur bacteria with long standing virus-host interactions. <i>ISME Journal</i> , 2021, 15, 1569-1584.	4.4	16
14	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborative's Workshop and Follow-On Activities. <i>MSystems</i> , 2021, 6, .	1.7	28
15	Ecology and molecular targets of hypermutation in the global microbiome. <i>Nature Communications</i> , 2021, 12, 3076.	5.8	35
16	Genomics, Exometabolomics, and Metabolic Probing Reveal Conserved Proteolytic Metabolism of <i>Thermoflexus hugenholtzii</i> and Three Candidate Species From China and Japan. <i>Frontiers in Microbiology</i> , 2021, 12, 632731.	1.5	8
17	Metagenome Sequencing to Explore Phylogenomics of Terrestrial Cyanobacteria. <i>Microbiology Resource Announcements</i> , 2021, 10, e0025821.	0.3	15
18	DOE JGI Metagenome Workflow. <i>MSystems</i> , 2021, 6, .	1.7	56

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19	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. <i>Nature Communications</i> , 2021, 12, 5483.	5.8	29
20	Insights into the dynamics between viruses and their hosts in a hot spring microbial mat. <i>ISME Journal</i> , 2020, 14, 2527-2541.	4.4	42
21	Diversity and Distribution of a Novel Genus of Hyperthermophilic Aquificae Viruses Encoding a Proof-Reading Family-A DNA Polymerase. <i>Frontiers in Microbiology</i> , 2020, 11, 583361.	1.5	7
22	Metagenomes from Experimental Hydrologic Manipulation of Restored Coastal Plain Wetland Soils (Tyrell County, North Carolina). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
23	Impact of Soil Salinity on the Cowpea Nodule-Microbiome and the Isolation of Halotolerant PGPR Strains to Promote Plant Growth under Salinity Stress. <i>Phytobiomes Journal</i> , 2020, 4, 364-374.	1.4	14
24	Influence of the polar light cycle on seasonal dynamics of an Antarctic lake microbial community. <i>Microbiome</i> , 2020, 8, 116.	4.9	32
25	Ecological and genomic analyses of candidate phylum <sc>WPS</sc> bacteria in an unvegetated soil. <i>Environmental Microbiology</i> , 2020, 22, 3143-3157.	1.8	42
26	COVID-19 pandemic reveals the peril of ignoring metadata standards. <i>Scientific Data</i> , 2020, 7, 188.	2.4	56
27	Shotgun metagenomic analysis of microbial communities from the Loxahatchee nature preserve in the Florida Everglades. <i>Environmental Microbiomes</i> , 2020, 15, 2.	2.2	20
28	Terabase-scale metagenome coassembly with MetaHipMer. <i>Scientific Reports</i> , 2020, 10, 10689.	1.6	34
29	Giant virus diversity and host interactions through global metagenomics. <i>Nature</i> , 2020, 578, 432-436.	13.7	207
30	The National Microbiome Data Collaborative: enabling microbiome science. <i>Nature Reviews Microbiology</i> , 2020, 18, 313-314.	13.6	42
31	Metagenomes and Metatranscriptomes of a Glucose-Amended Agricultural Soil. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
32	Metatranscriptomic Sequencing of a Cyanobacterial Soil-Surface Consortium with and without a Diverse Underlying Soil Microbiome. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
33	Genomes From Uncultivated Microorganisms. , 2019, , .		4
34	Microbiomes of Velloziaceae from phosphorus-impooverished soils of the campos rupestres, a biodiversity hotspot. <i>Scientific Data</i> , 2019, 6, 140.	2.4	10
35	Genome gazing in ammonia-oxidizing archaea. <i>Nature Reviews Microbiology</i> , 2019, 17, 531-531.	13.6	3
36	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. <i>Nature Microbiology</i> , 2019, 4, 1895-1906.	5.9	206

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37	Towards a genome-based virus taxonomy. <i>Nature Microbiology</i> , 2019, 4, 1249-1250.	5.9	7
38	Microbial metagenomes and metatranscriptomes during a coastal phytoplankton bloom. <i>Scientific Data</i> , 2019, 6, 129.	2.4	36
39	Unexpected host dependency of Antarctic Nanohaloarchaeota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14661-14670.	3.3	134
40	Metagenomes and metatranscriptomes from boreal potential and actual acid sulfate soil materials. <i>Scientific Data</i> , 2019, 6, 207.	2.4	6
41	Expansion of <i>Thaumarchaeota</i> habitat range is correlated with horizontal transfer of ATPase operons. <i>ISME Journal</i> , 2019, 13, 3067-3079.	4.4	59
42	Triplicate PCR reactions for 16S rRNA gene amplicon sequencing are unnecessary. <i>BioTechniques</i> , 2019, 67, 29-32.	0.8	48
43	Position-Specific Metabolic Probing and Metagenomics of Microbial Communities Reveal Conserved Central Carbon Metabolic Network Activities at High Temperatures. <i>Frontiers in Microbiology</i> , 2019, 10, 1427.	1.5	12
44	Advancing Genome-Resolved Metagenomics beyond the Shotgun. <i>MSystems</i> , 2019, 4, .	1.7	14
45	Spatial, Temporal, and Phylogenetic Scales of Microbial Ecology. <i>Trends in Microbiology</i> , 2019, 27, 662-669.	3.5	105
46	Genomic Characterization of Candidate Division LCP-89 Reveals an Atypical Cell Wall Structure, Microcompartment Production, and Dual Respiratory and Fermentative Capacities. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	14
47	Contrasting Pathways for Anaerobic Methane Oxidation in Gulf of Mexico Cold Seep Sediments. <i>MSystems</i> , 2019, 4, .	1.7	27
48	Carboxydrotrophy potential of uncultivated Hydrothermarchaeota from the seafloor crustal biosphere. <i>ISME Journal</i> , 2019, 13, 1457-1468.	4.4	31
49	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , 2019, 7, 157.	4.9	53
50	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
51	IMG/VR v.2.0: an integrated data management and analysis system for cultivated and environmental viral genomes. <i>Nucleic Acids Research</i> , 2019, 47, D678-D686.	6.5	174
52	IMG/M v.5.0: an integrated data management and comparative analysis system for microbial genomes and microbiomes. <i>Nucleic Acids Research</i> , 2019, 47, D666-D677.	6.5	799
53	Functional Signatures of the Epiphytic Prokaryotic Microbiome of Agaves and Cacti. <i>Frontiers in Microbiology</i> , 2019, 10, 3044.	1.5	41
54	Optimizing <i>de novo</i> genome assembly from PCR-amplified metagenomes. <i>PeerJ</i> , 2019, 7, e6902.	0.9	28

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55	Towards optimized viral metagenomes for double-stranded and single-stranded DNA viruses from challenging soils. PeerJ, 2019, 7, e7265.	0.9	48
56	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. Nature Biotechnology, 2018, 36, 359-367.	9.4	414
57	Metabolic versatility of small archaea Micrarchaeota and Parvarchaeota. ISME Journal, 2018, 12, 756-775.	4.4	91
58	Genomic variation and biogeography of Antarctic haloarchaea. Microbiome, 2018, 6, 113.	4.9	32
59	Metagenomic insights into diazotrophic communities across Arctic glacier forefields. FEMS Microbiology Ecology, 2018, 94, .	1.3	36
60	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. Nature Biotechnology, 2017, 35, 676-683.	9.4	222
61	Adaptations of Cold- and Pressure-Loving Bacteria to the Deep-Sea Environment: Cell Envelope and Flagella. , 2017, , 51-80.		6
62	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. Nature Biotechnology, 2017, 35, 725-731.	9.4	1,512
63	Towards a balanced view of the bacterial tree of life. Microbiome, 2017, 5, 140.	4.9	102
64	Benchmarking viromics: an <i>in silico</i> evaluation of metagenome-enabled estimates of viral community composition and diversity. PeerJ, 2017, 5, e3817.	0.9	235
65	Microbiome Data Science: Understanding Our Microbial Planet. Trends in Microbiology, 2016, 24, 425-427.	3.5	47
66	Uncovering Earth's virome. Nature, 2016, 536, 425-430.	13.7	880
67	Metagenomics uncovers gaps in amplicon-based detection of microbial diversity. Nature Microbiology, 2016, 1, 15032.	5.9	207
68	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. Nature Communications, 2016, 7, 10476.	5.8	189
69	Functional Dynamics of the Gut Microbiome in Elderly People during Probiotic Consumption. MBio, 2015, 6, .	1.8	126
70	Aerosol Mycobacterium tuberculosis Infection Causes Rapid Loss of Diversity in Gut Microbiota. PLoS ONE, 2014, 9, e97048.	1.1	124
71	Ecotype Diversity and Conversion in Photobacterium profundum Strains. PLoS ONE, 2014, 9, e96953.	1.1	15
72	The Human Microbiome: From Symbiosis to Pathogenesis. Annual Review of Medicine, 2013, 64, 145-163.	5.0	175

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73	Impact of Oral Typhoid Vaccination on the Human Gut Microbiota and Correlations with S. Typhi-Specific Immunological Responses. PLoS ONE, 2013, 8, e62026.	1.1	82
74	Differential Response of the Cynomolgus Macaque Gut Microbiota to Shigella Infection. PLoS ONE, 2013, 8, e64212.	1.1	52
75	Medicago root nodule microbiomes: insights into a complex ecosystem with potential candidates for plant growth promotion. Plant and Soil, 0, , 1.	1.8	4