

Jed A Fuhrman

List of Publications by Year in descending order

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220
papers

43,997
citations

3149

92
h-index

2375

198
g-index

246
all docs

246
docs citations

246
times ranked

28657
citing authors

#	ARTICLE	IF	CITATIONS
1	Every base matters: assessing small subunit <scp>rRNA</scp> primers for marine microbiomes with mock communities, time series and global field samples. <i>Environmental Microbiology</i> , 2016, 18, 1403-1414.	1.8	2,618
2	Microbial biogeography: putting microorganisms on the map. <i>Nature Reviews Microbiology</i> , 2006, 4, 102-112.	13.6	2,434
3	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
4	Marine viruses and their biogeochemical and ecological effects. <i>Nature</i> , 1999, 399, 541-548.	13.7	1,895
5	Improved Bacterial 16S rRNA Gene (V4 and V4-5) and Fungal Internal Transcribed Spacer Marker Gene Primers for Microbial Community Surveys. <i>MSystems</i> , 2016, 1, .	1.7	1,364
6	Beyond biogeographic patterns: processes shaping the microbial landscape. <i>Nature Reviews Microbiology</i> , 2012, 10, 497-506.	13.6	1,299
7	Thymidine incorporation as a measure of heterotrophic bacterioplankton production in marine surface waters: Evaluation and field results. <i>Marine Biology</i> , 1982, 66, 109-120.	0.7	1,246
8	Relationships between Biovolume and Biomass of Naturally Derived Marine Bacterioplankton. <i>Applied and Environmental Microbiology</i> , 1987, 53, 1298-1303.	1.4	1,156
9	Microbial community structure and its functional implications. <i>Nature</i> , 2009, 459, 193-199.	13.7	1,061
10	Defining seasonal marine microbial community dynamics. <i>ISME Journal</i> , 2012, 6, 298-308.	4.4	928
11	Use of SYBR Green I for rapid epifluorescence counts of marine viruses and bacteria. <i>Aquatic Microbial Ecology</i> , 1998, 14, 113-118.	0.9	906
12	Viral mortality of marine bacteria and cyanobacteria. <i>Nature</i> , 1990, 343, 60-62.	13.7	865
13	Novel major archaeobacterial group from marine plankton. <i>Nature</i> , 1992, 356, 148-149.	13.7	825
14	Bacterioplankton Secondary Production Estimates for Coastal Waters of British Columbia, Antarctica, and California. <i>Applied and Environmental Microbiology</i> , 1980, 39, 1085-1095.	1.4	804
15	Marine microbial community dynamics and their ecological interpretation. <i>Nature Reviews Microbiology</i> , 2015, 13, 133-146.	13.6	681
16	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	9.4	608
17	A latitudinal diversity gradient in planktonic marine bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7774-7778.	3.3	599
18	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016, 10, 1669-1681.	4.4	593

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19	Annually reoccurring bacterial communities are predictable from ocean conditions. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13104-13109.	3.3	578
20	Marine bacterial, archaeal and protistan association networks reveal ecological linkages. ISME Journal, 2011, 5, 1414-1425.	4.4	560
21	Global Patterns of Bacterial Beta-Diversity in Seafloor and Seawater Ecosystems. PLoS ONE, 2011, 6, e24570.	1.1	525
22	Significance of Size and Nucleic Acid Content Heterogeneity as Measured by Flow Cytometry in Natural Planktonic Bacteria. Applied and Environmental Microbiology, 1999, 65, 4475-4483.	1.4	473
23	Phylogenetic diversity of subsurface marine microbial communities from the Atlantic and Pacific Oceans. Applied and Environmental Microbiology, 1993, 59, 1294-1302.	1.4	466
24	VirFinder: a novel k-mer based tool for identifying viral sequences from assembled metagenomic data. Microbiome, 2017, 5, 69.	4.9	433
25	Minimum Information about an Uncultivated Virus Genome (MIUViG). Nature Biotechnology, 2019, 37, 29-37.	9.4	414
26	Viruses and protists cause similar bacterial mortality in coastal seawater. Limnology and Oceanography, 1995, 40, 1236-1242.	1.6	397
27	Pronounced daily succession of phytoplankton, archaea and bacteria following a spring bloom. Nature Microbiology, 2016, 1, 16005.	5.9	384
28	Global declines in oceanic nitrification rates as a consequence of ocean acidification. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 208-213.	3.3	316
29	Marine Planktonic Archaea Take Up Amino Acids. Applied and Environmental Microbiology, 2000, 66, 4829-4833.	1.4	313
30	Identifying viruses from metagenomic data using deep learning. Quantitative Biology, 2020, 8, 64-77.	0.3	302
31	Combined Microautoradiography and 16S rRNA Probe Technique for Determination of Radioisotope Uptake by Specific Microbial Cell Types In Situ. Applied and Environmental Microbiology, 1999, 65, 1746-1752.	1.4	302
32	Top-down controls on bacterial community structure: microbial network analysis of bacteria, T4-like viruses and protists. ISME Journal, 2014, 8, 816-829.	4.4	300
33	Marine viruses and global climate change. FEMS Microbiology Reviews, 2011, 35, 993-1034.	3.9	297
34	Local similarity analysis reveals unique associations among marine bacterioplankton species and environmental factors. Bioinformatics, 2006, 22, 2532-2538.	1.8	292
35	Dominance of bacterial biomass in the Sargasso Sea and its ecological implications. Marine Ecology - Progress Series, 1989, 57, 207-217.	0.9	290
36	Extraction from Natural Planktonic Microorganisms of DNA Suitable for Molecular Biological Studies. Applied and Environmental Microbiology, 1988, 54, 1426-1429.	1.4	277

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37	Virus and prokaryote enumeration from planktonic aquatic environments by epifluorescence microscopy with SYBR Green I. <i>Nature Protocols</i> , 2007, 2, 269-276.	5.5	272
38	Re-examination of the relationship between marine virus and microbial cell abundances. <i>Nature Microbiology</i> , 2016, 1, 15024.	5.9	264
39	Viruses in Marine Planktonic Systems. <i>Oceanography</i> , 1993, 6, 51-63.	0.5	259
40	Unlocking the potential of metagenomics through replicated experimental design. <i>Nature Biotechnology</i> , 2012, 30, 513-520.	9.4	250
41	Alignment-free d_2 oligonucleotide frequency dissimilarity measure improves prediction of hosts from metagenomically-derived viral sequences. <i>Nucleic Acids Research</i> , 2017, 45, 39-53.	6.5	245
42	<i>Silicibacter pomeroyi</i> sp. nov. and <i>Roseovarius nubinhibens</i> sp. nov., dimethylsulfoniopropionate-demethylating bacteria from marine environments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 1261-1269.	0.8	231
43	Coupling 16S-ITS rDNA clone libraries and automated ribosomal intergenic spacer analysis to show marine microbial diversity: development and application to a time series. <i>Environmental Microbiology</i> , 2005, 7, 1466-1479.	1.8	230
44	Microbial community structure in the North Pacific ocean. <i>ISME Journal</i> , 2009, 3, 1374-1386.	4.4	224
45	A COMPARISON OF TAXON CO-OCCURRENCE PATTERNS FOR MACRO- AND MICROORGANISMS. <i>Ecology</i> , 2007, 88, 1345-1353.	1.5	223
46	Extended local similarity analysis (eLSA) of microbial community and other time series data with replicates. <i>BMC Systems Biology</i> , 2011, 5, S15.	3.0	223
47	A multitrophic model to quantify the effects of marine viruses on microbial food webs and ecosystem processes. <i>ISME Journal</i> , 2015, 9, 1352-1364.	4.4	223
48	Widespread Archaea and novel Bacteria from the deep sea as shown by 16S rRNA gene sequences. <i>Marine Ecology - Progress Series</i> , 1997, 150, 275-285.	0.9	222
49	Proteorhodopsins: an array of physiological roles?. <i>Nature Reviews Microbiology</i> , 2008, 6, 488-494.	13.6	220
50	Seasonal and interannual variability of the marine bacterioplankton community throughout the water column over ten years. <i>ISME Journal</i> , 2015, 9, 563-580.	4.4	219
51	Global biogeography of SAR11 marine bacteria. <i>Molecular Systems Biology</i> , 2012, 8, 595.	3.2	215
52	Community structure of marine bacterioplankton: patterns, networks, and relationships to function. <i>Aquatic Microbial Ecology</i> , 2008, 53, 69-81.	0.9	211
53	Richness and Diversity of Bacterioplankton Species along an Estuarine Gradient in Moreton Bay, Australia. <i>Applied and Environmental Microbiology</i> , 2004, 70, 3425-3433.	1.4	210
54	Global distribution and diversity of marine <i>Verrucomicrobia</i> . <i>ISME Journal</i> , 2012, 6, 1499-1505.	4.4	196

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55	The ocean sampling day consortium. <i>GigaScience</i> , 2015, 4, 27.	3.3	185
56	Ecosystem Services for 2020. <i>Science</i> , 2010, 330, 323-324.	6.0	178
57	Bacterioplankton growth in seawater: I. Growth kinetics and cellular characteristics in seawater cultures. <i>Marine Ecology - Progress Series</i> , 1984, 18, 31-39.	0.9	172
58	Bacterioplankton Roles in Cycling of Organic Matter: The Microbial Food Web. , 1992, , 361-383.		167
59	Virus-like particle distribution and abundance in sediments and overlying waters along eutrophication gradients in two subtropical estuaries. <i>Limnology and Oceanography</i> , 2001, 46, 1734-1746.	1.6	167
60	Temporal variability and coherence of euphotic zone bacterial communities over a decade in the Southern California Bight. <i>ISME Journal</i> , 2013, 7, 2259-2273.	4.4	162
61	Time- and sediment depth-related variations in bacterial diversity and community structure in subtidal sands. <i>ISME Journal</i> , 2009, 3, 780-791.	4.4	159
62	Millions of reads, thousands of taxa: microbial community structure and associations analyzed via marker genes. <i>FEMS Microbiology Reviews</i> , 2016, 40, 686-700.	3.9	159
63	Close coupling between release and uptake of dissolved free amino acids in seawater studied by an isotope dilution approach. <i>Marine Ecology - Progress Series</i> , 1987, 37, 45-52.	0.9	159
64	Ecological dynamics and co-occurrence among marine phytoplankton, bacteria and myoviruses shows microdiversity matters. <i>ISME Journal</i> , 2017, 11, 1614-1629.	4.4	158
65	Roles of viral infection in organic particle flux. <i>Marine Ecology - Progress Series</i> , 1991, 69, 133-142.	0.9	158
66	Burrowing deeper into benthic nitrogen cycling: the impact of bioturbation on nitrogen fixation coupled to sulfate reduction. <i>Marine Ecology - Progress Series</i> , 2010, 409, 1-15.	0.9	157
67	Bacterioplankton in the coastal euphotic zone: Distribution, activity and possible relationships with phytoplankton. <i>Marine Biology</i> , 1980, 60, 201-207.	0.7	154
68	Tiered Approach for Identification of a Human Fecal Pollution Source at a Recreational Beach: A Case Study at Avalon Bay, Catalina Island, California. <i>Environmental Science & Technology</i> , 2003, 37, 673-680.	4.6	154
69	Multitiered Approach Using Quantitative PCR To Track Sources of Fecal Pollution Affecting Santa Monica Bay, California. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1604-1612.	1.4	145
70	Short-term observations of marine bacterial and viral communities: patterns, connections and resilience. <i>ISME Journal</i> , 2013, 7, 1274-1285.	4.4	144
71	Microzones surrounding phytoplankton form the basis for a stratified marine microbial ecosystem. <i>Nature</i> , 1985, 316, 58-59.	13.7	143
72	Microbial microdiversity. <i>Nature</i> , 1998, 393, 410-411.	13.7	137

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73	Title is missing!. <i>Hydrobiologia</i> , 2001, 460, 175-184.	1.0	137
74	Efficient statistical significance approximation for local similarity analysis of high-throughput time series data. <i>Bioinformatics</i> , 2013, 29, 230-237.	1.8	137
75	Bacterial viruses in coastal seawater: lytic rather than lysogenic production. <i>Marine Ecology - Progress Series</i> , 1994, 114, 35-45.	0.9	136
76	Influence of Method on the Apparent Size Distribution of Bacterioplankton Cells: Epifluorescence Microscopy Compared to Scanning Electron Microscopy. <i>Marine Ecology - Progress Series</i> , 1981, 5, 103-106.	0.9	132
77	Dependent coupling of inorganic and organic nitrogen uptake and regeneration in the plume of the Chesapeake Bay estuary and its regulation by large heterotrophs. <i>Limnology and Oceanography</i> , 1991, 36, 895-909.	1.6	131
78	COCACOLA: binning metagenomic contigs using sequence COmposition, read CoverAge, CO-alignment and paired-end read LinkAge. <i>Bioinformatics</i> , 2017, 33, 791-798.	1.8	130
79	Estimating maximal microbial growth rates from cultures, metagenomes, and single cells via codon usage patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	130
80	Do Bacteria-Sized Marine Eukaryotes Consume Significant Bacterial Production?. <i>Science</i> , 1984, 224, 1257-1260.	6.0	125
81	Marine bacterial microdiversity as revealed by internal transcribed spacer analysis. <i>Aquatic Microbial Ecology</i> , 2005, 41, 15-23.	0.9	123
82	Radioactively labeling of natural assemblages of bacterioplankton for use in trophic studies1. <i>Limnology and Oceanography</i> , 1980, 25, 172-181.	1.6	120
83	Nanomolar concentrations and rapid turnover of dissolved free amino acids in seawater: agreement between chemical and microbiological measurements. <i>Marine Ecology - Progress Series</i> , 1986, 33, 237-242.	0.9	116
84	Microbial uptake of dissolved organic matter in Mcmurdo Sound, Antarctica. <i>Marine Biology</i> , 1981, 61, 89-94.	0.7	114
85	Rapid Virus Production and Removal as Measured with Fluorescently Labeled Viruses as Tracers. <i>Applied and Environmental Microbiology</i> , 2000, 66, 3790-3797.	1.4	112
86	Biological considerations in the measurement of dissolved free amino acids in seawater and implications for chemical and microbiological studies. <i>Marine Ecology - Progress Series</i> , 1985, 25, 13-21.	0.9	112
87	Dissolved free amino acids in the Sargasso Sea: uptake and respiration rates, turnover times, and concentrations. <i>Marine Ecology - Progress Series</i> , 1991, 70, 189-199.	0.9	111
88	Bacterial secondary production in freshwater measured by ³ H-thymidine incorporation method. <i>Microbial Ecology</i> , 1982, 8, 101-113.	1.4	107
89	Wide-ranging abundances of aerobic anoxygenic phototrophic bacteria in the world ocean revealed by epifluorescence microscopy and quantitative PCR. <i>Limnology and Oceanography</i> , 2005, 50, 620-628.	1.6	107
90	Accurate Genome Relative Abundance Estimation Based on Shotgun Metagenomic Reads. <i>PLoS ONE</i> , 2011, 6, e27992.	1.1	105

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91	Cross-depth analysis of marine bacterial networks suggests downward propagation of temporal changes. <i>ISME Journal</i> , 2015, 9, 2573-2586.	4.4	105
92	Bacterial Diversity in Shallow Oligotrophic Marine Benthos and Overlying Waters: Effects of Virus Infection, Containment, and Nutrient Enrichment. <i>Microbial Ecology</i> , 2003, 46, 322-336.	1.4	104
93	Temporal and spatial scales of variation in bacterioplankton assemblages of oligotrophic surface waters. <i>Marine Ecology - Progress Series</i> , 2006, 311, 67-77.	0.9	104
94	Discovery of several novel, widespread, and ecologically distinct marine <i>Thaumarchaeota</i> viruses that encode <i>amoC</i> nitrification genes. <i>ISME Journal</i> , 2019, 13, 618-631.	4.4	103
95	Diel variations in bacterioplankton, phytoplankton, and related parameters in the Southern California Bight. <i>Marine Ecology - Progress Series</i> , 1985, 27, 9-20.	0.9	101
96	Rapid ammonium cycling and concentration-dependent partitioning of ammonium and phosphate: Implications for carbon transfer in planktonic communities. <i>Limnology and Oceanography</i> , 1990, 35, 424-433.	1.6	98
97	Microbial rhodopsins are major contributors to the solar energy captured in the sea. <i>Science Advances</i> , 2019, 5, eaaw8855.	4.7	97
98	Control of marine bacterioplankton populations: Measurement and significance of grazing. <i>Hydrobiologia</i> , 1988, 159, 51-62.	1.0	96
99	Viriobenthos Production and Virioplankton Sorptive Scavenging by Suspended Sediment Particles in Coastal and Pelagic Waters. <i>Microbial Ecology</i> , 2003, 46, 337-347.	1.4	96
100	Population ecology of nitrifying <i>Archaea</i> and <i>Bacteria</i> in the Southern California Bight. <i>Environmental Microbiology</i> , 2010, 12, 1282-1292.	1.8	96
101	Rapid Detection of Enteroviruses in Small Volumes of Natural Waters by Real-Time Quantitative Reverse Transcriptase PCR. <i>Applied and Environmental Microbiology</i> , 2005, 71, 4523-4530.	1.4	93
102	Viral effects on bacterial community composition in marine plankton microcosms. <i>Aquatic Microbial Ecology</i> , 2004, 34, 117-127.	0.9	93
103	Bacterivory in seawater studied with the use of inert fluorescent particles ¹ . <i>Limnology and Oceanography</i> , 1986, 31, 420-426.	1.6	92
104	Ecosystem services, targets, and indicators for the conservation and sustainable use of biodiversity. <i>Frontiers in Ecology and the Environment</i> , 2011, 9, 512-520.	1.9	91
105	Mortality of marine bacteria in response to enrichments of the virus size fraction from seawater. <i>Marine Ecology - Progress Series</i> , 1992, 87, 283-293.	0.9	90
106	Viral Influence on Aquatic Bacterial Communities. <i>Biological Bulletin</i> , 2003, 204, 192-195.	0.7	88
107	Spatial and temporal variation of natural bacterioplankton assemblages studied by total genomic DNA cross-hybridization. <i>Limnology and Oceanography</i> , 1991, 36, 1277-1287.	1.6	87
108	Improved Strategy for Comparing Microbial Assemblage Fingerprints. <i>Microbial Ecology</i> , 2006, 51, 147-153.	1.4	87

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109	Co-occurrence patterns for abundant marine archaeal and bacterial lineages in the deep chlorophyll maximum of coastal California. <i>ISME Journal</i> , 2011, 5, 1077-1085.	4.4	85
110	Remarkable heterogeneity in meso- and bathypelagic bacterioplankton assemblage composition. <i>Limnology and Oceanography</i> , 2006, 51, 1274-1283.	1.6	84
111	Short-term dynamics and interactions of marine protist communities during the springâ€“summer transition. <i>ISME Journal</i> , 2018, 12, 1907-1917.	4.4	84
112	Photosynthetic pigments in the ciliate <i>Laboea strobila</i> from Long Island Sound, USA. <i>Journal of Plankton Research</i> , 1986, 8, 317-327.	0.8	83
113	Breakdown and microbial uptake of marine viruses and other lysis products. <i>Aquatic Microbial Ecology</i> , 1999, 20, 1-11.	0.9	83
114	Seasonality and monthly dynamics of marine myovirus communities. <i>Environmental Microbiology</i> , 2012, 14, 2171-2183.	1.8	82
115	Marine archaeal dynamics and interactions with the microbial community over 5 years from surface to seafloor. <i>ISME Journal</i> , 2017, 11, 2510-2525.	4.4	80
116	Diversity and biogeography of bacterial assemblages in surface sediments across the San Pedro Basin, Southern California Borderlands. <i>Environmental Microbiology</i> , 2007, 9, 923-933.	1.8	79
117	Characterization of marine prokaryotic communities via DNA and RNA. <i>Microbial Ecology</i> , 1994, 28, 133-145.	1.4	76
118	Evidence of <i>Trichodesmium</i> viral lysis and potential significance for biogeochemical cycling in the oligotrophic ocean. <i>Aquatic Microbial Ecology</i> , 2004, 36, 1-8.	0.9	76
119	Possible biogeochemical consequences of ocean fertilization. <i>Limnology and Oceanography</i> , 1991, 36, 1951-1959.	1.6	75
120	Beta diversity of marine bacteria depends on temporal scale. <i>Ecology</i> , 2013, 94, 1898-1904.	1.5	75
121	Performance of viruses and bacteriophages for fecal source determination in a multi-laboratory, comparative study. <i>Water Research</i> , 2013, 47, 6929-6943.	5.3	75
122	Origins of Dissolved Organic Matter in Southern California Coastal Waters: Experiments on the Role of Zooplankton. <i>Marine Ecology - Progress Series</i> , 1981, 6, 149-159.	0.9	74
123	Genome and epigenome of a novel marine Thaumarchaeota strain suggest viral infection, phosphorothioation DNA modification and multiple restriction systems. <i>Environmental Microbiology</i> , 2017, 19, 2434-2452.	1.8	71
124	Title is missing!. <i>Aquatic Ecology</i> , 1998, 32, 3-15.	0.7	70
125	A comparative study of culture-independent, library-independent genotypic methods of fecal source tracking. <i>Journal of Water and Health</i> , 2003, 1, 181-194.	1.1	69
126	A network-based integrated framework for predicting virusâ€“prokaryote interactions. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa044.	1.5	69

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127	Dynamics and interactions of highly resolved marine plankton via automated high-frequency sampling. ISME Journal, 2018, 12, 2417-2432.	4.4	66
128	Diel changes in bacterial biomass and growth rates in coastal environments, determined by means of thymidine incorporation into DNA, frequency of dividing cells (FDC), and microautoradiography. Marine Ecology - Progress Series, 1984, 17, 227-235.	0.9	65
129	Production, consumption and nutrient cycling in a laboratory mesocosm. Marine Ecology - Progress Series, 1988, 42, 39-52.	0.9	65
130	Dissolved free amino acid cycling in an estuarine outflow plume. Marine Ecology - Progress Series, 1990, 66, 197-203.	0.9	64
131	Imperfect retention of natural bacterioplankton cells by glass fiber filters. Marine Ecology - Progress Series, 1995, 119, 285-290.	0.9	64
132	Taxon Disappearance from Microbiome Analysis Reinforces the Value of Mock Communities as a Standard in Every Sequencing Run. MSystems, 2018, 3, .	1.7	62
133	Dynamic marine viral infections and major contribution to photosynthetic processes shown by spatiotemporal picoplankton metatranscriptomes. Nature Communications, 2019, 10, 1169.	5.8	62
134	Long-term stability and Red Queen-like strain dynamics in marine viruses. Nature Microbiology, 2020, 5, 265-271.	5.9	62
135	Spatial and vertical biogeography of coral reef sediment bacterial and diazotroph communities. Marine Ecology - Progress Series, 2006, 306, 79-86.	0.9	62
136	Genome sequences from the sea. Nature, 2003, 424, 1001-1002.	13.7	61
137	Whither or wither geomicrobiology in the era of 'community metagenomics'. Nature Reviews Microbiology, 2005, 3, 572-578.	13.6	59
138	CAFE: aCcelerated Alignment-FrEe sequence analysis. Nucleic Acids Research, 2017, 45, W554-W559.	6.5	59
139	Mosaic patterns of B12 vitamin synthesis and utilization in a natural marine microbial community. Environmental Microbiology, 2018, 20, 2809-2823.	1.8	59
140	Proteorhodopsin light-enhanced growth linked to vitamin-B1 acquisition in marine Flavobacteria. ISME Journal, 2016, 10, 1102-1112.	4.4	58
141	Centimeter scale vertical heterogeneity in bacteria and chlorophyll a. Marine Ecology - Progress Series, 1989, 54, 141-148.	0.9	57
142	Mechanoreception in calanoid copepods. Marine Biology, 1986, 90, 529-535.	0.7	56
143	Macroecological patterns of marine bacteria on a global scale. Journal of Biogeography, 2013, 40, 800-811.	1.4	53
144	Effects of viral enrichment on the mortality and growth of heterotrophic bacterioplankton. Aquatic Microbial Ecology, 1999, 18, 1-13.	0.9	53

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145	Benchmarking microbial growth rate predictions from metagenomes. <i>ISME Journal</i> , 2021, 15, 183-195.	4.4	52
146	The founding charter of the Genomic Observatories Network. <i>GigaScience</i> , 2014, 3, 2.	3.3	51
147	Zooplankton induced changes in dissolved free amino acids and in production rates of freshwater bacteria. <i>Microbial Ecology</i> , 1986, 12, 247-258.	1.4	49
148	Impact of light on marine bacterioplankton community structure. <i>Aquatic Microbial Ecology</i> , 2005, 39, 235-245.	0.9	49
149	Use of ¹³ N as tracer for bacterial and algal uptake of ammonium from sea-water. <i>Marine Ecology - Progress Series</i> , 1988, 45, 271-278.	0.9	49
150	Covariation of viral parameters with bacterial assemblage richness and diversity in the water column and sediments. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2007, 54, 811-830.	0.6	47
151	Viral impacts upon marine bacterioplankton assemblage structure. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2006, 86, 577-589.	0.4	45
152	Multi-year dynamics of fine-scale marine cyanobacterial populations are more strongly explained by phage interactions than abiotic, bottom-up factors. <i>Environmental Microbiology</i> , 2019, 21, 2948-2963.	1.8	45
153	Clearance of bacteria-sized particles by natural populations of nanoplankton in the Chesapeake Bay outflow plume. <i>Marine Ecology - Progress Series</i> , 1988, 42, 199-206.	0.9	43
154	Species composition shift of confined bacterioplankton studied at the level of community DNA. <i>Marine Ecology - Progress Series</i> , 1991, 79, 195-201.	0.9	43
155	Genomics and Physiology of a Marine Flavobacterium Encoding a Proteorhodopsin and a Xanthorhodopsin-Like Protein. <i>PLoS ONE</i> , 2013, 8, e57487.	1.1	42
156	Long-term nitrogen and phosphorus fertilization effects on N ₂ fixation rates and <i>nifH</i> gene community patterns in mangrove sediments. <i>Marine Ecology</i> , 2012, 33, 117-127.	0.4	41
157	Systematic, continental scale temporal monitoring of marine pelagic microbiota by the Australian Marine Microbial Biodiversity Initiative. <i>Scientific Data</i> , 2018, 5, 180130.	2.4	41
158	Cycling of organic nitrogen in marine plankton communities studied in enclosed water columns. <i>Marine Biology</i> , 1980, 59, 15-21.	0.7	40
159	Structure of microbial communities in ethanol biofilters. <i>Chemical Engineering Journal</i> , 2005, 113, 135-143.	6.6	40
160	Dilution reveals how viral lysis and grazing shape microbial communities. <i>Limnology and Oceanography</i> , 2016, 61, 889-905.	1.6	39
161	Measurement of Bacterioplankton Growth in the Sea and Its Regulation by Environmental Conditions. , 1984, , 179-196.		39
162	Prokaryotic and viral diversity patterns in marine plankton. <i>Ecological Research</i> , 2002, 17, 183-194.	0.7	38

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163	Prediction of virus-host infectious association by supervised learning methods. BMC Bioinformatics, 2017, 18, 60.	1.2	38
164	Strong Seasonality and Interannual Recurrence in Marine Myovirus Communities. Applied and Environmental Microbiology, 2013, 79, 6253-6259.	1.4	37
165	Characterizing Chemoautotrophy and Heterotrophy in Marine Archaea and Bacteria With Single-Cell Multi-isotope NanoSIP. Frontiers in Microbiology, 2019, 10, 2682.	1.5	37
166	Comprehensive single-cell PCR 16S and 18S rRNA community analysis validated with mock communities, and estimation of sequencing bias against 18S. Environmental Microbiology, 2021, 23, 3240-3250.	1.8	35
167	Evaluating and Improving Small Subunit rRNA PCR Primer Coverage for Bacteria, Archaea, and Eukaryotes Using Metagenomes from Global Ocean Surveys. MSystems, 2021, 6, e0056521.	1.7	35
168	Distribution of Extracellular Flavins in a Coastal Marine Basin and Their Relationship to Redox Gradients and Microbial Community Members. Environmental Science & Technology, 2018, 52, 12265-12274.	4.6	34
169	Growth efficiencies of freshwater bacterioplankton. Microbial Ecology, 1992, 24, 145-60.	1.4	31
170	Microbiological water quality at non-human influenced reference beaches in southern California during wet weather. Marine Pollution Bulletin, 2010, 60, 500-508.	2.3	30
171	Community structure and function in prokaryotic marine plankton. Antonie Van Leeuwenhoek, 2002, 81, 521-527.	0.7	28
172	The Vertical Distribution and Diversity of Marine Bacteriophage at a Station off Southern California. Microbial Ecology, 2003, 45, 399-410.	1.4	28
173	Optimizing <i>de novo</i> genome assembly from PCR-amplified metagenomes. PeerJ, 2019, 7, e6902.	0.9	28
174	Does adenine incorporation into nucleic acids measure total microbial production?1. Limnology and Oceanography, 1986, 31, 627-636.	1.6	27
175	Viral and bacterial assemblage covariance in oligotrophic waters of the West Florida Shelf (Gulf of Mexico). <i>Journal of Plankton Research</i> , 2014, 36, 1073-1084.	0.4	27
176	Diversity of virus-like agents killing <i>Microcystis aeruginosa</i> in a hyper-eutrophic pond. Journal of Plankton Research, 2006, 28, 407-412.	0.8	26
177	Planktonic food web structure at a coastal time-series site: I. Partitioning of microbial abundances and carbon biomass. Deep-Sea Research Part I: Oceanographic Research Papers, 2017, 121, 14-29.	0.6	25
178	Vertical and Seasonal Patterns Control Bacterioplankton Communities at Two Horizontally Coherent Coastal Upwelling Sites off Galicia (NW Spain). Microbial Ecology, 2018, 76, 866-884.	1.4	25
179	Marine alga <i>Platymonas</i> sp. accumulates silicon without apparent requirement. Nature, 1978, 272, 244-246.	13.7	24
180	Characterization of Lysogens in Bacterioplankton Assemblages of the Southern California Borderland. Microbial Ecology, 2007, 53, 631-638.	1.4	24

#	ARTICLE	IF	CITATIONS
181	Influence of Light on Particulate Organic Matter Utilization by Attached and Free-Living Marine Bacteria. <i>Frontiers in Microbiology</i> , 2019, 10, 1204.	1.5	24
182	Loss rate of an oligotrophic bacterial assemblage as measured by H-thymidine and PO ₄ (4): good agreement and near-balance with production. <i>Aquatic Microbial Ecology</i> , 1996, 10, 29-36.	0.9	23
183	Mesoscale and seasonal variability of heterotrophic nanoflagellate abundance in an estuarine outflow plume. <i>Marine Ecology - Progress Series</i> , 1990, 61, 207-213.	0.9	22
184	Proteorhodopsins dominate the expression of phototrophic mechanisms in seasonal and dynamic marine picoplankton communities. <i>PeerJ</i> , 2018, 6, e5798.	0.9	22
185	Influence of Amazon and Orinoco offshore surface water plumes on oligotrophic bacterioplankton diversity in the west tropical Atlantic. <i>Aquatic Microbial Ecology</i> , 2006, 43, 11-22.	0.9	21
186	Contrasting diversity patterns of prokaryotes and protists over time and depth at the San-Pedro Ocean Time series. <i>ISME Communications</i> , 2022, 2, .	1.7	21
187	Gyrotaxis as a new mechanism for generating spatial heterogeneity and migration in microplankton. <i>Limnology and Oceanography</i> , 1990, 35, 123-130.	1.6	20
188	A dynamic programming algorithm for binning microbial community profiles. <i>Bioinformatics</i> , 2006, 22, 1508-1514.	1.8	18
189	The Earth Microbiome Project: The Meeting Report for the 1st International Earth Microbiome Project Conference, Shenzhen, China, June 13th-15th 2011. <i>Standards in Genomic Sciences</i> , 2011, 5, 243-247.	1.5	18
190	Assessment of metagenomic assemblers based on hybrid reads of real and simulated metagenomic sequences. <i>Briefings in Bioinformatics</i> , 2020, 21, 777-790.	3.2	18
191	Adaptations of bacteria to marine subsurface waters studied by temperature response. <i>Marine Ecology - Progress Series</i> , 1983, 13, 95-98.	0.9	18
192	Metagenomics and its connection to microbial community organization. <i>F1000 Biology Reports</i> , 2012, 4, 15.	4.0	16
193	Microbial tropicalization driven by a strengthening western ocean boundary current. <i>Global Change Biology</i> , 2020, 26, 5613-5629.	4.2	16
194	Metagenomics and Quantitative Stable Isotope Probing Offer Insights into Metabolism of Polycyclic Aromatic Hydrocarbon Degraders in Chronically Polluted Seawater. <i>MSystems</i> , 2021, 6, .	1.7	16
195	A comparative study of culture-independent, library-independent genotypic methods of fecal source tracking. <i>Journal of Water and Health</i> , 2003, 1, 181-94.	1.1	15
196	Statistical significance approximation in local trend analysis of high-throughput time-series data using the theory of Markov chains. <i>BMC Bioinformatics</i> , 2015, 16, 301.	1.2	13
197	Biodiversity Transcends Servicesâ€™ Response. <i>Science</i> , 2010, 330, 1745-1745.	6.0	11
198	A hydrocarbon-contaminated aquifer reveals a Piggyback-the-Persistent viral strategy. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	11

#	ARTICLE	IF	CITATIONS
199	Effects of four organic pollutants on the growth of natural marine bacterioplankton populations. <i>Marine Ecology - Progress Series</i> , 1988, 47, 185-194.	0.9	11
200	Nifty nanoplankton. <i>Nature</i> , 2001, 412, 593-594.	13.7	10
201	Phylogenetic Diversity of Diazotrophs along an Experimental Nutrient Gradient in Mangrove Sediments. <i>Journal of Marine Science and Engineering</i> , 2015, 3, 699-719.	1.2	10
202	Adenine and total microbial production: A reply. <i>Limnology and Oceanography</i> , 1986, 31, 1395-1400.	1.6	8
203	Relationships between biovolume and biomass of naturally derived marine bacterioplankton. <i>Deep Sea Research Part B Oceanographic Literature Review</i> , 1987, 34, 1069.	0.1	8
204	Heterotrophic Planktonic Microbes: Virus, Bacteria, Archaea, and Protozoa. , 2015, , 4.2.2-1-4.2.2-34.		8
205	Mineralization potentials of aromatic hydrocarbons by estuarine microorganisms: variations with season, location, and bacterioplankton production. <i>Marine Ecology - Progress Series</i> , 1988, 47, 97-102.	0.9	7
206	Viruses, Bacteria, and the Microbial Loop. , 2008, , 1097-1134.		6
207	Immune lag is a major cost of prokaryotic adaptive immunity during viral outbreaks. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20211555.	1.2	5
208	Composition and Biogeography of Planktonic Pro- and Eukaryotic Communities in the Atlantic Ocean: Primer Choice Matters. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
209	Enteroviruses detected by reverse transcriptase polymerase chain reaction from the coastal waters of Santa Monica Bay, California: low correlation to bacterial indicator levels. , 2001, , 175-184.		4
210	A non-tailed twist in the viral tale. <i>Nature</i> , 2018, 554, 38-39.	13.7	3
211	Oceans of Crenarchaeota: a Personal History Describing This Paradigm Shift. <i>Microbe Magazine</i> , 2011, 6, 531-537.	0.4	3
212	Phageâ€“bacterial contig association prediction with a convolutional neural network. <i>Bioinformatics</i> , 2022, 38, i45-i52.	1.8	3
213	The contribution of phytoplankton to ocean density gradients. <i>Deep-sea Research Part A, Oceanographic Research Papers</i> , 1989, 36, 1277-1282.	1.6	2
214	Computational methods for the analysis of tag sequences in metagenomics studies. <i>Frontiers in Bioscience - Scholar</i> , 2012, S4, 1333-1343.	0.8	2
215	Marine Bacterial, Archaeal, and Protistan Association Networks. , 2013, , 1-10.		2
216	Microbial Biogeography. , 2013, , 271-279.		1

#	ARTICLE	IF	CITATIONS
217	Towards enhanced and interpretable clustering/classification in integrative genomics. <i>Nucleic Acids Research</i> , 2017, 45, e169-e169.	6.5	1
218	Marine Planktonic Archaea Take Up Amino Acids. <i>Applied and Environmental Microbiology</i> , 2001, 67, 1023-1023.	1.4	1
219	Measuring Diversity. , 0, , 131-151.		1
220	Microbiological Water Quality at Non-Human Impacted Reference Beaches in Southern California During wet Weather. <i>Proceedings of the Water Environment Federation</i> , 2009, 2009, 1193-1212.	0.0	0