

Jed A Fuhrman

List of Publications by Year in descending order

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Version: 2024-02-01

220
papers

43,997
citations

3668

92
h-index

2750

198
g-index

246
all docs

246
docs citations

246
times ranked

31941
citing authors

#	ARTICLE	IF	CITATIONS
1	Phageâ€“bacterial contig association prediction with a convolutional neural network. <i>Bioinformatics</i> , 2022, 38, i45-i52.	1.8	3
2	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
3	Benchmarking microbial growth rate predictions from metagenomes. <i>ISME Journal</i> , 2021, 15, 183-195.	4.4	52
4	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
5	Comprehensive <scp>singleâ€“PCR 16S</scp> and <scp>18S rRNA</scp> community analysis validated with mock communities, and estimation of sequencing bias against <scp>18S</scp>. <i>Environmental Microbiology</i> , 2021, 23, 3240-3250.	1.8	35
6	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
7	Evaluating and Improving Small Subunit rRNA PCR Primer Coverage for Bacteria, Archaea, and Eukaryotes Using Metagenomes from Global Ocean Surveys. <i>MSystems</i> , 2021, 6, e0056521.	1.7	35
8	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
9	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
10	Long-term stability and Red Queen-like strain dynamics in marine viruses. <i>Nature Microbiology</i> , 2020, 5, 265-271.	5.9	62
11	Microbial tropicalization driven by a strengthening western ocean boundary current. <i>Global Change Biology</i> , 2020, 26, 5613-5629.	4.2	16
12	A network-based integrated framework for predicting virusâ€“prokaryote interactions. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa044.	1.5	69
13	Identifying viruses from metagenomic data using deep learning. <i>Quantitative Biology</i> , 2020, 8, 64-77.	0.3	302
14	Microbial rhodopsins are major contributors to the solar energy captured in the sea. <i>Science Advances</i> , 2019, 5, eaaw8855.	4.7	97
15	A hydrocarbon-contaminated aquifer reveals a Piggyback-the-Persistent viral strategy. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	11
16	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
17	Multiâ€“year dynamics of fineâ€“scale marine cyanobacterial populations are more strongly explained by phage interactions than abiotic, bottomâ€“up factors. <i>Environmental Microbiology</i> , 2019, 21, 2948-2963.	1.8	45
18	Dynamic marine viral infections and major contribution to photosynthetic processes shown by spatiotemporal picoplankton metatranscriptomes. <i>Nature Communications</i> , 2019, 10, 1169.	5.8	62

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19	Characterizing Chemoautotrophy and Heterotrophy in Marine Archaea and Bacteria With Single-Cell Multi-isotope NanoSIP. <i>Frontiers in Microbiology</i> , 2019, 10, 2682.	1.5	37
20	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
21	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
22	Optimizing <i>de novo</i> genome assembly from PCR-amplified metagenomes. <i>PeerJ</i> , 2019, 7, e6902.	0.9	28
23	Vertical and Seasonal Patterns Control Bacterioplankton Communities at Two Horizontally Coherent Coastal Upwelling Sites off Galicia (NW Spain). <i>Microbial Ecology</i> , 2018, 76, 866-884.	1.4	25
24	Mosaic patterns of B vitamin synthesis and utilization in a natural marine microbial community. <i>Environmental Microbiology</i> , 2018, 20, 2809-2823.	1.8	59
25	Short-term dynamics and interactions of marine protist communities during the spring–summer transition. <i>ISME Journal</i> , 2018, 12, 1907-1917.	4.4	84
26	Distribution of Extracellular Flavins in a Coastal Marine Basin and Their Relationship to Redox Gradients and Microbial Community Members. <i>Environmental Science & Technology</i> , 2018, 52, 12265-12274.	4.6	34
27	Taxon Disappearance from Microbiome Analysis Reinforces the Value of Mock Communities as a Standard in Every Sequencing Run. <i>MSystems</i> , 2018, 3, .	1.7	62
28	A non-tailed twist in the viral tale. <i>Nature</i> , 2018, 554, 38-39.	13.7	3
29	Dynamics and interactions of highly resolved marine plankton via automated high-frequency sampling. <i>ISME Journal</i> , 2018, 12, 2417-2432.	4.4	66
30	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
31	Proteorhodopsins dominate the expression of phototrophic mechanisms in seasonal and dynamic marine picoplankton communities. <i>PeerJ</i> , 2018, 6, e5798.	0.9	22
32	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
33	Planktonic food web structure at a coastal time-series site: I. Partitioning of microbial abundances and carbon biomass. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2017, 121, 14-29.	0.6	25
34	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
35	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
36	CAFE: aCcelerated Alignment-FrEe sequence analysis. <i>Nucleic Acids Research</i> , 2017, 45, W554-W559.	6.5	59

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37	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
38	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
39	Prediction of virus-host infectious association by supervised learning methods. <i>BMC Bioinformatics</i> , 2017, 18, 60.	1.2	38
40	Towards enhanced and interpretable clustering/classification in integrative genomics. <i>Nucleic Acids Research</i> , 2017, 45, e169-e169.	6.5	1
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	VirFinder: a novel k-mer based tool for identifying viral sequences from assembled metagenomic data. <i>Microbiome</i> , 2017, 5, 69.	4.9	433
43	Every base matters: assessing small subunit rRNA 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
44	Re-examination of the relationship between marine virus and microbial cell abundances. <i>Nature Microbiology</i> , 2016, 1, 15024.	5.9	264
45	Pronounced daily succession of phytoplankton, archaea and bacteria following a spring bloom. <i>Nature Microbiology</i> , 2016, 1, 16005.	5.9	384
46	Dilution reveals how viral lysis and grazing shape microbial communities. <i>Limnology and Oceanography</i> , 2016, 61, 889-905.	1.6	39
47	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
48	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
49	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016, 10, 1669-1681.	4.4	593
50	Proteorhodopsin light-enhanced growth linked to vitamin-B1 acquisition in marine Flavobacteria. <i>ISME Journal</i> , 2016, 10, 1102-1112.	4.4	58
51	Heterotrophic Planktonic Microbes: Virus, Bacteria, Archaea, and Protozoa. , 2015, , 4.2.2-1-4.2.2-34.		8
52	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
53	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
54	Cross-depth analysis of marine bacterial networks suggests downward propagation of temporal changes. <i>ISME Journal</i> , 2015, 9, 2573-2586.	4.4	105

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55	Marine microbial community dynamics and their ecological interpretation. <i>Nature Reviews Microbiology</i> , 2015, 13, 133-146.	13.6	681
56	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
57	The ocean sampling day consortium. <i>GigaScience</i> , 2015, 4, 27.	3.3	185
58	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
59	The founding charter of the Genomic Observatories Network. <i>GigaScience</i> , 2014, 3, 2.	3.3	51
60	Top-down controls on bacterial community structure: microbial network analysis of bacteria, T4-like viruses and protists. <i>ISME Journal</i> , 2014, 8, 816-829.	4.4	300
61	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
62	Beta diversity of marine bacteria depends on temporal scale. <i>Ecology</i> , 2013, 94, 1898-1904.	1.5	75
63	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
64	Short-term observations of marine bacterial and viral communities: patterns, connections and resilience. <i>ISME Journal</i> , 2013, 7, 1274-1285.	4.4	144
65	Macroecological patterns of marine bacteria on a global scale. <i>Journal of Biogeography</i> , 2013, 40, 800-811.	1.4	53
66	<i>Microbial Biogeography</i> . , 2013, , 271-279.		1
67	Efficient statistical significance approximation for local similarity analysis of high-throughput time series data. <i>Bioinformatics</i> , 2013, 29, 230-237.	1.8	137
68	Strong Seasonality and Interannual Recurrence in Marine Myovirus Communities. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6253-6259.	1.4	37
69	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
70	<i>Marine Bacterial, Archaeal, and Protistan Association Networks</i> . , 2013, , 1-10.		2
71	Global biogeography of SAR11 marine bacteria. <i>Molecular Systems Biology</i> , 2012, 8, 595.	3.2	215
72	Metagenomics and its connection to microbial community organization. <i>F1000 Biology Reports</i> , 2012, 4, 15.	4.0	16

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73	Defining seasonal marine microbial community dynamics. <i>ISME Journal</i> , 2012, 6, 298-308.	4.4	928
74	Computational methods for the analysis of tag sequences in metagenomics studies. <i>Frontiers in Bioscience - Scholar</i> , 2012, S4, 1333-1343.	0.8	2
75	Global distribution and diversity of marine <i>Verrucomicrobia</i> . <i>ISME Journal</i> , 2012, 6, 1499-1505.	4.4	196
76	Beyond biogeographic patterns: processes shaping the microbial landscape. <i>Nature Reviews Microbiology</i> , 2012, 10, 497-506.	13.6	1,299
77	Unlocking the potential of metagenomics through replicated experimental design. <i>Nature Biotechnology</i> , 2012, 30, 513-520.	9.4	250
78	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
79	Seasonality and monthly dynamics of marine myovirus communities. <i>Environmental Microbiology</i> , 2012, 14, 2171-2183.	1.8	82
80	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
81	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MlxS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	9.4	608
82	Global Patterns of Bacterial Beta-Diversity in Seafloor and Seawater Ecosystems. <i>PLoS ONE</i> , 2011, 6, e24570.	1.1	525
83	Accurate Genome Relative Abundance Estimation Based on Shotgun Metagenomic Reads. <i>PLoS ONE</i> , 2011, 6, e27992.	1.1	105
84	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
85	Marine viruses and global climate change. <i>FEMS Microbiology Reviews</i> , 2011, 35, 993-1034.	3.9	297
86	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
87	Marine bacterial, archaeal and protistan association networks reveal ecological linkages. <i>ISME Journal</i> , 2011, 5, 1414-1425.	4.4	560
88	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
89	Global declines in oceanic nitrification rates as a consequence of ocean acidification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 208-213.	3.3	316
90	Oceans of Crenarchaeota: a Personal History Describing This Paradigm Shift. <i>Microbe Magazine</i> , 2011, 6, 531-537.	0.4	3

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91	Microbiological water quality at non-human influenced reference beaches in southern California during wet weather. <i>Marine Pollution Bulletin</i> , 2010, 60, 500-508.	2.3	30
92	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
93	Biodiversity Transcends Services' Response. <i>Science</i> , 2010, 330, 1745-1745.	6.0	11
94	Ecosystem Services for 2020. <i>Science</i> , 2010, 330, 323-324.	6.0	178
95	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
96	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
97	Microbial community structure in the North Pacific ocean. <i>ISME Journal</i> , 2009, 3, 1374-1386.	4.4	224
98	Microbial community structure and its functional implications. <i>Nature</i> , 2009, 459, 193-199.	13.7	1,061
99	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
100	Proteorhodopsins: an array of physiological roles?. <i>Nature Reviews Microbiology</i> , 2008, 6, 488-494.	13.6	220
101	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
102	Community structure of marine bacterioplankton: patterns, networks, and relationships to function. <i>Aquatic Microbial Ecology</i> , 2008, 53, 69-81.	0.9	211
103	Viruses, Bacteria, and the Microbial Loop. , 2008, , 1097-1134.		6
104	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
105	A COMPARISON OF TAXON CO-OCCURRENCE PATTERNS FOR MACRO- AND MICROORGANISMS. <i>Ecology</i> , 2007, 88, 1345-1353.	1.5	223
106	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
107	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
108	Characterization of Lysogens in Bacterioplankton Assemblages of the Southern California Borderland. <i>Microbial Ecology</i> , 2007, 53, 631-638.	1.4	24

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109	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
110	Remarkable heterogeneity in meso- and bathypelagic bacterioplankton assemblage composition. <i>Limnology and Oceanography</i> , 2006, 51, 1274-1283.	1.6	84
111	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
112	Microbial biogeography: putting microorganisms on the map. <i>Nature Reviews Microbiology</i> , 2006, 4, 102-112.	13.6	2,434
113	Improved Strategy for Comparing Microbial Assemblage Fingerprints. <i>Microbial Ecology</i> , 2006, 51, 147-153.	1.4	87
114	Viral and bacterial assemblage covariance in oligotrophic waters of the West Florida Shelf (Gulf of Mexico). <i>Journal of Marine Research</i> , 2006, 64, 101-117.	0.4	27
115	A dynamic programming algorithm for binning microbial community profiles. <i>Bioinformatics</i> , 2006, 22, 1508-1514.	1.8	18
116	Diversity of virus-like agents killing <i>Microcystis aeruginosa</i> in a hyper-eutrophic pond. <i>Journal of Plankton Research</i> , 2006, 28, 407-412.	0.8	26
117	Local similarity analysis reveals unique associations among marine bacterioplankton species and environmental factors. <i>Bioinformatics</i> , 2006, 22, 2532-2538.	1.8	292
118	Annually reoccurring bacterial communities are predictable from ocean conditions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 13104-13109.	3.3	578
119	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
120	Spatial and vertical biogeography of coral reef sediment bacterial and diazotroph communities. <i>Marine Ecology - Progress Series</i> , 2006, 306, 79-86.	0.9	62
121	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
122	Structure of microbial communities in ethanol biofilters. <i>Chemical Engineering Journal</i> , 2005, 113, 135-143.	6.6	40
123	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
124	Whither or wither geomicrobiology in the era of 'community metagenomics'. <i>Nature Reviews Microbiology</i> , 2005, 3, 572-578.	13.6	59
125	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
126	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

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127	Impact of light on marine bacterioplankton community structure. <i>Aquatic Microbial Ecology</i> , 2005, 39, 235-245.	0.9	49
128	Marine bacterial microdiversity as revealed by internal transcribed spacer analysis. <i>Aquatic Microbial Ecology</i> , 2005, 41, 15-23.	0.9	123
129	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
130	Viral effects on bacterial community composition in marine plankton microcosms. <i>Aquatic Microbial Ecology</i> , 2004, 34, 117-127.	0.9	93
131	Evidence of Trichodesmium viral lysis and potential significance for biogeochemical cycling in the oligotrophic ocean. <i>Aquatic Microbial Ecology</i> , 2004, 36, 1-8.	0.9	76
132	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
133	The Vertical Distribution and Diversity of Marine Bacteriophage at a Station off Southern California. <i>Microbial Ecology</i> , 2003, 45, 399-410.	1.4	28
134	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
135	Genome sequences from the sea. <i>Nature</i> , 2003, 424, 1001-1002.	13.7	61
136	Viral Influence on Aquatic Bacterial Communities. <i>Biological Bulletin</i> , 2003, 204, 192-195.	0.7	88
137	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
138	<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
139	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
140	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
141	Prokaryotic and viral diversity patterns in marine plankton. <i>Ecological Research</i> , 2002, 17, 183-194.	0.7	38
142	Community structure and function in prokaryotic marine plankton. <i>Antonie Van Leeuwenhoek</i> , 2002, 81, 521-527.	0.7	28
143	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
144	Title is missing!. <i>Hydrobiologia</i> , 2001, 460, 175-184.	1.0	137

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145	Nifty nanoplankton. <i>Nature</i> , 2001, 412, 593-594.	13.7	10
146	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
147	Marine Planktonic Archaea Take Up Amino Acids. <i>Applied and Environmental Microbiology</i> , 2001, 67, 1023-1023.	1.4	1
148	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
149	Marine Planktonic Archaea Take Up Amino Acids. <i>Applied and Environmental Microbiology</i> , 2000, 66, 4829-4833.	1.4	313
150	Significance of Size and Nucleic Acid Content Heterogeneity as Measured by Flow Cytometry in Natural Planktonic Bacteria. <i>Applied and Environmental Microbiology</i> , 1999, 65, 4475-4483.	1.4	473
151	Marine viruses and their biogeochemical and ecological effects. <i>Nature</i> , 1999, 399, 541-548.	13.7	1,895
152	Breakdown and microbial uptake of marine viruses and other lysis products. <i>Aquatic Microbial Ecology</i> , 1999, 20, 1-11.	0.9	83
153	Combined Microautoradiography and ¹⁴ C-16S rRNA Probe Technique for Determination of Radioisotope Uptake by Specific Microbial Cell Types In Situ. <i>Applied and Environmental Microbiology</i> , 1999, 65, 1746-1752.	1.4	302
154	Effects of viral enrichment on the mortality and growth of heterotrophic bacterioplankton. <i>Aquatic Microbial Ecology</i> , 1999, 18, 1-13.	0.9	53
155	Title is missing!. <i>Aquatic Ecology</i> , 1998, 32, 3-15.	0.7	70
156	Microbial microdiversity. <i>Nature</i> , 1998, 393, 410-411.	13.7	137
157	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
158	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
159	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
160	Viruses and protists cause similar bacterial mortality in coastal seawater. <i>Limnology and Oceanography</i> , 1995, 40, 1236-1242.	1.6	397
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164	Viruses in Marine Planktonic Systems. <i>Oceanography</i> , 1993, 6, 51-63.	0.5	259
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166	Bacterioplankton Roles in Cycling of Organic Matter: The Microbial Food Web. , 1992, , 361-383.		167
167	Growth efficiencies of freshwater bacterioplankton. <i>Microbial Ecology</i> , 1992, 24, 145-60.	1.4	31
168	Novel major archaeobacterial group from marine plankton. <i>Nature</i> , 1992, 356, 148-149.	13.7	825
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180	Dissolved free amino acid cycling in an estuarine outflow plume. <i>Marine Ecology - Progress Series</i> , 1990, 66, 197-203.	0.9	64

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