

# Jed A Fuhrman

## List of Publications by Year in descending order

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Version: 2024-02-01

220  
papers

43,997  
citations

3159

92  
h-index

2385

198  
g-index

246  
all docs

246  
docs citations

246  
times ranked

28657  
citing authors

#	ARTICLE	IF	CITATIONS
1	Phageâ€“bacterial contig association prediction with a convolutional neural network. <i>Bioinformatics</i> , 2022, 38, i45-i52.	4.1	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, .	4.2	21
3	Benchmarking microbial growth rate predictions from metagenomes. <i>ISME Journal</i> , 2021, 15, 183-195.	9.8	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, .	7.1	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.	3.8	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, .	3.8	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.	3.8	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.	2.6	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.	6.5	18
10	Long-term stability and Red Queen-like strain dynamics in marine viruses. <i>Nature Microbiology</i> , 2020, 5, 265-271.	13.3	62
11	Microbial tropicalization driven by a strengthening western ocean boundary current. <i>Global Change Biology</i> , 2020, 26, 5613-5629.	9.5	16
12	A network-based integrated framework for predicting virusâ€“prokaryote interactions. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa044.	3.2	69
13	Identifying viruses from metagenomic data using deep learning. <i>Quantitative Biology</i> , 2020, 8, 64-77.	0.5	302
14	Microbial rhodopsins are major contributors to the solar energy captured in the sea. <i>Science Advances</i> , 2019, 5, eaaw8855.	10.3	97
15	A hydrocarbon-contaminated aquifer reveals a Piggyback-the-Persistent viral strategy. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	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.	3.5	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.	3.8	45
18	Dynamic marine viral infections and major contribution to photosynthetic processes shown by spatiotemporal picoplankton metatranscriptomes. <i>Nature Communications</i> , 2019, 10, 1169.	12.8	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.	3.5	37
20	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	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.	9.8	103
22	Optimizing <i>de novo</i> genome assembly from PCR-amplified metagenomes. <i>PeerJ</i> , 2019, 7, e6902.	2.0	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.	2.8	25
24	Mosaic patterns of B-vitamin synthesis and utilization in a natural marine microbial community. <i>Environmental Microbiology</i> , 2018, 20, 2809-2823.	3.8	59
25	Short-term dynamics and interactions of marine protist communities during the spring-summer transition. <i>ISME Journal</i> , 2018, 12, 1907-1917.	9.8	84
26	Distribution of Extracellular Flavins in a Coastal Marine Basin and Their Relationship to Redox Gradients and Microbial Community Members. <i>Environmental Science &amp; Technology</i> , 2018, 52, 12265-12274.	10.0	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, .	3.8	62
28	A non-tailed twist in the viral tale. <i>Nature</i> , 2018, 554, 38-39.	27.8	3
29	Dynamics and interactions of highly resolved marine plankton via automated high-frequency sampling. <i>ISME Journal</i> , 2018, 12, 2417-2432.	9.8	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.	5.3	41
31	Proteorhodopsins dominate the expression of phototrophic mechanisms in seasonal and dynamic marine picoplankton communities. <i>PeerJ</i> , 2018, 6, e5798.	2.0	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.	4.1	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.	1.4	25
34	Ecological dynamics and co-occurrence among marine phytoplankton, bacteria and myoviruses shows microdiversity matters. <i>ISME Journal</i> , 2017, 11, 1614-1629.	9.8	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.	3.8	71
36	CAFE: aCcelerated Alignment-FrEe sequence analysis. <i>Nucleic Acids Research</i> , 2017, 45, W554-W559.	14.5	59

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37	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	27.8	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.	9.8	80
39	Prediction of virus-host infectious association by supervised learning methods. <i>BMC Bioinformatics</i> , 2017, 18, 60.	2.6	38
40	Towards enhanced and interpretable clustering/classification in integrative genomics. <i>Nucleic Acids Research</i> , 2017, 45, e169-e169.	14.5	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.	14.5	245
42	VirFinder: a novel k-mer based tool for identifying viral sequences from assembled metagenomic data. <i>Microbiome</i> , 2017, 5, 69.	11.1	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.	3.8	2,618
44	Re-examination of the relationship between marine virus and microbial cell abundances. <i>Nature Microbiology</i> , 2016, 1, 15024.	13.3	264
45	Pronounced daily succession of phytoplankton, archaea and bacteria following a spring bloom. <i>Nature Microbiology</i> , 2016, 1, 16005.	13.3	384
46	Dilution reveals how viral lysis and grazing shape microbial communities. <i>Limnology and Oceanography</i> , 2016, 61, 889-905.	3.1	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.	8.6	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, .	3.8	1,364
49	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016, 10, 1669-1681.	9.8	593
50	Proteorhodopsin light-enhanced growth linked to vitamin-B1 acquisition in marine Flavobacteria. <i>ISME Journal</i> , 2016, 10, 1102-1112.	9.8	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.	2.6	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.	2.6	10
54	Cross-depth analysis of marine bacterial networks suggests downward propagation of temporal changes. <i>ISME Journal</i> , 2015, 9, 2573-2586.	9.8	105

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55	Marine microbial community dynamics and their ecological interpretation. Nature Reviews Microbiology, 2015, 13, 133-146.	28.6	681
56	A multitrophic model to quantify the effects of marine viruses on microbial food webs and ecosystem processes. ISME Journal, 2015, 9, 1352-1364.	9.8	223
57	The ocean sampling day consortium. GigaScience, 2015, 4, 27.	6.4	185
58	Seasonal and interannual variability of the marine bacterioplankton community throughout the water column over ten years. ISME Journal, 2015, 9, 563-580.	9.8	219
59	The founding charter of the Genomic Observatories Network. GigaScience, 2014, 3, 2.	6.4	51
60	Top-down controls on bacterial community structure: microbial network analysis of bacteria, T4-like viruses and protists. ISME Journal, 2014, 8, 816-829.	9.8	300
61	Temporal variability and coherence of euphotic zone bacterial communities over a decade in the Southern California Bight. ISME Journal, 2013, 7, 2259-2273.	9.8	162
62	Beta diversity of marine bacteria depends on temporal scale. Ecology, 2013, 94, 1898-1904.	3.2	75
63	Performance of viruses and bacteriophages for fecal source determination in a multi-laboratory, comparative study. Water Research, 2013, 47, 6929-6943.	11.3	75
64	Short-term observations of marine bacterial and viral communities: patterns, connections and resilience. ISME Journal, 2013, 7, 1274-1285.	9.8	144
65	Macroecological patterns of marine bacteria on a global scale. Journal of Biogeography, 2013, 40, 800-811.	3.0	53
66	Microbial Biogeography. , 2013, , 271-279.		1
67	Efficient statistical significance approximation for local similarity analysis of high-throughput time series data. Bioinformatics, 2013, 29, 230-237.	4.1	137
68	Strong Seasonality and Interannual Recurrence in Marine Myovirus Communities. Applied and Environmental Microbiology, 2013, 79, 6253-6259.	3.1	37
69	Genomics and Physiology of a Marine Flavobacterium Encoding a Proteorhodopsin and a Xanthorhodopsin-Like Protein. PLoS ONE, 2013, 8, e57487.	2.5	42
70	Marine Bacterial, Archaeal, and Protistan Association Networks. , 2013, , 1-10.		2
71	Global biogeography of SAR11 marine bacteria. Molecular Systems Biology, 2012, 8, 595.	7.2	215
72	Metagenomics and its connection to microbial community organization. F1000 Biology Reports, 2012, 4, 15.	4.0	16

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73	Defining seasonal marine microbial community dynamics. ISME Journal, 2012, 6, 298-308.	9.8	928
74	Computational methods for the analysis of tag sequences in metagenomics studies. Frontiers in Bioscience - Scholar, 2012, S4, 1333-1343.	2.1	2
75	Global distribution and diversity of marine <i>Verrucomicrobia</i> . ISME Journal, 2012, 6, 1499-1505.	9.8	196
76	Beyond biogeographic patterns: processes shaping the microbial landscape. Nature Reviews Microbiology, 2012, 10, 497-506.	28.6	1,299
77	Unlocking the potential of metagenomics through replicated experimental design. Nature Biotechnology, 2012, 30, 513-520.	17.5	250
78	Long-term nitrogen and phosphorus fertilization effects on $N_2$ fixation rates and <i>nifH</i> gene community patterns in mangrove sediments. Marine Ecology, 2012, 33, 117-127.	1.1	41
79	Seasonality and monthly dynamics of marine myovirus communities. Environmental Microbiology, 2012, 14, 2171-2183.	3.8	82
80	Ecosystem services, targets, and indicators for the conservation and sustainable use of biodiversity. Frontiers in Ecology and the Environment, 2011, 9, 512-520.	4.0	91
81	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MlxS) specifications. Nature Biotechnology, 2011, 29, 415-420.	17.5	608
82	Global Patterns of Bacterial Beta-Diversity in Seafloor and Seawater Ecosystems. PLoS ONE, 2011, 6, e24570.	2.5	525
83	Accurate Genome Relative Abundance Estimation Based on Shotgun Metagenomic Reads. PLoS ONE, 2011, 6, e27992.	2.5	105
84	The Earth Microbiome Project: The Meeting Report for the 1st International Earth Microbiome Project Conference, Shenzhen, China, June 13th-15th 2011. Standards in Genomic Sciences, 2011, 5, 243-247.	1.5	18
85	Marine viruses and global climate change. FEMS Microbiology Reviews, 2011, 35, 993-1034.	8.6	297
86	Co-occurrence patterns for abundant marine archaeal and bacterial lineages in the deep chlorophyll maximum of coastal California. ISME Journal, 2011, 5, 1077-1085.	9.8	85
87	Marine bacterial, archaeal and protistan association networks reveal ecological linkages. ISME Journal, 2011, 5, 1414-1425.	9.8	560
88	Extended local similarity analysis (eLSA) of microbial community and other time series data with replicates. BMC Systems Biology, 2011, 5, S15.	3.0	223
89	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.	7.1	316
90	Oceans of Crenarchaeota: a Personal History Describing This Paradigm Shift. Microbe Magazine, 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. Marine Pollution Bulletin, 2010, 60, 500-508.	5.0	30
92	Population ecology of nitrifying <i>Archaea</i> and <i>Bacteria</i> in the Southern California Bight. Environmental Microbiology, 2010, 12, 1282-1292.	3.8	96
93	Biodiversity Transcends Services' Response. Science, 2010, 330, 1745-1745.	12.6	11
94	Ecosystem Services for 2020. Science, 2010, 330, 323-324.	12.6	178
95	Burrowing deeper into benthic nitrogen cycling: the impact of bioturbation on nitrogen fixation coupled to sulfate reduction. Marine Ecology - Progress Series, 2010, 409, 1-15.	1.9	157
96	Time- and sediment depth-related variations in bacterial diversity and community structure in subtidal sands. ISME Journal, 2009, 3, 780-791.	9.8	159
97	Microbial community structure in the North Pacific ocean. ISME Journal, 2009, 3, 1374-1386.	9.8	224
98	Microbial community structure and its functional implications. Nature, 2009, 459, 193-199.	27.8	1,061
99	Microbiological Water Quality at Non-Human Impacted Reference Beaches in Southern California During wet Weather. Proceedings of the Water Environment Federation, 2009, 2009, 1193-1212.	0.0	0
100	Proteorhodopsins: an array of physiological roles?. Nature Reviews Microbiology, 2008, 6, 488-494.	28.6	220
101	A latitudinal diversity gradient in planktonic marine bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7774-7778.	7.1	599
102	Community structure of marine bacterioplankton: patterns, networks, and relationships to function. Aquatic Microbial Ecology, 2008, 53, 69-81.	1.8	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. Deep-Sea Research Part I: Oceanographic Research Papers, 2007, 54, 811-830.	1.4	47
105	A COMPARISON OF TAXON CO-OCCURRENCE PATTERNS FOR MACRO- AND MICROORGANISMS. Ecology, 2007, 88, 1345-1353.	3.2	223
106	Virus and prokaryote enumeration from planktonic aquatic environments by epifluorescence microscopy with SYBR Green I. Nature Protocols, 2007, 2, 269-276.	12.0	272
107	Diversity and biogeography of bacterial assemblages in surface sediments across the San Pedro Basin, Southern California Borderlands. Environmental Microbiology, 2007, 9, 923-933.	3.8	79
108	Characterization of Lysogens in Bacterioplankton Assemblages of the Southern California Borderland. Microbial Ecology, 2007, 53, 631-638.	2.8	24

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109	Multitiered Approach Using Quantitative PCR To Track Sources of Fecal Pollution Affecting Santa Monica Bay, California. Applied and Environmental Microbiology, 2006, 72, 1604-1612.	3.1	145
110	Remarkable heterogeneity in meso- and bathypelagic bacterioplankton assemblage composition. Limnology and Oceanography, 2006, 51, 1274-1283.	3.1	84
111	Viral impacts upon marine bacterioplankton assemblage structure. Journal of the Marine Biological Association of the United Kingdom, 2006, 86, 577-589.	0.8	45
112	Microbial biogeography: putting microorganisms on the map. Nature Reviews Microbiology, 2006, 4, 102-112.	28.6	2,434
113	Improved Strategy for Comparing Microbial Assemblage Fingerprints. Microbial Ecology, 2006, 51, 147-153.	2.8	87
114	Viral and bacterial assemblage covariance in oligotrophic waters of the West Florida Shelf (Gulf of Mexico). Environmental Microbiology, 2006, 8, 107-117.	0.8	27
115	A dynamic programming algorithm for binning microbial community profiles. Bioinformatics, 2006, 22, 1508-1514.	4.1	18
116	Diversity of virus-like agents killing Microcystis aeruginosa in a hyper-eutrophic pond. Journal of Plankton Research, 2006, 28, 407-412.	1.8	26
117	Local similarity analysis reveals unique associations among marine bacterioplankton species and environmental factors. Bioinformatics, 2006, 22, 2532-2538.	4.1	292
118	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.	7.1	578
119	Influence of Amazon and Orinoco offshore surface water plumes on oligotrophic bacterioplankton diversity in the west tropical Atlantic. Aquatic Microbial Ecology, 2006, 43, 11-22.	1.8	21
120	Spatial and vertical biogeography of coral reef sediment bacterial and diazotroph communities. Marine Ecology - Progress Series, 2006, 306, 79-86.	1.9	62
121	Temporal and spatial scales of variation in bacterioplankton assemblages of oligotrophic surface waters. Marine Ecology - Progress Series, 2006, 311, 67-77.	1.9	104
122	Structure of microbial communities in ethanol biofilters. Chemical Engineering Journal, 2005, 113, 135-143.	12.7	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. Environmental Microbiology, 2005, 7, 1466-1479.	3.8	230
124	Whither or wither geomicrobiology in the era of 'community metagenomics'. Nature Reviews Microbiology, 2005, 3, 572-578.	28.6	59
125	Rapid Detection of Enteroviruses in Small Volumes of Natural Waters by Real-Time Quantitative Reverse Transcriptase PCR. Applied and Environmental Microbiology, 2005, 71, 4523-4530.	3.1	93
126	Wide-ranging abundances of aerobic anoxygenic phototrophic bacteria in the world ocean revealed by epifluorescence microscopy and quantitative PCR. Limnology and Oceanography, 2005, 50, 620-628.	3.1	107



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127	Impact of light on marine bacterioplankton community structure. <i>Aquatic Microbial Ecology</i> , 2005, 39, 235-245.	1.8	49
128	Marine bacterial microdiversity as revealed by internal transcribed spacer analysis. <i>Aquatic Microbial Ecology</i> , 2005, 41, 15-23.	1.8	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.	3.1	210
130	Viral effects on bacterial community composition in marine plankton microcosms. <i>Aquatic Microbial Ecology</i> , 2004, 34, 117-127.	1.8	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.	1.8	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.	2.8	96
133	The Vertical Distribution and Diversity of Marine Bacteriophage at a Station off Southern California. <i>Microbial Ecology</i> , 2003, 45, 399-410.	2.8	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.	2.8	104
135	Genome sequences from the sea. <i>Nature</i> , 2003, 424, 1001-1002.	27.8	61
136	Viral Influence on Aquatic Bacterial Communities. <i>Biological Bulletin</i> , 2003, 204, 192-195.	1.8	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 &amp; Technology</i> , 2003, 37, 673-680.	10.0	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.	1.7	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.	2.6	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.	2.6	15
141	Prokaryotic and viral diversity patterns in marine plankton. <i>Ecological Research</i> , 2002, 17, 183-194.	1.5	38
142	Community structure and function in prokaryotic marine plankton. <i>Antonie Van Leeuwenhoek</i> , 2002, 81, 521-527.	1.7	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.	3.1	167
144	Title is missing!. <i>Hydrobiologia</i> , 2001, 460, 175-184.	2.0	137

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145	Nifty nanoplankton. Nature, 2001, 412, 593-594.	27.8	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. Applied and Environmental Microbiology, 2001, 67, 1023-1023.	3.1	1
148	Rapid Virus Production and Removal as Measured with Fluorescently Labeled Viruses as Tracers. Applied and Environmental Microbiology, 2000, 66, 3790-3797.	3.1	112
149	Marine Planktonic Archaea Take Up Amino Acids. Applied and Environmental Microbiology, 2000, 66, 4829-4833.	3.1	313
150	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.	3.1	473
151	Marine viruses and their biogeochemical and ecological effects. Nature, 1999, 399, 541-548.	27.8	1,895
152	Breakdown and microbial uptake of marine viruses and other lysis products. Aquatic Microbial Ecology, 1999, 20, 1-11.	1.8	83
153	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.	3.1	302
154	Effects of viral enrichment on the mortality and growth of heterotrophic bacterioplankton. Aquatic Microbial Ecology, 1999, 18, 1-13.	1.8	53
155	Title is missing!. Aquatic Ecology, 1998, 32, 3-15.	1.5	70
156	Microbial microdiversity. Nature, 1998, 393, 410-411.	27.8	137
157	Use of SYBR Green I for rapid epifluorescence counts of marine viruses and bacteria. Aquatic Microbial Ecology, 1998, 14, 113-118.	1.8	906
158	Widespread Archaea and novel Bacteria from the deep sea as shown by 16S rRNA gene sequences. Marine Ecology - Progress Series, 1997, 150, 275-285.	1.9	222
159	Loss rate of an oligotrophic bacterial assemblage as measured by H-thymidine and PO <sub>4</sub> (4): good agreement and near-balance with production. Aquatic Microbial Ecology, 1996, 10, 29-36.	1.8	23
160	Viruses and protists cause similar bacterial mortality in coastal seawater. Limnology and Oceanography, 1995, 40, 1236-1242.	3.1	397
161	Imperfect retention of natural bacterioplankton cells by glass fiber filters. Marine Ecology - Progress Series, 1995, 119, 285-290.	1.9	64
162	Characterization of marine prokaryotic communities via DNA and RNA. Microbial Ecology, 1994, 28, 133-145.	2.8	76

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163	Bacterial viruses in coastal seawater: lytic rather than lysogenic production. Marine Ecology - Progress Series, 1994, 114, 35-45.	1.9	136
164	Viruses in Marine Planktonic Systems. Oceanography, 1993, 6, 51-63.	1.0	259
165	Phylogenetic diversity of subsurface marine microbial communities from the Atlantic and Pacific Oceans. Applied and Environmental Microbiology, 1993, 59, 1294-1302.	3.1	466
166	Bacterioplankton Roles in Cycling of Organic Matter: The Microbial Food Web. , 1992, , 361-383.		167
167	Growth efficiencies of freshwater bacterioplankton. Microbial Ecology, 1992, 24, 145-60.	2.8	31
168	Novel major archaeobacterial group from marine plankton. Nature, 1992, 356, 148-149.	27.8	825
169	Mortality of marine bacteria in response to enrichments of the virus size fraction from seawater. Marine Ecology - Progress Series, 1992, 87, 283-293.	1.9	90
170	Spatial and temporal variation of natural bacterioplankton assemblages studied by total genomic DNA cross-hybridization. Limnology and Oceanography, 1991, 36, 1277-1287.	3.1	87
171	Dependent coupling of inorganic and organic nitrogen uptake and regeneration in the plume of the Chesapeake Bay estuary and its regulation by large heterotrophs. Limnology and Oceanography, 1991, 36, 895-909.	3.1	131
172	Possible biogeochemical consequences of ocean fertilization. Limnology and Oceanography, 1991, 36, 1951-1959.	3.1	75
173	Roles of viral infection in organic particle flux. Marine Ecology - Progress Series, 1991, 69, 133-142.	1.9	158
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