

Curtis Suttle

List of Publications by Year in descending order

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186
papers

21,443
citations

15504

65
h-index

11052

137
g-index

215
all docs

215
docs citations

215
times ranked

13907
citing authors

#	ARTICLE	IF	CITATIONS
1	Marine viruses are major players in the global ecosystem. <i>Nature Reviews Microbiology</i> , 2007, 5, 801-812.	28.6	2,602
2	Viruses in the sea. <i>Nature</i> , 2005, 437, 356-361.	27.8	1,906
3	Viruses and Nutrient Cycles in the Sea. <i>BioScience</i> , 1999, 49, 781-788.	4.9	996
4	The Marine Viromes of Four Oceanic Regions. <i>PLoS Biology</i> , 2006, 4, e368.	5.6	867
5	Virus taxonomy in the age of metagenomics. <i>Nature Reviews Microbiology</i> , 2017, 15, 161-168.	28.6	590
6	Infection of phytoplankton by viruses and reduction of primary productivity. <i>Nature</i> , 1990, 347, 467-469.	27.8	472
7	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
8	Mechanisms and Rates of Decay of Marine Viruses in Seawater. <i>Applied and Environmental Microbiology</i> , 1992, 58, 3721-3729.	3.1	413
9	The significance of viruses to mortality in aquatic microbial communities. <i>Microbial Ecology</i> , 1994, 28, 237-243.	2.8	379
10	Metagenomic Analysis of Coastal RNA Virus Communities. <i>Science</i> , 2006, 312, 1795-1798.	12.6	334
11	Giant virus with a remarkable complement of genes infects marine zooplankton. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19508-19513.	7.1	317
12	Dynamics and Distribution of Cyanophages and Their Effect on Marine <i>Synechococcus</i> spp. <i>Applied and Environmental Microbiology</i> , 1994, 60, 3167-3174.	3.1	310
13	Marine viruses and global climate change. <i>FEMS Microbiology Reviews</i> , 2011, 35, 993-1034.	8.6	297
14	Re-examination of the relationship between marine virus and microbial cell abundances. <i>Nature Microbiology</i> , 2016, 1, 15024.	13.3	264
15	Viruses in Marine Planktonic Systems. <i>Oceanography</i> , 1993, 6, 51-63.	1.0	259
16	A Virophage at the Origin of Large DNA Transposons. <i>Science</i> , 2011, 332, 231-234.	12.6	258
17	Grazing by marine nanoflagellates on viruses and virus-sized particles: ingestion and digestion. <i>Marine Ecology - Progress Series</i> , 1993, 94, 1-10.	1.9	239
18	Global-scale processes with a nanoscale drive: the role of marine viruses. <i>ISME Journal</i> , 2008, 2, 575-578.	9.8	226

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19	Exploring the Vast Diversity of Marine Viruses. <i>Oceanography</i> , 2007, 20, 135-139.	1.0	224
20	Marine T4-type bacteriophages, a ubiquitous component of the dark matter of the biosphere. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12471-12476.	7.1	223
21	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.	9.8	223
22	High diversity of unknown picorna-like viruses in the sea. <i>Nature</i> , 2003, 424, 1054-1057.	27.8	213
23	Nearly Identical Bacteriophage Structural Gene Sequences Are Widely Distributed in both Marine and Freshwater Environments. <i>Applied and Environmental Microbiology</i> , 2005, 71, 480-486.	3.1	206
24	A Dilution Technique For The Direct Measurement Of Viral Production: A Comparison In Stratified And Tidally Mixed Coastal Waters. <i>Microbial Ecology</i> , 2002, 43, 168-173.	2.8	205
25	Direct counts of viruses in natural waters and laboratory cultures by epifluorescence microscopy. <i>Limnology and Oceanography</i> , 1995, 40, 1050-1055.	3.1	192
26	Use of Ultrafiltration To Isolate Viruses from Seawater Which Are Pathogens of Marine Phytoplankton. <i>Applied and Environmental Microbiology</i> , 1991, 57, 721-726.	3.1	189
27	Deposition rates of viruses and bacteria above the atmospheric boundary layer. <i>ISME Journal</i> , 2018, 12, 1154-1162.	9.8	178
28	The virosphere, diversity, and genetic exchange within phage communities. <i>Current Opinion in Microbiology</i> , 2005, 8, 444-450.	5.1	172
29	Accurate Estimation of Viral Abundance by Epifluorescence Microscopy. <i>Applied and Environmental Microbiology</i> , 2004, 70, 3862-3867.	3.1	168
30	Previously unknown and highly divergent ssDNA viruses populate the oceans. <i>ISME Journal</i> , 2013, 7, 2169-2177.	9.8	160
31	The role of sunlight in the removal and repair of viruses in the sea. <i>Limnology and Oceanography</i> , 1998, 43, 586-592.	3.1	152
32	Dynamics of lytic virus infecting the photosynthetic marine picoflagellate <i>Micromonas pusilla</i> . <i>Limnology and Oceanography</i> , 1995, 40, 730-739.	3.1	149
33	Sequence Analysis of Marine Virus Communities Reveals that Groups of Related Algal Viruses Are Widely Distributed in Nature. <i>Applied and Environmental Microbiology</i> , 2002, 68, 1290-1296.	3.1	135
34	Lysogeny and prophage induction in coastal and offshore bacterial communities. <i>Aquatic Microbial Ecology</i> , 1999, 18, 217-225.	1.8	130
35	Ammonium and phosphate uptake rates, N: P supply ratios, and evidence for N and P limitation in some oligotrophic lakes. <i>Limnology and Oceanography</i> , 1988, 33, 186-202.	3.1	128
36	To kill or not to kill: The balance between lytic and lysogenic viral infection is driven by trophic status. <i>Limnology and Oceanography</i> , 2013, 58, 465-474.	3.1	122

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37	Evolutionary Relationships among Large Double-Stranded DNA Viruses That Infect Microalgae and Other Organisms as Inferred from DNA Polymerase Genes. <i>Virology</i> , 1996, 219, 170-178.	2.4	115
38	The Effect of Cyanophages on the Mortality of <i>Synechococcus</i> spp. and Selection for UV Resistant Viral Communities. <i>Microbial Ecology</i> , 1998, 36, 281-292.	2.8	112
39	CHARACTERIZATION OF HaRNAV, A SINGLE-STRANDED RNA VIRUS CAUSING LYSIS OF <i>HETEROSIGMA AKASHIWO</i> (RAPHIDOPHYCEAE). <i>Journal of Phycology</i> , 2003, 39, 343-352.	2.3	105
40	Evidence that viral abundance across oceans and lakes is driven by different biological factors. <i>Freshwater Biology</i> , 2008, 53, 1090-1100.	2.4	101
41	Lysogeny and Lytic Viral Production during a Bloom of the Cyanobacterium <i>Synechococcus</i> spp.. <i>Microbial Ecology</i> , 2002, 43, 225-231.	2.8	100
42	Evolving paradigms in biological carbon cycling in the ocean. <i>National Science Review</i> , 2018, 5, 481-499.	9.5	100
43	Viruses in Antarctic lakes. <i>Limnology and Oceanography</i> , 1998, 43, 1754-1761.	3.1	99
44	Ecological, Evolutionary, and Geochemical Consequences of Viral Infection of Cyanobacteria and Eukaryotic Algae. , 2000, , 247-296.		99
45	High abundances of viruses in a deep-sea hydrothermal vent system indicates viral mediated microbial mortality. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2005, 52, 1515-1527.	1.4	99
46	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.	3.1	98
47	Comparison of epifluorescence and transmission electron microscopy for counting viruses in natural marine waters. <i>Aquatic Microbial Ecology</i> , 1997, 13, 225-232.	1.8	97
48	Biogeography of Viruses in the Sea. <i>Annual Review of Virology</i> , 2015, 2, 41-66.	6.7	96
49	Discrimination by freshwater zooplankton between single algal cells differing in nutritional status. <i>Oecologia</i> , 1989, 78, 368-372.	2.0	93
50	Development of <i>phoH</i> as a Novel Signature Gene for Assessing Marine Phage Diversity. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7730-7739.	3.1	90
51	Phylogenetic Diversity of Sequences of Cyanophage Photosynthetic Gene <i>psbA</i> in Marine and Freshwaters. <i>Applied and Environmental Microbiology</i> , 2008, 74, 5317-5324.	3.1	89
52	Effects of environmental variation and spatial distance on <i>Bacteria</i> , <i>Archaea</i> and viruses in sub-polar and arctic waters. <i>ISME Journal</i> , 2013, 7, 1507-1518.	9.8	88
53	Genome sequence and characterization of a virus (HaRNAV) related to picorna-like viruses that infects the marine toxic bloom-forming alga <i>Heterosigma akashiwo</i> . <i>Virology</i> , 2004, 320, 206-217.	2.4	86
54	A comprehensive method for amplicon-based and metagenomic characterization of viruses, bacteria, and eukaryotes in freshwater samples. <i>Microbiome</i> , 2016, 4, 20.	11.1	86

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55	Virus-driven nitrogen cycling enhances phytoplankton growth. <i>Aquatic Microbial Ecology</i> , 2012, 66, 41-46.	1.8	84
56	Isolation and Phylogenetic Analysis of Novel Viruses Infecting the Phytoplankton <i>Phaeocystis globosa</i> (Prymnesiophyceae). <i>Applied and Environmental Microbiology</i> , 2004, 70, 3700-3705.	3.1	83
57	DESCRIPTION AND CHARACTERIZATION OF THE ALGAL SPECIES AUREOUMBRA LAGUNENSIS GEN. ET SP. NOV. AND REFERRAL OF AUREOUMBRA AND AUREOCOCCUS TO THE PELAGOPHYCEAE1. <i>Journal of Phycology</i> , 1997, 33, 1042-1048.	2.3	80
58	Metagenomic Analysis Suggests Modern Freshwater Microbialites Harbor a Distinct Core Microbial Community. <i>Frontiers in Microbiology</i> , 2016, 6, 1531.	3.5	78
59	Metagenomic characterization of viral communities in corals: mining biological signal from methodological noise. <i>Environmental Microbiology</i> , 2015, 17, 3440-3449.	3.8	75
60	Metagenomic and whole-genome analysis reveals new lineages of gokushoviruses and biogeographic separation in the sea. <i>Frontiers in Microbiology</i> , 2013, 4, 404.	3.5	74
61	Eye-like ocelloids are built from different endosymbiotically acquired components. <i>Nature</i> , 2015, 523, 204-207.	27.8	74
62	Viruses infecting the marine Prymnesiophyte <i>Chrysochromulina</i> spp.: isolation, preliminary characterization and natural abundance. <i>Marine Ecology - Progress Series</i> , 1995, 118, 275-282.	1.9	73
63	Combining genomic sequencing methods to explore viral diversity and reveal potential virus-host interactions. <i>Frontiers in Microbiology</i> , 2015, 6, 265.	3.5	72
64	A NOVEL VIRUS (HaNIV) CAUSES LYSIS OF THE TOXIC BLOOM-FORMING ALGA HETEROSIGMA AKASHIWO (RAPHIDOPHYCEAE). <i>Journal of Phycology</i> , 2001, 37, 216-222.	2.3	71
65	Effects of patch connectivity and heterogeneity on metacommunity structure of planktonic bacteria and viruses. <i>ISME Journal</i> , 2013, 7, 533-542.	9.8	71
66	The kinetoplastid-infecting Bodo saltans virus (BsV), a window into the most abundant giant viruses in the sea. <i>ELife</i> , 2018, 7, .	6.0	71
67	Genetic richness of vibriophages isolated in a coastal environment. <i>Environmental Microbiology</i> , 2006, 8, 1164-1176.	3.8	70
68	The complete sequence of marine bacteriophage VpV262 infecting <i>Vibrio parahaemolyticus</i> indicates that an ancestral component of a T7 viral supergroup is widespread in the marine environment. <i>Virology</i> , 2003, 310, 359-371.	2.4	68
69	Effects of Nutrient Pulses on Community Structure and Cell Size of a Freshwater Phytoplankton Assemblage in Culture. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 1987, 44, 1768-1774.	1.4	66
70	<i>Synechococcus</i> growth in the ocean may depend on the lysis of heterotrophic bacteria. <i>Journal of Plankton Research</i> , 2011, 33, 1465-1476.	1.8	66
71	Endangered wild salmon infected by newly discovered viruses. <i>ELife</i> , 2019, 8, .	6.0	66
72	THE INABILITY OF THE TEXAS "BROWN TIDE" ALGA TO USE NITRATE AND THE ROLE OF NITROGEN IN THE INITIATION OF A PERSISTENT BLOOM OF THIS ORGANISM1. <i>Journal of Phycology</i> , 1994, 30, 800-806.	2.3	65

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73	Viruses causing lysis of the toxic bloom-forming alga <i>Heterosigma akashiwo</i> (Raphidophyceae) are widespread in coastal sediments of British Columbia, Canada. <i>Limnology and Oceanography</i> , 2002, 47, 545-550.	3.1	63
74	The complete genomes of three viruses assembled from shotgun libraries of marine RNA virus communities. <i>Virology Journal</i> , 2007, 4, 69.	3.4	63
75	Physical and biological correlates of virus dynamics in the southern Beaufort Sea and Amundsen Gulf. <i>Journal of Marine Systems</i> , 2008, 74, 933-945.	2.1	63
76	The same strain of <i>Piscine orthoreovirus</i> (PRV-1) is involved in the development of different, but related, diseases in Atlantic and Pacific Salmon in British Columbia. <i>Facets</i> , 2018, 3, 599-641.	2.4	63
77	Adsorption and precipitation of iron from seawater on a marine bacteriophage (PWH3A-P1). <i>Marine Chemistry</i> , 2004, 91, 101-115.	2.3	62
78	Metagenomic analysis reveals that modern microbialites and polar microbial mats have similar taxonomic and functional potential. <i>Frontiers in Microbiology</i> , 2015, 6, 966.	3.5	62
79	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2021, 166, 3513-3566.	2.1	62
80	Measurements of DNA damage and photoreactivation imply that most viruses in marine surface waters are infective. <i>Aquatic Microbial Ecology</i> , 1998, 14, 215-222.	1.8	62
81	Polar freshwater cyanophage S-EIV1 represents a new widespread evolutionary lineage of phages. <i>ISME Journal</i> , 2015, 9, 2046-2058.	9.8	61
82	Active and diverse viruses persist in the deep sub-seafloor sediments over thousands of years. <i>ISME Journal</i> , 2019, 13, 1857-1864.	9.8	61
83	Year-Long Metagenomic Study of River Microbiomes Across Land Use and Water Quality. <i>Frontiers in Microbiology</i> , 2015, 6, 1405.	3.5	60
84	Effect of viral infection on sinking rates of <i>Heterosigma akashiwo</i> and its implications for bloom termination. <i>Aquatic Microbial Ecology</i> , 2004, 37, 1-7.	1.8	60
85	<i>Chromulinavorax destructans</i> , a pathogen of microzooplankton that provides a window into the enigmatic candidate phylum Dependistia. <i>PLoS Pathogens</i> , 2019, 15, e1007801.	4.7	59
86	Large double-stranded DNA viruses which cause the lysis of a marine heterotrophic nanoflagellate (<i>Bodo</i> sp.) occur in natural marine viral communities. <i>Aquatic Microbial Ecology</i> , 1995, 9, 203-210.	1.8	59
87	Phages Infecting <i>Vibrio vulnificus</i> Are Abundant and Diverse in Oysters (<i>Crassostrea</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 346-351.	3.1	56
88	The Physical Environment Affects Cyanophage Communities in British Columbia Inlets. <i>Microbial Ecology</i> , 2003, 46, 348-357.	2.8	56
89	Enumeration of virus particles in aquatic or sediment samples by epifluorescence microscopy. , 0, , 145-153.		56
90	Genetic Diversity of Algal Viruses Which Lyse the Photosynthetic Picoflagellate <i>Micromonas pusilla</i> (Prasinophyceae). <i>Applied and Environmental Microbiology</i> , 1995, 61, 3088-3091.	3.1	56

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91	Arctic microbial ecosystems and impacts of extreme warming during the International Polar Year. <i>Polar Science</i> , 2009, 3, 171-180.	1.2	55
92	The Sensitivity of Massively Parallel Sequencing for Detecting Candidate Infectious Agents Associated with Human Tissue. <i>PLoS ONE</i> , 2011, 6, e19838.	2.5	55
93	Viruses: unlocking the greatest biodiversity on Earth. <i>Genome</i> , 2013, 56, 542-544.	2.0	54
94	Generating viral metagenomes from the coral holobiont. <i>Frontiers in Microbiology</i> , 2014, 5, 206.	3.5	54
95	Grazing of planktonic diatoms by microflagellates. <i>Journal of Plankton Research</i> , 1986, 8, 393-398.	1.8	53
96	Phylogenetic Analysis Indicates Evolutionary Diversity and Environmental Segregation of Marine Podovirus DNA Polymerase Gene Sequences. <i>Applied and Environmental Microbiology</i> , 2009, 75, 3634-3640.	3.1	53
97	Dynamics of Heterotrophic Bacterial Assemblages within <i>Synechococcus</i> Cultures. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	52
98	Cyanophages and Their Role in the Ecology of Cyanobacteria. , 2000, , 563-589.		51
99	Eukaryotic virus composition can predict the efficiency of carbon export in the global ocean. <i>IScience</i> , 2021, 24, 102002.	4.1	50
100	Sunlight-induced DNA damage and resistance in natural viral communities. <i>Aquatic Microbial Ecology</i> , 1999, 17, 111-120.	1.8	49
101	Effects of viral infection on photosynthetic processes in the bloom-forming alga <i>Heterosigma akashiwo</i> . <i>Aquatic Microbial Ecology</i> , 2003, 31, 9-17.	1.8	48
102	Temporal dynamics of natural communities of marine algal viruses and eukaryotes. <i>Aquatic Microbial Ecology</i> , 2003, 32, 107-119.	1.8	48
103	Viruses Infecting a Freshwater Filamentous Cyanobacterium (<i>Nostoc</i> sp.) Encode a Functional CRISPR Array and a Proteobacterial DNA Polymerase B. <i>MBio</i> , 2016, 7, .	4.1	47
104	Time-courses of size-fractionated phosphate uptake: are larger cells better competitors for pulses of phosphate than smaller cells?. <i>Oecologia</i> , 1988, 74, 571-576.	2.0	46
105	Environmental microbiology: Viral diversity on the global stage. <i>Nature Microbiology</i> , 2016, 1, 16205.	13.3	46
106	The virosphere: the greatest biological diversity on Earth and driver of global processes. <i>Environmental Microbiology</i> , 2005, 7, 481-482.	3.8	43
107	A Persistent, Productive, and Seasonally Dynamic Vibriophage Population within Pacific Oysters (<i>Tj ETQq1</i>)	1.0784314	43
108	High temporal and spatial diversity in marine RNA viruses implies that they have an important role in mortality and structuring plankton communities. <i>Frontiers in Microbiology</i> , 2014, 5, 703.	3.5	42

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109	The virion of Cafeteria roenbergensis virus (CroV) contains a complex suite of proteins for transcription and DNA repair. <i>Virology</i> , 2014, 466-467, 82-94.	2.4	41
110	Cryo-EM reconstruction of the Cafeteria roenbergensis virus capsid suggests novel assembly pathway for giant viruses. <i>Scientific Reports</i> , 2017, 7, 5484.	3.3	41
111	The Genome of the Beluga Whale (<i>Delphinapterus leucas</i>). <i>Genes</i> , 2017, 8, 378.	2.4	39
112	Enumeration and Isolation of Viruses. , 2018, , 121-134.		39
113	Virus-Specific Responses of <i>Heterosigma akashiwo</i> to Infection. <i>Applied and Environmental Microbiology</i> , 2006, 72, 7829-7834.	3.1	38
114	PHYLOGENY OF AUREOCOCCUS ANOPHAGEFFERENS AND A MORPHOLOGICALLY SIMILAR BLOOM-FORMING ALGA FROM TEXAS AS DETERMINED BY 18S RIBOSOMAL RNA SEQUENCE ANALYSIS1. <i>Journal of Phycology</i> , 1995, 31, 413-418.	2.3	37
115	Correcting a major error in assessing organic carbon pollution in natural waters. <i>Science Advances</i> , 2021, 7, .	10.3	37
116	PRODUCTION OF AXENIC CULTURES OF MICROMONAS PUSILLA (PRASINOPHYCEAE) USING ANTIBIOTIC 1. <i>Journal of Phycology</i> , 1993, 29, 385-387.	2.3	36
117	Marine RNA Virus Quasispecies Are Distributed throughout the Oceans. <i>MSphere</i> , 2019, 4, .	2.9	36
118	Estimation of Biologically Damaging UV Levels in Marine Surface Waters with DNA and Viral Dosimeters. <i>Photochemistry and Photobiology</i> , 2002, 76, 268.	2.5	35
119	A compendium of multi-omic sequence information from the Saanich Inlet water column. <i>Scientific Data</i> , 2017, 4, 170160.	5.3	35
120	Nutrients and Other Environmental Factors Influence Virus Abundances across Oxidic and Hypoxic Marine Environments. <i>Viruses</i> , 2017, 9, 152.	3.3	33
121	Draft Genome Sequence of <i>Exiguobacterium pavilionensis</i> Strain RW-2, with Wide Thermal, Salinity, and pH Tolerance, Isolated from Modern Freshwater Microbialites. <i>Genome Announcements</i> , 2013, 1, .	0.8	32
122	Diversity and Host Specificity Revealed by Biological Characterization and Whole Genome Sequencing of Bacteriophages Infecting <i>Salmonella enterica</i> . <i>Viruses</i> , 2019, 11, 854.	3.3	32
123	The Complete Genome and Physiological Analysis of the Eurythermal Firmicute <i>Exiguobacterium chiriquicha</i> Strain RW2 Isolated From a Freshwater Microbialite, Widely Adaptable to Broad Thermal, pH, and Salinity Ranges. <i>Frontiers in Microbiology</i> , 2018, 9, 3189.	3.5	32
124	Title is missing!. , 1999, 401, 19-33.		31
125	A compendium of geochemical information from the Saanich Inlet water column. <i>Scientific Data</i> , 2017, 4, 170159.	5.3	29
126	Flamingos and drought as drivers of nutrients and microbial dynamics in a saline lake. <i>Scientific Reports</i> , 2017, 7, 12173.	3.3	28

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127	A historical overview of the Pavilion Lake Research Project—Analog science and exploration in an underwater environment. , 2011, , .		27
128	Identification of Freshwater <i>Phycodnaviridae</i> and Their Potential Phytoplankton Hosts, Using DNA Sequence Fragments and a Genetic-Distance Analysis. Applied and Environmental Microbiology, 2009, 75, 991-997.	3.1	26
129	Determination of Virus Abundance by Epifluorescence Microscopy. Methods in Molecular Biology, 2009, 501, 87-95.	0.9	26
130	A New Freshwater Cyanosiphovirus Harboring Integrase. Frontiers in Microbiology, 2018, 9, 2204.	3.5	26
131	Size-Dependent Ammonium and Phosphate Uptake, and N:P Supply Ratios in an Oligotrophic Lake. Canadian Journal of Fisheries and Aquatic Sciences, 1991, 48, 1226-1234.	1.4	25
132	Who Owns the Ocean? Policy Issues Surrounding Marine Genetic Resources. Limnology and Oceanography Bulletin, 2016, 25, 29-35.	0.4	25
133	Transcriptional responses of the marine green alga <i>Micromonas pusilla</i> and an infecting prasinovirus under different phosphate conditions. Environmental Microbiology, 2018, 20, 2898-2912.	3.8	25
134	Phosphate Uptake Rates of Phytoplankton Assemblages Grown at Different Dilution Rates in Semicontinuous Culture. Canadian Journal of Fisheries and Aquatic Sciences, 1986, 43, 1474-1481.	1.4	24
135	The use of degenerate-primed random amplification of polymorphic DNA (DP-RAPD) for strain-typing and inferring the genetic similarity among closely related viruses. Journal of Virological Methods, 2004, 118, 95-100.	2.1	24
136	Functional Diversity: An Epistemic Roadmap. BioScience, 2019, 69, 800-811.	4.9	23
137	The Complete Genome and Physiological Analysis of the Microbialite-Dwelling <i>Agrococcus pavilionensis</i> sp. nov; Reveals Genetic Promiscuity and Predicted Adaptations to Environmental Stress. Frontiers in Microbiology, 2018, 9, 2180.	3.5	22
138	Virus-mediated transfer of nitrogen from heterotrophic bacteria to phytoplankton. Biogeosciences, 2018, 15, 809-819.	3.3	22
139	Metagenomes of a Freshwater Charavirus from British Columbia Provide a Window into Ancient Lineages of Viruses. Viruses, 2019, 11, 299.	3.3	21
140	Nested PCR with three highly degenerate primers for amplification and identification of DNA from related organisms. BioTechniques, 1995, 18, 609-12.	1.8	21
141	Milne Fiord epishelf lake: A coastal Arctic ecosystem vulnerable to climate change. Ecoscience, 2011, 18, 304-316.	1.4	20
142	Single-cell transcriptomics using spliced leader PCR: Evidence for multiple losses of photosynthesis in polykrikoid dinoflagellates. BMC Genomics, 2015, 16, 528.	2.8	20
143	Phylogenetics and movement of Phycodnaviruses among aquatic environments. ISME Journal, 2012, 6, 237-247.	9.8	19
144	A Virus Infecting Marine Photoheterotrophic Alphaproteobacteria (<i>Citromicrobium</i> spp.) Defines a New Lineage of ssDNA Viruses. Frontiers in Microbiology, 2018, 9, 1418.	3.5	19

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145	Application of a sequence-based taxonomic classification method to uncultured and unclassified marine single-stranded RNA viruses in the order Picornavirales. <i>Virus Evolution</i> , 2019, 5, vez056.	4.9	19
146	Previously unknown evolutionary groups dominate the ssDNA gokushoviruses in oxic and anoxic waters of a coastal marine environment. <i>Frontiers in Microbiology</i> , 2015, 6, 315.	3.5	18
147	Ammonium and phosphate uptake kinetics of size-fractionated plankton from an oligotrophic freshwater lake. <i>Journal of Plankton Research</i> , 1988, 10, 133-149.	1.8	17
148	Denaturing Gradient Gel Electrophoresis Resolves Virus Sequences Amplified with Degenerate Primers. <i>BioTechniques</i> , 2000, 28, 20-26.	1.8	16
149	RAPID AMMONIUM UPTAKE BY FRESHWATER PHYTOPLANKTON. <i>Journal of Phycology</i> , 1988, 24, 13-16.	2.3	15
150	Contrasting Ecosystem-Effects of Morphologically Similar Copepods. <i>PLoS ONE</i> , 2011, 6, e26700.	2.5	15
151	First Draft Genome Sequence from a Member of the Genus <i>Agrococcus</i> , Isolated from Modern Microbialites. <i>Genome Announcements</i> , 2013, 1, .	0.8	15
152	Variation in the Genetic Repertoire of Viruses Infecting <i>Micromonas pusilla</i> Reflects Horizontal Gene Transfer and Links to Their Environmental Distribution. <i>Viruses</i> , 2017, 9, 116.	3.3	15
153	The Environment and Cyanophage Diversity: Insights From Environmental Sequencing of DNA Polymerase. <i>Frontiers in Microbiology</i> , 2019, 10, 167.	3.5	14
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