

Curtis Suttle

List of Publications by Year in descending order

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Version: 2024-02-01

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	Patterns of microbial abundance and heterotrophic activity along nitrogen and salinity gradients in coastal wetlands. <i>Aquatic Sciences</i> , 2022, 84, 1.	1.5	2
2	Discovery and surveillance of viruses from salmon in British Columbia using viral immune-response biomarkers, metatranscriptomics, and high-throughput RT-PCR. <i>Virus Evolution</i> , 2021, 7, veaa069.	4.9	13
3	Algal Marnaviruses (Marnaviridae)., 2021, , 671-676.		1
4	Eukaryotic virus composition can predict the efficiency of carbon export in the global ocean. <i>IScience</i> , 2021, 24, 102002.	4.1	50
5	Correcting a major error in assessing organic carbon pollution in natural waters. <i>Science Advances</i> , 2021, 7, .	10.3	37
6	Role of Phylogenetic Structure in the Dynamics of Coastal Viral Assemblages. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	6
7	Moderate Seasonal Dynamics Indicate an Important Role for Lysogeny in the Red Sea. <i>Microorganisms</i> , 2021, 9, 1269.	3.6	6
8	ICTV Virus Taxonomy Profile: Marnaviridae 2021. <i>Journal of General Virology</i> , 2021, 102, .	2.9	13
9	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
10	Viral Characteristics of the Warm Atlantic and Cold Arctic Water Masses in the Nordic Seas. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0116021.	3.1	12
11	Revealing the composition of the eukaryotic microbiome of oyster spat by CRISPR-Cas Selective Amplicon Sequencing (CCSAS). <i>Microbiome</i> , 2021, 9, 230.	11.1	6
12	Saline lakes on the Qinghai-Tibet Plateau harbor unique viral assemblages mediating microbial environmental adaption. <i>IScience</i> , 2021, 24, 103439.	4.1	13
13	Relative genomic impacts of translocation history, hatchery practices, and farm selection in Pacific oyster <i>Crassostrea gigas</i> throughout the Northern Hemisphere. <i>Evolutionary Applications</i> , 2020, 13, 1380-1399.	3.1	13
14	From the Inside Out: an Epibiotic <i>Bdellovibrio</i> Predator with an Expanded Genomic Complement. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	14
15	Functional Diversity: An Epistemic Roadmap. <i>BioScience</i> , 2019, 69, 800-811.	4.9	23
16	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
17	<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
18	Distribution and Phylogeny of Erythrocytic Necrosis Virus (ENV) in Salmon Suggests Marine Origin. <i>Viruses</i> , 2019, 11, 358.	3.3	11

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19	Metagenomes of a Freshwater Charavirus from British Columbia Provide a Window into Ancient Lineages of Viruses. <i>Viruses</i> , 2019, 11, 299.	3.3	21
20	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
21	VHost-Classifer: virus-host classification using natural language processing. <i>Bioinformatics</i> , 2019, 35, 3867-3869.	4.1	4
22	Marine RNA Virus Quasispecies Are Distributed throughout the Oceans. <i>MSphere</i> , 2019, 4, .	2.9	36
23	The Environment and Cyanophage Diversity: Insights From Environmental Sequencing of DNA Polymerase. <i>Frontiers in Microbiology</i> , 2019, 10, 167.	3.5	14
24	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
25	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
26	Endangered wild salmon infected by newly discovered viruses. <i>ELife</i> , 2019, 8, .	6.0	66
27	Deposition rates of viruses and bacteria above the atmospheric boundary layer. <i>ISME Journal</i> , 2018, 12, 1154-1162.	9.8	178
28	Dynamics of Heterotrophic Bacterial Assemblages within <i>Synechococcus</i> Cultures. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	52
29	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. <i>Frontiers in Microbiology</i> , 2018, 9, 2180.	3.5	22
30	A New Freshwater Cyanosiphovirus Harboring Integrase. <i>Frontiers in Microbiology</i> , 2018, 9, 2204.	3.5	26
31	Transcriptional responses of the marine green alga <i>Micromonas pusilla</i> and an infecting prasinovirus under different phosphate conditions. <i>Environmental Microbiology</i> , 2018, 20, 2898-2912.	3.8	25
32	Virus-mediated transfer of nitrogen from heterotrophic bacteria to phytoplankton. <i>Biogeosciences</i> , 2018, 15, 809-819.	3.3	22
33	The kinetoplastid-infecting <i>Bodo saltans</i> virus (BsV), a window into the most abundant giant viruses in the sea. <i>ELife</i> , 2018, 7, .	6.0	71
34	A Virus Infecting Marine Photoheterotrophic Alphaproteobacteria (<i>Citromicrobium</i> spp.) Defines a New Lineage of ssDNA Viruses. <i>Frontiers in Microbiology</i> , 2018, 9, 1418.	3.5	19
35	Editorial for the special issue on marine carbon sequestration and climate change. <i>National Science Review</i> , 2018, 5, 456-457.	9.5	1
36	Evolving paradigms in biological carbon cycling in the ocean. <i>National Science Review</i> , 2018, 5, 481-499.	9.5	100

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37	The Complete Genome and Physiological Analysis of the Eurythermal Firmicute <i>Exiguobacterium chiriqhucha</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
38	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
39	Enumeration and Isolation of Viruses. , 2018, , 121-134.		39
40	Virus taxonomy in the age of metagenomics. <i>Nature Reviews Microbiology</i> , 2017, 15, 161-168.	28.6	590
41	Flamingos and drought as drivers of nutrients and microbial dynamics in a saline lake. <i>Scientific Reports</i> , 2017, 7, 12173.	3.3	28
42	Cryo-EM reconstruction of the <i>Cafeteria roenbergensis</i> virus capsid suggests novel assembly pathway for giant viruses. <i>Scientific Reports</i> , 2017, 7, 5484.	3.3	41
43	From Farm to Sea: A Tribute to Paul J. Harrison. <i>Limnology and Oceanography Bulletin</i> , 2017, 26, 58-59.	0.4	1
44	A compendium of geochemical information from the Saanich Inlet water column. <i>Scientific Data</i> , 2017, 4, 170159.	5.3	29
45	A compendium of multi-omic sequence information from the Saanich Inlet water column. <i>Scientific Data</i> , 2017, 4, 170160.	5.3	35
46	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
47	Nutrients and Other Environmental Factors Influence Virus Abundances across Oxic and Hypoxic Marine Environments. <i>Viruses</i> , 2017, 9, 152.	3.3	33
48	The Genome of the Beluga Whale (<i>Delphinapterus leucas</i>). <i>Genes</i> , 2017, 8, 378.	2.4	39
49	Metagenomic Analysis Suggests Modern Freshwater Microbialites Harbor a Distinct Core Microbial Community. <i>Frontiers in Microbiology</i> , 2016, 6, 1531.	3.5	78
50	Who Owns the Ocean? Policy Issues Surrounding Marine Genetic Resources. <i>Limnology and Oceanography Bulletin</i> , 2016, 25, 29-35.	0.4	25
51	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
52	Environmental microbiology: Viral diversity on the global stage. <i>Nature Microbiology</i> , 2016, 1, 16205.	13.3	46
53	Re-examination of the relationship between marine virus and microbial cell abundances. <i>Nature Microbiology</i> , 2016, 1, 15024.	13.3	264
54	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

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55	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
56	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
57	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
58	Year-Long Metagenomic Study of River Microbiomes Across Land Use and Water Quality. <i>Frontiers in Microbiology</i> , 2015, 6, 1405.	3.5	60
59	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
60	Metagenomic characterization of viral communities in corals: mining biological signal from methodological noise. <i>Environmental Microbiology</i> , 2015, 17, 3440-3449.	3.8	75
61	Eye-like ocelloids are built from different endosymbiotically acquired components. <i>Nature</i> , 2015, 523, 204-207.	27.8	74
62	Polar freshwater cyanophage S-EIV1 represents a new widespread evolutionary lineage of phages. <i>ISME Journal</i> , 2015, 9, 2046-2058.	9.8	61
63	Single-cell transcriptomics using spliced leader PCR: Evidence for multiple losses of photosynthesis in polykrikoid dinoflagellates. <i>BMC Genomics</i> , 2015, 16, 528.	2.8	20
64	Biogeography of Viruses in the Sea. <i>Annual Review of Virology</i> , 2015, 2, 41-66.	6.7	96
65	Generating viral metagenomes from the coral holobiont. <i>Frontiers in Microbiology</i> , 2014, 5, 206.	3.5	54
66	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
67	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
68	Viral infection of bacteria and phytoplankton in the Arctic Ocean as viewed through the lens of fingerprint analysis. <i>Aquatic Microbial Ecology</i> , 2014, 72, 47-61.	1.8	8
69	Dissecting the role of viruses in marine nutrient cycling: bacterial uptake of D- and L-amino acids released by viral lysis. <i>Aquatic Microbial Ecology</i> , 2014, 73, 235-243.	1.8	11
70	Previously unknown and highly divergent ssDNA viruses populate the oceans. <i>ISME Journal</i> , 2013, 7, 2169-2177.	9.8	160
71	Viruses: unlocking the greatest biodiversity on Earth. <i>Genome</i> , 2013, 56, 542-544.	2.0	54
72	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

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73	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
74	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
75	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
76	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
77	Prevalence of psbA-containing cyanobacterial podoviruses in the ocean. <i>Scientific Reports</i> , 2013, 3, 3207.	3.3	12
78	The Draft Genome Sequence of <i>Sphingomonas paucimobilis</i> Strain HER1398 (<i>Proteobacteria</i>), Host to the Giant PAU Phage, Indicates That It Is a Member of the Genus <i>Sphingobacterium</i> ()	3.1	10
79	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
80	Phylodynamics and movement of Phycodnaviruses among aquatic environments. <i>ISME Journal</i> , 2012, 6, 237-247.	9.8	19
81	Modeling the Winter-to-Summer Transition of Prokaryotic and Viral Abundance in the Arctic Ocean. <i>PLoS ONE</i> , 2012, 7, e52794.	2.5	12
82	Virus-driven nitrogen cycling enhances phytoplankton growth. <i>Aquatic Microbial Ecology</i> , 2012, 66, 41-46.	1.8	84
83	Milne Fiord epishelf lake: A coastal Arctic ecosystem vulnerable to climate change. <i>Ecoscience</i> , 2011, 18, 304-316.	1.4	20
84	Contrasting Ecosystem-Effects of Morphologically Similar Copepods. <i>PLoS ONE</i> , 2011, 6, e26700.	2.5	15
85	Marine viruses and global climate change. <i>FEMS Microbiology Reviews</i> , 2011, 35, 993-1034.	8.6	297
86	<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
87	A Virophage at the Origin of Large DNA Transposons. <i>Science</i> , 2011, 332, 231-234.	12.6	258
88	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
89	A historical overview of the Pavilion Lake Research Project—Analog science and exploration in an underwater environment. , 2011, , .		27
90	Marnavirus. , 2011, , 835-837.		2

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91	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
92	Pymnesiovirus. , 2011, , 1269-1273.		1
93	Prasinovirusâ€™. , 2011, , 1265-1268.		1
94	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
95	Identification of Freshwater <i>Phycodnaviridae</i> and Their Potential Phytoplankton Hosts, Using DNA <i>pol</i> Sequence Fragments and a Genetic-Distance Analysis. <i>Applied and Environmental Microbiology</i> , 2009, 75, 991-997.	3.1	26
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	Arctic microbial ecosystems and impacts of extreme warming during the International Polar Year. <i>Polar Science</i> , 2009, 3, 171-180.	1.2	55
98	Determination of Virus Abundance by Epifluorescence Microscopy. <i>Methods in Molecular Biology</i> , 2009, 501, 87-95.	0.9	26
99	Isolation Independent Methods of Characterizing Phage Communities I: Strain Typing Using Fingerprinting Methods. <i>Methods in Molecular Biology</i> , 2009, 502, 255-278.	0.9	2
100	Viruses: a vast reservoir of genetic diversity and driver of global processes. <i>Retrovirology</i> , 2009, 6, .	2.0	3
101	Global-scale processes with a nanoscale drive: the role of marine viruses. <i>ISME Journal</i> , 2008, 2, 575-578.	9.8	226
102	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
103	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
104	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
105	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
106	Exploring the Vast Diversity of Marine Viruses. <i>Oceanography</i> , 2007, 20, 135-139.	1.0	224
107	Marine viruses â€™ major players in the global ecosystem. <i>Nature Reviews Microbiology</i> , 2007, 5, 801-812.	28.6	2,602
108	Distribution, genetic richness and phage sensitivity of <i>Vibriosp.</i> from coastal British Columbia. <i>Environmental Microbiology</i> , 2007, 9, 1790-1800.	3.8	11

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109	Estimation of Biologically Damaging UV Levels in Marine Surface Waters with DNA and Viral Dosimeters. <i>Photochemistry and Photobiology</i> , 2007, 76, 268-273.	2.5	7
110	Metagenomic Analysis of Coastal RNA Virus Communities. <i>Science</i> , 2006, 312, 1795-1798.	12.6	334
111	Genetic richness of vibriophages isolated in a coastal environment. <i>Environmental Microbiology</i> , 2006, 8, 1164-1176.	3.8	70
112	The Marine Viromes of Four Oceanic Regions. <i>PLoS Biology</i> , 2006, 4, e368.	5.6	867
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	The virosphere: the greatest biological diversity on Earth and driver of global processes. <i>Environmental Microbiology</i> , 2005, 7, 481-482.	3.8	43
115	Viruses in the sea. <i>Nature</i> , 2005, 437, 356-361.	27.8	1,906
116	A Persistent, Productive, and Seasonally Dynamic Vibriophage Population within Pacific Oysters (<i>Crassostrea gigas</i>). <i>Journal of Virology</i> , 2005, 79, 1071-1079.	3.1	43
117	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
118	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
119	The virosphere, diversity, and genetic exchange within phage communities. <i>Current Opinion in Microbiology</i> , 2005, 8, 444-450.	5.1	172
120	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
121	Accurate Estimation of Viral Abundance by Epifluorescence Microscopy. <i>Applied and Environmental Microbiology</i> , 2004, 70, 3862-3867.	3.1	168
122	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
123	The use of degenerate-primed random amplification of polymorphic DNA (DP-RAPD) for strain-typing and inferring the genetic similarity among closely related viruses. <i>Journal of Virological Methods</i> , 2004, 118, 95-100.	2.1	24
124	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
125	Adsorption and precipitation of iron from seawater on a marine bacteriophage (PWH3A-P1). <i>Marine Chemistry</i> , 2004, 91, 101-115.	2.3	62
126	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

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127	The Physical Environment Affects Cyanophage Communities in British Columbia Inlets. <i>Microbial Ecology</i> , 2003, 46, 348-357.	2.8	56
128	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
129	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
130	High diversity of unknown picorna-like viruses in the sea. <i>Nature</i> , 2003, 424, 1054-1057.	27.8	213
131	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
132	Temporal dynamics of natural communities of marine algal viruses and eukaryotes. <i>Aquatic Microbial Ecology</i> , 2003, 32, 107-119.	1.8	48
133	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
134	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
135	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
136	DNA polymerase gene sequences indicate western and forest tent caterpillar viruses form a new taxonomic group within baculoviruses. <i>Journal of Invertebrate Pathology</i> , 2002, 81, 131-147.	3.2	5
137	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
138	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
139	Prasinovirus. , 2002, , 737-740.		0
140	A NOVEL VIRUS (HaNIV) CAUSES LYSIS OF THE TOXIC BLOOM-FORMING ALGA <i>HETEROSIGMA AKASHIWO</i> (RAPHIDOPHYCEAE). <i>Journal of Phycology</i> , 2001, 37, 216-222.	2.3	71
141	Denaturing Gradient Gel Electrophoresis Resolves Virus Sequences Amplified with Degenerate Primers. <i>BioTechniques</i> , 2000, 28, 20-26.	1.8	16
142	Ecological, Evolutionary, and Geochemical Consequences of Viral Infection of Cyanobacteria and Eukaryotic Algae. , 2000, , 247-296.		99
143	Cyanophages and Their Role in the Ecology of Cyanobacteria. , 2000, , 563-589.		51
144	Viruses and Nutrient Cycles in the Sea. <i>BioScience</i> , 1999, 49, 781-788.	4.9	996

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145	Title is missing!. , 1999, 401, 19-33.		31
146	Sunlight-induced DNA damage and resistance in natural viral communities. <i>Aquatic Microbial Ecology</i> , 1999, 17, 111-120.	1.8	49
147	Lysogeny and prophage induction in coastal and offshore bacterial communities. <i>Aquatic Microbial Ecology</i> , 1999, 18, 217-225.	1.8	130
148	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
149	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
150	Viruses in Antarctic lakes. <i>Limnology and Oceanography</i> , 1998, 43, 1754-1761.	3.1	99
151	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
152	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
153	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
154	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
155	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
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