## Declan C Schroeder

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	New perspectives for evaluating relative risks of African swine fever virus contamination in global feed ingredient supply chains. Transboundary and Emerging Diseases, 2022, 69, 31-56.	3.0	18
2	Uses of molecular taxonomy in identifying phytoplankton communities from the Continuous Plankton Recorder Survey. , 2022, , 47-79.		2
3	Phycodnaviruses (Phycodnaviridae). , 2021, , 687-695.		7
4	Ten Years of Deformed Wing Virus (DWV) in Hawaiian Honey Bees (Apis mellifera), the Dominant DWV-A Variant Is Potentially Being Replaced by Variants with a DWV-B Coding Sequence. Viruses, 2021, 13, 969.	3.3	13
5	Phylogenetic Structure and Sequential Dominance of Sub-Lineages of PRRSV Type-2 Lineage 1 in the United States. Vaccines, 2021, 9, 608.	4.4	38
6	Deformed wing virus variant shift from 2010 to 2016 in managed and feral UK honey bee colonies. Archives of Virology, 2021, 166, 2693-2702.	2.1	14
7	Phylogenetically Distinct Near-Complete Genome Sequences of Porcine Reproductive and Respiratory Syndrome Virus Type 2 Variants from Four Distinct Disease Outbreaks at U.S. Swine Farms over the Past 6 Years. Microbiology Resource Announcements, 2021, 10, e0026021.	0.6	4
8	Tracing Viral Transmission and Evolution of Bovine Leukemia Virus through Long Read Oxford Nanopore Sequencing of the Proviral Genome. Pathogens, 2021, 10, 1191.	2.8	5
9	Molecular and phylogenetic analysis reveals new diversity of <i>Dunaliella salina</i> from hypersaline environments. Journal of the Marine Biological Association of the United Kingdom, 2021, 101, 27-37.	0.8	9
10	A longitudinal study on PRRSV detection in swine herds with different demographics and PRRSV management strategies. Transboundary and Emerging Diseases, 2021, , .	3.0	1
11	Flexible genes establish widespread bacteriophage pan-genomes in cryoconite hole ecosystems. Nature Communications, 2020, 11, 4403.	12.8	36
12	Implications of increasing Atlantic influence for Arctic microbial community structure. Scientific Reports, 2020, 10, 19262.	3.3	11
13	RNAseq of Deformed Wing Virus and Other Honey Bee-Associated Viruses in Eight Insect Taxa with or without Varroa Infestation. Viruses, 2020, 12, 1229.	3.3	19
14	Bee Viruses: Routes of Infection in Hymenoptera. Frontiers in Microbiology, 2020, 11, 943.	3.5	76
15	Detection and Replication of Moku Virus in Honey Bees and Social Wasps. Viruses, 2020, 12, 607.	3.3	20
16	The Pathogen Profile of a Honey Bee Queen Does Not Reflect That of Her Workers. Insects, 2020, 11, 382.	2.2	9
17	Meta-analysis of honey bee neurogenomic response links Deformed wing virus type A to precocious behavioral maturation. Scientific Reports, 2020, 10, 3101.	3.3	35
18	Day length as a key factor moderating the response of coccolithophore growth to elevated <i>p</i> CO <sub>2</sub> . Limnology and Oceanography, 2019, 64, 1284-1296.	3.1	7

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19	RNAseq Analysis Reveals Virus Diversity within Hawaiian Apiary Insect Communities. Viruses, 2019, 11, 397.	3.3	28
20	DWV-A Lethal to Honey Bees (Apis mellifera): A Colony Level Survey of DWV Variants (A, B, and C) in England, Wales, and 32 States across the US. Viruses, 2019, 11, 426.	3.3	62
21	Temporal Dynamics of Co-circulating Lineages of Porcine Reproductive and Respiratory Syndrome Virus. Frontiers in Microbiology, 2019, 10, 2486.	3.5	56
22	Pentaplacodinium saltonense gen. et sp. nov. (Dinophyceae) and its relationship to the cyst-defined genus Operculodinium and yessotoxin-producing Protoceratium reticulatum. Harmful Algae, 2018, 71, 57-77.	4.8	20
23	Distinct Oceanic Microbiomes From Viruses to Protists Located Near the Antarctic Circumpolar Current. Frontiers in Microbiology, 2018, 9, 1474.	3.5	23
24	Phaeoviral Infections Are Present in Macrocystis, Ecklonia and Undaria (Laminariales) and Are Influenced by Wave Exposure in Ectocarpales. Viruses, 2018, 10, 410.	3.3	12
25	Phaeoviruses discovered in kelp (Laminariales). ISME Journal, 2017, 11, 2869-2873.	9.8	24
26	Integrated biological responses and tissue-specific expression of <i>p53</i> and <i>ras</i> genes in marine mussels following exposure to benzo(α)pyrene and C <sub>60</sub> fullerenes, either alone or in combination. Mutagenesis, 2017, 32, 77-90.	2.6	33
27	A Comparison of Deformed Wing Virus in Deformed and Asymptomatic Honey Bees. Insects, 2017, 8, 28.	2.2	45
28	Isolation and Characterization of a Double Stranded DNA Megavirus Infecting the Toxin-Producing Haptophyte Prymnesium parvum. Viruses, 2017, 9, 40.	3.3	20
29	Change in Emiliania huxleyi Virus Assemblage Diversity but Not in Host Genetic Composition during an Ocean Acidification Mesocosm Experiment. Viruses, 2017, 9, 41.	3.3	10
30	Schrödinger's Cheshire Cat: Are Haploid Emiliania huxleyi Cells Resistant to Viral Infection or Not?. Viruses, 2017, 9, 51.	3.3	10
31	A Pelagic Microbiome (Viruses to Protists) from a Small Cup of Seawater. Viruses, 2017, 9, 47.	3.3	17
32	ABC Assay: Method Development and Application to Quantify the Role of Three DWV Master Variants in Overwinter Colony Losses of European Honey Bees. Viruses, 2017, 9, 314.	3.3	62
33	Environmental carbonate chemistry selects for phenotype of recently isolated strains of Emiliania huxleyi. Deep-Sea Research Part II: Topical Studies in Oceanography, 2016, 127, 28-40.	1.4	34
34	Choice of molecular barcode will affect species prevalence but not bacterial community composition. Marine Genomics, 2016, 29, 39-43.	1.1	10
35	Opening the door to new virus interactions in the aquatic world. Journal of Phycology, 2016, 52, 491-492.	2.3	1
36	Moku virus; a new Iflavirus found in wasps, honey bees and Varroa. Scientific Reports, 2016, 6, 34983.	3.3	55

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37	A role for diatom-like silicon transporters in calcifying coccolithophores. Nature Communications, 2016, 7, 10543.	12.8	78
38	Diversity in a honey bee pathogen: first report of a third master variant of the Deformed Wing Virus quasispecies. ISME Journal, 2016, 10, 1264-1273.	9.8	147
39	Superinfection exclusion and the long-term survival of honey bees in Varroa-infested colonies. ISME Journal, 2016, 10, 1182-1191.	9.8	88
40	Key metabolic pathways involved in xenobiotic biotransformation and stress responses revealed by transcriptomics of the mangrove oyster Crassostrea brasiliana. Aquatic Toxicology, 2015, 166, 10-20.	4.0	53
41	The ocean sampling day consortium. GigaScience, 2015, 4, 27.	6.4	185
42	The Continuous Plankton Recorder survey: How can long-term phytoplankton datasets contribute to the assessment of Good Environmental Status?. Estuarine, Coastal and Shelf Science, 2015, 162, 88-97.	2.1	42
43	More to Phaeovirus infections than first meets the eye. Perspectives in Phycology, 2015, 2, 105-109.	1.9	9
44	A Novel Evolutionary Strategy Revealed in the Phaeoviruses. PLoS ONE, 2014, 9, e86040.	2.5	14
45	Genotyping an <i>Emiliania huxleyi</i> (prymnesiophyceae) bloom event in the North Sea reveals evidence of asexual reproduction. Biogeosciences, 2014, 11, 5215-5234.	3.3	35
46	The Marine Microbial Eukaryote Transcriptome Sequencing Project (MMETSP): Illuminating the Functional Diversity of Eukaryotic Life in the Oceans through Transcriptome Sequencing. PLoS Biology, 2014, 12, e1001889.	5.6	885
47	How many Coccolithovirus genotypes does it take to terminate an Emiliania huxleyi bloom?. Virology, 2014, 466-467, 138-145.	2.4	16
48	The CO2 microalgae biorefinery: high value products and biofuels using halophilic microalgae in the "D-Factoryâ€: New Biotechnology, 2014, 31, S14-S15.	4.4	1
49	A light in the darkness: New biotransformation genes, antioxidant parameters and tissue-specific responses in oysters exposed to phenanthrene. Aquatic Toxicology, 2014, 152, 324-334.	4.0	71
50	Pan genome of the phytoplankton Emiliania underpins its global distribution. Nature, 2013, 499, 209-213.	27.8	448
51	Dissecting the impact of CO <sub>2</sub> and <scp>pH</scp> on the mechanisms of photosynthesis and calcification in the coccolithophore <i>Emiliania huxleyi</i> . New Phytologist, 2013, 199, 121-134.	7.3	171
52	On the description of Tisochrysis lutea gen. nov. sp. nov. and Isochrysis nuda sp. nov. in the Isochrysidales, and the transfer of Dicrateria to the Prymnesiales (Haptophyta). Journal of Applied Phycology, 2013, 25, 1763-1776.	2.8	169
53	Deformed wing virus. Virulence, 2012, 3, 589-591.	4.4	58
54	Effect of Metals on the Lytic Cycle of the Coccolithovirus, EhV86. Frontiers in Microbiology, 2012, 3, 155.	3.5	11

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55	The Ectocarpus Genome and Brown Algal Genomics. Advances in Botanical Research, 2012, 64, 141-184.	1.1	18
56	Dynamics and genotypic composition of Emiliania huxleyi and their co-occurring viruses during a coccolithophore bloom in the North Sea. FEMS Microbiology Ecology, 2012, 81, 315-323.	2.7	27
57	Global Honey Bee Viral Landscape Altered by a Parasitic Mite. Science, 2012, 336, 1304-1306.	12.6	548
58	Tissue-Specific Expression of <i>p53</i> and <i>ras</i> Genes in Response to the Environmental Genotoxicant Benzo(α)pyrene in Marine Mussels. Environmental Science & Technology, 2011, 45, 8974-8981.	10.0	49
59	Molecular tools separate harmful algal bloom species, Karenia mikimotoi, from different geographical regions into distinct sub-groups. Harmful Algae, 2011, 10, 636-643.	4.8	26
60	Expression of biomineralizationâ€related ion transport genes in <i>Emiliania huxleyi</i> . Environmental Microbiology, 2011, 13, 3250-3265.	3.8	82
61	Genetic diversity of <i>Ectocarpus</i> (Ectocarpales, Phaeophyceae) in Peru and northern Chile, the area of origin of the genomeâ€sequenced strain. New Phytologist, 2010, 188, 30-41.	7.3	20
62	The Ectocarpus genome and the independent evolution of multicellularity in brown algae. Nature, 2010, 465, 617-621.	27.8	774
63	Reinstatement of Ectocarpus crouaniorum Thuret in Le Jolis as a third common species of Ectocarpus (Ectocarpales, Phaeophyceae) in Western Europe, and its phenology at Roscoff, Brittany. Phycological Research, 2010, 58, 157-170.	1.6	38
64	Molecular Mechanisms Underlying Calcification in Coccolithophores. Geomicrobiology Journal, 2010, 27, 585-595.	2.0	110
65	Sequencing and characterization of virus genomes. , 2010, , 134-144.		1
66	A unicellular algal virus, Emiliania huxleyi virus 86, exploits an animal-like infection strategy. Journal of General Virology, 2009, 90, 2306-2316.	2.9	119
67	Novel virus dynamics in an Emiliania huxleyi bloom. Journal of Plankton Research, 2009, 31, 787-791.	1.8	19
68	Deformed Wing Virus Implicated in Overwintering Honeybee Colony Losses. Applied and Environmental Microbiology, 2009, 75, 7212-7220.	3.1	247
69	Genomic analysis of the smallest giant virus — Feldmannia sp. virus 158. Virology, 2009, 384, 223-232.	2.4	27
70	Global-scale processes with a nanoscale drive: the role of marine viruses. ISME Journal, 2008, 2, 575-578.	9.8	226
71	The use of RNA-dependent RNA polymerase for the taxonomic assignment of Picorna-like viruses (order) Tj ETQq1	1 0.7843 3.4	14 rgBT /Ov
72	Occurrence and genetic analysis of picorna-like viruses infecting worker bees of Apis mellifera L. populations in Devon, South West England. Journal of Invertebrate Pathology, 2008, 98, 239-242.	3.2	43

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73	Development and validation of a molecular technique for the analysis of archived formalin-preserved phytoplankton samples permits retrospective assessment of Emiliania huxleyi communities. Journal of Microbiological Methods, 2008, 73, 118-124.	1.6	18
74	Molecular Dynamics of Emiliania huxleyi and Cooccurring Viruses during Two Separate Mesocosm Studies. Applied and Environmental Microbiology, 2007, 73, 554-562.	3.1	90
75	Use of microarrays to assess viral diversity: from genotype to phenotype. Environmental Microbiology, 2007, 9, 971-982.	3.8	42
76	Genome comparison of two Coccolithoviruses. Virology Journal, 2006, 3, 15.	3.4	32
77	Phylogenetic analysis of PgV-102P, a new virus from the English Channel that infects Phaeocystis globosa. Journal of the Marine Biological Association of the United Kingdom, 2006, 86, 485-490.	0.8	19
78	Preliminary characterisation of repeat families in the genome of EhV-86, a giant algal virus that infects the marine microalga Emiliania huxleyi. Archives of Virology, 2006, 151, 525-535.	2.1	26
79	Locus-Specific Gene Expression Pattern Suggests a Unique Propagation Strategy for a Giant Algal Virus. Journal of Virology, 2006, 80, 7699-7705.	3.4	49
80	Evolutionary History of the Coccolithoviridae. Molecular Biology and Evolution, 2006, 23, 86-92.	8.9	57
81	Identification of a Diagnostic Marker To Detect Freshwater Cyanophages of Filamentous Cyanobacteria. Applied and Environmental Microbiology, 2006, 72, 5713-5719.	3.1	31
82	Variability in microbial population dynamics between similarly perturbed mesocosms. Journal of Plankton Research, 2006, 28, 783-791.	1.8	23
83	A GENETIC MARKER TO SEPARATE EMILIANIA HUXLEYI (PRYMNESIOPHYCEAE) MORPHOTYPES1. Journal of Phycology, 2005, 41, 874-879.	2.3	67
84	Complete Genome Sequence and Lytic Phase Transcription Profile of a <i>Coccolithovirus</i> . Science, 2005, 309, 1090-1092.	12.6	270
85	Investigation of the role of a β(1–4) agarase produced by Pseudoalteromonas gracilis B9 in eliciting disease symptoms in the red alga Gracilaria gracilis. Microbiology (United Kingdom), 2003, 149, 2919-2929.	1.8	57
86	Virus Succession Observed during an Emiliania huxleyi Bloom. Applied and Environmental Microbiology, 2003, 69, 2484-2490.	3.1	108
87	Isolation of viruses responsible for the demise of an Emiliania huxleyi bloom in the English Channel. Journal of the Marine Biological Association of the United Kingdom, 2002, 82, 369-377.	0.8	173
88	Coccolithovirus (Phycodnaviridae): Characterisation of a new large dsDNA algal virus that infects Emiliana huxleyi. Archives of Virology, 2002, 147, 1685-1698.	2.1	168
89	Fingerprinting aquatic virus communities. , 0, , 9-18.		8
90	Detection of Multiple Lineages of PRRSV in Breeding and Growing Swine Farms. Frontiers in Veterinary Science, 0, 9, .	2.2	10