

Ruth-Anne Sandaa

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

1,757
citations

361413

20
h-index

289244

40
g-index

45
all docs

45
docs citations

45
times ranked

1998
citing authors

#	ARTICLE	IF	CITATIONS
1	Reproducing the virusâ€œcopepod link in Arctic mesocosms using host fitness optimization. <i>Limnology and Oceanography</i> , 2021, 66, S303.	3.1	6
2	A Persistent Giant Algal Virus, with a Unique Morphology, Encodes an Unprecedented Number of Genes Involved in Energy Metabolism. <i>Journal of Virology</i> , 2021, 95, .	3.4	31
3	Going to extremes â€œ a metagenomic journey into the dark matter of life. <i>FEMS Microbiology Letters</i> , 2021, 368, .	1.8	16
4	Adaptive evolution of viruses infecting marine microalgae (haptophytes), from acute infections to stable coexistence. <i>Biological Reviews</i> , 2021, , .	10.4	3
5	Algal Mimiviruses (Mimiviridae). , 2021, , 677-683.		3
6	Removal of large viruses and their dispersal through fecal pellets of the appendicularian <i>Oikopleura dioica</i> during <i>Emiliana huxleyi</i> bloom conditions. <i>Limnology and Oceanography</i> , 2021, 66, 3963.	3.1	1
7	Seasonal Dynamics of Algae-Infecting Viruses and Their Inferred Interactions with Protists. <i>Viruses</i> , 2019, 11, 1043.	3.3	10
8	Seasonality Drives Microbial Community Structure, Shaping both Eukaryotic and Prokaryotic Hostâ€œViral Relationships in an Arctic Marine Ecosystem. <i>Viruses</i> , 2018, 10, 715.	3.3	26
9	Is the Virus Important? And Some Other Questions. <i>Viruses</i> , 2018, 10, 442.	3.3	4
10	Water Masses and Depth Structure Prokaryotic and T4-Like Viral Communities Around Hydrothermal Systems of the Nordic Seas. <i>Frontiers in Microbiology</i> , 2018, 9, 1002.	3.5	6
11	Simple models combining competition, defence and resource availability have broad implications in pelagic microbial food webs. <i>Ecology Letters</i> , 2018, 21, 1440-1452.	6.4	33
12	<i>Micromonas</i> versus virus: New experimental insights challenge viral impact. <i>Environmental Microbiology</i> , 2017, 19, 2068-2076.	3.8	2
13	Linking bacterial community structure to advection and environmental impact along a coast-fjord gradient of the Sognefjord, western Norway. <i>Progress in Oceanography</i> , 2017, 159, 13-30.	3.2	18
14	Emerging Interaction Patterns in the <i>Emiliana huxleyi</i> -EhV System. <i>Viruses</i> , 2017, 9, 61.	3.3	12
15	Seasonal Dynamics of Haptophytes and dsDNA Algal Viruses Suggest Complex Virus-Host Relationship. <i>Viruses</i> , 2017, 9, 84.	3.3	31
16	The Response of Heterotrophic Prokaryote and Viral Communities to Labile Organic Carbon Inputs Is Controlled by the Predator Food Chain Structure. <i>Viruses</i> , 2017, 9, 238.	3.3	16
17	<i>Synechococcus</i> in the Atlantic Gateway to the Arctic Ocean. <i>Frontiers in Marine Science</i> , 2016, 3, .	2.5	103
18	The 474-Kilobase-Pair Complete Genome Sequence of CeV-01B, a Virus Infecting <i>Haptolina</i> (<i>Haptolina</i>)	0.8	17

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19	Tsv-N1: A Novel DNA Algal Virus that Infects <i>Tetraselmis striata</i> . <i>Viruses</i> , 2015, 7, 3937-3953.	3.3	28
20	Seasonal diversity and dynamics of haptophytes in the <sc>S</sc>lagerrak, <sc>N</sc>orway, explored by high-throughput sequencing. <i>Molecular Ecology</i> , 2015, 24, 3026-3042.	3.9	90
21	Characterisation of three novel giant viruses reveals huge diversity among viruses infecting Prymnesiales (Haptophyta). <i>Virology</i> , 2015, 476, 180-188.	2.4	35
22	Top-down and bottom-up control on bacterial diversity in a western Norwegian deep-silled fjord. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv076.	2.7	29
23	A theoretical analysis of how strain-specific viruses can control microbial species diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7813-7818.	7.1	130
24	Virus infection of <i>Haptolina ericina</i> and <i>Phaeocystis pouchetii</i> implicates evolutionary conservation of programmed cell death induction in marine haptophyte-virus interactions. <i>Journal of Plankton Research</i> , 2014, 36, 943-955.	1.8	8
25	Dip in the gene pool: Metagenomic survey of natural coccolithovirus communities. <i>Virology</i> , 2014, 466-467, 129-137.	2.4	10
26	Effects of differences in organic supply on bacterial diversity subject to viral lysis. <i>FEMS Microbiology Ecology</i> , 2013, 83, 202-213.	2.7	13
27	Effect of increased pCO_2 on bacterial assemblage shifts in response to glucose addition in Fram Strait seawater mesocosms. <i>FEMS Microbiology Ecology</i> , 2012, 82, 713-723.	2.7	17
28	Finding a Needle in the Virus Metagenome Haystack - Micro-Metagenome Analysis Captures a Snapshot of the Diversity of a Bacteriophage Armoire. <i>PLoS ONE</i> , 2012, 7, e34238.	2.5	23
29	Diversity of airborne bacteria in samples collected using different devices for aerosol collection. <i>Aerobiologia</i> , 2011, 27, 107-120.	1.7	66
30	Bacterial community composition in an Arctic phytoplankton mesocosm bloom: the impact of silicate and glucose. <i>Polar Biology</i> , 2010, 33, 1557-1565.	1.2	24
31	Viral control of bacterial biodiversity - evidence from a nutrient-enriched marine mesocosm experiment. <i>Environmental Microbiology</i> , 2009, 11, 2585-2597.	3.8	78
32	Photosynthetic genes in viral populations with a large genomic size range from Norwegian coastal waters. <i>FEMS Microbiology Ecology</i> , 2008, 63, 2-11.	2.7	22
33	Marine mimivirus relatives are probably large algal viruses. <i>Virology Journal</i> , 2008, 5, 12.	3.4	104
34	Burden or benefit? Virus-host interactions in the marine environment. <i>Research in Microbiology</i> , 2008, 159, 374-381.	2.1	43
35	Seasonal Variations in Virus-Host Populations in Norwegian Coastal Waters: Focusing on the Cyanophage Community Infecting Marine <i>Synechococcus</i> spp. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4610-4618.	3.1	91
36	Spring phytoplankton bloom dynamics in Norwegian coastal waters: Microbial community succession and diversity. <i>Limnology and Oceanography</i> , 2004, 49, 180-190.	3.1	126

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37	Virioplankton community structure along a salinity gradient in a solar saltern. <i>Extremophiles</i> , 2003, 7, 347-351.	2.3	38
38	ISOLATION AND CHARACTERIZATION OF A VIRUS THAT INFECTS <i>EMILIANA HUXLEYI</i> (HAPTOPHYTA). <i>Journal of Phycology</i> , 2002, 38, 767-774.	2.3	86
39	Isolation and Characterization of Two Viruses with Large Genome Size Infecting <i>Chrysochromulina ericina</i> (Prymnesiophyceae) and <i>Pyramimonas orientalis</i> (Prasinophyceae). <i>Virology</i> , 2001, 290, 272-280.	2.4	133
40	Abundance and Diversity of <i>Archaea</i> in Heavy-Metal-Contaminated Soils. <i>Applied and Environmental Microbiology</i> , 1999, 65, 3293-3297.	3.1	147
41	Analysis of bacterial communities in heavy metal-contaminated soils at different levels of resolution. <i>FEMS Microbiology Ecology</i> , 1999, 30, 237-251.	2.7	10
42	Transfer in Marine Sediments of the Naturally Occurring Plasmid pRAS1 Encoding Multiple Antibiotic Resistance. <i>Applied and Environmental Microbiology</i> , 1994, 60, 4234-4238.	3.1	67