Grieg F Steward

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/472821/publications.pdf

Version: 2024-02-01

80 papers

7,819 citations

71061 41 h-index 71651 76 g-index

86 all docs 86 docs citations

86 times ranked 6885 citing authors

#	Article	IF	Citations
1	Nitrogenase gene diversity and microbial community structure: a cross-system comparison. Environmental Microbiology, 2003, 5, 539-554.	1.8	844
2	Unicellular cyanobacteria fix N2 in the subtropical North Pacific Ocean. Nature, 2001, 412, 635-638.	13.7	678
3	Dynamics of Bacterial Community Composition and Activity during a Mesocosm Diatom Bloom. Applied and Environmental Microbiology, 2000, 66, 578-587.	1.4	592
4	Minimum Information about an Uncultivated Virus Genome (MIUViG). Nature Biotechnology, 2019, 37, 29-37.	9.4	414
5	Variability in ectohydrolytic enzyme activities of pelagic marine bacteria and its significance for substrate processing in the sea. Aquatic Microbial Ecology, 1996, 10, 223-230.	0.9	309
6	Bacteria-organic matter coupling and its significance for oceanic carbon cycling. Microbial Ecology, 1994, 28, 167-179.	1.4	263
7	Abundance and production of bacteria and viruses in the Bering and Chukchi Seas. Marine Ecology - Progress Series, 1996, 131, 287-300.	0.9	262
8	Bacterial mediation of carbon fluxes during a diatom bloom in a mesocosm. Deep-Sea Research Part II: Topical Studies in Oceanography, 1995, 42, 75-97.	0.6	235
9	Variations in bacterial community structure during a dinoflagellate bloom analyzed by DGGE and 16S rDNA sequencing. Aquatic Microbial Ecology, 2001, 23, 119-130.	0.9	223
10	Microbial food web structure in the Arabian Sea: a US JGOFS study. Deep-Sea Research Part II: Topical Studies in Oceanography, 2000, 47, 1387-1422.	0.6	198
11	Spatial distribution of viruses, bacteria and chlorophyll a in nentic, oceanic and estuarme environments. Marine Ecology - Progress Series, 1993, 92, 77-87.	0.9	187
12	Nitrogenase Gene Amplicons from Global Marine Surface Waters Are Dominated by Genes of Non-Cyanobacteria. PLoS ONE, 2011, 6, e19223.	1.1	176
13	Nitrogenase genes in non-cyanobacterial plankton: prevalence, diversity and regulation in marine waters. Aquatic Microbial Ecology, 2010, 61, 235-247.	0.9	165
14	Are we missing half of the viruses in the ocean?. ISME Journal, 2013, 7, 672-679.	4.4	164
15	The complete genomic sequence of the marine phage Roseophage SIO1 shares homology with nonmarine phages. Limnology and Oceanography, 2000, 45, 408-418.	1.6	154
16	Genome size distributions indicate variability and similarities among marine viral assemblages from diverse environments. Limnology and Oceanography, 2000, 45, 1697-1706.	1.6	153
17	Glucose fluxes and concentrations of dissolved combined neutral sugars (polysaccharides) in the Ross Sea and Polar Front Zone, Antarctica. Deep-Sea Research Part II: Topical Studies in Oceanography, 2001, 48, 4179-4197.	0.6	146
18	RNA viruses in the sea. FEMS Microbiology Reviews, 2009, 33, 295-323.	3.9	136

#	Article	IF	Citations
19	Bacterial community composition during two consecutive NE Monsoon periods in the Arabian Sea studied by denaturing gradient gel electrophoresis (DGGE) of rRNA genes. Deep-Sea Research Part II: Topical Studies in Oceanography, 1999, 46, 1791-1811.	0.6	105
20	Phylogenetic Screening of Ribosomal RNA Gene-Containing Clones in Bacterial Artificial Chromosome (BAC) Libraries from Different Depths in Monterey Bay. Microbial Ecology, 2004, 48, 473-488.	1.4	101
21	The seasonal development of the bacterioplankton bloom in the Ross Sea, Antarctica, 1994–1997. Deep-Sea Research Part II: Topical Studies in Oceanography, 2001, 48, 4199-4221.	0.6	100
22	Development and Testing of a DNA Macroarray To Assess Nitrogenase (nifH) Gene Diversity. Applied and Environmental Microbiology, 2004, 70, 1455-1465.	1.4	99
23	Impacts of Hurricanes Katrina and Rita on the microbial landscape of the New Orleans area. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9029-9034.	3.3	97
24	RNA viruses as major contributors to Antarctic virioplankton. Environmental Microbiology, 2016, 18, 3714-3727.	1.8	92
25	A giant virus infecting green algae encodes key fermentation genes. Virology, 2018, 518, 423-433.	1.1	92
26	Virus-induced transfer of organic carbon between marine bacteria in a model community. Aquatic Microbial Ecology, 2003, 33, 1-10.	0.9	87
27	Fingerprinting Diazotroph Communities in the Chesapeake Bay by Using a DNA Macroarray. Applied and Environmental Microbiology, 2004, 70, 1767-1776.	1.4	82
28	Cryptic Blooms: Are Thin Layers the Missing Connection?. Estuaries and Coasts, 2008, 31, 396-401.	1.0	78
29	Constraining bacterial production, conversion efficiency and respiration in the Ross Sea, Antarctica, January–February, 1997. Deep-Sea Research Part II: Topical Studies in Oceanography, 2000, 47, 3227-3247.	0.6	76
30	New Genera of RNA Viruses in Subtropical Seawater, Inferred from Polymerase Gene Sequences. Applied and Environmental Microbiology, 2007, 73, 5937-5944.	1.4	75
31	The Characterization of RNA Viruses in Tropical Seawater Using Targeted PCR and Metagenomics. MBio, 2014, 5, e01210-14.	1.8	69
32	Abundance, Distribution, and Diversity of Viruses in Alkaline, Hypersaline Mono Lake, California. Microbial Ecology, 2004, 47, 9-17.	1.4	68
33	Sufentanil, Morphine, Met-enkephalin, and k-Agonist (U-50,488H) Inhibit Substance P Release from Primary Sensory Neurons. Anesthesiology, 1989, 70, 672-677.	1.3	66
34	Viruses in the Oceanic Basement. MBio, 2017, 8, .	1.8	63
35	Heterotrophic bacterioplankton in the Arabian Sea:. Deep-Sea Research Part II: Topical Studies in Oceanography, 2001, 48, 1303-1323.	0.6	57
36	Bromodeoxyuridine as an alternative to 3H-thymidine for measuring bacterial productivity in aquatic samples. Aquatic Microbial Ecology, 1999, 19, 57-66.	0.9	52

#	Article	IF	Citations
37	A Simple, Rapid Method for Demonstrating Bacterial Flagella. Applied and Environmental Microbiology, 2000, 66, 3632-3636.	1.4	50
38	Purification of viruses by centrifugation., 0,, 166-181.		50
39	Vertical Distribution of Nitrogen-Fixing Phylotypes in a Meromictic, Hypersaline Lake. Microbial Ecology, 2004, 47, 30-40.	1.4	48
40	Temporal and Spatial Variability in Culturable Pathogenic Vibrio spp. in Lake Pontchartrain, Louisiana, following Hurricanes Katrina and Rita. Applied and Environmental Microbiology, 2011, 77, 5384-5393.	1.4	48
41	Application of a nifH oligonucleotide microarray for profiling diversity of N2-fixing microorganisms in marine microbial mats. Environmental Microbiology, 2006, 8, 1721-1735.	1.8	46
42	Population dynamics of Cytophaga-Flavobacteria during marine phytoplankton blooms analyzed by real-time quantitative PCR. Aquatic Microbial Ecology, 2005, 40, 251-257.	0.9	46
43	Nucleic acids from the host bacterium as a major source of nucleotides for three marine bacteriophages. FEMS Microbiology Ecology, 1993, 12, 237-248.	1.3	42
44	Microbial biomass and viral infections of heterotrophic prokaryotes in the sub-surface layer of the central Arctic Ocean. Deep-Sea Research Part I: Oceanographic Research Papers, 2007, 54, 1744-1757.	0.6	40
45	Analysis of a viral metagenomic library from 200 m depth in Monterey Bay, California constructed by direct shotgun cloning. Virology Journal, 2011, 8, 287.	1.4	40
46	Draft genome sequence of marine alphaproteobacterial strain HIMB11, the first cultivated representative of a unique lineage within the Roseobacter clade possessing an unusually small genome. Standards in Genomic Sciences, 2014, 9, 632-645.	1.5	40
47	Spatial and temporal variability of prokaryotes, viruses, and viral infections of prokaryotes in an alkaline, hypersaline lake. Aquatic Microbial Ecology, 2005, 41, 247-260.	0.9	38
48	Morphological Characterization of Viruses in the Stratified Water Column of Alkaline, Hypersaline Mono Lake. Microbial Ecology, 2010, 60, 636-643.	1.4	33
49	Making sense of virus size and the tradeoffs shaping viral fitness. Ecology Letters, 2021, 24, 363-373.	3.0	31
50	Variables influencing the efficiency and interpretation of reverse transcription quantitative PCR (RT-qPCR): An empirical study using Bacteriophage MS2. Journal of Virological Methods, 2017, 241, 1-10.	1.0	28
51	Plasticity in the grazing ecophysiology of <i>Florenciella</i> (Dichtyochophyceae), a mixotrophic nanoflagellate that consumes <i>Prochlorococcus</i> and other bacteria. Limnology and Oceanography, 2021, 66, 47-60.	1.6	28
52	Draft genome sequence of strain HIMB100, a cultured representative of the SAR116 clade of marine Alphaproteobacteria. Standards in Genomic Sciences, 2011, 5, 269-278.	1.5	27
53	Host Traits Drive Viral Life Histories across Phytoplankton Viruses. American Naturalist, 2018, 191, 566-581.	1.0	27
54	Detection of inteins among diverse DNA polymerase genes of uncultivated members of the <i>Phycodnaviridae</i> . ISME Journal, 2009, 3, 409-418.	4.4	26

#	Article	IF	CITATIONS
55	Overlooked and widespread pennate diatom-diazotroph symbioses in the sea. Nature Communications, 2022, 13, 799.	5.8	26
56	Fingerprinting viral assemblages by Pulsed Field Gel Electrophoresis (PFGE). Methods in Microbiology, 2001, , 85-103.	0.4	25
57	Complete genome sequence of bacteriophage VvAW1, which infects Vibrio vulnificus. Standards in Genomic Sciences, 2012, 6, 415-426.	1.5	24
58	Variables Influencing Extraction of Nucleic Acids from Microbial Plankton (Viruses, Bacteria, and) Tj ETQq0 0 0 rgB 2014, 80, 3930-3942.	T /Overloo 1.4	ck 10 Tf 50 6 24
59	Broad phylogenetic and functional diversity among mixotrophic consumers of <i>Prochlorococcus</i> . ISME Journal, 2022, 16, 1557-1569.	4.4	24
60	Significance of bacteria in carbon fluxes in the Arabian Sea. Journal of Earth System Science, 1994, 103, 341-351.	0.6	24
61	Estimating viral proliferation in aquatic samples. Methods in Microbiology, 2001, 30, 67-84.	0.4	23
62	Extraction and purification of nucleic acids from viruses., 0,, 154-165.		20
63	Assembly of a Marine Viral Metagenome after Physical Fractionation. PLoS ONE, 2013, 8, e60604.	1.1	18
64	A novel method for the measurement of dissolved deoxyribonucleic acid in seawater. Limnology and Oceanography: Methods, 2004, 2, 248-255.	1.0	16
65	What's the â€~meta' with metagenomics?. ISME Journal, 2007, 1, 100-102.	4.4	15
66	Towards an integrative view of virus phenotypes. Nature Reviews Microbiology, 2022, 20, 83-94.	13.6	15
67	haracterizing the Effects of Two Storms on the Coastal Waters of O ahu, Hawai i, Using Data from the Pacific Islands Ocean Observing System. Oceanography, 2011, 24, 182-199.	0.5	14
68	Differential specificity of selective culture media for enumeration of pathogenic vibrios: Advantages and limitations of multi-plating methods. Journal of Microbiological Methods, 2015, 111, 24-30.	0.7	12
69	Bacteria in Oceanic Carbon Cycling as a Molecular Problem. , 1995, , 39-54.		12
70	Characterization of the diversity of marine RNA viruses., 0,, 193-201.		12
71	CoCoNet: an efficient deep learning tool for viral metagenome binning. Bioinformatics, 2021, 37, 2803-2810.	1.8	11
72	A method for characterizing dissolved <scp>DNA</scp> and its application to the North Pacific Subtropical Gyre. Limnology and Oceanography: Methods, 2021, 19, 210-221.	1.0	9

#	Article	IF	CITATIONS
73	Characterizing the effluence near Waikiki, Hawaii with a coupled biophysical model. Continental Shelf Research, 2013, 54, 1-13.	0.9	7
74	Divide and Conquer: Enriching Environmental Sequencing Data. PLoS ONE, 2007, 2, e830.	1.1	6
75	Variable Freshwater Influences on the Abundance of <i>Vibrio vulnificus</i> in a Tropical Urban Estuary. Applied and Environmental Microbiology, 2022, 88, AEM0188421.	1.4	5
76	Refining real-time predictions of Vibrio vulnificus concentrations in a tropical urban estuary by incorporating dissolved organic matter dynamics. Science of the Total Environment, 2022, 829, 154075.	3.9	5
77	Physical fractionation of aquatic viral assemblages. Limnology and Oceanography: Methods, 2011, 9, 150-163.	1.0	4
78	Marine Viruses. , 2013, , 127-144.		4
79	Real-Time Observations of the February 2010 Chile and March 2011 Japan Tsunamis Recorded in Honolulu by the Pacific Islands Ocean Observing System. Oceanography, 2014, 27, .	0.5	3
80	A Functional K+ Channel from Tetraselmis Virus 1, a Member of the Mimiviridae. Viruses, 2020, 12, 1107.	1.5	3