

Harriet Alexander

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

13,244
citations

471509

17
h-index

501196

28
g-index

40
all docs

40
docs citations

40
times ranked

16603
citing authors

#	ARTICLE	IF	CITATIONS
1	Bio-GO-SHIP: The Time Is Right to Establish Global Repeat Sections of Ocean Biology. <i>Frontiers in Marine Science</i> , 2022, 8, .	2.5	9
2	Microbiomes of bloom-forming <i>Phaeocystis</i> algae are stable and consistently recruited, with both symbiotic and opportunistic modes. <i>ISME Journal</i> , 2022, 16, 2255-2264.	9.8	19
3	EUKulele: Taxonomic annotation of the unsung eukaryotic microbes. <i>Journal of Open Source Software</i> , 2021, 6, 2817.	4.6	19
4	The Osmolyte Ties That Bind: Genomic Insights Into Synthesis and Breakdown of Organic Osmolytes in Marine Microbes. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	17
5	<i>DMS</i> synthesis genes distinguish two types of <i>DMS</i> producer phenotypes. <i>Environmental Microbiology</i> , 2021, 23, 1656-1669.	3.8	6
6	Seasonal and Geographical Transitions in Eukaryotic Phytoplankton Community Structure in the Atlantic and Pacific Oceans. <i>Frontiers in Microbiology</i> , 2020, 11, 542372.	3.5	22
7	Auxotrophic interactions: a stabilizing attribute of aquatic microbial communities?. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	31
8	Transcriptional response of <i>Emiliana huxleyi</i> under changing nutrient environments in the North Pacific Subtropical Gyre. <i>Environmental Microbiology</i> , 2020, 22, 1847-1860.	3.8	13
9	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	17.5	11,167
10	Transcriptional Shifts Highlight the Role of Nutrients in Harmful Brown Tide Dynamics. <i>Frontiers in Microbiology</i> , 2019, 10, 136.	3.5	19
11	Keeping it light: (re)analyzing community-wide datasets without major infrastructure. <i>GigaScience</i> , 2019, 8, .	6.4	2
12	Re-assembly, quality evaluation, and annotation of 678 microbial eukaryotic reference transcriptomes. <i>GigaScience</i> , 2019, 8, .	6.4	61
13	Transcriptional patterns identify resource controls on the diazotroph <i>Trichodesmium</i> in the Atlantic and Pacific oceans. <i>ISME Journal</i> , 2018, 12, 1486-1495.	9.8	17
14	Shifting metabolic priorities among key protistan taxa within and below the euphotic zone. <i>Environmental Microbiology</i> , 2018, 20, 2865-2879.	3.8	32
15	Phosphorus availability regulates intracellular nucleotides in marine eukaryotic phytoplankton. <i>Limnology and Oceanography Letters</i> , 2017, 2, 119-129.	3.9	38
16	Transcriptional response of the harmful raphidophyte <i>Heterosigma akashiwo</i> to nitrate and phosphate stress. <i>Harmful Algae</i> , 2017, 68, 258-270.	4.8	32
17	Integrating "Big Data" into Aquatic Ecology: Challenges and Opportunities. <i>Limnology and Oceanography Bulletin</i> , 2017, 26, 101-108.	0.4	40
18	What are the type, direction, and strength of species, community, and ecosystem responses to warming in aquatic mesocosm studies and their dependency on experimental characteristics? A systematic review protocol. <i>Environmental Evidence</i> , 2017, 6, .	2.7	3

#	ARTICLE	IF	CITATIONS
19	Virus-host relationships of marine single-celled eukaryotes resolved from metatranscriptomics. <i>Nature Communications</i> , 2017, 8, 16054.	12.8	100
20	Probing the evolution, ecology and physiology of marine protists using transcriptomics. <i>Nature Reviews Microbiology</i> , 2017, 15, 6-20.	28.6	176
21	Conserved Transcriptional Responses to Nutrient Stress in Bloom-Forming Algae. <i>Frontiers in Microbiology</i> , 2017, 8, 1279.	3.5	31
22	Variable depth distribution of <i>Trichodesmium</i> clades in the North Pacific Ocean. <i>Environmental Microbiology Reports</i> , 2016, 8, 1058-1066.	2.4	16
23	Functional group-specific traits drive phytoplankton dynamics in the oligotrophic ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5972-9.	7.1	118
24	Metatranscriptome analyses indicate resource partitioning between diatoms in the field. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2182-90.	7.1	166
25	Sixty Years of Sverdrup: A Retrospective of Progress in the Study of Phytoplankton Blooms. <i>Oceanography</i> , 2014, 27, 222-235.	1.0	47
26	Identifying reference genes with stable expression from high throughput sequence data. <i>Frontiers in Microbiology</i> , 2012, 3, 385.	3.5	40
27	The Transcriptome and Proteome of the Diatom <i>Thalassiosira pseudonana</i> Reveal a Diverse Phosphorus Stress Response. <i>PLoS ONE</i> , 2012, 7, e33768.	2.5	296
28	Marine Microeukaryote Metatranscriptomics: Sample Processing and Bioinformatic Workflow Recommendations for Ecological Applications. <i>Frontiers in Marine Science</i> , 0, 9, .	2.5	8