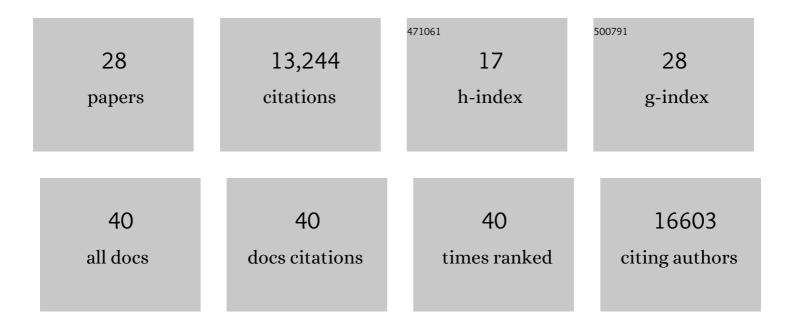
Harriet Alexander

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Bio-GO-SHIP: The Time Is Right to Establish Global Repeat Sections of Ocean Biology. Frontiers in Marine Science, 2022, 8, .	1.2	9
2	Microbiomes of bloom-forming <i>Phaeocystis</i> algae are stable and consistently recruited, with both symbiotic and opportunistic modes. ISME Journal, 2022, 16, 2255-2264.	4.4	19
3	EUKulele: Taxonomic annotation of the unsung eukaryotic microbes. Journal of Open Source Software, 2021, 6, 2817.	2.0	19
4	The Osmolyte Ties That Bind: Genomic Insights Into Synthesis and Breakdown of Organic Osmolytes in Marine Microbes. Frontiers in Marine Science, 2021, 8, .	1.2	17
5	<scp>DMSP</scp> synthesis genes distinguish two types of <scp>DMSP</scp> producer phenotypes. Environmental Microbiology, 2021, 23, 1656-1669.	1.8	6
6	Seasonal and Geographical Transitions in Eukaryotic Phytoplankton Community Structure in the Atlantic and Pacific Oceans. Frontiers in Microbiology, 2020, 11, 542372.	1.5	22
7	Auxotrophic interactions: a stabilizing attribute of aquatic microbial communities?. FEMS Microbiology Ecology, 2020, 96, .	1.3	31
8	Transcriptional response of Emiliania huxleyi under changing nutrient environments in the North Pacific Subtropical Gyre. Environmental Microbiology, 2020, 22, 1847-1860.	1.8	13
9	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	9.4	11,167
10	Transcriptional Shifts Highlight the Role of Nutrients in Harmful Brown Tide Dynamics. Frontiers in Microbiology, 2019, 10, 136.	1.5	19
11	Keeping it light: (re)analyzing community-wide datasets without major infrastructure. GigaScience, 2019, 8, .	3.3	2
12	Re-assembly, quality evaluation, and annotation of 678 microbial eukaryotic reference transcriptomes. GigaScience, 2019, 8, .	3.3	61
13	Transcriptional patterns identify resource controls on the diazotroph <i>Trichodesmium</i> in the Atlantic and Pacific oceans. ISME Journal, 2018, 12, 1486-1495.	4.4	17
14	Shifting metabolic priorities among key protistan taxa within and below the euphotic zone. Environmental Microbiology, 2018, 20, 2865-2879.	1.8	32
15	Phosphorus availability regulates intracellular nucleotides in marine eukaryotic phytoplankton. Limnology and Oceanography Letters, 2017, 2, 119-129.	1.6	38
16	Transcriptional response of the harmful raphidophyte Heterosigma akashiwo to nitrate and phosphate stress. Harmful Algae, 2017, 68, 258-270.	2.2	32
17	Integrating "Big Data―into Aquatic Ecology: Challenges and Opportunities. Limnology and Oceanography Bulletin, 2017, 26, 101-108.	0.2	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. Environmental Evidence, 2017, 6, .	1.1	3

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#	Article	IF	CITATIONS
19	Virus-host relationships of marine single-celled eukaryotes resolved from metatranscriptomics. Nature Communications, 2017, 8, 16054.	5.8	100
20	Probing the evolution, ecology and physiology of marine protists using transcriptomics. Nature Reviews Microbiology, 2017, 15, 6-20.	13.6	176
21	Conserved Transcriptional Responses to Nutrient Stress in Bloom-Forming Algae. Frontiers in Microbiology, 2017, 8, 1279.	1.5	31
22	Variable depth distribution of <i>Trichodesmium</i> clades in the North Pacific Ocean. Environmental Microbiology Reports, 2016, 8, 1058-1066.	1.0	16
23	Functional group-specific traits drive phytoplankton dynamics in the oligotrophic ocean. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5972-9.	3.3	118
24	Metatranscriptome analyses indicate resource partitioning between diatoms in the field. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2182-90.	3.3	166
25	Sixty Years of Sverdrup: A Retrospective of Progress in the Study of Phytoplankton Blooms. Oceanography, 2014, 27, 222-235.	0.5	47
26	Identifying reference genes with stable expression from high throughput sequence data. Frontiers in Microbiology, 2012, 3, 385.	1.5	40
27	The Transcriptome and Proteome of the Diatom Thalassiosira pseudonana Reveal a Diverse Phosphorus Stress Response. PLoS ONE, 2012, 7, e33768.	1.1	296
28	Marine Microeukaryote Metatranscriptomics: Sample Processing and Bioinformatic Workflow Recommendations for Ecological Applications. Frontiers in Marine Science, 0, 9, .	1.2	8