HARRIET ALEXANDER

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EDUCATION

PhD, Biological Oceanography, MIT-WHOI Joint Program, Cambridge / Woods Hole, MA	2016
Advisor: Dr. Sonya Dyhrman	
BA, Biological Sciences, Wellesley College, Wellesley, MA	2010
Departmental Honors in Biological Sciences, Minor in Mathematics, cum laude	

PROFESSIONAL EXPERIENCE

Assistant Scientist , Biology Department, Woods Hole Oceanographic Institution Woods Hole, MA	2018-present
Postdoctoral Fellow, University of California, Davis, Davis, CA Advisor: Dr. C. Titus Brown	2016-2018
Postdoctoral Investigator , Lamont-Doherty Earth Observatory, Palisades, NY Advisor: Dr. Sonya Dyhrman	2016

SELECTED AWARDS AND FELLOWSHIPS

Simons Early Career Investigator in Marine Microbial Ecology and Evolution Av	ward 2022
GigaScience Paper Prize ICG13	2018
EMBL Travel Award	2016
NSF ECOGEO Workshop Travel Award	2015
OCB Trait-based Ecology Conference Travel Award	2015
Ocean Life Institute Fellowship	2014–2015
OCB Scoping Workshop Travel Award	2014
National Defense Science and Engineering Fellowship	2011-2014
National Science Foundation Graduate Research Fellowship	2011 (declined for NDSEG)
MIT Presidential Fellowship	2010–2011
Lucy Allen Branch Prize in Natural History	2010
Jane Harris Schneider Prize in Sculpture	2010

PUBLICATIONS

Mentored students and postdocs are <u>underlined</u>. * indicates equal contribution and authorship.

[30] <u>Krinos AI</u>, Cohen NR, Follows MJ, **Alexander H**. (2023). Reverse engineering environmental metatranscriptomes clarifies best practices for eukaryotic assembly. *BMC bioinformatics* 24:1–36.

Role: Conceived of the project, designed pipeline and associated test datasets with AIK, analyzed and interpreted data, co-wrote the manuscript.

[29] Mars Brisbin M, Mitarai S, Saito MA, **Alexander H**. (2022). Microbiomes of bloom-forming phaeocystis algae are stable and consistently recruited, with both symbiotic and opportunistic modes. *The ISME Journal* pp 1–10. doi:10.1038/s41396-022-01263-2.

Role: Contributed to experimental design and data analysis and interpretation. Contributed to paper editing.

[28] Cohen NR, **Alexander H**, <u>Krinos AI</u>, Hu SK, Lampe RH. (2022). Marine microeukaryote metatranscriptomics: Sample processing and bioinformatic workflow recommendations for ecological applications. *Frontiers in Marine Science* 9. doi:10.3389/fmars.2022.867007.

Role: Co-conceived of the paper, co-wrote paper.

[27] *Clayton S, *Alexander H, Graff JR, Poulton NJ, Thompson LR, Benway H, Boss E, Martiny A. (2022). Bio-go-ship: The time is right to establish global repeat sections of ocean biology. Frontiers in Marine Science 8. doi:10.3389/fmars.2021.767443.

Role: Equal authorship with Clayton, co-wrote paper, designed figures.

[26] *McParland EL, *Alexander H, *Johnson WM. (2021). The osmolyte ties that bind: genomic insights into synthesis and breakdown of organic osmolytes in marine microbes. Frontiers in Marine Science 8:732. doi:10.3389/fmars.2021.689306.

Role: Equal co-authorship with other two authors (a fun pandemic computational project). Co-conceived of project, designed and carried out bioinformatic analyses, co-wrote the paper.

[25] Krinos Al, Hu SK, Cohen NR, **Alexander H**. (2021). Eukulele: Taxonomic annotation of the unsung eukaryotic microbes. *Journal of Open Source Software* 6:2817. doi:10.21105/joss.02817.

Role: Conceived of project, wrote the original software, co-wrote the paper.

[24] McParland EL, Lee MD, Webb EA, **Alexander H**, Levine NM. (2021). DMSP synthesis genes distinguish two types of DMSP producer phenotypes. *Environmental Microbiology* 23:1656–1669. doi:10.1111/1462-2920.15393.

Role: Contributed to bioinformatics data analysis and interpretation, and contributed to paper editing.

[23] Fiore CL, **Alexander H**, Soule MCK, Kujawinski EB. (2021). A phosphate starvation response gene (psr1-like) is present and expressed in micromonas pusilla and other marine algae. *Aquatic Microbial Ecology* 86:29–46. doi:10.3354/ame01955.

Role: Performed to metagenomic data analysis, contributed to interpretation and paper editing.

- [22] Alexander H, Rouco M, Haley ST, Dyhrman ST. (2020). Transcriptional response of *Emiliania huxleyi* under changing nutrient environments in the North Pacific Subtropical Gyre. *Environmental Microbiology*. doi:doi:10.1111/1462-2920.14942.
- [21] Johnson WM, **Alexander H**, Bier RL, Miller DR, Muscarella ME, Pitz KJ, Smith H. (2020). Auxotrophic interactions: A stabilizing attribute of aquatic microbial communities? *FEMS Microbiology Ecology*. doi:10.1093/femsec/fiaa115.

Role: Co-conceived of the manuscript, contributed to writing of the paper and designed figures.

[20] Choi CJ, Jimenez V, Needham DM, Poirier C, Bachy C, **Alexander H**, Wilken S, Chavez FP, Sudek S, Giovannoni SJ, Worden AZ. (2020). Seasonal and geographical transitions in eukary-otic phytoplankton community structure in the atlantic and pacific oceans. *Front. Microbiol.* 11. doi:10.3389/fmicb.2020.542372.

Role: Contributed to data analysis, collection, and interpretation and edited manuscript.

[19] Bolyen E, et al. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology* 37:852–857. doi:10.1038/s41587-019-0209-9.

Role: Wrote and documented a giime2 plugin application.

[18] Wurch LL, **Alexander H**, Frischkorn KR, Haley ST, Gobler CJ, Dyhrman ST. (2019). Transcriptional shifts highlight the role of nutrients in harmful brown tide dynamics. *Frontiers in Microbiology* 10:136. doi:10.3389/fmicb.2019.00136.

Role: Contributed to bioinformatics data analysis and interpretation, and contributed to paper editing.

- [17] **Alexander H**, Johnson LK, Brown CT. (2018). Keeping it light: (Re)analyzing community-wide datasets without major infrastructure. *GigaScience*. doi:10.1093/gigascience/giy159.
- [16] Johnson LK, **Alexander H**, Brown CT. (2018). Re-assembly, quality evaluation, and annotation of 678 microbial eukaryotic reference transcriptomes. *GigaScience*. doi:10.1093/gigascience/giy158.

Role: Contributed transcriptomic and metatranscriptomic data to the paper, ran bioinformatic analyses and created figures.

[15] Hu SK, Liu Z, Alexander H, Campbell V, Connell PE, Dyhrman ST, Heidelberg KB, Caron DA. (2018). Shifting metabolic priorities among key protistan taxa within and below the euphotic zone. Environmental Microbiology. doi:10.1111/1462-2920.14259.

Role: Designed and ran bioinformatic analyses, and contributed to interpretation and manuscript preparation.

[14] Rouco M, Frischkorn KR, Haley ST, **Alexander H**, Dyhrman ST. (2018). Transcriptional patterns identify resource controls on the diazotroph *Trichodesmium* in the Atlantic and Pacific oceans. *The ISME Journal* 12:1486–1495. doi:10.1038/s41396-018-0087-z.

Role: Collected samples for analysis, assisted in bioinformatics analysis and interpretation, commented on manuscript.

[13] Haley ST, **Alexander H**, Juhl AR, Dyhrman ST. (2017). Transcriptional response of the harmful raphidophyte *Heterosigma akashiwo* to nitrate and phosphate stress. *Harmful Algae* 68:258–270. doi:10.1016/j.hal.2017.07.001.

Role: Performed bioinformatic analyses, contributed to biological interpretation and paper writing.

[12] Harke MJ, Juhl AR, Haley ST, **Alexander H**, Dyhrman ST. (2017). Conserved transcriptional responses to nutrient stress in bloom-forming algae. *Frontiers in Microbiology* 8. doi:10.3389/fmicb.2017.01279.

Role: Contributed to data analysis and interpretation, provided comments on paper.

[11] Moniruzzaman M, Wurch LL, **Alexander H**, Dyhrman ST, Gobler CJ, Wilhelm SW. (2017). Virus-host relationships of marine single-celled eukaryotes resolved from metatranscriptomics. *Nature Communications* 8:16054. doi:10.1038/ncomms16054.

Role: Contributed metatranscriptomic data to the paper, contributed to data analysis and interpretation.

[10] Kujawinski EB, Longnecker K, Alexander H, Dyhrman ST, Fiore CL, Haley ST, Johnson WM. (2017). Phosphorus availability regulates intracellular nucleotides in marine eukaryotic phytoplankton. *Limnology and Oceanography Letters* 2:119–129.

Role: Contributed transcriptomic and metatranscriptomic data to the paper, ran bioinformatic analyses and created figures.

[9] Guy-Haim T, Alexander H, Bell TW, Bier RL, Bortolotti LE, Briseño-Avena C, Dong X, Flanagan AM, Grosse J, Grossmann L, Hasnain S, Hovel R, Johnston CA, Miller DR, Muscarella M, Noto AE, Reisinger AJ, Smith HJ, Stamieszkin K. (2017). 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* 6:6. doi:10.1186/s13750-017-0084-0.

Role: Contributed to experimental design, performed literature review, and contributed to paper writing.

[8] Durden J, Luo J, **Alexander H**, Flanagan A, Grossmann L. (2017). Integrating "big data" into aquatic ecology: Challenges and opportunities. *Limnology and Oceanography Bulletin*. doi:10.1002/lob.10213.

Role: Conceived of paper and contributed to paper writing.

[7] Caron DA, **Alexander H**, Allen AE, Archibald JM, Armbrust EV, Bachy C, Bell CJ, Bharti A, Dyhrman ST, Guida SM, Heidelberg KB, Kaye JZ, Metzner J, Smith SR, Worden AZ. (2016). Probing the evolution, ecology and physiology of marine protists using transcriptomics. *Nature Reviews Microbiology* 15:6–20. doi:10.1038/nrmicro.2016.160.

Role: Contributed a figure and co-wrote a section of the paper.

[6] Rouco M, Haley ST, Alexander H, Wilson ST, Karl DM, Dyhrman ST. (2016). Variable depth distribution of *Trichodesmium* clades in the North Pacific Ocean. *Environmental Microbiology Reports*. doi:10.1111/1758-2229.12488.

Role: Collected and processed samples on cruises and contributed to data analysis and paper editing.

- [5] **Alexander H**, Rouco M, Haley ST, Wilson ST, Karl DM, Dyhrman ST. (2015). Functional group-specific traits drive phytoplankton dynamics in the oligotrophic ocean. *Proceedings of the National Academy of Sciences* 112:E5972–E5979. doi:10.1073/pnas.1518165112.
- [4] **Alexander H**, Jenkins BD, Rynearson TA, Dyhrman ST. (2015). Metatranscriptome analyses indicate resource partitioning between diatoms in the field. *Proceedings of the National Academy of Sciences* 112:E2182–E2190. doi:10.1073/pnas.1421993112.
- [3] Fischer A, Moberg E, **Alexander H**, Brownlee E, Hunter-Cevera K, Pitz K, Rosengard S, Sosik H. (2014). Sixty Years of Sverdrup: A Retrospective of Progress in the Study of Phytoplankton Blooms. *Oceanography* 27:222–235. doi:10.5670/oceanog.2014.26.

Role: Contributed to paper conception and writing.

- [2] **Alexander H**, Jenkins BD, Rynearson TA, Saito MA, Mercier ML, Dyhrman ST. (2012). Identifying reference genes with stable expression from high throughput sequence data. *Frontiers in Microbiology* 3:385. doi:10.3389/fmicb.2012.00385.
- [1] Dyhrman ST, Jenkins BD, Rynearson TA, Saito MA, Mercier ML, **Alexander H**, Whitney LP, Drzewianowski A, Bulygin VV, Bertrand EM, Wu Z, Benitez-Nelson C, Heithoff A. (2012). The transcriptome and proteome of the diatom *Thalassiosira pseudonana* reveal a diverse phosphorus stress response. *PloS one* 7:e33768. doi:10.1371/journal.pone.0033768.

Role: Performed bioinformatic analyses and contributed to figure design, commented on paper.

INVITED PRESENTATIONS

- [12] Alexander H. A eukaryotic heist: scalable and automated approaches for the study of eukaryotic genomes. Rutgers Department of Marine and Coastal Sciences, New Brunswick, NJ. April 2023.
- [11] Alexander H. A eukaryotic heist: scalable and automated approaches for the discovery of eukaryotic genomes. Bioinformatics Virtual Coordination Network Conference, Online. June 2021.

- [10] Alexander H. A eukaryotic heist: scalable and automated approaches for the discovery of eukaryotic genomes. Marine and Environmental Biology Seminar, University of Southern California, Online. April 2021.
- [9] Alexander H. A eukaryotic heist: scalable and automated approaches for the discovery of eukaryotic genomes. University of Georgia MARS Seminar, Online. October 2020.
- [8] Alexander H. A eukaryotic heist: scalable and automated approaches for the discovery of eukaryotic genomes. Simons Foundation CBIOMES Meeting, Online. June 2020.
- [7] Alexander H. Bioinformatics in light of intercalibration. OCB NA Omics Standardization and Intercalibration Workshop, Chapel Hill, NC. January 2020.
- [6] Alexander H. Computational approaches to the study of marine protists. Biology Seminar, Graduate School of Oceanography, University of Rhode Island, Narragansett, RI. May 2019.
- [5] Alexander H. Computational approaches to the study of marine protists. Parsons Microbial Systems Seminar, Massachusetts Institute of Technology, Cambridge, MA. April 2019.
- [4] Alexander H. The role of intra-specific diversity on the physiological ecology of phytoplankton. Marine Science Department, Old Dominion University, Norfolk, VA. March 2019.
- [3] Alexander H. Combining in situ and culture-based approaches to characterize the physiological ecology of blooming and sinking diatoms. The Molecular Life of Diatoms, Kobe, Japan. July 2017.
- [2] Alexander H. The role of intra-specific diversity on the physiological ecology of phytoplankton. Interdepartmental Graduate Program in Marine Science, University of California, Santa Barbra, Santa Barbra, CA. May 2017.
- [1] Alexander H. Strain variation and transcriptional response of the *Emiliania huxleyi* species complex under changing nutrient environments. ASLO, Honolulu, HI. February 2017.

SELECTED ABSTRACTS

- [21] <u>Krinos AI</u>, Shapiro SK, Follows M, **Alexander H**. Thermal acclimation experiments highlight intraspecific differences in the flexibility of Emiliania huxleyi to thermal stimuli. International Society of Evolutionary Protistologists (ISEP), Virtual. January 2023.
- [20] <u>Krinos AI</u>, Cohen NR, Follows M, **Alexander H**. eukrhythmic: leveraging the metatranscriptomic landscape to reproduciblity detect and describe marine protistan communities. Association for the Sciences of Limnology and Oceanography Aquatic Sciences Meeting, Virtual. May 2021.
- [19] Krinos Al, Cohen NR, Hu S, Gast R, Follows M, Dyhrman S, Alexander H. Exploring the ecology of marine cryptophytes with metatranscriptomics. Gordon Research Conference on Marine Microbes, Les Diablerets, Switzerland. June 2022.
- [18] **Alexander H**, Hu S. Eukaryotic genome discovery: Scalable and automated retrieval of eukaryotic metagenome assembled genomes (MAGs) from a global-scale dataset. Ocean Sciences, San Diego, CA. February 2020.
- [17] <u>Blum L</u>, Pachiadaki M, **Alexander H**. Microbial drivers of nitrogen metabolism: Searching Tara Oceans metagenomes. Ocean Sciences, San Diego, CA. February 2020.
- [16] Alexander H, Phillips J, Thomas M, Chisholm C, Craft K, Galindo V, Neveu M, Laney S, Karenz D, Manahan D. Antarctic Biology Training II: Automatic image classification and colony morphology of Phaeocystis antarctica. Polar Marine Science GRC, Lucca, Italy. March 2019.
- [15] **Alexander H**, Brown CT. Reference- and assembly-independent, scalable discovery of shared content between metagenomic datasets. Ocean Sciences, Portland, OR. February 2018.

- [14] **Alexander H**, Durkin C, Dyhrman ST. Combining *in situ* and culture-based 'omic and biogeochemical measures to identify the physiological ecology of a blooming diatom in the Amazon River Plume. Ocean Sciences, New Orleans, LA. February 2016.
- [13] Kujawinski E, Longnecker K, **Alexander H**, Dyhrman S, Jenkins B, Rynearson T. Multi-omics profiling of phytoplankton community metabolism: linking metatranscriptomics and metabolomics to elucidate phytoplankton physiology in a model coastal system. Ocean Sciences, New Orleans, LA. February 2016.
- [12] Rosengard SZ, **Alexander H**, Cramer C. SUBMERGE! Bringing the ocean closer to New York City. Ocean Sciences, New Orleans, LA. February 2016.
- [11] Alexander H, Dyhrman ST. Nutrient pulses uniquely drive physiological ecology of cosmopolitan phytoplankton strains. A New Age of Discovery for Aquatic Microeukaryotes, Heidelberg, Germany. January 2016.
- [10] Alexander H, Rouco M, Haley ST, Wilson ST, Karl DM, Dyhrman ST. Functional group-specific traits drive phytoplankton dynamics in the oligotrophic ocean. Trait-based Approaches to Ocean Life, Waterville, NH. October 2015.
- [9] **Alexander H**, Jenkins BD, Rynearson TA, Dyhrman ST. Metatranscriptome analyses indicate resource partitioning between diatoms in the field. The Molecular Life of Diatoms, Seattle, WA. July 2015.
- [8] **Alexander H**, Rouco M, Haley ST, Dyhrman ST. Eukaryotic metatranscriptome profiling identifies the unique response of phytoplankton functional groups to deep water upwelling at Station ALOHA. ASLO, Granada, Spain. February 2015.
- [7] Alexander H. Sixty years of Sverdrup. Wellesley College, Wellesley, MA. June 2014. Invited talk.
- [6] Alexander H, Jenkins BD, Rynearson TA, Dyhrman ST. Eukaryotic metatranscriptomics reveals niche differentiation between two diatoms in Narragansett Bay,. Marine Microbes Gordon Research Conference, Waltham, MA. June 2014.
- [5] Alexander H, Rouco M, Haley ST, Dyhrman ST. Eukaryotic metatranscriptomics illuminates physiological response of phytoplankton to nutrient pulses at Station ALOHA. Ocean Carbon and Biogeochemistry Summer Workshop, Woods Hole, MA. July 2013.
- [4] **Alexander H**, Jenkins B, Rynearson T, Saito M, Mercier M, Dyhrman S. Identifying reference genes with stable expression from high throughput sequence data. ASLO, New Orleans, LA. February 2013.
- [3] **Alexander H**, Dyhrman S. Assessing patterns in expression from transcriptome data. Town Hall: Marine Microbial Transcriptome Project, ASLO, New Orleans, LA. February 2013. *Invited talk*.
- [2] **Alexander H**, Monier A, McRose D, Wilcox H, Worden A. Prasinophyte phylogenetic characterization along a transect from Monterey Bay to oligotrophic waters. Rhulman Conference, Wellesley, MA. April 2010.
- [1] **Alexander H**, Monier A, McRose D, Wilcox H, Worden A. Prasionphytae phylogenetic characterization along a transect from Monterey Bay to oligotrophic waters and application to 454-TAG sequence analysis. Ocean Sciences, Portland, OR. February 2010.

SUPERVISION AT WHOI

MIT-WHOI Joint Program Graduate Students

Miah Manning, June 2023-present.

Jo Hickman, NSF Graduate Fellow, June 2023-present.

Arianna Krinos, co-advised with Mick Follows, Computational Science Graduate Fellowship, June 2019-present.

WHOI Postdoctoral Scholars

Margaret Mars Brisbin, November 2020-present, co-advised with Mak Saito, WHOI Postdoctoral Scholar and Simons Foundation Postdoctoral Fellow in Marine Microbial Ecology.

Other Students

Alese Schofield, CC-CREW, Summer 2022

Patrick White, Guest Student, MSc Student at University of Alberta, 2021-2023

Celeste Nobrega, Guest Student, Summer 2021

Kevin Rice, Guest Student, Summer 2021

Laura Blum, Summer Student Fellow, Summer 2019

Thesis Committees

Serena Sung-Clarke, MIT Thesis Committee member (MIT-WHOI), 2021-present

Max Jahns, Thesis Committee member, 2021-present

David Geller-McGrath, Thesis Committee member, 2019-present

Cynthia Becker, Thesis Committee member, 2018-2023

Technical Staff

Sara Shapiro, Research Assistant II, 2021-present

EDUCATIONAL ACTIVITIES

Instructor, 12.756 Environmental Bioinformatics, MIT-WHOI Joint Program Fall 2019-present Co-created and instructed 12-credit graduate course on environmental and non-model bioinformatic approaches with M. Pachiadaki and C. Tepolt. Taught in alternating years.

Instructor, MBL Physiology Course, Marine Biological Laboratory

Organized and taught an introduction to bioinformatics for the MBL Physiology course with a focus on transcriptomics and phylogenetics.

Instructor, Software Carpentry, Woods Hole Oceanographic Institution

June 2021

Organized and taught Software Carpentry course for WHOI SSFs and incoming JP students, teaching introductory UNIX shell scripting and Python programming.

Instructor, Software Carpentry, Woods Hole Oceanographic Institution

June 2020

Organized and taught Software Carpentry course for WHOI SSFs and incoming JP students, teaching introductory UNIX shell scripting, Python programming, and Git versioning.

Lead Instructor, Environmental Metagenomics Workshop, Data Intensive Biology Summer Institute *July* 2017

Organized and taught workshop on environmental metagenomic analysis and interpretation.

Instructor, Metagenomics Workshop, University of California, Santa Cruz

April 2017

Taught workshop on environmental metagenomic analysis and interpretation.

Instructor, Metagenomics Workshop, Scripps Institute of Oceanography

Taught workshop on environmental metagenomic analysis and interpretation.

Instructor, Software Carpentry, Woods Hole Oceanographic Institution September 2015
Organized and taught Software Carpentry course at WHOI, teaching introductory UNIX shell scripting, Python programming, and Git versioning.

Teaching Assistant, Biological Oceanography, MIT-WHOI Joint Program

Conducted recitation sections, wrote and graded tests, problem sets, and daily assignments, advised professors on student performance.

Writing Tutor, Pforzheimer Learning and Teaching Center, Wellesley College 2007-2010 Peer tutor trained to assist in all aspects of the writing process- specialized in writing for the sciences and social sciences. Math Tutor and Grader, Mathematics Department, Wellesley College 2009-2010 Grader for multivariable calculus and number theory. Tutor and assistant for number theory. **PROFESSIONAL ACTIVITIES** Woods Hole Oceanographic Institution Co-Chair, HPC Committee 2019-present Member, SciSec 2019-2022 Member, Biology Chair Search Committee 2019 Member, HPC Committee 2018-present Outside WHOI Member, BCO-DMO Strategic Planning Committee 2019-present Session Convener, ASLO Meeting, Co-chair of session titled "Molecular Insights into 2017 Adaptive Microbial Physiology" at ASLO Meeting, Honolulu, HI. Session Convener, SciPy, Co-chair of mini-symposium on "Computational Reproducibility" 2016 at SciPy, Austin, TX. Professional Development and Workshop Participation Participant, UNOLS Chief Scientist Training Cruise, Honolulu HI. 2019 Invited Participant, BioGeoScapes Scoping Workshop, Woods Hole, MA. 2018 Participant, National Academies Keck Futures Initiative (NAKFI): Discovering the Fall 2018 Deep Blue Sea, Irvine, CA. Participant, EcoDAS XII: Ecological Dissertations in the Aquatic Sciences, Honolulu, HI. 2016 Invited Participant, Plant Science Research Network Scenario Modeling Workshop, Chevy Chase, MD. 2016 Participant, OCB Scoping Workshop: Trait-based approaches to ocean life, Waterville Valley, NH. 2015 Participant, OCB Scoping Workshop: Improving predictive biogeochemical models through single cell-based analyses of marine plankton, Boothbay, ME. 2014 Reviewer National Science Foundation, NSF Graduate Research Fellowship Program, National Defense Science and Engineering Graduate Fellowshp Program, Moore Foundation, Nature Communications, ISME Journal, Environmental Microbiology, Limnology and Oceanography, Journal of Phycology, GigaScience RESEARCH CRUISES **UNOLS Chief Scientist Training Cruise; KN19-10**, R/V Kilo Moana 14-23 June 2019 Seasonal Trophic Roles of *Euphasia suberba* (STRES); NBP14-10, R/V Palmer December 2014 Chief Scientist: Edward Durbin Deep Dissolved Organic Matter (DeepDOM); KN210-04, R/V Knorr March-May 2013 Chief Scientists: Elizabeth Kujawinski Krista Longnecker Hawaii Ocean Experiment (HOE-DYLAN 9); KM12-19, R/V Kilo Moana August-September 2012 Chief Scientist: Sam Wilson

OUTREACH

August 2012

Hawaii Ocean Experiment (HOE-DYLAN 7); KM12-17, R/V Kilo Moana

Chief Scientist: Sonya Dyhrman

Skype a scientist, Skyped directly with various elementary - high school classrooms	2018-present
to share about research and ocean science.	
Submerge!, New York City marine science festival. Designed and manned booth of hands-on	2014
activities focused on the biological pump (>4000 in attendance).	
Women in Ocean Engineering, Volunteered weekends to work with middle school age girls	2014
introducing them to engineering concepts in a marine environment.	
Artistic Oceanographer Program, Combining science and art to teach science concepts.	2011-2014
Falmouth Public School Science Fair, Judged middle and high school science fair.	2011-2013
STEM for Girls at the New England Aquarium, Mentored and volunteered for a	2012
program to encourage girls to pursue math and science.	

SKILLS AND CERTIFICATIONS

Certifications Software Carpentry Instructor Training, PADI SCUBA Open Water **Computation** Python (language of choice), Matlab, R, shell script **Languages** English, French (conversational)