

PROFESSIONAL PREPARATION

- University of Southampton, United Kingdom, Molecular Biology, Ph.D. 2010
- King's College London, United Kingdom, Biological Sciences, B.Sc. 2005

APPOINTMENTS

- 2015 – Project Scientist, Center for Genomics and Systems Biology, New York University (Lab of Jane Carlton; as of Oct 2015)
- 2014 – 2015 Birmingham Fellow, School of Biosciences, University of Birmingham, UK
- 2012 – 2014 Postdoctoral researcher, University of California, Davis; UCD Genome Center & Associate with the Center for Population Biology (Advisor: Jonathan Eisen)
- 2010 – 2011 Postdoctoral researcher, Hubbard Center for Genome Studies, University of New Hampshire (Advisor: W. Kelley Thomas)

RESEACH GRANTS AWARDED

- Principal Investigator, “RCN EukHiTS: Eukaryotic biodiversity research using high-throughput sequencing”, DBI-1262480 awarded by the National Science Foundation (\$296,485; Sept 2013 – Aug 2018)
- Principal Investigator, “A Research-Driven Data Visualization Framework for High-Throughput Environmental Sequence Data”, awarded by the Alfred P. Sloan Foundation (\$247,189; July 2013 – Aug 2014)
- Co-PI, “Genomic Responses to the Deepwater Horizon event and development of high-throughput biological assays for oil spills”, awarded by the Gulf of Mexico Research Initiative (\$119,834; Jan 2016 – Dec 2018)
- Co-PI, “Assessing benthic meiofaunal community structure in the Alaskan Arctic: A high-throughput DNA sequencing approach”, awarded by the North Pacific Research Board (\$40,906; July 2013 – August 2016)
- Co-PI, Amazon AWS cloud computing support for the analysis of microbial eukaryote Illumina datasets (\$5,000; Apr 2012 – Sept 2014)
- Co-PI, “SMBE Satellite Meeting on Eukaryotic –Omics” (\$27,741 awarded by the Society for Molecular Biology and Evolution; meeting held April 29-May 2, 2013 at UC Davis)
- Co-PI, NESCent Catalysis Meeting on “High-Throughput Biodiversity Assessment using Eukaryotic Metagenetics” awarded through the National Evolutionary Synthesis Center (NESCent), Durham, NC. (24 participants funded to attend meeting in January 2011)

AWARDS & HONORS

- Recipient of a 2014 Birmingham Fellowship in Bioinformatics
- “Professors for the Future” Fellowship (2013-14 cohort at UC Davis)

ACADEMIC SERVICE

- Subject Editor, mSystems, an American Society for Microbiology journal (2015—present)
- Subject Editor, Molecular Ecology and Molecular Ecology Resources (2014—present)
- Executive Board, Deep-Sea Biology Society (2014—present)
- Deep Carbon Observatory, External Midterm Review Committee (reporting to the President of the Alfred P. Sloan Foundation; October 2014)
- Ad hoc reviewer, Alfred P. Sloan Foundation (2014—present)
- Ad hoc reviewer and panel service, National Science Foundation (2012—present)
- DOE JGI reviewer for community sequencing proposals (2013—present)
- Journal Review Work: *Aquatic Microbial Ecology*, *Bioinformatics*, *BMC Biology*, *BMC Bioinformatics*, *BMC Evolutionary Biology*, *BMC Ecology*, *Diversity*, *Environmental Science and Pollution Research*, *Experimental Marine Biology*, *Freshwater Biology*, *Frontiers in Zoology*, *Journal of Biogeography*, *Molecular Ecology*, *Molecular Ecology Resources*, *PLoS Biology*, *PLOS ONE*, *Proceedings of the Royal Society B*, *The ISME Journal*

PUBLICATIONS – Submitted or in preparation

1. **Bik HM**, Darling A. Biodiversity and phylogeography of sediment microbial eukaryote communities on the Mid-Atlantic Ridge, *in preparation*
2. **Bik HM**, Sharma J, Halanych K, Thomas WK. Illumina sequencing reveals long-term community shifts in sediment microbial eukaryote communities impacted by the Deepwater Horizon oil spill, *in preparation*
3. **Bik HM**, Alexiev A, Lang JM, Neufeld J, Sauder L, Jospin G, Eisen JA, Flanagan J, Haggerty M, Shaver A, Bharadwaj L, Aulakh S, Hird S, Sethi A, Coil D. Microbial biogeography and community succession in aquariums, *submitted*
4. **Bik HM**, Pitch Interactive (2014) Phinch: An interactive, exploratory data visualization framework for –Omic datasets, *bioRxiv*, doi: <http://dx.doi.org/10.1101/009944> (preprint); *preprint manuscript submitted and in review at GigaScience*
5. Creer S, Deiner K, Frey S, Porazinska D, Taberlet P, Thomas WK, Potter C, **Bik HM**. The Ecologist's 2015 field guide to sequence-based identification of biodiversity, *invited review submitted to Methods in Ecology and Evolution*
6. Derycke S, De Meester N, Rigaux A, Creer S, **Bik H**, Thomas WK, Moens T. Coexisting cryptic species of the *Litoditis marina* complex (Nematoda) have distinct microbiomes with high intraspecific variability, *in revision at Molecular Ecology*

PUBLICATIONS – Peer-reviewed research articles

7. Adams R[#], Bateman AC[#], **Bik HM**[#], Meadow JF[#] (2015) Microbiota of the indoor environment: a meta-analysis, *Microbiome*, 3:49. ([#] all authors contributed equally)
8. Chariton A, Ho K, Proestou D, **Bik H**, Simpson S, Portis L, Cantwell M, Baguley J, Burgess R, Pelletier M, Perron M, Gunsch C (2014) A molecular-based approach for examining responses of microcosm-contained eukaryotes to contaminant-spiked estuarine sediments, *Environmental Toxicology and Chemistry*, 33(2): 359-369.
9. Darling A, Jospin G, Lowe E, Matsen FA, **Bik HM**, Eisen JA (2014) PhyloSift: phylogenetic analysis of genomes and metagenomes, *PeerJ*, 2:e243.
10. **Bik HM**, Fournier D, Bergeron RD, Sung W, Thomas WK (2013) Intra-Genomic Variation in the Ribosomal Repeats of Nematodes, *PLoS ONE*, 8(10): e78230
11. Stoltzfus A, Lapp H, Matasci N, Deus H, Sidlauskas B, Zmasek CM, Vaidya G, Pontelli E, Cranston K, Vos R, Webb CO, Harmon LJ, Pirrung M, O'Meara B, Pennell MW, Mirarab S, Rosenberg MS, Balhoff JP, **Bik HM**, Heath T, Midford P, Brown JW, McTavish EJ, Sukumaran J, Westneat M, Alfaro ME, Steele A (2013) Phylotastic! Making Tree-of-Life Knowledge Accessible, Re-usable and Convenient, *BMC Bioinformatics*, 14(1):158.
12. Ho KT, Chariton AA, Portis LM, Proestou D, Cantwell MG, Baguley JG, Burgess RM, Simpson S, Pelletier MC, Perron MM, Gunsch CK, **Bik HM**, Katz D, Kamikawa A (2013) Use of a novel sediment exposure to determine the effects of triclosan on estuarine benthic communities. *Environmental Toxicology and Chemistry*, 32(2):384–92.
13. **Bik HM**, Halanych KM, Sharma J, Thomas WK (2012) Dramatic shifts in benthic microbial eukaryote communities following the Deepwater Horizon oil spill. *PLoS ONE*, 7(6):e38550.
14. **Bik HM**, Sung W, De Ley P, Baldwin JG, Sharma J, Rocha-Olivares A, Thomas WK (2012) Metagenetic community analysis of microbial eukaryotes illuminates biogeographic patterns in deep-sea and shallow water sediments. *Molecular Ecology*, 21(5):1048-1059. (*“From the Cover” paper*)
15. Bhadury P[#], **Bik H**[#], Lamshead PJD, Austen MC, Smerdon GR, Rogers AD (2011) Molecular diversity of fungal phylotypes co-amplified alongside nematodes from coastal and deep-sea marine environments. *PLOS One*, 6 (10):e26445. ([#] joint first author)

16. **Bik HM**, Lunt DH, Thomas WK, Lamshead PJD (2010) Low endemism, continued deep-shallow interchanges, and evidence for cosmopolitan distributions in free-living marine nematodes (order Enoplida). *BMC Evolutionary Biology*, 10:389.
17. **Bik HM**, Thomas WKT, Lamshead PJD, Lunt DH (2010) Moving towards a complete molecular framework of the Nematoda: A focus on the Enoplida and early-branching clades. *BMC Evolutionary Biology*, 10:353.
18. **Bik HM**, Hawkins LE, Hughes JA, Lamshead PJD (2009) Rapid decline of PCR amplification from genomic extracts of DESS-preserved, slide-mounted nematodes. *Nematology*, 11(6):827-34.

PUBLICATIONS – Peer-reviewed reviews and perspectives

17. **Bik HM**, Dove ADM, Goldstein MC, Helm RR, MacPherson R, Martini K, Warneke A, McClain C (2015) Ten Simple Rules for Effective Online Outreach. *PLoS Computational Biology* 11(4): e1003906.
18. NESCent Working Group on the Evolutionary Biology of the Built Environment, Martin LJ, Adams RI, Bateman A, **Bik HM**, Hawks J, Hird SM, Hughes D, Kembel SW, Kinney K, Kolokotronis SO, Levy G, McClain C, Meadow JF, Medina RF, Mhuireach G, Moreau CS, Munshi-South J, Nichols LM, Palmer C, Popova L, Schal C, Täubel M, Trautwein M, Ugalde JA, Dunn RR (2015) Evolution of the Indoor Biome, *Trends in Ecology and Evolution*, 30(4): 223–232.
19. **Bik HM** (2014) Deciphering diversity and ecological function from marine metagenomes, *Biological Bulletin*, 227:107-116. (invited review)
20. **Bik HM**, Coil D, Eisen JA (2014) microBEnet: Lessons learned from building an interdisciplinary scientific community in the online sphere, *PLoS Biology*, 12(6): e1001884.
21. Morgan MJ, Bass D, Birky CW, **Bik H**, Blaxter M, Crisp MD, Derycke S, Fitch D, Fontaneto D, Hardy CM, King AJ, Kiontke KC, Moens T, Pawlowski JW, Porazinska D, Tang CQ, Thomas WK, Yeates DK, Creer S (2014) A critique of Rossberg et al.: noise obscures the genetic signal of meiobiotal ecospecies in ecogenomic datasets, *Proceedings of the Royal Society B*, 281: 20133076.
22. Burleigh JG, Alphonse K, Alverson AJ, **Bik HM**, Blank CE, Cirranello AL, Cui H, Daly M, Dietterich TG, Gasparich G, Irvine J, Julius M, Kaufman S, Law E, Liu J, Moore LR, O’Leary MA, Passarotti M, Ranade S, Simmons NB, Stevenson DW, Thacker RW, Theriot EC, Todorovic S, Velazco PM, Walls RL, Wolfe JM, Yu A (2013) Next Generation Phenomics for the Tree of Life, *PLOS Currents Tree of Life*, [doi:10.1371/currents.tol.085c713acafc8711b2ff7010a4b03733](https://doi.org/10.1371/currents.tol.085c713acafc8711b2ff7010a4b03733)
23. **Bik HM**, Goldstein MC (2013) An Introduction to Social Media for Scientists, *PLoS Biology*, 11(4): e1001535.
24. **Bik HM**, Thomas WK (2012) Metagenomics will highlight and drive links to taxonomic data: reply to Murray, *Trends in Ecology and Evolution*, 27(12): 652-653.
25. **Bik HM**, Porazinska DL, Creer S, Caporaso JG, Knight R, Thomas WK (2012) Sequencing our way towards understanding global eukaryotic biodiversity. *Trends in Ecology and Evolution*, 27(4):233-243.
26. **Bik HM** (2010) Small worms, big ideas: Evolutionary inferences from nematode DNA. *Journal of Biogeography*. 37(1):1-2.
27. **Bik HM** (2009) Unraveling post-glacial colonization through molecular techniques: new insight from estuarine invertebrates. *Journal of Biogeography*, 36:16-17.

PUBLICATIONS – Book chapters

- **Bik HM**, Thomas WK (in press) Biodiversity and the (data) Beast. In: Hughes J., Cotton, J., and Olson, P. (eds.) *Next Generation Systematics: Studying Evolution and Diversity in the Era of Ubiquitous Genomics*, Cambridge University Press, UK.

- Thaler AD, Zelnio KA, Freitag A, MacPherson R, Shiffman D, **Bik H**, Goldstein MC, McClain C (2012) Digital Environmentalism: Tools and strategies for the evolving online ecosystem. In: D. Gallagher (ed.) *Environmental Leadership: A Reference Handbook*, SAGE Publications, London.

PUBLICATIONS – Meeting Reports

- Bates ST, Ahrendt S, **Bik HM**, Bruns TD, Caporaso JG, Cole J, Dwan M, Fierer N, Gu D, Houston S, Knight R, Leff J, Lewis C, Maestre JP, McDonald D, Nilsson RH, Porras-Alfaro A, Robert V, Schoch C, Scott J, Taylor DL, Wegener Parfrey L, Stajich JE (2013) Meeting Report: Fungal ITS Workshop (October 2012), *Standards in Genomic Sciences*, 8(1): [doi:10.4056/sigs.3737409](https://doi.org/10.4056/sigs.3737409)
- Robbins RJ, Amaral-Zettler L, **Bik H**, Blum S, Edwards J, Field D, Garrity G, Gilbert JA, Kottmann R, Krishtalka L, Lapp H, Lawrence C, Morrison N, Tuama EO, Parr C, San Gil I, Schindel D, Schriml L, Vieglas D, Wooley J. (2012) RCN4GSC Workshop Report: Managing data at the interface of biodiversity and (meta)genomics, March 2011. *Standards in Genomic Sciences*, 7(1): [doi:10.4056/sigs.3156511](https://doi.org/10.4056/sigs.3156511)

OTHER SCIENTIFIC PRODUCTS

- Phinch (<http://phinch.org>) – an interactive, exploratory data visualization framework for high-throughput sequence data; open source code available on Github
- Github, open source software repository – <https://github.com/hollybik>
- Bik HM et al. (2012) Data from: Dramatic shifts in benthic microbial eukaryote communities following the Deepwater Horizon oil spill. Dryad Digital Repository. [doi:10.5061/dryad.4sd51d4b](https://doi.org/10.5061/dryad.4sd51d4b) (environmental 18S rRNA dataset)
- Bik HM et al. (2011) Data from: Metagenetic community analysis of microbial eukaryotes illuminates biogeographic patterns in deep-sea and shallow water sediments. Dryad Digital Repository. [doi:10.5061/dryad.vd094](https://doi.org/10.5061/dryad.vd094) (environmental 18S rRNA dataset)

INVITED TALKS (selected)

- 2015 Invited speaker, Gordon Research Conference on Ecological and Evolutionary Genomics, Biddeford, ME
- 2015 Keynote speaker, Bioinformatics Open Source Conference, Dublin, Ireland
- 2015 Invited seminar, Department of Engineering, University of Glasgow, Scotland
- 2015 Invited speaker, NGS Bioinformatics User Group, James Hutton Institute, Scotland
- 2014 Invited speaker, World Conference on Marine Biodiversity, Qingdao, China
- 2014 Invited speaker, Oxford Genome Science Meeting, Oxford, UK
- 2014 Invited speaker, Joint Aquatic Sciences Meeting, Portland, OR
- 2014 Invited seminar, Monterey Bay Aquarium Research Institute, Moss Landing, CA
- 2014 Invited seminar, IBEST seminar series, University of Idaho, ID
- 2014 Invited seminar, Dept of Integrative Biology, Oregon State University, Corvallis, OR
- 2013 Session Chair, Gordon Research Conference on Ecological and Evolutionary Genomics, Biddeford, ME
- 2013 Invited speaker, SMBE annual meeting, Chicago, IL
- 2013 Keynote speaker, iEvoBio Conference, Snowbird, UT
- 2013 Invited speaker, Int'l Assoc. for Great Lakes Research meeting, Lafayette, IN
- 2013 Invited speaker, 2nd Microbiology of the Built Environment meeting, Boulder, CO
- 2013 Invited seminar, Institute of Ecology & Evolution, Univ. of Oregon, Eugene, OR
- 2012 Invited speaker and Session Chair, Evolution of *C. elegans* and other Nematodes meeting, Cold Spring Harbor, NY
- 2012 Invited speaker, Assoc. of Biomolecular Research Facilities meeting, Orlando, FL
- 2011 Invited seminar, Univ. of South Florida/US Geological Survey, St. Petersburg, FL
- 2011 Invited speaker, Society of Nematologists Annual Meeting, Corvallis, OR
- 2011 Invited speaker, iEvoBio conference, Norman, OK
- 2010 Invited seminar, US Environmental Protection Agency, Cincinnati, OH

TEACHING EXPERIENCE

- Graduate Student Supervision: Alexis Walker (MSc, University of Alaska Fairbanks), Hollie Marshall (MSc, University of Birmingham)
- Students and Undergraduates Mentored: Jordan Ramsdell (Undergraduate, work-study project at UNH), Evan Dube (High School student, summer project at UNH), Alison Federer (Undergraduate, meeting mentor at SMBE Kyoto 2011), Tamar Dickerson and Kayla Hinson (ASLO Multicultural Program, meeting mentor at 2012 Ocean Sciences Meeting), bioinformatics advisor for undergraduate research projects at UC Davis (2012-2014).
- Instructor and course organizer: “Bioinformatics & Biodiversity” undergraduate workshops at Auburn University (2011) and the University of New Hampshire (2014, 2015) – courses focused on the intersection of taxonomy and high-throughput sequencing methods, in the context of the Deepwater Horizon oil spill.
- Seminar on College Teaching: Semester-long course on pedagogy and practical teaching techniques, completed at UC Davis in 2014.
- UC Davis GradPathways Workshops, “Using Social Media to promote your research” (2012-2014)
- Math/Science Tutor for private clients, New Hampshire (2010-11) and London (2007-10)

LEADERSHIP ACTIVITIES

- Co-organizer, “Bioinformatics & Biodiversity Undergraduate Workshop” at the University of New Hampshire (Durham, NH – July 27-30, 2015)
- Lead Organizer, Symposium at the Joint 2014 British/French Ecological Society Annual Meeting, “Accelerating ecology and biodiversity research via ecometagenomics: species, communities and environmental DNA” (Lille, France – December 9-12, 2014)
- Lead Organizer, “Ecometagenomics” Special Session and full-day workshop, Ecological Society of America 2014 Annual Meeting (Sacramento, CA, August 10-15, 2014)
- Co-organizer, “Bioinformatics & Biodiversity Undergraduate Workshop” at the University of New Hampshire (Durham, NH – July 28-31, 2014)
- Lead Organizer, UC Davis Genome Assembly Masterclass (Davis, CA, Dec 16-20, 2013)
- Organizing Committee, Evolution of *Caenorhabditis* and Other Nematodes 2014 Meeting (Hinxton, UK – June 14-17, 2014)
- Organizing Committee, iEvoBio 2013 (Snowbird, UT – June 25-26, 2013)
- Co-Convener (“Phylogenomics and Microbial Species Concepts” Session at the American Society for Microbiology Annual Meeting (Denver, CO – May 18-21, 2013)
- Lead Organizer and Co-PI, SMBE Satellite Meeting on Eukaryotic -Omics and QIIME software workshop (Davis, CA – April 29-May 4, 2013)
- Council Member, UC Davis Postdoc Association (2012-2014)
- Lead Organizer, “Bioinformatics of Biodiversity Undergraduate Workshop” at Auburn University (Auburn, AL – March 31-April 3, 2011)
- Lead Organizer, NESCent Catalysis Meeting, “High-throughput biodiversity assessment using Eukaryotic Metagenetics” (Durham, NC – January 24-26, 2011)
- Lead Organizer, “UNH Metageniuses” data analysis discussion group (2010-2011, University of New Hampshire)
- Organizing Committee, Natural History Museum Annual Postgraduate Conferences, London Evolutionary Research Network Annual Conferences, NHM Phylogenetics and Genomics Workshop, and London (2007-2009)
- Council Member and Representative, The Natural History Museum London Students’ Association, London Evolutionary Research Network (2007-2009)

WORKING GROUPS

- Invited Participant, NEON Advanced Analysis of Genomic Data in Microbial Ecology Research Workshop (July 14-16, 2014 – NEON headquarters, Boulder, CO)

- Invited Participant, Evolution of the Indoor Biome (June 11-13, 2013 – NESCent, Durham, NC) and Indoor Evolution Meta-analysis working group (ongoing)
- Data Provider, NSF AVAToL Project “Next-generation Phenomics for the Tree of Life” (3-year project, 2012-2014; <http://avatol.org>)
- Invited Participant, Phylotastic Hackathon (June 4-8, 2012 - NESCent, Durham, NC)
- Invited Participant, NSF Ideas Lab for Advancing and Visualizing the Tree of Life, (August 22-26, 2011 – Lake Placid, NY)
- Invited Participant, Genomic Standards Consortium, Biodiversity Working Group (March 21-22, 2011 – San Diego, CA; activities are ongoing)
- Invited Participant, Ecogenomics, environmental barcoding and biomonitoring workshop, hosted at Biodiversity Institute of Ontario (August 12-13, 2010 – Guelph, Canada)
- Invited Participant, Natural Resource Damage Assessment (NRDA) in Arctic Waters, sponsored by UNH Coastal Response Research Center and Alaska’s Oil Spill Response Institute (April 20-22, 2010 – Anchorage, AK)

SCIENTIFIC & PROFESSIONAL TRAINING

- Software Carpentry Workshop (NERC Advanced Training Short Course) – University of Leeds, United Kingdom (2015)
- UC Davis Genome Assembly Masterclass – Davis, CA (2013)
- Advancing Towards Professorship in Biology, Ecology, and Earth Systems Sciences – Oregon State University, Corvallis, OR (2012)
- NIGMS Workshop for Postdocs Transitioning to Independent Positions – NIH campus, Bethesda, MD (2012)
- Perl programming for Bioinformatics, 3-week intensive course – University of New Hampshire (2011)
- ARB/SILVA training workshop – Bremen, Germany, (2010)
- Deep-sea DNA Barcoding Workshop sponsored by Census for the Diversity of Marine Life (CeDAMar) – Senckenberg Research Institute, Wilhelmshaven, Germany (2008)
- Benthic Marine Invertebrate Workshop sponsored by the Royal Society of the UK – University of the Western Cape, Cape Town, South Africa (2007)
- Deep-sea Nematode Taxonomy Workshop sponsored by MarBEF – University of Ghent, Belgium (2007)

CONFERENCE PRESENTATIONS (selected)

- International Environmental Omics Synthesis Conference (iEOS 2014), Liverpool, UK, September 15-17, 2014 – “Phinch: An interactive, exploratory data visualization framework for environmental sequence data” (Contributed Talk)
- SMBE 2014 Annual Meeting, San Juan, Puerto Rico, June 8-12, 2014 – “Phinch: An interactive, exploratory data visualization framework for metagenomic datasets” (Contributed Talk)
- VIZBI 2014, Heidelberg, Germany, March 5-7, 2014 – “Phinch: An interactive, exploratory data visualization framework for metagenomic datasets” (Poster and Software Demo)
- Evolution 2013, Snowbird, UT, June 21-25, 2013 – “Phylosift: phylogenetic analysis of genomes and metagenomes” (Contributed Talk)
- American Society for Microbiology Annual Meeting, Denver, CO, May 18-21 2013 – “Phylosift: phylogenetic analysis of genomes and metagenomes” (Poster)
- SMBE 2012 Annual Meeting, Dublin, Ireland, June 23-26, 2012 – “Phylosift: phylogenetic taxonomy assignments from environmental metagenome data” (Poster)
- Ocean Sciences 2012 Meeting, Salt Lake City, UT, February 20-24, 2012 – “Rapid biodiversity assessment of microbial eukaryotes using High-Throughput Sequencing: A case study from the BP oil spill” (Poster)

- World Conference on Marine Biodiversity, Aberdeen, Scotland, Sept 26-30, 2011 – “Rapid biodiversity assessment of marine meiofauna using high-throughput sequencing: A case study from the BP oil spill” (Contributed Talk)
- SMBE 2011 Annual Meeting, Kyoto, Japan, July 26-30, 2011 – “Rapid biodiversity assessment of microbial eukaryotes using high-throughput sequencing: A case study from the BP oil spill” (Contributed Talk)
- Deepwater Horizon Oil Spill Principal Investigator (PI) Conference sponsored by the NSTC Joint Sub-Committee on Ocean Science and Technology, St. Petersburg, FL, October 5-6, 2010 – “RAPID: Taxonomic and metagenetic test of species distributions for marine meiofauna in the Gulf of Mexico” (Poster)
- 12th International Deep-sea Biology Symposium, Reykjavik, Iceland, June 7-11, 2010 – “Metagenetic analysis of biodiversity patterns in deep-sea benthic meiofaunal communities” (Contributed Talk)
- SMBE 2009 Annual Meeting, Iowa City, IA, June 3-7, 2009 – “Resolving phylogenetic relationships within the basal clade Enoplida (Phylum Nematoda): an integrative approach combining molecular and morphological data” (Contributed Talk)

OUTREACH & BROADER IMPACTS (selected)

- Contributing Scientist and Associate Editor, “Deep-sea News” Blog (2010 to present) – Utilizing social media (Blogs, Twitter) to disseminate my research and highlight important publications in marine biology and genomics.
- Radio segment on the "Academic Minute" (July 2014) – I gave an “elevator pitch” of my research on this two-minute segment produced by WAMC Northeast Public Radio
- “Girls Who Code” guest speaker (August 2013) – an 8-week summer immersion program in computer science, web design, and mobile apps for high school girls. Sponsored by Intel and held at UC Davis.
- US National Commission on the BP Deepwater Horizon Oil Spill and Offshore Drilling: Report to the President (2011), NSF RAPID project highlighted
- “Open Lab: Best Science Writing on the Web” (2010), my online blog posts were selected for inclusion in this edited print anthology
- “Nature Live” Events, The Natural History Museum, London, UK (2007-2010) – Half-hour “behind the scenes” events run for the general public.
- A-Level Biology days, The Natural History Museum, London, UK (2008-2010) – Hour-long session bringing high-school students into contact with active researchers.
- “Researchers in Residence” Program, St James’ Senior Girls School, London, UK (2008-2009) – National UK program placing early-career researchers into secondary schools.