

Luke R. Thompson, Ph.D.

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Associate Research Professor & NGI Program Coordinator
Northern Gulf Institute (NGI), Mississippi State University
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RESEARCH INTERESTS

Microbial ecology and biogeography | eDNA | Biodiversity monitoring | Biological big data | Environmental metadata

EDUCATION

MASSACHUSETTS INSTITUTE OF TECHNOLOGY, *Cambridge, Massachusetts*

Ph.D. Biology 2003–2010
Microbiology *Specialization*
Thesis: Auxiliary metabolic genes in viruses infecting marine cyanobacteria ([link to full text](#))
Advisors: Sallie W. Chisholm and JoAnne Stubbe

STANFORD UNIVERSITY, *Stanford, California*

B.S. Biological Sciences *with Honors* 1998–2002
Chemistry *Minor*

PREVIOUS POSITIONS

SCRIPPS INSTITUTION OF OCEANOGRAPHY, *La Jolla, California*

Lecturer (part-time) Graduate-level Python course 2015–2018

UNIVERSITY OF CALIFORNIA, *San Diego, California* & UNIVERSITY OF COLORADO, *Boulder, Colorado*

Postdoctoral Scholar Rob Knight Lab 2013–2016

KING ABDULLAH UNIVERSITY OF SCIENCE AND TECHNOLOGY, *Thuwal, Saudi Arabia*

Postdoctoral Fellow Red Sea Research Center 2010–2013

PUBLICATIONS

Google Scholar Profile: [goo.gl/Te4va1](https://scholar.google.com/citations?user=Te4va1)

ORCID ID: orcid.org/0000-0002-3911-1280

52. Park, H., S.J. Lim, J. Cosme, K. O'Connell, J. Sandeep, F. Gayanilo, G.R. Cutter, E. Montes, C. Nitikitpaiboon, S. Fisher, H. Moustahfid & **L.R. Thompson**. (2023). Investigation of machine learning algorithms for taxonomic classification of marine metagenomes. *Microbiology Spectrum*, in press.
51. **Thompson, L.R.** & P. Thielen. (2023). Decoding dissolved information: environmental DNA sequencing at global scale to monitor a changing ocean. *Current Opinion in Biotechnology* 81(June):102936, <https://doi.org/10.1016/j.copbio.2023.102936>.
50. Gold, Z., R.P. Kelly, A.O. Shelton, A. Thompson, K.D. Goodwin, R. Gallego, K. Parsons, **L.R. Thompson**, D. Kacev & P.H. Barber. (2023). Message in a bottle: archived DNA reveals marine heatwave-associated shifts in fish assemblages. *Environmental DNA*, <https://doi.org/10.1002/edn3.400>.

49. Lim, S.J., **L.R. Thompson**, K.D. Goodwin. (2023). Genetic features of the marine polychaete *Sirsoe methanicola* from metagenomic data. **Frontiers in Marine Science**, <https://doi.org/10.3389/fmars.2022.1067482>.
48. Shaffer, J., L.F. Nothias, **L.R. Thompson**, J.G. Sanders, R. Salido, S. Couvillion, A. Brejnrod, S. Huang, F. Lejzerowicz, N. Haiminen, S. Huang, H. Lutz, Q. Zhu, C. Martino, J. Morton, S. Karthikeyan, M. Nothias-Esposito, K. Dührkop, S. Böcker, H. Kim, A. Aksenov, W. Bittremieux, J. Minich, C. Marotz, M. Bryant, K. Sanders, T. Schwartz, G. Humphrey, Y. Vázquez-Baeza, A. Tripathi, L. Parida, A.P. Carrieri, K. Beck, P. Das, A. Gonzalez, D. McDonald, S. Karst, M. Albertsen, G. Ackermann, J. DeReus, T. Thomas, D. Petras, A. Shade, J. Stegen, S. Song, T. Metz, A. Swafford, P. Dorrestein, J. Jansson, J. Gilbert, R. Knight & Earth Microbiome Project 500 (EMP500) Consortium. (2022). Standardized multi-omics of Earth's microbiomes reveals microbial and metabolite diversity. **Nature Microbiology**, 7, 2128–2150, <https://doi.org/10.1038/s41564-022-01266-x>.
47. Den Uyl, P.A., **L.R. Thompson**, R.M. Errera, J.M. Birch, C.M. Preston, W. Ussler, C.E. Yancey, S.R. Chaganti, S.A. Ruberg, G.J. Doucette, G.J. Dick, C.A. Scholin & K.D. Goodwin. (2022). Lake Erie field trials to advance autonomous monitoring of cyanobacterial harmful algal blooms. **Frontiers in Marine Science**, <https://doi.org/10.3389/fmars.2022.1021952>.
46. **Thompson, L.R.**, S.R. Anderson, P.A. Den Uyl, N.V. Patin, S.J. Lim, G. Sanderson & K.D. Goodwin. (2022). Tourmaline: a containerized workflow for rapid and iterable amplicon sequence analysis using QIIME 2 and Snakemake. **GigaScience**, <https://doi.org/10.1093/gigascience/giac066>.
45. Lim, S.J., **L.R. Thompson**, C.M. Young, T. Gaasterland, K.D. Goodwin. (2022). Dominance of *Sulfurospirillum* in metagenomes associated with the methane ice worm (*Sirsoe methanicola*). **Applied and Environmental Microbiology**, <https://doi.org/10.1128/aem.00290-22>.
44. Truelove, N.K., N.V. Patin, M. Min, K.J. Pitz, C. Preston, K. Yamahara, Y. Zhang, B. Raanan, B. Kieft, B. Hobson, **L.R. Thompson**, K.D. Goodwin, F.P. Chavez. (2022). Expanding the temporal and spatial scales of environmental DNA research with autonomous sampling. **Environmental DNA**, <https://doi.org/10.1002/edn3.299>.
43. Jorge, F., J.C. Brealey, P.J. Brindley, C. Cantacessi, O. Duron, C.R. Fitzpatrick, M. Hahn, V. Hervé, L.J. Knoll, K.D. Kohl, M. Lalle, J. Lukeš, J. Martínez Martínez, S.L. Perkins, R. Poulin, K. Rosario, A.C. Schneider, L.M. Schriml, **L.R. Thompson** & N.M. Dheilly. (2022). MlxS-SA: a MlxS extension defining the minimum information standard for sequence data from symbiont-associated micro-organisms. **ISME Communications**, <https://doi.org/10.1038/s43705-022-00092-w>.
42. Clayton, S., H. Alexander, J. Graff, N. Poulton, **L.R. Thompson**, H. Benway, E. Boss & A. Martiny. (2022). Bio-GO-SHIP: the time is right to establish global repeat sections of ocean biology. **Frontiers in Marine Science** 8:767443, <https://doi.org/10.3389/fmars.2021.767443>.
41. Formel, N., I.C. Enochs, C. Sinigalliano, S.R. Anderson & **L.R. Thompson**. (2021). Subsurface Automated Samplers for eDNA (SASe) for biological monitoring and research. **HardwareX** 10:e00239, <https://doi.org/10.1016/j.ohx.2021.e00239>.
40. Anderson, S.R. & **L.R. Thompson**. (2021). Optimizing an enclosed bead beating extraction method for microbial and fish environmental DNA. **Environmental DNA**, <https://doi.org/10.1002/edn3.251>.
39. Vangay, P., J. Burgin, A. Johnston, K. Beck, D. Berrios, K. Blumberg, S. Canon, P. Chain, J. Chandonia, D. Christianson, S. Costes, J. Damerow, W. Duncan, J. P. Dundore-Arias, K. Fagnan, J. Galazka, S. Gibbons, D. Hays, W. Hervey, B. Hu, B. Hurwitz, P. Jaiswal, M. Joachimiak, L. Kinkel, J. Ladau, S. Martin, L.A. McCue, K. Miller, N. Mouncey, C. Mungall, E. Pafilis, T.B.K. Reddy, L. Richardson, S. Roux, J. Shaffer, J. Sundaramurthi, **L.R. Thompson**, R. Timme, J. Zheng, E. Wood-Charlson, and E. Eloie-Fadrosh. (2021). Microbiome metadata standards: report of the National Microbiome Data Collaborative's workshop and follow-on activities. **mSystems** 6(1):e01194-20, <https://doi.org/10.1128/mSystems.01194-20>.
38. Lim, S.J. & **L.R. Thompson**. (2021). Mitohelper: a mitochondrial reference sequence analysis tool for fish eDNA studies. **Environmental DNA**, <https://doi.org/10.1002/edn3.187>.
37. Lavrinienko, A., E. Tukalenko, T.A. Mousseau, **L.R. Thompson**, R. Knight, T. Mappes & P.C. Watts. (2020). Two hundred and fifty-four metagenome-assembled bacterial genomes from the bank vole gut microbiota. **Scientific Data**, <https://doi.org/10.1038/s41597-020-00656-2>.

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35. Cao, L., A. Gurevich, K.L. Alexander, C.B. Naman, T. Leão, E. Glukhov, T. Luzzatto-Knaan, F. Vargas, R. Quinn, A. Bouslimani, L.F. Nothias, N.K. Singh, J.G. Sanders, R.A.S. Benitez, **L.R. Thompson**, M. Hamid, J.T. Morton, A. Mikheenko, A. Shlemov, A. Korobeynikov, I. Friedberg, R. Knight, K. Venkateswaran, W. Gerwick, L. Gerwick, P.C. Dorrestein, P.A. Pevzner & H. Mohimani. (2019). MetaMiner: a scalable peptidogenomics approach for discovery of ribosomal peptide natural products with blind modifications from microbial communities. *Cell Systems*, <https://doi.org/10.1016/j.cels.2019.09.004>.
34. Dheilly, N.M., J. Martínez Martínez, K. Rosario, P.J. Brindley, R.N. Fichorova, J.Z. Kaye, K. Kohl, L.J. Knoll, J. Lukeš, S. Perkins, R. Poulin, L. Schriml & **L.R. Thompson**. (2019). Parasite microbiome project: grand challenges. *PLOS Pathogens*, <https://doi.org/10.1371/journal.ppat.1008028>.
33. Bolyen, E., J.R. Rideout, M.R. Dillon, N.A. Bokulich, C.C. Abnet, G.A. Al-Ghalith, H. Alexander, E.J. Alm, M. Arumugam, F. Asnicar, Y. Bai, J.E. Bisanz, K. Bittinger, A. Brejnrod, C.J. Brislawn, C.T. Brown, B.J. Callahan, A.M. Caraballo-Rodríguez, J. Chase, E.K. Cope, R. Da Silva, C. Diener, P.C. Dorrestein, G.M. Douglas, D.M. Durall, C. Duvallet, C.F. Edwardson, M. Ernst, M. Estaki, J. Fouquier, J.M. Gauglitz, S.M. Gibbons, D.L. Gibson, A. González, K. Gorlick, J. Guo, B. Hillmann, S. Holmes, H. Holste, C. Huttenhower, G.A. Huttley, S. Janssen, A.K. Jarmusch, L. Jiang, B.D. Kaehler, K.B. Kang, C.R. Keefe, P. Keim, S.T. Kelley, D. Knights, I. Koester, T. Kosciulek, J. Kreps, M.G.I. Langille, J. Lee, R. Ley, Y. Liu, E. Lofffield, C. Lozupone, M. Maher, C. Marotz, B.D. Martin, D. McDonald, L.J. McIver, A.V. Melnik, J.L. Metcalf, S.C. Morgan, J.T. Morton, A.T. Naimey, J.A. Navas-Molina, L.F. Nothias, S.B. Orchanian, T. Pearson, S.L. Peoples, D. Petras, M.L. Preuss, E. Priesse, L.B. Rasmussen, A. Rivers, M.S. Robeson, P. Rosenthal, N. Segata, M. Shaffer, A. Shiffer, R. Sinha, S. Song, J.R. Spear, A.D. Swafford, **L.R. Thompson**, P.J. Torres, P. Trinh, A. Tripathi, P.J. Turnbaugh, S. Ul-Hasan, J.J.J. van der Hooft, F. Vargas, Y. Vázquez-Baeza, E. Vogtmann, M. von Hippel, W. Walters, Y. Wan, M. Wang, J. Warren, K.C. Weber, C.H.D. Williamson, A.D. Willis, Z.Z. Xu, J.R. Zaneveld, Y. Zhang, Q. Zhu, R. Knight & J.G. Caporaso. (2019). QIIME 2: reproducible, interactive, scalable, and extensible microbiome data science. *Nature Biotechnology*, <https://doi.org/10.1038/s41587-019-0209-9>.
32. **Thompson, L.R.**, M.F. Haroon, A.A. Shibl, M.J. Cahill, D.K. Ngugi, G.J. Williams, J.T. Morton, R. Knight, K.D. Goodwin & U. Stingl. (2019). Red Sea SAR11 and *Prochlorococcus* single-cell genomes reflect globally distributed pangenomes. *Applied and Environmental Microbiology*, <https://doi.org/10.1128/AEM.00369-19>.
31. Martino, C., J.T. Morton, C.A. Marotz, **L.R. Thompson**, A. Tripathi, R. Knight & K. Zengler. (2019). A novel sparse compositional technique reveals microbial perturbations. *mSystems*, <https://doi.org/10.1128/mSystems.00016-19>.
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29. Shibl, A.A., D.K. Ngugi, A. Talarmin, **L.R. Thompson**, J. Blom & U. Stingl. (2018). The genome of a novel isolate of *Prochlorococcus* from the Red Sea contains transcribed genes for compatible solute biosynthesis. *FEMS Microbiology Ecology*, <https://doi.org/10.1093/femsec/fiy182>.
28. Amato, K.R., J.G. Sanders, S. Song, M. Nute, J.L. Metcalf, **L.R. Thompson**, J.T. Morton, A. Amir, V. McKenzie, G. Humphrey, G. Gogul, J. Gaffney, A. Baden, G. Britton, F. Cuozzo, A. Di Fiore, N. Dominy, T. Goldberg, A. Gomez, M.M. Kowalewski, R. Lewis, A. Link, M. Sauter, S. Tecot, B. White, K. Nelson, R. Stumpf, R. Knight & S. Leigh. (2018). Evolutionary trends in host physiology outweigh dietary niche in structuring primate gut microbiomes. *The ISME Journal*, <https://doi.org/10.1038/s41396-018-0175-0>.
27. Lavrinienko, A., T. Mappes, E. Tukalenko, T.A. Mousseau, A.P. Møller, R. Knight, J.T. Morton, **L.R. Thompson** & P.C. Watts. (2018). Environmental radiation alters the gut microbiome of the bank vole *Myodes glareolus*. *The ISME Journal*, <https://doi.org/10.1038/s41396-018-0214-x>.
26. Knight, R., A. Vrbnac, B.C. Taylor, A. Aksenov, C. Callewaert, J. Debelius, A. Gonzalez, T. Kosciulek, L. McCall, D. McDonald, A.V. Melnik, J.T. Morton, J. Navas, R.A. Quinn, J.G. Sanders, A.D. Swafford, **L.R. Thompson**, A. Tripathi, Z.Z. Xu, J.R. Zaneveld, Q. Zhu, J.G. Caporaso & P.C. Dorrestein. (2018). Best practices for analyzing microbiomes. *Nature Reviews Microbiology* 16:410–422, <https://doi.org/10.1038/s41579-018-0029-9>.

25. Michaud, J.M., **L.R. Thompson**, D. Kaul, J. Espinoza, R.A. Richter, Z.Z. Xu, C. Lee, K.M. Pham, C.M. Beall, F. Malfatti, F. Azam, R. Knight, K.A. Prather, C.L. Dupont & M.D. Burkart. (2018). Taxon-specific aerosolization of bacteria and viruses in an experimental ocean–atmosphere mesocosm. *Nature Communications* 9(1):2017, <https://doi.org/10.1038/s41467-018-04409-z>.
24. McDonald, D., E.R. Hyde, J.W. Debelius, J.T. Morton, A. González, G. Ackermann, A.A. Aksenov, B. Behsaz, C. Brennan, Y. Chen, L. DeRight-Goldasich, P.C. Dorrestein, R.R. Dunn, A.K. Fahimipour, J. Gaffney, J.A. Gilbert, G. Gogul, J.L. Green, P. Hugenholtz, G. Humphrey, C. Huttenhower, M.A. Jackson, S. Janssen, D.V. Jeste, L. Jiang, S.T. Kelley, D. Knights, T. Kosciolk, J. Ladau, J. Leach, C. Marotz, D. Meleshko, A.V. Melnik, J.L. Metcalf, H. Mohimani, E. Montassier, J. Navas-Molina, T.T. Nguyen, S. Peddada, P. Pevzner, K.S. Pollard, G. Rahnavard, A. Robbins-Pianka, N. Sangwan, J. Shorenstein, L. Smarr, S. Song, T. Spector, A.D. Swafford, V.G. Thackray, **L.R. Thompson**, A. Tripathi, Y. Vázquez-Baeza, A. Vrbanc, P. Wischmeyer, E. Wolfe, Q. Zhu, The American Gut Consortium & R. Knight. (2018). American Gut: an open platform for citizen-science microbiome research. *mSystems* 3(3):e00031–18, <https://doi.org/10.1128/mSystems.00031-18>.
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20. Amir, A., D. McDonald, J.A. Navas-Molina, E. Kopylova, J. Morton, Z.Z. Xu, E.P. Kightley, **L.R. Thompson**, E.R. Hyde, A. Gonzalez & R. Knight. (2017). Deblur rapidly resolves single-nucleotide community sequence patterns. *mSystems* 2(2):e00191–16, <https://doi.org/10.1128/mSystems.00191-16>.
19. **Thompson, L.R.**, K. Nikolakakis, S. Pan, J. Reed, R. Knight & E.G. Ruby. (2017). Transcriptional characterization of *Vibrio fischeri* during colonization of juvenile *Euprymna scolopes*. *Environmental Microbiology* 19(5):1845–1856, <https://doi.org/10.1111/1462-2920.13684>.
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16. Haroon, M.F., **L.R. Thompson**, D.H. Parks, P. Hugenholtz & U. Stingl. (2016). A catalogue of 136 microbial draft genomes from the Red Sea. *Scientific Data* 3:160050, <https://doi.org/10.1038/sdata.2016.50>.
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14. Haroon, M.F., **L.R. Thompson** & U. Stingl. (2016). Draft genome sequence of uncultured SAR324 bacterium lautmerah10, binned from a Red Sea metagenome. *Genome Announcements* 4(1):e01711–15, <https://doi.org/10.1128/genomeA.01711-15>.
13. Metcalf, J.L., Z.Z. Xu, S. Weiss, S. Lax, T. Vanreuren W, E.R. Hyde, S. Song, A. Amir, P. Larsen, N. Sangwan, D. Haarmann, G.C. Humphrey, G. Ackermann, **L.R. Thompson**, C. Lauber, A. Bibat, C. Nicholas, M.J. Gebert, J.F. Petrosino, S.C. Reed, J.A. Gilbert, A.M. Lynne, S.R. Bucheli, D.O. Carter & R. Knight. (2016). Microbial community assembly and metabolic function during mammalian corpse decomposition. *Science* 351:158–162, <https://doi.org/10.1126/science.aad2646>.

12. Luo, H., **L.R. Thompson**, U. Stingl & A.L. Hughes. (2015). Selection maintains low genomic GC content in marine SAR11 lineages. *Molecular Biology and Evolution* 32(10):2738–2748, <https://doi.org/10.1093/molbev/msv149>.
11. Berube, P.M., S.J. Biller, A.G. Kent, J.W. Berta-Thompson, S.E. Roggensack, K.H. Roache-Johnson, M. Ackerman, L.R. Moore, J.D. Meisel, D. Sher, **L.R. Thompson**, L. Campbell, A.C. Martiny & S.W. Chisholm. (2015). Physiology and evolution of nitrogen acquisition in *Prochlorococcus*. *The ISME Journal* 9:1195–1207. <https://doi.org/10.1038/ismej.2014.211>.
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9. **Thompson, L.** (2013). Red Sea Metagenomics. In: K. Nelson (Ed.) *Encyclopedia of Metagenomics*. Springer-Verlag, Berlin Heidelberg, ISBN: 978-1-4614-6418-1. URL: <https://www.springer.com/us/book/9781461446743>.
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5. Sullivan, M.B., K.H. Huang, J.C. Ignacio-Espinoza, A. Berlin, L. Kelly, P.R. Weigele, A.S. DeFrancesco, S.E. Kern, **L.R. Thompson**, S. Young, W. Lee, M. Weiland, R. Fu, B. Krastins, M. Chase, D. Sarracino, M.S. Osburne, M.R. Henn & S.W. Chisholm. (2010). Genomic analysis of oceanic cyanobacterial myoviruses compared to T4-like myoviruses from diverse hosts and environments. *Environmental Microbiology* 12:3035–3056. <https://doi.org/10.1111/j.1462-2920.2010.02280.x>.
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INVITED & CONTRIBUTED TALKS

38. Ocean Carbon and Biogeochemistry 2023 Summer Workshop, Woods Hole, Massachusetts, June 15, 2023, “Sustained observations of global ocean biology – session introduction” (invited).
37. Metabolomics Association of North America Microbiome Interest Group, February 13, 2023, “Behind the Paper from the Knight Lab and EMP Group at UC San Diego” (invited).
36. Atlantic International Research Centre (AIR Centre) Marine Biodiversity Networking Fridays, December 9, 2022, “Bio-GO-SHIP: expanding biological ocean observations for plankton ecosystem science and monitoring to the global scale” (invited).
35. ICES Annual Science Conference, Dublin, Ireland, September 19, 2022, “Machine learning-based taxonomic classification of DNA sequences in marine metagenomes” (contributed).
34. World Aquatic Veterinary Medical Association (WAVMA), August 26, 2022, “Environmental DNA for the study of ocean biodiversity from microbes to vertebrates” (invited).
33. NOAA 'Omics Seminar Series, July 20, 2022, “Global marine biodiversity monitoring through partnership and innovation” (contributed).
32. American Society for Microbiology General Meeting (ASM Microbe 2022), Washington, DC, June 12, 2022, “Crowdsourcing the microbiome: no guts, no glory” (invited).
31. Michigan State University, East Lansing, Michigan, April 21, 2022, “Environmental DNA for the study of ocean biodiversity from microbes to vertebrates” (invited).
30. Introduction to Environmental DNA for Applications in Florida, Webinar, January 28 and February 4, 2021, “NOAA eDNA Research in South Florida and the Gulf of Mexico” (invited).
29. Institute of Food and Agricultural Sciences, University of Florida, Davie, March 4, 2020, “Environmental DNA tools and applications for oceans and the Great Lakes” (invited).
28. Scripps Institution of Oceanography, November 1, 2019, “Environmental DNA tools and applications for oceans and the Great Lakes” (invited).
27. University of Southern Mississippi, Hattiesburg, October 18, 2019, “Applications and tools for environmental DNA” (invited).
26. OceanObs'19, Honolulu, Hawaii, September 18, 2019, Panelist for Special Session “Incorporating environmental DNA into global ocean observing systems: opportunities and challenges” (invited).
25. 1st Parasite Microbiome Project Workshop, Clearwater, Florida, January 11, 2019, “Standards-enabled large-scale surveys of Earth's microbial communities” (invited).
24. International Microbiome and Metagenomics Standards Alliance, November 8, 2018, “Standards-enabled metagenomics and metabolomics of Earth's microbial communities” (invited).
23. San Diego State University, October 18, 2018, “Multi-omics of Earth's microbial communities” (invited).
22. 148th Annual Meeting of the American Fisheries Society, Atlantic City, August 20, 2018, “Computational workflows for rapid and customizable analysis of amplicon sequencing data from environmental DNA” (contributed).
21. 17th International Symposium on Microbial Ecology, Leipzig, Germany, August 16, 2018, “EMP500: multi-omics of diverse microbial environments in the Earth Microbiome Project” (invited).
20. Department of Earth System Science, Stanford University, May 30, 2018, “The Earth Microbiome Project: investigating the structure of microbial diversity on Earth” (invited).
19. DOE Joint Genome Institute, Walnut Creek, May 29, 2018, “The Earth Microbiome Project: lessons from a scientifically crowdsourced microbiome survey” (invited).
18. University of Oulu, Finland, March 22, 2018, “The Earth Microbiome Project: revealing global patterns of microbial distribution” (invited).
17. 'Omic Biomonitoring Workshop, Max-Planck-Institute for Marine Microbiology, Bremen, Germany, February 21, 2018, “Global characterization of microbial taxonomic and functional diversity in the Earth Microbiome Project” (invited).
16. San Diego Microbiology Group, January 11, 2018, “Mapping the microbes of Earth” (invited).
15. Scripps Institution of Oceanography, December 1, 2017, “A communal catalogue of Earth's microbes” (invited).
14. TDWG 2017: Biodiversity Information Standards, Ottawa, Canada, October 2, 2017 (contributed).

- Sachs, J., **L. Thompson**, N. El-Kayssi & S. Bilkhu. (2017). Using MiXS: an implementation report from two metagenomic information systems. *Biodivers Inform Sci Stand* 1:e20637, <https://doi.org/10.3897/tdwgproceedings.1.20637>.
13. ICES Annual Science Conference, Fort Lauderdale, September 18, 2017, “The Earth Microbiome Project: lessons from a massive metagenetic survey” (contributed).
 12. GRDI-Ecobiomics: Workshop on Environmental and Protocol Metadata, Ottawa, Canada, May 31, 2016, “Environmental metadata and the Earth Microbiome Project” (invited/webinar).
 11. Sharp HealthCare Obesity Crisis Conference, San Diego, May 13, 2016, “Healthy gut and microbiomes” (invited).
 10. Microbiome Connections to the Environment and Health, University of California, Irvine, September 25, 2015, “Computational tools for environmental genomics and the Earth Microbiome Project” (invited).
 9. Scripps Institution of Oceanography, February 13, 2015, “Metagenomic analysis and the Earth Microbiome Project” (invited).
 8. 2nd International Symposium on Sponge Microbiology, Baltimore, October 27, 2014, “The Earth Microbiome Project: early successes and challenges” and panel member of “Group discussion: Where to from here?” (invited).
 7. 15th International Symposium on Microbial Ecology, Seoul, South Korea, August 29, 2014, “Mapping the genetic diversity and physicochemical space of the Red Sea basin” (contributed).
 6. Pacific Northwest National Laboratory, November 1, 2013, “Marine metagenomics: the Red Sea and the Earth Microbiome Project” (invited).
 5. Woods Hole Oceanographic Institution, July 30, 2012, “Let my microbes go! The Red Sea and stress tolerance strategies of *Prochlorococcus*, cyanophage, and SAR11” (invited).
 4. Winter Enrichment Program, KAUST, January 23, 2012, “The coming big data singularity” (invited).
 3. Integrative Microbial Ecology Workshop, KAUST, June 26, 2010, “Auxiliary metabolic genes in viruses infecting marine cyanobacteria” (invited).
 2. DOE Genomics:GTL (Genomes-To-Life) Contractor–Grantee Workshop VII, Bethesda, February 9, 2009, “Viruses hijacking cyanobacterial carbon metabolism” (contributed).
 1. Boston Bacterial Meeting, June 22, 2007, “Transaldolase in viruses infecting *Prochlorococcus*: hijacking host carbon metabolism with a non-cyanobacterial enzyme” (contributed).

NEWS FEATURES

- Interviewed for article in The Guardian, “How eDNA technology is changing the game for protecting ocean species”, June 2023
- Interviewed for American Blue Economy Podcast episode “Exploring the Wonders of Biotechnology in the American Blue Economy”, February 2023
- UC San Diego News Center on 2018 *Nature Communications* article “Taxon-specific aerosolization of bacteria and viruses in an experimental ocean–atmosphere mesocosm”
- News features on 2017 *Nature* article “A communal catalogue reveals Earth’s multiscale microbial diversity”:
 - *Nature News & Views*: J. Raes. (2017). Microbiology: Crowdsourcing Earth’s microbes. *Nature* 551:446–447, <https://doi.org/10.1038/nature24756>.
 - *WIRED*, *The Scientist*, *Science Friday*, *Ars Technica*, and others.
- PNAS Plus Author Summary of 2011 *PNAS* article “Phage auxiliary metabolic genes and the redirection of cyanobacterial host carbon metabolism”
- Faculty of 1000 recommendation for 2011 *PNAS* article “Phage auxiliary metabolic genes and the redirection of cyanobacterial host carbon metabolism”

AWARDS & HONORS

- Graduate Teaching Award, Scripps Institution of Oceanography, 2019
- NOAA/OAR Outstanding Scientific Paper Award for Oceans and Great Lakes, 2018
- Ranked First in Selection Process for Visiting Professor in Environmental Science, University of Brasilia, 2018 (declined position)
- SABIC Postdoctoral Fellowship, King Abdullah University of Science and Technology, 2012
- SABIC Postdoctoral Fellowship, King Abdullah University of Science and Technology, 2011
- 2011 *PNAS* article selected by Faculty of 1000 as a “must read” article (FFa score of 8)
- Poster Award, Cells, Circuits, and Computation Conference, Harvard University, 2009
- Student Travel Grant, Genomics: GTL Conference, U.S. Department of Energy, 2009
- Praecis Presidential Fellowship, Massachusetts Institute of Technology, 2003
- Howard Hughes Summer Research Fellowship, Stanford University Department of Biological Sciences, 2001
- Semifinalist, Westinghouse Science Talent Search, 1998

RESEARCH CRUISES

- Institute for Marine Research (Norway) cruise number 2019703. “Characterizing mesopelagic fish populations using environmental DNA (eDNA).” R/V *Kronprins Haakon*, Cape Verde to Oslo, May 1–27, 2019.
- California Cooperative Oceanic Fisheries Investigations (CalCOFI) 1704SH. “eAUV mobile ’omics platform to reduce ship time.” NOAA Ship *Bell M. Shimada*, Monterey to San Francisco, Apr 15–20, 2017.
- KAUST Red Sea Expedition 2013. “Gene expression of marine bacterial communities in the Eastern Mediterranean and Northern Red Sea.” R/V *Aegaeo*, Athens to Thuwal, Feb 14–Mar 6 and Mar 9–17, 2013.
- KAUST Red Sea Expedition 2011. “Population genomics of marine bacteria along physicochemical gradients in the Eastern Red Sea.” R/V *Aegaeo*, Southern to Northern Red Sea, Sep 15–Oct 10, 2011.
- Hawaii Ocean Time-series HOT-181. “Cultivation of *Prochlorococcus* from the North Pacific Subtropical Gyre.” R/V *Kilo Moana*, Station ALOHA, May 24–29, 2006.

CHAired SESSIONS

- OCB2023 Summer Workshop, Woods Hole Oceanographic Institution, Woods Hole, Massachusetts, June 12–15, 2023. “Sustained observations of global ocean biology.”
- ASLO Aquatic Sciences Meeting 2023, Palma de Mallorca, Spain, June 4–9, 2023. “Linking Ocean Microbiomes and Ecosystem Functions.”
- TDWG 2017: Biodiversity Information Standards, Ottawa, Canada, October 2017. “Towards robust interoperability in multi-omic approaches to biodiversity monitoring.”

COMMITTEE APPOINTMENTS, WORKING GROUPS & CONSORTIA

- Earth HoloGenome Initiative (EHI) Scientific Committee, 2021–present
- NOS–OAR Summit Steering Committee, 2021–present
- NOAA OAR Cloud Computing Strategy Document Writing Team, 2020
- National Microbiome Data Collaborative (NMDC) Champion, 2020–present
- National Microbiome Data Collaborative (NMDC) Research Coordination Network (RCN) steering committee, 2018–present
- EMOSE Inter-Comparison of Marine Plankton Metagenomic Analysis Methods, 2017, <https://doi.org/10.17605/osf.io/u93qm>

PEER REVIEW

Publons ID: publons.com/a/1456009/

- Associate Editor, *Proceedings of the Royal Society B*, 2020–2022
- Review Editor, *Frontiers in Marine Science*
- Reviewer for *Nature*, *Proceedings of the Royal Society B*, *Ecology Letters*, *The ISME Journal*, *Genes*, *Bacteriophage*, National Science Foundation, NOAA Office of Ocean Exploration and Research, and United States–Israel Binational Science Foundation

PROTOCOLS

- EMP Sample Submission Guide: <https://doi.org/10.17504/protocols.io.pfqdjmw>
- EMP DNA Extraction Protocol (current): <https://doi.org/10.17504/protocols.io.pcydixw>
- EMP DNA Extraction Protocol (previous): <https://doi.org/10.17504/protocols.io.nutdewn>
- EMP 16S Illumina Amplicon Protocol: <https://doi.org/10.17504/protocols.io.nuudeww>
- EMP 18S Illumina Amplicon Protocol: <https://doi.org/10.17504/protocols.io.nuvdew6>
- EMP ITS Illumina Amplicon Protocol: <https://doi.org/10.17504/protocols.io.pa7dihn>

WEBSITES

- **L. Thompson**, P. Vangay, K. Blumberg, D. Christianson, J.P. Dundore-Arias, B. Hu, R. Timme, and E. Wood-Charlson. (2020). Introduction to Metadata and Ontologies: Everything You Always Wanted to Know About Metadata and Ontologies (But Were Afraid to Ask). United States. Web. <https://doi.org/10.25979/1607365>.

GITHUB REPOSITORIES

- Earth Microbiome Project: <https://github.com/biocore/emp>
- Tourmaline – Amplicon sequence processing workflow using QIIME 2 and Snakemake: <https://github.com/NOAA-AOML/tourmaline>
- Labelmaker – Printable QR-coded labels for samples: <https://github.com/NOAA-AOML/labelmaker>
- Python for Data Analysis – Online course for data science: <https://github.com/cuttlefishh/python-for-data-analysis>
- Papers – Code for manuscripts published by Thompson and colleagues: <https://github.com/cuttlefishh/papers>

TEACHING EXPERIENCE

- Lecturer and Course Developer, “Python for Data Analysis”, Scripps Institution of Oceanography, 2015–18
 - GitHub repository: <https://github.com/cuttlefishh/python-for-data-analysis>
 - YouTube channel: <https://www.youtube.com/channel/UCVZrIrWtcvTzYlRnX7RcDyg>
- Guest Lecturer, Gut Check: Exploring Your Microbiome, Coursera, 2018
- Instructor, Advanced Bioinformatics for Metagenomics and Population Genomics, University of Oulu, Finland, March 2018
- Instructor, SIO Transcriptomics Workshop, Scripps Institution of Oceanography, October 2017
- Instructor, QIIME Workshop, University of Costa Rica, January 2016

- Guest Lecturer, Gut Check: Exploring Your Microbiome, Coursera, 2014
- Co-Supervisor of Ph.D. Student, KAUST, 2011–13
- Mentor of Undergraduate Students, Chisholm Lab, MIT, 2005–10
- Head Teaching Assistant, General Biochemistry, MIT, 2007
- Teaching Assistant, Introductory Biology, MIT, 2005
- Biology Tutor for Undergraduate Students, Boston Area, 2005–08
- Science Explorers Program, Fletcher–Maynard Academy and Cambridge Community Center, 2005–08
- Radio Talk Show Co-Host, *Biologue*, WMBR-FM Cambridge, 2005–08