

Jon G Sanders, PhD

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Education

2015 **Harvard University**

PhD, Organismic and Evolutionary Biology; Naomi Pierce and Peter Girguis, Advisors

2006 **Stanford University**

BS, Earth Systems

Research Experience

2018–2022 **The genomics of host specificity in gut microbes**

CIHMID Postdoctoral Fellow, Cornell University

I am developing approaches to construct genome-centric analyses of evolution in host-associated microbiomes. By combining long-read sequencing, short-read sequencing, and anaerobic culture, I am creating genomic resources that will enable us to investigate how evolution shapes microbial genomes as a function of host specificity. Current projects include a new open-source protocol for inexpensively generating high-throughput bacterial isolate genome sequences, an approach for prototype selection of representative samples for differential coverage profiles for efficient binning of high-N metagenomics studies, and a project combining long- and short-read sequencing primate metagenomes to demonstrate deep patterns of host fidelity and codiversification in primate gut microbiomes.

2015–2018 **Codiversification in host-associated microbiomes**

Postdoctoral scholar, Rob Knight lab, University of California San Diego

I developed open source tools for characterizing phylogenetic signal in complex host-associated microbial communities, helping to answer the question of what it means for a microbiome to 'evolve' with its host. I applied these tools to large datasets of vertebrate-associated microbiomes, using both amplicon sequencing and shotgun metagenomics.

Additionally, I developed novel approaches for the high-throughput sequencing and analysis of metagenomes. These tools leverage advances in automation and miniaturization to decrease library prep costs by an order of magnitude, allowing a shift from low-N to high-N strategies in shotgun metagenomics studies, with corresponding improvements in statistical power.

2008–2015 Symbiotic Microbial Evolution, Ecology, and Physiology

Graduate Student, Pierce and Girguis Labs, Harvard University

I used a variety of recently developed techniques in microbial community sequencing and analysis to investigate the evolution and ecology of symbiotic microbial communities, using chemoautotrophic hydrothermal vent gastropods and the gut communities of arboreal neotropical ants and baleen whales as model systems. I developed novel computational approaches to characterizing phylogenetic signal in complex host-associated microbial communities.

2006–2008 Ecological Physiology, Transcriptomics, and Proteomics

Research Technician, George N Somero Lab, Hopkins Marine Station

Responsible for a wide range of duties, from lab organization and equipment maintenance/repair to independent, self-directed research. I was involved in experiments in transcriptomics (using both printed cDNA and Agilent oligo microarray platforms), proteomics (Western blotting), and whole-organism physiology. I lead the development of a new oligonucleotide expression array for intra- and interspecific transcriptomics in *Mytilus* mussels, as well as establishing an in-house bioinformatics pipeline for the processing, annotation, and databasing of target organism ESTs.

2005–2007 Phylogeography of Zooxanthellae in Intertidal Anemones

Student, Stephen R Palumbi Lab, Hopkins Marine Station

Constructed a fine-scale phylogeny of dinoflagellate symbionts inhabiting the intertidal anemone *Anthopleura elegantissima* along the entire coast of California. Characterized symbionts at four loci using direct sequencing, PCR cloning, and RFLP.

2005–2006 Biogeography as a signal of mass extinction in reef ecosystems

Student, under Elizabeth Hadly, Stanford University

Performed a novel biogeographic meta-analysis of mass extinctions in Phanerozoic reefs. Tested various hypotheses about generalized response to mass extinction using ancient and modern georeferenced reef databases and ArcGIS software.

2005–2006 Molecular Forensics and Phylogeography of Seahorses

Student, Stephen R Palumbi Lab, Hopkins Marine Station

Investigated market composition of the central California medicinal seahorse trade using mitochondrial DNA sequencing (control region). Created a rough phylogeography for the most widely traded species using location-referenced museum specimens.

Computational Expertise

End-to-end bioinformatics workflows with Snakemake

Six years of experience writing genomics and metagenomics workflows in the Snakemake workflow language. These workflows have been deployed locally and in HPC cluster environments, and have processed studies comprising tens of thousands of novel samples. See <https://github.com/biocore/oecophylla> for one example.

Data management, analysis, and interface programming in Python

I have seven years of writing collaborative open-source PyCodeStyle-compliant bioinformatics software in Python, including unit and integration testing in a public-facing production environment. I am proficient with Pandas, NumPy, Matplotlib, Scikit-Bio, and other common bioinformatics and data science libraries, and have experience writing web app backends with Tornado.

Statistical analysis in R

I have more than a decade of experience doing basic data processing and statistical analysis in R. I am familiar with both Jupyter and R-markdown based notebook scripting and sharing.

CAD modeling and simulation in Fusion360

I have two years of experience designing and creating custom laboratory equipment (and other tools) using the Autodesk Fusion360 CAD platform, including basic FEA simulation. See <https://github.com/CUMoellerLab/Labware> for some examples.

Collaborative software development

I enjoy constructive and collaborative software development, in both junior and mentorship roles. I use Git and GitHub extensively for both personal and shared projects, and contribute pull requests to open-source projects when I can.

Industry Experience

2018-2019 Consultant, Biota Technologies, Inc.

Completed 290 billable hours developing novel applications in low-biomass microbiome DNA sequencing. Introduced new technique adopted in standard processing workflow to enhance reliability and traceability of samples. Resulted in one coauthored patent application, in process.

2020-2021 Consultant, BiomeSense, Inc.

2021-now Founder, Lightweight Labware, LLC.

Founded small business designing and selling open-source laboratory equipment to enable high-throughput genomics protocols at low cost, as well as engaging in bioinformatics and laboratory consulting services.

Publications

* Equal contribution

- Liu Y, Ritchie SC, Teo SM, Ruuskanen MO, Kambur O, Zhu Q, **Sanders JG** *et al.* (2023). Integration of polygenic and gut metagenomic risk prediction for common diseases. *medRxiv*. DOI: 10.1101/2023.07.30.23293396
- Palmu J, Börschel CS, Ortega-Alonso A, Markó L, ... **Sanders JG** *et al.* (2023). Gut microbiome and atrial fibrillation—results from a large population-based study. *EBioMedicine*. 91.
- Sanders JG**, Sprocket DD, Li YY, Mjungo D, Lonsdorf E, *et al.* (2023). Widespread extinctions of co-diversified primate gut bacterial symbionts from humans. *Nature Microbiology*. 8, 1039-1050.
- Sanders JG**, Yan W, Mjungo D, Lonsdorf E *et al.* (2022). A low-cost genomics workflow enables isolate screening and strain-level analyses within microbiomes. *Genome Biology*. 23(1): 212.
- Liu Y, Teo SM, Meric G, Tang HHF, Zhu Q, **Sanders JG**, Vazquez-Baeza Y, *et al.* (2022). The gut microbiome is a significant risk factor for future chronic lung disease. *Journal of Allergy and Clinical Immunology*. 4: 943-952.
- Goldman SL, **Sanders JG**, Yan W, Denice A, Cornwall M, Ivey KN, *et al.* (2022). Culture-enriched community profiling improves resolution of the vertebrate gut microbiota. *Molecular Ecology Resources*. 22(1), 122-136.
- Qin Y, Havulinna AS, Liu Y, Jousilahti P, Ritchie SC, Tokolyi A, **Sanders JG**, *et al.* (2022). Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort. *Nature Genetics*. 54(2): 134-142.
- Liu Y, Méric G, Havulinna AS, Teo SM, Ruuskanen M, **Sanders JG**, *et al.* (2022). Early prediction of incident liver disease using conventional risk factors and gut-microbiome-augmented gradient boosting. *Cell Metabolism*. 34: 1-12.
- Béchade B, Hu Y, **Sanders JG**, Cabuslay CS, Łukasik P, *et al.* (2022). Turtle ants harbor metabolically versatile microbiomes with conserved functions across development and phylogeny. *FEMS Microbiology Ecology*. 98(9): fiac068
- Hu Y, D'Amelio C, Béchade B, Łukasik P, **Sanders JG**, *et al.* (2023). Partner fidelity and environmental filtering preserve stage-specific turtle ant gut symbioses for over 40 million years. *Ecological Monographs*. 93(1): e1560.
- Shaffer JP, Nothias L-F, Thompson LR, **Sanders JG**, Salido RA, Couvillion SP, *et al.* (2022). Standardized multi-omics of Earth's microbiomes reveals microbial and metabolite diversity. *Nature Microbiology*. 7(12): 2128-2150.
- Leonard J, Mitchell J, Beinart RA, Delaney JA, **Sanders JG**, Ellis G, *et al.* (2021). Co-occurring activity of two autotrophic pathways in symbionts of hydrothermal vent tubeworm *Riftia pachyptila*. *Applied and Environmental Microbiology*. 87(17), e00794-21.

- Koponen KK, Salosensaari A, Ruuskanen MO, Havulinna AS, Männistö S, Jousilahti P, ... **Sanders JG**, *et al.* (2021). Associations of healthy food choices with gut microbiota profiles. *American Journal of Clinical Nutrition*, 114(2), 605–16.
- Salosensaari A, Laitinen V, Havulinna AS, Méric G, Cheng S, Perola M, ... **Sanders JG** *et al.* (2021). Taxonomic signatures of cause-specific mortality risk in human gut microbiome. *Nature Communications*, 12(1), 2671–8.
- Houtz JL, **Sanders JG**, Denice A, Moeller AH. (2021). Predictable and host-species specific humanization of the gut microbiota in captive primates. *Molecular Ecology*, 30(15), 3677–87.
- Cantrell K, Fedarko MW, Rahman G, McDonald D, Yang Y, Zaw T, ... **Sanders JG** *et al.* (2021). EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. *mSystems*, 6(2).
- Flynn PJ, D'Amelio CL, **Sanders JG**, Russell JA, Moreau CS. (2021). Localization of bacterial communities within gut compartments across Cephalotes turtle ants. *Applied and Environmental Microbiology*.
- Leão T, Silva R, Moss NA, Wang M, **Sanders JG**, Nurk S, *et al.* (2021). A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. *Marine Drugs*, 19(1), 20.
- Cantrell K, Fedarko MW, Rahman G, McDonald D, Yang Y, Zaw T, ... **Sanders JG** *et al.* (2021). EMPress enables tree-guided, interactive, and exploratory analyses of multi-omic datasets. *bioRxiv*. DOI: 10.1101/2020.10.06.327080
- Palmu J, Salosensaari A, Havulinna AS, Cheng S, Inouye M, Jain M, ... **Sanders JG** *et al.* (2020). Association between the gut microbiota and blood pressure in a population cohort of 6953 individuals. *Journal of the American Heart Association Journal of the American Heart Association* 9(15), e016641.
- Asnicar F, Maltez Thomas A, Beghini F, Mengoni C, Manara S, Mangh P, ... **Sanders JG** *et al.* (2020). Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. *Nature Communications* 11(1), 2500.
- Fang X, Vázquez-Baeza Y, Elijah E, Vargas F, Ackermann G, Humphrey GC, ... **Sanders JG** *et al.* (2020). Gastrointestinal surgery for inflammatory bowel disease persistently lowers microbiome and metabolome diversity. *Inflammatory Bowel Diseases* 27(5).
- Moeller AH, **Sanders JG**. (2020). Roles for the gut microbiota in the adaptive evolution of mammalian species. *Philosophical Transactions Of The Royal Society B-Biological Sciences* 375(1808).
- Salosensaari A, Laitinen V, Havulinna AS, Méric G, Cheng S, Perola M, ... **Sanders JG**, *et al.* (2020). Taxonomic signatures of long-term mortality risk in human gut microbiota. *medRxiv*. DOI: 10.1101/2019.12.30.19015842
- Song SJ*, **Sanders JG***, Delsuc F, Metcalf J, Amato K, Taylor MW, *et al.* (2020). Comparative analyses of vertebrate gut microbiomes reveal convergence between birds and bats. *MBio* 11(1), 3229.

- Cao L, Gurevich A, Alexander KL, Naman CB, Leão T, Glukhov E, ... **Sanders JG**, *et al.* (2019). Metaminer: a scalable peptidogenomics approach for discovery of ribosomal peptide natural products with blind modifications from microbial communities. *Cell Systems*, 9(6), 600–4.
- Glenn TC, Nilsen RA, Kieran TJ, **Sanders JG**, Bayona-Vásquez NJ, Finger JW, *et al.* (2019). Adapterama I: universal stubs and primers for 384 unique dual-indexed or 147,456 combinatorially-indexed Illumina libraries (iTru & iNext). *PeerJ*, 7, e7755.
- Zhu Q, Mai U, Pfeiffer W, Janssen S, Asnicar F, **Sanders JG**, *et al.* (2019). Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. *Nature Communications*, 10(1), 5477–14.
- Sanders JG**, Nurk S, Salido RA, Minich J, Xu ZZ, Zhu Q, *et al.* (2019). Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. *Genome Biology*, 20(1), 226.
- Amato KR, **Sanders JG**, Song SJ *et al.* (2019) Evolutionary trends in host physiology outweigh dietary niche in structuring primate gut microbiomes. *The ISME Journal*, 13, 576–587.
- Hammer TJ, **Sanders JG**, Fierer N (2019) Not all animals need a microbiome. *FEMS Microbiology Letters*, 366, 1–11.
- Lloyd CJ, King ZA, Sandberg TE... **Sanders JG** *et al.* (2019) The genetic basis for adaptation of model-designed syntrophic co-cultures. *PLoS Computational Biology*, 15, e1006213.
- Minich JJ, **Sanders JG**, Amir A *et al.* (2019) Quantifying and understanding well-to-well contamination in microbiome research. *mSystems*, 4, 457.
- Song SJ, **Sanders JG**, Baldassarre DT *et al.* (2019) Is there convergence of gut microbes in blood-feeding vertebrates? *Philosophical Transactions Of The Royal Society B-Biological Sciences*, 374, 20180249.
- Xu ZZ, Amir A, **Sanders JG** *et al.* (2019) Calour: an interactive, microbe-centric analysis tool. *mSystems*, 4, 581.
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- Donaldson GP, Ladinsky MS, Yu KB... **Sanders JG** *et al.* (2018) Gut microbiota utilize immunoglobulin A for mucosal colonization. *Science*, 360, 795–800.
- Fang X, Monk JM, Nurk S... **Sanders JG** *et al.* (2018) Metagenomics-based, strain-level analysis of *Escherichia coli* from a time-series of microbiome samples from a crohn's disease patient. *Frontiers in Microbiology*, 9, 2559.
- González A, Navas-Molina JA, Kosciolk T... **Sanders JG** *et al.* (2018) Qiita: rapid, web-enabled microbiome meta-analysis. *Nature Methods*, 15, 1–6.

- Hu Y*, **Sanders JG***, Łukasik P *et al.* (2018) Herbivorous turtle ants obtain essential nutrients from a conserved nitrogen-recycling gut microbiome. *Nature Communications*, 9, 964.
- Knight R, Vrbanac A, Taylor BC ... **Sanders JG** *et al.* (2018) Best practices for analysing microbiomes. *Nature Reviews Microbiology*, 16, 410–422.
- Marotz CA, **Sanders JG**, Zuniga C *et al.* (2018) Improving saliva shotgun metagenomics by chemical host DNA depletion. *Microbiome*, 6, 42.
- Minich JJ, Humphrey G, Benitez RAS ... **Sanders JG** *et al.* (2018) High-Throughput Miniaturized 16S rRNA Amplicon Library Preparation Reduces Costs while Preserving Microbiome Integrity. *mSystems*, 3.
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- Tripathi A, Marotz C, González A ... **Sanders JG** *et al.* (2018) Are microbiome studies ready for hypothesis-driven research? *Current Opinion In Microbiology*, 44, 61–69.
- Washburne AD, Morton JT, **Sanders JG** *et al.* (2018) Methods for phylogenetic analysis of microbiome data. *Nature Microbiology*, 3, 652–661.
- Davenport ER*, **Sanders JG***, Song SJ *et al.* (2017) The human microbiome in evolution. *BMC Biology*, 15, 127
- Thompson LR, **Sanders JG**, McDonald D *et al.* (2017) A communal catalogue reveals Earth's multiscale microbial diversity. *Nature*, 104, 1–24.
- Arcila Hernández LM, **Sanders JG**, Miller GA, Ravenscraft A, Frederickson ME (2017) Ant-plant mutualism: a dietary by-product of a tropical ant's macronutrient requirements. *Ecology*, 98, 3141–3151.
- McKenzie VJ, Song SJ, Delsuc F... **Sanders JG** *et al.* (2017) The effects of captivity on the mammalian gut microbiome. *Integrative And Comparative Biology*, 57, 690–704.
- Sanders JG**, Łukasik P, Frederickson ME *et al.* (2017) Dramatic differences in gut bacterial densities correlate with diet and habitat in rainforest ants. *Integrative And Comparative Biology*, 57, 705-722.
- Navas-Molina JA, Hyde ER, **Sanders JG**, Knight R (2017) The microbiome and big data. *Current Opinion in Systems Biology*, 1–5.
- Morton JT, **Sanders JG**, Quinn RA *et al.* (2017) Balance trees reveal microbial niche differentiation. *mSystems*, 2.
- Groussin M, Mazel F, **Sanders JG** *et al.* (2017) Unraveling the processes shaping mammalian gut microbiomes over evolutionary time. *Nature Communications*, 8, 14319.

- Hu Y, Holway DA, Łukasik P, ... **Sanders JG**, *et al.* (2017) By their own devices: invasive Argentine ants have shifted diet without clear aid from symbiotic microbes. *Molecular Ecology*, 26, 1608–1630.
- Russell JA, **Sanders JG**, Moreau CS (2017) Hotspots for symbiosis: Function, evolution, and specificity of ant-microbe associations from trunk to tips of the ant phylogeny (Hymenoptera: Formicidae). *Myrmecological News*, 2, 43–69.
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- Baker CCM, Bittleston LS, **Sanders JG**, Pierce NE (2016) Dissecting host-associated communities with DNA barcodes. *Philosophical Transactions Of The Royal Society B-Biological Sciences*, 371.
- Lin JY, Russell JA, **Sanders JG**, Wertz JT (2016) *Cephaloticoccus* gen. nov., a new genus of “Verrucomicrobia” containing two novel species isolated from *Cephalotes* ant guts. *International Journal Of Systematic And Evolutionary Microbiology*, 66, 3034–3040.
- Shukla SP, **Sanders JG**, Byrne MJ, Pierce NE (2016) Gut microbiota of dung beetles correspond to dietary specializations of adults and larvae. *Molecular Ecology*, 25, 6092–6106.
- Whitaker MRL, Salzman S, **Sanders JG**, Kaltenpoth M, Pierce NE (2016) Microbial communities of lycaenid butterflies do not correlate with larval diet. *Frontiers in Microbiology*, 7, 1920.
- Sanders JG**, Beichman AC, Roman J *et al.* (2015) Baleen whales host a unique gut microbiome with similarities to both carnivores and herbivores. *Nature Communications*, 6, 8285.
- Beinart RA, Gartman A, **Sanders JG**, Luther GW, Girguis PR (2015) The uptake and excretion of partially oxidized sulfur expands the repertoire of energy resources metabolized by hydrothermal vent symbioses. *Proceedings Of The Royal Society B-Biological Sciences*, 282, 20142811.
- Cembrowski AR, Reurink G, **Sanders JG** *et al.* (2015) Sporadic pollen consumption among tropical ants. *Insectes Sociaux*, 62, 379–382.
- Rubin BER, **Sanders JG**, Hampton-Marcell J *et al.* (2014) DNA extraction protocols cause differences in 16S rRNA amplicon sequencing efficiency but not in community profile composition or structure. *MicrobiologyOpen*, 3, 910–921.
- Sanders JG**, Powell S, Kronauer DJC *et al.* (2014) Stability and phylogenetic correlation in gut microbiota: lessons from ants and apes. *Molecular Ecology*, 23, 1268–1283.
- Sanders JG***, Beinart RA*, Stewart FJ, DeLong EF, Girguis PR (2013) Metatranscriptomics reveal differences in in situ energy and nitrogen metabolism among hydrothermal vent snail symbionts. *The ISME Journal*, 7, 1556–1567.

- McFall-Ngai M, Hadfield MG, Bosch TCG... **Sanders JG**, *et al.* (2013) Animals in a bacterial world, a new imperative for the life sciences. *Proceedings of the National Academy of Sciences*, 110, 3229–3236.
- Beinart RA, **Sanders JG**, Faure B *et al.* (2012) Evidence for the role of endosymbionts in regional-scale habitat partitioning by hydrothermal vent symbioses. *Proceedings of the National Academy of Sciences*, 109, E3241–50.
- Sanders JG**, Palumbi SR (2011) Populations of *Symbiodinium muscatinei* show strong biogeographic structuring in the intertidal anemone *Anthopleura elegantissima*. *Biological Bulletin*, 220, 199–208.
- Lockwood BL, **Sanders JG**, Somero GN (2010) Transcriptomic responses to heat stress in invasive and native blue mussels (genus *Mytilus*): molecular correlates of invasive success. *Journal of Experimental Biology*, 213, 3548–3558.
- Sanders JG** (2010) Program note: Cladescan, a program for automated phylogenetic sensitivity analysis. *Cladistics-The International Journal Of The Willi Hennig Society*, 26, 114–116.
- Dong Y, Miller LP, **Sanders JG**, Somero GN (2008) Heat-shock protein 70 (Hsp70) expression in four limpets of the genus *Lottia*: interspecific variation in constitutive and inducible synthesis correlates with in situ exposure to heat stress. *Biological Bulletin*, 215, 173–181.
- Sanders JG**, Cribbs JE, Fienberg HG *et al.* (2008) The tip of the tail: molecular identification of seahorses for sale in apothecary shops and curio stores in California. *Conservation Genetics*, 9, 65–71.

Invited Talks

- Towards a genomic perspective on evolution in non-model gut microbiomes.* Penn State University, 2021.
- Towards a genomic perspective on evolution in non-model gut microbiomes.* Microbiome Centers Consortium, 2021.
- Towards a distributed framework for microbial ecophylogenomics.* Penn State University, 2020.
- Agglomerating data to study major trends in the ecology and evolution of microbiomes.* San Diego State University, 2020.
- Agglomerating data to study major trends in the ecology and evolution of microbiomes.* Duke University, 2019.
- Agglomerating data to study major trends in the ecology and evolution of microbiomes.* North Carolina State University microbiology seminar series, 2019.

The evolution of the tetrapod gut microbiome. Gordon Research Seminar on Animal-Microbial Symbioses, 2018.

Changing the scale of inquiry with the Earth Microbiome Project. Keynote lecture, IEEE Aerospace Conference, Big Sky, MT, 2018.

The evolution of the tetrapod gut microbiome. Departmental seminar, Biological Sciences, Binghamton University, 2018.

The Earth Microbiome Project and the critical challenges of democratized metagenomics. University of British Columbia, 2018.

The evolution of the tetrapod gut microbiome. Joint Congress on Evolutionary Biology, Montpellier, 2018.

The Earth Microbiome Project and the critical challenges of democratized metagenomics. Polar Microbes Symposium, Tvarminne, 2018.

Democratizing metagenomics with leaderboard sequencing. Critical Assessment of Metagenomic Interpretation / Mid-Atlantic Microbiome Meetup, University of Maryland, 2017.

Carried through the trees: gut bacteria and rainforest ants. Departmental seminar, Microbiology, UC Riverside, 2017.

The evolution of the tetrapod gut microbiome. Society for Integrative and Comparative Biology, 2017.

Working below the OTU: codiversification in microbiomes and deblur and Heatsequer: improving 16S resolution to find and track contaminants. Standards, Precautions, and Advances in Ancient Metagenomics. Max Planck Institute for the Science of Human History, Jena, 2016.

Abundance and codiversification in ant gut microbiomes. Rowland Institute at Harvard, 2016.

Gut microbiomic consequences of dietary shifts in animals great and small. Scripps Institute for Oceanography, 2015.

Gut microbiomic consequences of dietary shifts in animals great and small. Gordon Research Conference on Animal-Microbe Symbioses, 2015.

Disentangling the coevolutionary histories of animal gut microbiota. Departmental seminar, Microbiology, Cornell University, 2014.

Disentangling the coevolutionary histories of animal gut microbiota. Evolution, Raleigh, NC, 2014

Detecting codiversification in an ant gut microbiome. ASM Beneficial Microbes, San Antonio, TX, 2012

Invited Posters

Comparative analyses of vertebrate gut microbiomes reveal convergence between birds and bats. Gordon Research Conference on Animal-Microbe Symbioses, 2019.

The whale gut reveals another axis of microbiome diversity. ASM General Meeting, Boston, MA, 2014.

Detecting codiversification in an ant gut microbiome. Evolution, Ottawa, ON, 2012.

Awards and Grants

- 2019 Best talk, Gordon Research Seminar on Animal-Microbial Symbiosis
- 2014 Certificate of Distinction in Teaching, Harvard University
- 2011 Putnam Field Grant, Harvard University
- 2011 Doctoral Dissertation Improvement Grant, National Science Foundation
- 2010 Putnam Field Grant, Harvard University
- 2008 Predoctoral Fellow, National Science Foundation
- 2004 Undergraduate Research Program Major Grant, Stanford University

Teaching Experience

- 2021 Workshop organizer, "3D printing for the lab," Penn State University
- 2020 Guest lecturer, "Microbial Genomics," Cornell Veterinary Medicine
- 2020 Guest lecturer, Phylogenetics, Cornell University
- 2018 Guest lecturer, "Microbial Genomics," Cornell Veterinary Medicine
- 2018 Guest lecturer and mentor, Microbiome Hackathon, Cornell University
- 2018 Workshop co-organizer, "Microbial Diversity analysis: methods and pipelines", University of British Columbia
- 2015 Guest lecturer, "Animal Behavior," Harvard University
- 2015 Guest lecturer, "Animal Behavior," Harvard University
- 2015 Guest lecturer, "Special Topics in Ecology: From Metacommunities to Microbiomes," University of Toronto
- 2015 Guest lecturer, "Biology of the Social Insects," Providence College
- 2015 Teaching Fellow, "Animal Behavior," Harvard University
- 2014 Teaching Fellow, "Writing Science," Harvard University
- 2011 Teaching Fellow, "Animal Behavior," Harvard University
- 2010 Teaching Fellow, "Lab Techniques in Ecological Physiology," Harvard University

2009 Head Teaching Fellow, Mentoring For Science
2005 Guest Science Teacher, Escondido Elementary, Stanford, CA
2005 Underwater Explorers Instructor, Monterey Bay Aquarium
2003–2004 Science Educator, Marine Science Institute, Redwood City, CA

Mentorship Experience

2019-2020 *Shanyah Mitchell, Cornell University*
Laboratory technician

2017-2018 *Rodolfo Salido, University of California San Diego*
Laboratory technician

2016-2018 *Jeremiah Minich, University of California San Diego*
PhD candidate

2013-2015 *Nathaniel Bresnick, Milton Academy and Yale University*
Visiting high school/undergraduate researcher

2013 *Aaron Behr, Brown University*
Visiting undergraduate researcher

2012 *Annabel Beichman, Harvard University*
Senior Thesis, “Gut Flora of the North Atlantic Right Whale”
Hoops Prize nominee
Coauthor of published peer-reviewed scientific paper

2012 *Nathan Fudenberg, Carleton College*
Visiting undergraduate researcher

2011 *Chung Yao Yu, Harvard University*
Senior Thesis, “Exploring differences in carbon metabolism between short-fat and long-skinny *Ridgeia piscesae*”
Hoops Prize award winner

Science Outreach and Service

2019-2021 *Board of Directors, Ithaca Generator Makerspace*

2015 *Science ambassador, Harvard Museum of Natural History*
Public outreach at HMNH I Heart Science festival

2013 *Science outreach, Cambridge Science Festival*
Designed public demonstration of DNA barcoding and molecular forensics of seafood

- 2012 *Guest teacher, Science & Cooking, Harvard University*
Designed and taught class for summer kids program
- 2012 *Public lecture, Science In The News, Harvard University*
Public lecture on species interactions / symbioses
- 2009 *Head Teaching Fellow, Mentoring For Science, Harvard University*
Organized weekly after-school science enrichment class for students from Boston Public Schools

Peer Review

Journals

- Applied and Environmental Microbiology
- BMC Evolutionary Biology
- Ecology Letters
- Environmental Microbiology
- FEMS Microbiology Ecology
- Genome Biology
- ISME Journal
- Marine Mammal Science
- Microbiology Open
- Microbiome
- Molecular Biology and Evolution
- Molecular Ecology
- Molecular Ecology Resources
- mSystems
- National Geographic
- Nature Biotechnology
- Nature Ecology and Evolution
- Nature Scientific Reports
- PeerJ
- PLoS Biology

- Proceedings of the National Academy of Sciences
- Royal Society Open Science

Funding agencies

- National Science Foundation