

Jesse McNichol

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Summary of Experience

I am an Assistant Professor in the department of Biology at St. Francis Xavier University, where I teach microbiology and run a research program in marine microbial ecology. My research is currently primarily funded by the Simons Foundation International as part of the [CBIOMES collaboration](#).

My academic background is in oceanography and microbial ecology, and I have experience in both wet-lab and *in silico* approaches for generating and analyzing high-throughput sequencing data. This includes 3-domain metabarcoding, shotgun metagenomics, as well as related approaches for quantifying microbial activity using fluorescence *in situ* hybridization.

Education

Massachusetts Institute of Technology - Woods Hole Oceanographic Institution, Cambridge/Woods Hole, Massachusetts, USA

Ph.D., Biological Oceanography

2011-2016

Thesis: [Productivity, Metabolism and Physiology of Free-Living Chemoautotrophic *Epsilonproteobacteria*](#) (Advisor: Dr. Stefan Sievert)

Mount Allison University, Sackville, New Brunswick, Canada

B.Sc., First Class Honours with Distinction, Biology

2003-2008

Thesis: Endophytic Fungi of Liverworts (*Bryophyta*) in a Copper-Contaminated Environment (Advisors: Drs. Robert Thompson and Felix Baerlocher)

Professional Experience

St. Francis Xavier University; Antigonish, NS, Canada

Assistant Professor

2023 - present

University of Southern California, Fuhrman Lab; Los Angeles, CA, USA

Postdoctoral Scholar

2018 - 2023

- Compiled an atlas of microbial biogeography ([GRUMP](#)) based on existing meta-'omics datasets and newly generated amplicon sequence libraries
- Developed software pipelines for the analysis of amplicon sequences, intercomparison with metagenomes, and *in-silico* evaluation of primer performance

Chinese University of Hong Kong, Luo Lab; Shatin, New Territories, HK

Research Assistant 2016 - 2017

- Developed plate-based isolation methods for high-throughput isolation of fastidious chemoautotrophic *Campylobacter*
- Isolated sulfur-oxidizing microorganisms from hydrothermal vents and coastal sediments for pangenome and population genetic analysis
- Developed a high-through put isolation system for selective enrichment of roseobacter group bacteria from local sediments

Woods Hole Oceanographic Institution, Sievert Lab; Woods Hole, MA, USA

Graduate Research Assistant 2011-2016

- Incubated deep-sea hydrothermal vent chemoautotrophic communities at *in-situ* pressure and temperature to infer their ecophysiology and biogeochemical impact
- Cultivated *Sulfurimonas denitrificans* in a custom-built chemostat to validate a theoretical model of energy conservation for this organism

National Research Council of Canada; Halifax, NS, Canada

Technical Officer 2009-2011

Environment Canada; Moncton, NB, Canada

Environmental Technician 2009

Atlantic Canada Conservation Data Center; Sackville, NB, Canada

Assistant Field Botanist 2008

Marine Macroecology and Biogeochemistry Lab; Sackville, NB, Canada

Summer Research Student 2007-2008

**Grants,
Fellowships
and Awards**

2025-2026: Dr. W.F. James Research Scholar (StFX; 4.5 credit teaching release)

2024-2026: NRC Ocean Cluster Support Program (\$88,384 CAD)

Effects of nano/microplastic exposure on zebrafish (Danio rerio) gut microbiome

2024-2027: CBIOMES Scholars Program, Simons Foundation International (\$359,396 USD)

Predicting Community Resilience to Environmental Perturbations by

Quantifying in situ Physiology of Microdiverse Subclusters of Uncultured Marine Prokaryotes

2023: StFX Startup Funding (\$27,000 CAD)

2016: JGI Small-Scale Microbial / Metagenome Program

Investigating the Genetic Basis of Differential Oxygen Tolerance in Sulfurimonas Ecotypes from the Subseafloor Biosphere Using Single-Cell Genomics

2014-2016: NASA Earth Systems Science Fellowship

Quantifying Energy Metabolism and Associating Function with Taxonomy for Chemosynthetic Microbial Communities at Deep-Sea Hydrothermal Vents

2013-2016: Natural Sciences and Engineering Research Council of Canada, Post-Graduate Scholarship (Doctoral level)

Quantifying Energy Metabolism and Associating Function with Taxonomy for Chemolithoautotrophic Microbial Communities at Deep-Sea Hydrothermal Vents

2013-2014: Canadian Meteorological and Oceanographic Society Scholarship Supplement

2011-2012: Natural Sciences and Engineering Research Council of Canada, Post-Graduate Scholarship (Master's level)

Psychrophilic bacteria in the Canadian Arctic

Research Impact Total citations: 865, 547 citations since 2020
h-index: 13 (source: [Google Scholar](#); last updated 2025-09-18)

Preprints & in-review publications **McNichol, J.***, Sievert, S.M.*, 2019. [Reconciling a Model of Core Metabolism with Growth Yield Predicts Biochemical Mechanisms and Efficiency for a Versatile Chemoautotroph](#). bioRxiv. *Co-corresponding authors.

Faria, L.C., Raut, Y., **McNichol, J.**, Williams, N.L.R., Fuhrman, J.A., Signori, C.N. 2025. [A Multidomain Lens on the Temporal Dynamics of Surface Microbial Communities in the Southern Ocean \(2013–2019\)](#). bioRxiv.

Jones-Kellett, A.E., **McNichol, J.**, Raut, Y., Fuhrman, J.A., Follows, M.J. 2025. Eukaryotic Phytoplankton are Sustained by Eddies and Lateral Mixing in a

Subtropical Gyre *PNAS*. Submitted (2025-09-18).

Publications in Prep Ser-Giacomi, E.*, **McNichol, J.***, Raut, Y., Yeh, Y.-C., Ribalet, F., Hassle., C., Rees, A., Tarran, G., Gradoville, M., Turk-Kubo, K., Zehr, J., Dutkiewicz, S., Follows, M., Fuhrman, J.A. Estimating Absolute Microbial Abundances By Combining Metabarcoding and Cell-Count Data. *Co-first authors.

Peer-Reviewed Publications **McNichol, J.***, Williams L.R.*, Raut, Y., Fuhrman, J.A. *et al.* 2025. Characterizing organisms from three domains of life with universal primers from throughout the global ocean. *Scientific Data*. 12, 1078.

Zakem, E.J., **McNichol, J.**, Weissman, J.L., Raut, Y., Xu, L., Halewood, E.R., Carlson, C.A., Dutkiewicz, S., Fuhrman, J.A., Levine, N.M., 2025. Functional biogeography of marine microbial heterotrophs. *Science*. 388, eado5323.

Mishra, A., **McNichol, J.**, Fuhrman, J., Blei, D., Müller, C.L., 2024. Variational inference for microbiome survey data with application to global ocean data. *ISME Communications*. 5(1), ycaf062.

Jones-Kellett, A.E., **McNichol, J.**, Raut, Y., Cain, K.R., Ribalet, F., Armbrust, E.V., Follows, M.J., Fuhrman, J.A., 2024. Amplicon Sequencing with Internal Standards Yields Accurate Absolute Picocyanobacteria Cell Abundances as Validated with Flow Cytometry. *ISME Communications*. 4(1), ycae115.

Mino, S., Fukazawa, S., Tsuchiya, J., **McNichol, J.**, Sievert, S.M., Yamaki, S., Ando, Y., Sawabe, T., 2023. *Hydrogenimonas cancrithermarum* sp. nov., a hydrogen- and thiosulfate-oxidizing mesophilic chemolithoautotroph isolated from diffuse-flow fluids on the East Pacific Rise, and an emended description of the genus *Hydrogenimonas*. *IJSEM*. 73, 006132.

Milke, F., Sanchez-Garcia, S., Dlugosch, L., **McNichol, J.**, Fuhrman J.A., Simon, M., Wagner-Döbler I., 2022. Composition and Biogeography of Pro- and Eukaryotic Communities in the Atlantic Ocean: Primer Choice Matters. *Frontiers in Microbiology*. 13, 895875.

McNichol, J.^{1,2}, Dyksma S.¹, Mußmann M., Seewald, J., Sylva, S., Sievert S.², 2022. Genus-Specific Carbon Fixation Activity Measurements Reveal Distinct Responses to Oxygen Among Hydrothermal Vent *Campylobacteria*. *Applied and Environmental Microbiology*. 88(2), e02083-21. ¹Co-first authors. ²Co-corresponding authors.

Lin, X.Q., Chu, X., **McNichol, J.**, Qian, Y., Luo, H.W., 2022. Cryptic Niche Differentiation of Novel Sediment Ecotypes of *Ruegeria pomeroyi* Correlates

with Nitrate Respiration. *Environmental Microbiology*. 24(1), 390-403.

McNichol, J.*, Berube, P., Biller, S., Fuhrman, J., 2021. Evaluating and Improving SSU rRNA PCR Primer Coverage for Bacteria, Archaea, and Eukaryotes Using Metagenomes from Global Ocean Surveys. *mSystems*. 6(3), e00565-21. *Corresponding author.

Yeh, Y.C., **McNichol, J.**, Needham, D., Fichot, E., Berdjeb, L., Fuhrman, J., 2021. Comprehensive single-PCR 16S and 18S rRNA community analysis validated with mock communities, and estimation of sequencing bias against 18S. *Environmental Microbiology*. doi: 10.1111/1462-2920.15553.

Götz, F., Pjevac, P., Markert, S., **McNichol, J.**, Becher, D., Schweder, T., Mußmann, M., Sievert, S.M., 2019. Transcriptomic and proteomic insight into the mechanism of cyclooctasulfur- versus thiosulfate-oxidation by the chemolithoautotroph *Sulfurimonas denitrificans*. *Environmental Microbiology* 21, 244–258.

Labonté, J.M., Pachiadaki, M., Fergusson, E., **McNichol, J.**, Grosche, A., Gulmann, L.K., Vetriani, C., Sievert, S.M., Stepanauskas, R., 2019. Single Cell Genomics-Based Analysis of Gene Content and Expression of Prophages in a Diffuse-Flow Deep-Sea Hydrothermal System. *Frontiers in Microbiology*. 10.

McNichol, J.*, Stryhanyuk, H., Sylva, S.P., Thomas, F., Musat, N., Seewald, J.S., Sievert, S.M.*, 2018. Primary Productivity Below the Seafloor at Deep-Sea Hot Springs. *Proceedings of the National Academy of Sciences*. 115, 6756-6761. *Co-corresponding authors.

Götz, F., Longnecker, K., Soule, M.C.K., Becker, K.W., **McNichol, J.**, Kujawinski, E.B., Sievert, S.M., 2018. Targeted metabolomics reveals proline as a major osmolyte in the chemolithoautotroph *Sulfurimonas denitrificans*. *Microbiology Open*. e586.

McNichol, J., Sylva, S.P., Thomas, F., Taylor, C.D., Sievert, S.M., Seewald, J.S., 2016. Assessing microbial processes in deep-sea hydrothermal systems by incubation at *in situ* temperature and pressure. *Deep Sea Research Part I: Oceanographic Research Papers*. 115, 221–232.

McNichol, J., MacDougall, K.M., Melanson, J.E., McGinn, P.J., 2012. Suitability of soxhlet extraction to quantify microalgal fatty acids as determined by comparison with *in situ* transesterification. *Lipids*. 47, 1–13.

MacDougall, K.M., **McNichol, J.**, McGinn, P.J., O'Leary, S.J.B., Melanson, J.E.,

2011. [Triacylglycerol profiling of microalgae strains for biofuel feedstock by liquid chromatography–high-resolution mass spectrometry](#). *Analytical and Bioanalytical Chemistry*. 401, 2609–2616.

Park, K.C., Whitney, C., **McNichol, J.**, Dickinson, K.E., MacQuarrie, S., Skrupski, B.P., Zou, J., Wilson, K.E., O’Leary, S.J.B., McGinn, P.J., 2011. [Mixotrophic and photoautotrophic cultivation of 14 microalgae isolates from Saskatchewan, Canada: potential applications for wastewater remediation for biofuel production](#). *Journal of Applied Phycology*. 24, 339–348.

**Book
Chapters &
Other
Scientific
Writing**

McNichol, J., 2024. [Mineral-eating microorganisms at extinct hydrothermal vents](#). "News and Views" for Nature Microbiology. 9, 589-590.

Sievert, S.M., **McNichol, J.**, Thomas, F., Panayotova, E., Watson R., 2018. [How Do Deep-Sea Hot Spring Ecosystems Work?](#) *Environmental Science Journal for Teens*.

McNichol, J., 2017. [Breaking the Oxygen Barrier in Microbial Cultivation](#), Small Things Considered Blog, American Society for Microbiology.

McNichol, J., 2014. [A First-Time Diver’s Experience](#). Blog for research cruise AT2623 (R/V *Atlantis*).

McNichol, J., 2014. “Mail Buoy” responses to gradeschool student questions about deep-sea hydrothermal vent ecosystems: [Jan 12th](#), [Jan 13th](#), [Jan 20th](#), [Jan 30th](#). Research cruise AT26-10 (R/V *Atlantis*).

McNichol, J., McGinn, P.J., 2012. [Adapting Mass Algalculture for a Northern Climate](#), in: Gordon, R., Seckbach, J. (Eds.), *The Science of Algal Fuels, Cellular Origin, Life in Extreme Habitats and Astrobiology*. Springer Netherlands, pp. 131–146.

McNichol, J., Gordon, R., 2012. [Are We from Outer Space?: A Critical Review of the Panspermia Hypothesis](#), in: Seckbach, J. (Ed.), *Genesis - In The Beginning, Cellular Origin, Life in Extreme Habitats and Astrobiology*. Springer Netherlands, pp. 591– 619.

McNichol, J., 2008. [Primordial soup, fool’s gold, and spontaneous generation](#). *Biochemistry and Molecular Biology Education* 36, 255–261.

Scientific Workflows & Tools **McNichol, J.**, Yeh Y.C., Aleman, M., Fuhrman J., 2019. A custom bash pipeline to process 515Y/926R mixed 16S/18S amplicons into ASVs ([protocol link](#)).

McNichol, J., 2021. *MGPrimerEval*: A reproducible snakemake pipeline to compare amplicon primer sequences with metagenomes to quantify their *in-silico* coverage and real-world performance by comparing metagenomes with amplicons ([pipeline link](#)).

Teaching Experience **St. Francis Xavier University**; Antigonish, NS, Canada
Biology 398: Exploring Native Microbiota (~8 students, taught yearly)
Biology 315: Introduction to Microbiology (~40 students, taught yearly)
Biology 115: Introduction to Microbiology for Nursing (~90 students, taught yearly)
Biology 215: Introduction to Microbiology for Nutrition (~20 students, taught yearly)

Woods Hole Oceanographic Institution; Woods Hole, MA, USA
Biological Oceanography (TA, Spring 2015)
Marine Microbiology and Biogeochemistry (TA, Fall 2013)

Mount Allison University; Sackville, NB, Canada
Native Flora (TA, Fall 2007)

Research Mentoring & Supervisory Experience **2025 - present:** Mentoring Honours student Julia Crean in microbial metabarcoding and bioinformatic analysis of peatland microorganisms (co-supervised with Dr. Graham Clark, StFX).

2025 - present: Mentoring Honours student Laura Riendeau in microbial metabarcoding and bioinformatic analysis of pegmatite-associated microorganisms (co-supervised with Dr. Donnelly Archibald, StFX).

2025 summer: Mentored summer student Shaye Close in bioinformatic analysis of metagenome data, as well as field protocols for marine microbial ecology.

2023 - present: Mentoring recent graduate Jillian Davies in microbial metabarcoding techniques for analyzing zebrafish microbiomes in collaboration with NRC colleagues, including DNA extraction, PCR library preparation, and bioinformatic data analysis.

2021 - 2024: Mentored PhD student Laiza Faria in laboratory techniques for metabarcoding, metagenomics, and associated data analysis. Also assisted with successful application for funding to the Scientific Committee on Antarctic Research (SCAR) to travel to Antigonish, NS for research collaboration (July-August 2024).

2021 - 2023, USC: Mentored postdoctoral scholar Yubin Raut in a project that aims to use bioinformatic data from global ocean basins to validate and improve with the global-scale biogeochemical model DARWIN.

2019 - 2021, USC: Mentored undergraduate Bruce Yanpui Chan in bioinformatic analyses and assisted with a successful funding application to the program Student Opportunities for Academic Research (SOAR).

2018 - 2022, USC: Assisted graduate students Selene Sanchez-Garcia (Technical University Braunschweig) and Felix Milke (University of Oldenburg) with amplicon analysis, data interpretation, and conference presentations.

2018 - 2023, USC: Assisted Fuhrman lab graduate students in implementing a qiime2 workflow for the analysis of PCR amplicon data.

2017 - 2018, CUHK: Guided the final-year undergraduate project* of Annie Wing-Yi Lo, which tested the effect of microoxic conditions on the isolation of sulfur-oxidizing microbes from shallow-water hydrothermal vents and local sediments. *Equivalent of Honours thesis.

2015 - 2016, WHOI: Supervised the independent research project of volunteer Dali Smolsky to isolate novel autotrophic *Campylobacteria* from salt marsh and hydrothermal vent environments.

2010, NRC: Taught students techniques for lipid extraction and transesterification of microalgal biomass with bio-compatible solvents.

Pedagogical and Research Training **Maple League of Universities**

The Maple League Micro-Certificate in Teaching and Learning (2023-2024)

edX Online Learning Platform

Becoming a More Equitable Educator: Mindsets and Practices (Spring 2021)

CyVerse Learning Network

Foundational Open Science Skills Online (Spring 2021)

University of Southern California, Center for Excellence in Teaching
Future Faculty Teaching Institute (Spring 2020)

Science Outreach & Other Educational Experience X-CHEM, Introduction to Environmental Microbiology (July 2024, grades 5-8, 2 hour class)
Fun Interactive Science Hour ([FISH](#)) Outreach Program (USC) / Los Angeles Public Library (Dec 2020 - 2023)

Chinese Summer Language Village, Mount Allison University (MtA; 2008)

Planet Performers environmental drama, MtA (2007-2008)

University and Department Service Chairs Selection Committee, Faculty of Science (2025 - present)

Faculty of Science Secretary (2023 - 2025)

Science Atlantic Representative (Biology, 2024 - present)

Joint Occupational Health and Safety Committee (January 2025 - present)

University Open House Day (Oct 2023, 2024)

3 Minute Thesis judge (2024, 2025)

Woods Hole Oceanographic Institution Joint Program Career Panel (2024)

Honours thesis second reader: 4 (2023-2024: 2; 2025-2026: 2)

Selected Data Products McNichol., J., Williams, N., Fuhrman, J.A., *et al.* 2025. [Global rRNA Universal Metabarcoding of Plankton Dataset](#).

McNichol, J., 2019. [Exact Amplicon Sequence Variant Abundances from the ANT28-5 Latitudinal Transect of the Atlantic Ocean](#).

McNichol, J., Dyksma S., Mußmann M., and Sievert S., 2020. [CARD-FISH Images from Incubations of Deep-Sea Hydrothermal Vent Fluid and Testing of Novel Probes for *Arcobacter*, *Sulfurimonas*, and *Sulfurovum*](#).

Technical Comments McNichol, J., Sievert, S.M. Comment on PMID 26929299: Carbon Fixation Driven by Molecular Hydrogen Results in Chemolithoautotrophically Enhanced Growth of *Helicobacter pylori*. In: PubMed Commons [Internet]. Bethesda (MD): National Library of Medicine; 2017 Feb 16. [Permalink](#).

Invited Talks **Atlantic Canada Coastal and Estuarine Science Society Annual Meeting May 2025;** Wolfville, NS, Canada (Invited Plenary Talk)

Towards Holistic Microbial Ecology: Integrating Across Domains, Scale, and Genetic Diversity to Track Microbial Ecosystem Function

Institute for Chemistry and Biology of the Marine Environment (ICBM); Oldenburg, Germany (COVID e-seminar, Nov 25th, 2020)

Using Global Metagenomes to Evaluate and Improve PCR Primer Coverage and the Application of 3-Domain Amplicon Data to Trait-Based Models

Scripps Institution of Oceanography; San Diego, CA (COVID e-seminar, June 17th, 2020).

Using Global Metagenomes to Quantify PCR Primer Coverage and Integrating 3-Domain Amplicon Data with Models

CBIOMES e-meeting; (online seminar, Dec 12th, 2018).

Biogeography of Exact Amplicon Sequence Variants

The Swire Institute of Marine Science; Hong Kong S.A.R., China (Mar 20th, 2016)

Brimstone Bacteria: Primary Productivity and Microbial Ecology of Deep-Sea Hydrothermal Vents

University of Hong Kong, School of Biological Sciences; Hong Kong S.A.R., China (Jan 29th, 2016)

Brimstone Bacteria: Primary Productivity and Microbial Ecology of Deep-Sea Hydrothermal Vents

Max Planck Institute for Marine Microbiology; Bremen, Germany (July 8th, 2014)

Insights into chemolithoautotrophy at deep-sea hydrothermal vents from in-situ experiments and metabolic modeling

**Conference &
Workshop
Activity**

Scientific Committee on Antarctic Research (2024), Pucón
Punta Arenas, Chile

Co-author on 2 presentations, representing active collaborations:

Unraveling the Antarctic Krill microbiome present in Krill internal and external body parts (Mireia Miestre, National Museum of Natural Sciences, Madrid, Spain)

Latitudinal Gradients and Vertical Connectivity in the Scotia Sea Microbiome (Mireia Miestre, National Museum of Natural Sciences, Madrid, Spain)

Ocean Sciences Meeting (2024) New Orleans, LA, USA

Co-author on 5 presentations, representing active collaborations:

Characterizing and comparing distributions of organisms within all 3-domains of life with universal primers from 1577 samples throughout the global ocean (Nathan Williams, collaborator at USC)

Using global rRNA metabarcoding datasets to assess a trait-based ecosystem model reveals the importance of missing and under-surveyed phytoplankton (Yubin Raut, collaborator at MIT)

The Fluid Dynamical Structuring of Microbial Communities Along an Eastern North Pacific Transect (Lexi Jones-Kellett, collaborator at MIT)

A mechanistic species coexistence theory explains the observed increase in marine microbial biodiversity with depth (Liang Xu, collaborator at Carnegie Institute)

Emergent structure and function of microbial heterotrophic communities in a model ocean (Emily Zakem, collaborator at Carnegie Institute)

Ocean Sciences Meeting (2020) San Diego, CA, USA

Testing model predictions and revealing basin-scale biogeography with whole-community PCR amplicons from GEOTRACES (Oral Presentation)

Atlantic and Pacific Ocean bacterioplankton diversity (Co-author on student presentation).

Ocean Nucleic Acids 'omics Intercalibration and Standardization Workshop (2020) UNC Chapel Hill, NC, USA (Invited Participant)

Gordon Research Conference/Seminar in Marine Molecular Ecology

(2017) Hong Kong S.A.R., China

Primary Productivity and Ecophysiology of Chemosynthetic Campylobacteria
(Poster Presentation)

International Society for Microbial Ecology (2016) Montreal, QC, Canada

Primary Productivity and Ecology of the Subseafloor Biosphere at Deep-Sea Hydrothermal Vents, 9 °N East Pacific Rise (Oral Presentation)

Gordon Research Conference in Marine Molecular Ecology (2015) Hong Kong S.A.R., China

Bacterial Chemosynthesis at Deep-Sea Hydrothermal Vents Quantified by Cultivation at in-situ Pressure and NanoSIMS Analysis (Poster Presentation)

Gordon Research Seminar in Marine Molecular Ecology (2015) Hong Kong S.A.R., China

Incubations of Hydrothermal Vent Communities at In-situ Pressure and Temperature Quantify Community Primary Productivity of the Subseafloor Biosphere (Oral Presentation)

American Society for Microbiology General Meeting (2015) New Orleans, LA, USA *Simulated Seafloor Conditions Reveal Epsilonproteobacteria as Dominant Chemoautotrophs in Fluids from the Subseafloor Biosphere at Deep-Sea Vents* (Young Investigator Oral Presentation)

American Society for Microbiology General Meeting (2014) Boston, MA, USA

A Genome-Scale Metabolic Model of Sulfurimonas denitrificans Provides Insight into the Process of Autotrophic Denitrification (Young Investigator Oral Presentation)

Department Seminars Woods Hole Oceanographic Institution (Aug 1st, 2016)

Productivity, Metabolism and Physiology of Free-Living Chemoautotrophic Epsilonproteobacteria (Thesis defense)

Woods Hole Oceanographic Institution (Feb 19th, 2015)

Simulated Seafloor Conditions Reveal Epsilonproteobacteria as Dominant Chemoautotrophs in Fluids from the Subseafloor Biosphere at Deep-Sea Vents

Professional Service **Reviewer for:** Scientific Reports, Scientific Data, PLoS One, Frontiers in Microbiology, International Journal of Systematic and Evolutionary Microbiology, Journal of Open-Source Science, Nature Communications, PeerJ, Molecular Ecology Resources, Environmental Microbiology, ISME Journal, Journal of Geophysical Research - Biogeosciences.

Professional Affiliations American Society for Microbiology (ASM), Canadian Society for Microbiology (CSM), The Oceanography Society (TOS)

Research Cruises **November 2014**, East Pacific Rise 9°N, R/V *Atlantis*: AT26-23, Chemoautotrophic Carbon Production at Deep-Sea Hydrothermal Vents
January 2014, East Pacific Rise 9°N, R/V *Atlantis*: AT26-10, Dimensions of Biodiversity, An Integrated Study of Energy Metabolism, Carbon Fixation, and Colonization Mechanisms in Chemosynthetic Microbial Communities at Deep-Sea Vents
July-Aug 2012, Rhode Island Continental Shelf, R/V Endeavor: Deep Ocean Benthic Sampler Cruise

Technical Research Skills & Experience

- Aquatic microbial field sampling, preservation, and DNA extraction
- SSU rRNA amplicon / metagenomic / -transcriptomic library preparation
- Microbial pure culture isolation, including for oxygen-sensitive microorganisms (Hungate technique)
- Physiological growth experiments, including both batch and chemostat
- Incubations for measuring biogeochemical rates and microbial growth, including stable/radioisotope methods
- Microscopic enumeration and identification of environmental microorganisms, including Fluorescence *In Situ* Hybridization methods (e.g. CARD-FISH) and subsequent single-cell activity measurements (e.g. NanoSIMS)

Software / Bioinformatic skills **Scripting and Plotting Languages:** Python, bash, R.
Selected Bioinformatics Software Experience: qiime2, jupyter, conda/mamba, snakemake, anvi'o, (meta)SPAdes, look@NanoSIMS, GTDB-tk, phyloFlash, bbtools.

Languages Written Chinese (functional with traditional and simplified characters),
Mandarin Chinese (conversational), Cantonese (basic spoken), French
(conversational), Spanish (functional)