Qiyun Zhu, Ph. D.

(Updated on Mar 11, 2022)

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EDUCATION

- **Ph. D.** in Biological Sciences (evolutionary biology focus)   2014
  University at Buffalo, The State University of New York
  Advisor: Katharina Dittmar
  Dissertation: Molecular evolution and ecology of fleas and flea-associated microbial organisms in light of horizontal gene transfer.

- **M. S.** in Biological Sciences (molecular biology focus)   2009
  University at Buffalo

- **B. S.**, in Biological Sciences   2007
  Fudan University

ACADEMIC APPOINTMENTS

- **Assistant Professor**   2020 – present
  Arizona State University, School of Life Sciences; Biodesign Center for Fundamental and Applied Microbiomics

- **Postdoctoral Scholar**   2016 – 2020
  University of California San Diego, Department of Pediatrics
  Supervisor: Rob Knight

- **Postdoctoral Fellow**   2014 – 2016
  J. Craig Venter Institute, Department of Genomic Medicine
  Supervisor: Sarah Highlander

- **Research Assistant**   2008 – 2011
  New York State Center of Excellence in Bioinformatics and Life Sciences

- **Undergraduate Researcher**   2005 – 2007
  Fudan University, Lab of Molecular Immunology

PEER-REVIEWED PUBLICATIONS

Google Scholar profile: https://scholar.google.com/citations?user=mjkV0pUAAAAJ

Total papers: **59**, citations: **9,810**, *h*-index: **28**, *i*10-index: **43**.

2022

- **Zhu Q** (**co-corresponding**), Huang S, Gonzalez A, McGrath I, McDonald M, Haiminen N, Armstrong G, et al. Phylogeny-aware analysis of metagenome community ecology based on matched reference genomes while bypassing taxonomy. *mSystems*. In press. *BioRxiv*.

- Armstrong G, Martino C, Morris J, Khaleghi B, Kang J, Dereus J, **Zhu Q**, et al. Swapping metagenomics preprocessing pipeline components offers speed and sensitivity increases. *mSystems*. In press.

- Liu Y, Meric G, Havulinna AS, Teo SM, Aberg F, Ruuskanen M, Sanders J, **Zhu Q**, et al. Early prediction of incident liver disease using conventional risk factors and gut microbiome-augmented gradient boosting. *Cell Metabolism*. Provisionally accepted. *MedRxiv*.

- Singh K, Pituch P, **Zhu Q**, Gu H, Ernst B, Tofthagen C, Brewer B, et al. Distinct Nausea Profiles Are Associated With Gastrointestinal Symptoms In Oncology Patients Receiving Chemotherapy. _Cancer Nursing_. 2022. doi: 10.1097/NCC.0000000000001076

- Jasbi P, Mohr AE, Shi X, Mahmood T, **Zhu Q**, Bruening M, Gu H, Whisner C. Microbiome and metabolome profiles of high screen time in a cohort of healthy college students. _Scientific Reports_. 2022. 12(1):1-17.

- Needham BD, Funabashi M, Adame MD, Wang Z, Boktor JC, Haney J, Wu WL, et al. A gut-derived metabolite alters brain activity and anxiety behavior in mice. _Nature_. 2022. 602(7898):647-53.

- Qin Y, Havulinna AS, Liu Y, Jousilahti P, Ritchie SC, Tokolyi A, et al. Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort. _Nature Genetics_. 2022. 54(2):134-42.

- Mills RH, Dulai PS, Vázquez-Baeza Y, Sauceda C, Daniel N, Gerner RR, Batachari LE, et al. Multi-omics analyses of the ulcerative colitis gut microbiome link Bacteroides vulgatus proteases with disease severity. _Nature Microbiology_. 2022. 7(2):262-76.

- Balaban M, Jiang Y, Roush D, **Zhu Q**, Mirarab S. Fast and Accurate Distance-based Phylogenetic Placement using Divide and Conquer. _Molecular Ecology Resources_. 2022. 22(3):1213-27.

2021

- Armstrong G, Cantrell K, Huang S, McDonald D, Haiminen N, Carrieri AP, **Zhu, Q**, et al. Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. _Genome Research_. 2021. 31(11):2131-37.

- **Zhu Q**, Hou Q, Huang S, Ou Q, Huo D, Vázquez-Baeza Y, Cen C, Cantu V, Estaki M, Chang H, Belda-Ferre P, Kim HC, Chen K, Knight R, Zhang J. Compositional and genetic alterations in Graves' disease gut microbiome reveal specific diagnostic biomarkers. _The ISME Journal_. 2021. 15(11):3399-411.

- Huang S, Jiang S, Huo D, Allaband C, Estaki M, Cantu V, Belda-Ferre P, et al. Candidate probiotic _Lactiplantibacillus plantarum_ HNU082 rapidly and convergently evolves within human, mice, and zebrafish gut but differentially influences the resident microbiome. _Microbiome_. 2021. 9(1):151.

- Singh KP, Kober KM, Ernst B, Sachdev J, Brewer M, **Zhu Q**, Gu H, et al. Multiple Gastrointestinal Symptoms Are Associated With Chemotherapy-Induced Nausea In Patients With Breast Cancer. _Cancer Nursing_. 2021. doi: 10.1097/NCC.0000000000000976.

- Sun Z, Huang S, Zhang M, **Zhu Q**, Haiminen M, Carrieri AP, Vázquez-Baeza Y, Parida L, Kim HC, Knight R, Liu YY. Challenges in Benchmarking Metagenomic Profilers. _Nature Methods_. 2021. 18(6):618-26.

- Jiao JY, Fu L, Hua ZS, Liu L, Salam N, Liu PF, Lv AP, et al. Insight into the function and evolution of Wood-Ljungdahl pathway in _Actinobacteria_. _The ISME Journal_. 2021. 15(10):3005-18.

- Karst SM, Ziels RM, Kirkegaard RH, Sørensen EA, McDonald D, **Zhu Q**, Knight R, Albertsen M. High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. _Nature Methods_. 2021. 18(2):165-9.

- Tripathi A, Vazquez-Baeza Y, Gauglitz JM, Wang M, Duhrkop K, Esposito-Nothias M, Acharya DD, et al. Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. _Nature Chemical Biology_. 2021. 17(2):146-51.

- Cantrell K, Fedarko MW, Rahman G, McDonald D, Yang Y, Zaw T, Gonzalez A, et al. EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. _mSystems_. 2021. 6(2):e01216-20.

- Bhagwat G, **Zhu Q**, O'Connor W, Subashchandrabose S, Grainge, I, Knight R, Palanisami T. Exploring the Composition and Functions of Plastic Microbiome Using Whole-Genome Sequencing. *Environmental Science & Technology.* 2021. 55(8):4899-913.

- Leão T, Wang M, Moss N, da Silva R, Sanders J, Nurk S, Gurevich A, et al. A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. *Marine Drugs*. 2021. 19(1):20.

2020

- Lin W, Zhang W, Paterson GA, **Zhu Q**, Zhao X, Knight R, Bazylinski DA, Roberts AP, Pan Y. Expanding magnetic organelle biogenesis in the domain Bacteria. *Microbiome*. 2020. 8(1):152. (video abstract)

- Asnicar F, Thomas AM, Beghini F, Mengoni C, Manara S, Manghi P, **Zhu Q**, Bolzan M, Cumbo F, May U, Sanders JG, Zolfo M, Kopylova E, Pasolli E, Knight R, Mirarab S, Huttenhower C, Segata N. Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. *Nature Communications*. 2020. 11(1):2500.

- Hillmann B, Al-Ghalith GA, Shields-Cutler RR, **Zhu Q**, Knight R, Knights D. SHOGUN: a modular, accurate, and scalable framework for microbiome quantification. *Bioinformatics*. 2020. 36(13):4088-90.

- Estaki M, Jiang L, Bokulich NA, McDonald D, González A, Kosciolek T, Martino C, **Zhu Q**, Birmingham A, Vázquez-Baeza Y, Dillon MR, Bolyen E, Caporaso JG, Knight R. QIIME 2 enables comprehensive end-to-end analysis of diverse microbiome data and comparative studies with publicly available data. *Current Protocols in Bioinformatics*. 2020. 70(1):e100.

- Poore GD, Kopylova E, **Zhu Q**, Carpenter C, Fraraccio S, Wandro S, Kosciolek T, Janssen S, Metcalf J, Song SJ, Kanbar J, Miller-Montgomery S, Heaton R, Mckay R, Patel SP, Swafford AD, Patel SP, Knight R. Microbiome analyses of blood and tissues suggest cancer diagnostic approach. *Nature*. 2020. 579(7800):567-74.

- McCall L, Callewaert C, **Zhu Q** (**co-first**), Song SJ, Bouslimani A, Minich JJ, Ernst M, Ruiz-Calderon JF, Cavallin H, Pereira HS, Novoselac A, Hernandez J, Rios R, Branch OH, Blaser MJ, Paulino LC, Dorrestein PC, Knight R, Dominguez-Bello MG. Home chemical and microbial transitions across urbanization. *Nature Microbiology*. 2020. 5(1):108-15.

2019

- **Zhu Q**, Mai U, Pfeiffer W, Janssen S, Asnicar F, Sanders JG, Belda-Ferre P, Al-Ghalith GA, Kopylova E, McDonald D, Kosciolek T, Yin JB, Huang S, Salam N, Jiao J, Wu Z, Xu ZZ, Sayyari E, Morton JT, Podell S, Knights D, Li W, Huttenhower C, Segata N, Smarr L, Mirarab S, Knight R. Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. *Nature Communications*. 2019. 10(1):5477. (among top 50 life and biological sciences articles in 2019)

- Sanders JG, Nurk S, Salido RA, Minich J, Xu ZZ, **Zhu Q**, Martino C, et al. Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. *Genome Biology*. 2019. 20(1):226.

- Bolyen E, Rideout JR, Dillon MR, Bokulich NA, Abnet CC, et al. Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*. 2019. 37(8):852-57.

- Fu T, Coulter S, Yoshihara E, Oh TG, Fang S, Cayabyab F, **Zhu Q**, et al. FXR Regulates Intestinal Cancer Stem Cell Proliferation. *Cell*. 2019. 176(5):1098-1112.e18.

- Mills RH, Vázquez-Baeza Y, **Zhu Q**, Jiang L, Gaffney J, Humphrey G, et al. Evaluating Metagenomic Prediction of the Metaproteome in a 4.5-Year Study of a Patient with Crohn's Disease. *mSystems*. 2019. 4(1):e00337-18.

- Xu ZZ, Amir A, Sanders J, **Zhu Q**, Morton JT, Bletz MC, Tripathi A, Huang S, McDonald D, Jiang L, Knight R. Calour: an Interactive, Microbe-Centric Analysis Tool. *mSystems*. 2019. 4(1):e00269-18.

2018

- **Zhu Q**, Dupont CL, Jones MB, Pham KM, Jiang ZD, DuPont HL, Highlander SK. Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. *Microbiome*. 2018. 6(1):201.

- Fang X, Monk J, Nurk S, Akseshina M, et al. Metagenomics-based, strain-level analysis of Escherichia coli from a time-series of microbiome samples from a Crohn's disease patient. *Frontiers in Microbiology*. 2018. 9:2559.

- Hillmann B, Al-Ghalith G, Shields-Cutler R, **Zhu Q**, Gohl D, Beckman K, Knight R, Knights D. Evaluating the information content of shallow shotgun metagenomics. *mSystems*. 2018. 3(6):e00069-18.

- Minich JJ, **Zhu Q**, Xu ZZ, Amir A, Ngochera M, Simwaka M, Allen EE, Zidana H, Knight R. Microbial effects of livestock manure fertilization on freshwater aquaculture ponds rearing tilapia (*Oreochromis shiranus*) and North African catfish (*Clarias gariepinus*). *MicrobiologyOpen*. 2018. e00716.

- Tripathi A, Marotz C, Gonzalez A, Vázquez-Baeza Y, Song SJ, et al. Are microbiome studies ready for hypothesis-driven research? *Current Opinion in Microbiology*. 2018. 44:61-69.

- Hua ZS, Qu YN, **Zhu Q**, Zhou EM, Qi YL, et al. Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. *Nature Communications*. 2018. 9(1):2832.

- McDonald D, Hyde E, Debelius JW, Morton JT, Gonzalez A, Ackermann G, Aksenov AA, et al. American Gut: an Open Platform for Citizen Science Microbiome Research. *mSystems*. 3(3):e00031-18.

- He Y, Kosciolek T, Tang J, Zhou Y, et al. Gut microbiome and magnetic resonance spectroscopy study of subjects at ultra-high risk for psychosis may support the membrane hypothesis. *European Psychiatry*. 2018. 53:37-45.

- Washburne AD, Morton JT, Sanders J, McDonald D, **Zhu Q**, Oliverio AM, Knight R. Methods for phylogenetic analysis of microbiome data. *Nature Microbiology*. 2018. 3(6):652.

- Knight R, Vrbanac A, Taylor BC, Aksenov A, Callewaert C, Debelius J, Gonzalez A, et al. Best practices for analysing microbiomes. *Nature Reviews Microbiology*. 2018. 16(7):410-422.

- Minich JJ, **Zhu Q**, Janssen S, Hendrickson R, Amir A, Vetter R, Hyde J, et al. KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples. *mSystems*. 2018. 3(3):e00218-17.

- Kapono CA, Morton JT, Bouslimani A, Melnik AV, Orlinsky K, Knaan TL, Garg N, et al. Creating a 3D microbial and chemical snapshot of a human habitat. *Scientific Reports*. 2018. 8(1):3669.

2017 and before

- Thompson LR, Sanders JG, McDonald D, Amir A, Ladau J, Locey KJ, Prill RJ, et al. A communal catalogue reveals Earth's multiscale microbial diversity. *Nature*. 2017. 551(7681):457-63.

- Lin W, Paterson GA, **Zhu Q**, Wang Y, Kopylov E, Li Y, Knight R, et al. Origin of microbial biomineralization and magnetotaxis during the Archean. *Proceedings of the National Academy of Sciences*. 2017. 114(9):2171-76.

- Yang Y, **Zhu Q**, Liu S, Zhao C, Wu C. The origin of Chinese domestic horses revealed with novel mtDNA variants. *Animal Science Journal*. 2017. 88(1):19-26.

- Li W, Richter RA, Jung Y, **Zhu Q**, Li RW. Web-based bioinformatics workflows for end-to-end RNA-seq data computation and analysis in agricultural animal species. *BMC Genomics*. 2016. 17(1):761.

- Dittmar K, **Zhu Q**, Hastriter MW, Whiting MF: On the probability of dinosaur fleas. _BMC Evolutionary Biology_. 2016. 16(1):9.

- Liu Y, Yu Y, Duan W, Qu Q, Zhang Q, Zhao M, **Zhu Q**. Home storage significantly impairs Bifidobacteria survival in powered formula for infants and young children in the Chinese market. _International Journal of Dairy Technology_. 2015. 68(4):495-502.

- Han X, Chen Y, Wang L, Fang W, Zhang N, **Zhu Q**. RNA: an expanding view of function and evolution. _Evolutionary Bioinformatics_. 2015. Suppl. 1:77-9.

- **Zhu Q**, Hastriter MW, Whiting MF, Dittmar K. Fleas (Siphonaptera) are Cretaceous, and evolved with Theria. _Molecular Phylogenetics and Evolution_. 2015. 90:129-39.

- Brook CE, Bai Y, Dobson AP, Osikowicz LM, Ranaivoson HC, Zhu Q, Kosoy MY, Dittmar K. _Bartonella_ spp. in fruit bats and blood-feeding ectoparasites in Madagascar. _PLOS Neglected Tropical Diseases_. 2015. 9(2):e0003532.

- **Zhu Q** (**co-corresponding**), Kosoy M, Dittmar K. HGTector: an automated method facilitating genome-wide discovery of putative horizontal gene transfers. _BMC Genomics_. 2014. 15:717.

- **Zhu Q** (**co-corresponding**), Kosoy M, Olival KJ, Dittmar K. Horizontal transfers and gene losses in the phospholipid pathway of _Bartonella_ reveal clues about early ecological niches. _Genome Biology and Evolution_. 2014. 6(8):2156-69.

- Kazemian M, **Zhu Q**, Halfon MS, Sinha S. Improved accuracy of supervised CRM discovery with interpolated Markov models and cross-species comparison. _Nucleic Acids Research_. 2011. 39(22):9463-72.

- Kantorovitz MR, Kazemian M, Kinston S, Miranda-Saavedra D, **Zhu Q**, Robinson GE, Göttgens B, Halfon MS, Sinha S. Motif-blind, genome-wide discovery of cis-regulatory modules in _Drosophila_ and mouse. _Developmental Cell_. 2009. 17(4):568-79.

- Liu Y, **Zhu Q** (**co-first**), Zhu N. Recent duplication and positive selection of the _GAGE_ gene family. _Genetica_. 2008. 133(1):31-5.

- Liu Y, **Zhu Q**, Zhu N. Rapid HLA-DR fluorotyping based on melting curve analysis. _Immunological Investigations_. 2007. 36(4):507-21.

MANUSCRIPTS IN REVIEW

- Gonzalez CG, Mills RH, Kordahi M, Carrillo-Terrazas M, Secaira-Morocho H, Widjaja CE, Tsai MS, Ulcerative Colitis Host-Microbiome Response to Hyperbaric Oxygen Therapy.

- Shaffer JP, Nothias LF, Thompson LR, Sanders JG, Salido RA, Couvillion SP, Brejnrod AD, et al. Multi-omics profiling of Earth's biomes reveals that microbial and metabolite composition are shaped by the environment. _BioRxiv_.

- Gauglitz JM, Bittremieux W, Williams CL, Weldon KC, Panitchpakdi M, Ottavio FD, Aceves CM, et al. Reference data based insights expand understanding of human metabolomes. _BioRxiv_.

- Martino C, Kellman BP, Sandoval DR, Clausen TM, Marotz CA, Song SJ, Wandro S, et al. Bacterial modification of the host glycosaminoglycan heparan sulfate modulates SARS-CoV-2 infectivity. _BioRxiv_.

- Jiang Y, Balaban M, **Zhu Q**, Mirarab S. DEPP: Deep Learning Enables Extending Species Trees using Single Genes. _BioRxiv_.

- Yoo BB, Griffiths JA, Thuy-Boun PS, Cantu V, Weldon KC, Challis C, Sweredoski MJ, et al. Targeted Activation of Enteric Neurons Shapes the Gut Environment of Mice. _SSRN_.

BOOK CHAPTERS

- **Zhu Q**,(**corresponding**), Mirarab S. Assembling a Reference Phylogenomic Tree of Bacteria and Archaea by Summarizing Many Gene Phylogenies. In *Environmental Microbial Evolution - Methods in Molecular Biology*. Ed. Luo H, et al. Springer Nature. In review.
- Dittmar K, **Zhu Q**, Hastriter MW, Whiting MF. Evolutionary history of Siphonaptera: fossils, origins, vectors. In *Parasite Diversity and Diversification - Evolutionary Ecology Meets Phylogenetics*. Ed. Morand S, Krasnov BR, Littlewood DTJ. Cambridge University Press. 2015.

PRESENTATIONS (SELECTED)

Talks

- **Zhu Q**, Belda-Ferre P. Discoveries and Insights from the Nucleotides to Neighborhoods Cohort. *CMI Research Summit*. San Diego. Mar. 2, 2020.
- **Zhu Q**, Mai U, Pfeiffer W, Janssen S, Asnicar F, et al. A Reference Phylogeny of More Than 10,000 Microbial Genomes. *ASM Microbe*. Atlanta, USA. June 7-11, 2018. (**oral and poster presentations**)
- McCall L, Callewaert C, **Zhu Q** (**presenter**), Song SJ, et al. Impact of Urbanization and Westernization on the Human-Environment Microbiome and Metabolome. *ASM Microbe*. Atlanta, USA. June 7-11, 2018.
- **Zhu Q**, Mai U, Janssen S, Pfeiffer W, Sanders JG, et al. A Reference Phylogeny of More Than 10,000 Microbial Genomes. *Center for Microbiome Innovation Research Summit*, San Diego, USA. Mar. 7, 2018.
- **Zhu Q**, Dittmar K. Systematic detection of horizontal gene transfer patterns in Rickettsia using a new method based on Blast hit distribution statistics. *Annual Conference of Society for Molecular Biology and Evolution (SMBE)*. Chicago, USA. July 8, 2013.
- **Zhu Q**, Dittmar K. Genome-wide detection of horizontal gene transfer based on Blast hit distribution statistics. *8Th Annual Graduate Student Symposium*. Buffalo, USA. March 12, 2013. (best presentation award)

Posters

- **Zhu Q**, Janssen S, Sanders JG, Kopylova E, McDonald D, et al. Taxon subsampling strategies for efficient profiling of microbial big data. *CMI Research Summit*, San Diego, USA. Mar. 15, 2017.
- **Zhu Q**, Jones MB, Highlander SK. Pathogen Discovery in Travelers' Diarrhea of Unknown Etiology by Metagenomic Sequencing. *1st ASM Conference on Rapid NGS Bioinformatic Pipelines for Enhanced Molecular Epidemiologic Investigation of Pathogens*, Washington D.C., USA. Sep. 24-27, 2015.
- **Zhu Q**, Dittmar K. HGTector: a new approach to prediction of horizontal gene transfer based on Blast hit distribution statistics. *Great Lakes Bioinformatics Conference (GLBIO)*. Pittsburgh, USA. May 14-16, 2013.

Invited talks

- Seminar. Animal Microbiome Research Group (ARMG). Virtual. Nov 10, 2021.
- Seminar. Chinese Genomics Meet-up (CGM). Virtual. Sep 1, 2021.
- Coffee chat. BioSci Southwest Symposium, Arizona State University. Virtual. Oct 30, 2020.
- Seminar. SOLS New Faculty Showcase, Arizona State University. Virtual. Sep 25, 2020.

BIOINFORMATICS TOOLS (SELECTED)

GitHub profile: https://github.com/qiyunzhu

Main developer of

- **Web of Life** (WoL): Reference phylogenetics tree of bacterial and archaeal genomes.
  Available at: https://biocore.github.io/wol/

- **Woltka**: Phylogeny-guided shotgun metagenomic data analysis tool.
  Available at: https://github.com/qiyunzhu/woltka

- **HGTector**: Genome-wide detection of horizontal gene transfer based on BLAST hit distribution statistics.
  Available at: https://github.com/qiyunlab/HGTector

- **Horizomer**: Integrated workflow and benchmark system for various horizontal gene transfer prediction tools.
  Available at: https://github.com/biocore/horizomer

- **BinaRena**: Interactive graphical interface for manual observation and binning of metagenomic contigs.
  Available at: https://qiyunzhu.github.io/binarena/demo.html

Contributed to

- scikit-bio, QIIME 2, Qiita, SHOGUN, PhyloPhlAn3, Empress, Qemistree, Oecophylla, DEPP, APPLES-2.

TEACHING & MENTORING

- Instructor at Arizona State University
  - BIO/MBB/MAT 355: Introduction to Computational Molecular Biology   Fall 2021
  - MIC 501: Foundations in Microbiology (guest lecturer)   Fall 2021
  - BIO/MIC 494/598: Microbiome Data Science   Spring 2022, Spring 2021
  - MIC 401: Research Paper (supervisor)   Spring 2022, Spring 2021

- Guest lecturer at Quantitative Research for the Life and Social Sciences Program (QRLSSP)   Summer 2021

- Research mentor at Arizona State University
  - Two postdoctoral fellows   2020 – 2021, 2020 – present
  - One Ph.D. student   2021 – present
  - One summer intern Ph.D. student   Summer 2020
  - One undergraduate researcher   2021 – present
  - One high school student researcher   2021 – present

- Thesis advisory committee at Arizona State University
  - Three PhD students   2021 – present
  - One MS student   2022 – present
  - One undergraduate student   2020 – present

- Mentor of 20 undergraduate, graduate students and visiting scholars in research labs   2008 – 2020

- Instructor at Qiita workshops hosted by the Center for Microbiome Innovation, San Diego   2019

- Mentor of a high school student, eMentor program, Del Lago Academy, San Diego   2015

- Teaching Assistant for undergraduate and graduate courses, University at Buffalo
  - BIO200 Evolutionary Biology   Fall 2013, Fall 2012, Fall 2011, Fall 2008, Summer 2008
  - BIO201 Cell Biology   Spring 2014, Spring 2013
  - BIO400/500 Bioinformatics and Genome Analysis   Spring 2012
  - BIO205/215 Biological Chemistry   Spring 2008
  - BIO302 Molecular Biology   Fall 2007

HONORS & AWARDS

- Darrell Doyle Travel Award for the best student presentation at Departmental Research Symposium   2013
- Graduate Student Employees Union Professional Development Award   2013
- Graduate Student Employees Union Doctoral Retention Award   2011 – 2012

RESEARCH GRANTS

- NSF XSEDE BIO210103   2021 – 2022
  - Title: Inference and application of a largest and hierarchically organized microbial reference phylogeny
  - Role: Lead PI. Co-PIs: Rob Knight, Siavash Mirarab, and Wayne Pfeiffer
  - Amount: $10,513.40 (computing resources equivalent to)

ACADEMIC SERVICES

Guest editor for journal

- *Evolutionary Bioinformatics*   2014 – 2015

Peer-reviewer for journals

- *Nature Biotechnology, Nature Communications, eLife, Genome Biology, Microbiome, Journal of Hazardous Materials, mSystems, npj Biofilms and Microbiomes, Molecular Metabolism, Bioinformatics, PLOS Computational Biology, Frontiers in Microbiology, Scientific Reports, Microbiological Research, Microbial Ecology, PLOS ONE, Gene* (Elsevier), *European Journal of Clinical Microbiology & Infectious Diseases, PeerJ, Evolutionary Bioinformatics, Journal of Molecular Evolution, Bioinformatics and Biology Insights, SOJ Genetic Science*

Peer-reviewer for funding agencies

- National Science Foundation (NSF), USA   2020
  - Division of Environmental Biology (DEB)
- German Research Foundation (DFG)   2021
  - Life Sciences 1: Molecular and Organismic Biology