

# Qiyun Zhu, Ph. D.

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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, 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: **38**, citations: **3,154**, *h*-index: **20**.

(\*co-first authors; ‡co-corresponding authors)

### 2020

- 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, Kosciulek 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, Kosciulek 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\*, Callewart C\*, Zhu Q\* (co-first author), 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<sup>‡</sup>, Knight R<sup>‡</sup>, Dominguez-Bello MG<sup>‡</sup>. 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, Kosciulek 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, Kosciolk 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. (cover paper)
- Lin W<sup>\*‡</sup>, 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<sup>‡</sup>, Kosoy M, Dittmar K<sup>‡</sup>. HGTector: an automated method facilitating genome-wide discovery of putative horizontal gene transfers. **BMC Genomics**. 2014. 15:717.
- Zhu Q<sup>‡</sup>, Kosoy M, Olival KJ, Dittmar K<sup>‡</sup>. 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<sup>‡</sup>, Sinha S<sup>‡</sup>. 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<sup>†</sup>, Halfon MS<sup>‡</sup>, Sinha S<sup>‡</sup>. Motif-blind, genome-wide discovery of cis-regulatory modules in *Drosophila* and mouse. ***Developmental Cell***. 2009. 17(4):568-79.
- Liu Y\*, Zhu Q\*, 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

- Mills RH\*, Dulai PS\*, Vázquez-Baeza Y, Zhu Q, Humphrey G, Goldasich LD, et al. Meta-omics reveals microbiome driven proteolysis as a contributing factor to severity of ulcerative colitis disease activity.
- Karst SM\*, Ziels RM\*, Kirkegaard RH, Sørensen EA, McDonald D, Zhu Q, Knight R, Albertsen M. Enabling high-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. [BioRxiv](#).
- Liu Y, Meric G, Havulinna AS, Teo SM, Ruuskanen M, Sanders J, Zhu Q, et al. Early prediction of liver disease using conventional risk factors and gut microbiome-augmented gradient boosting. [MedRxiv](#).
- Tripathi A\*, Vazquez-Baeza Y\*, Gauglitz JM, Wang M, Duhrkop K, Esposito-Nothias M, Acharya D, et al. Chemically-informed Analyses of Metabolomics Mass Spectrometry Data with Qemistree. [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](#).
- 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. [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](#).

## BOOK CHAPTERS

- 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.

### 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/DittmarLab/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](#), [Qiiita](#), [SHOGUN](#), [PhyloPhlAn3](#), [Empress](#), [Qemistree](#), [Oecophylla](#).

### TEACHING & MENTORING

- Supervisor of a summer intern Ph.D. student in bioinformatics, Arizona State University 2020
- 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
- BIO302 Molecular Biology

Spring 2008  
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

## ACADEMIC SERVICES

### Guest editor for

- *Evolutionary Bioinformatics* 2014 – 2015

### Peer-reviewer for

- *Nature Biotechnology, 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*