Chengqi Wang, PhD

CONTACT INFORMATION

Genomics Program
College of Public Health
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RESEARCH SUMMARY

My research focuses on the intersection of functional genomics, cell biology, and molecular parasitology. I employ integrative approaches such as epigenomics, transcriptomics, proteomics, high-throughput genome editing, single-cell genomics, microbial genomics, and long-read sequencing to understand how biological systems, which underpin health and disease, respond to genetic variations and environmental factors (such as drugs).

I also utilize statistical inference methods (including MCMC and Bayesian modeling), optimization algorithms, and machine learning to uncover patterns in large datasets (such as multi-omics data), decipher underlying mechanisms, and leverage predictive and causal relationships to address key questions in genomics and molecular medicine.

APPOINTMENTS

9/2024-Now	**Director,** USF Genomics Program Sequencing Core. **Assistant Professor**, University of South Florida, College of Public Health, Tampa, FL.
8/2020-9/2024	**Research Assistant Professor**, University of South Florida, College of Public Health, Tampa, FL.
8/2014-8/2020	**Research Associate**, University of South Florida, College of Public Health, Tampa, FL.

EDUCATION

7/2012-6/2014	**Postdoctoral Fellow**, Beijing Institute of Genomics (BGI), Chinese Academy of Sciences.
9/2007-6/2012	**Ph.D.** in Cheminformatics/Bioinformatics, Lanzhou University, China. Area of Concentration: Protein Structure Prediction by Using Machine Learning Algorithms.
9/2002-6/2006	**B.S.** School of Chemical Engineering, Lanzhou University, China.

AWARDS AND HONORS

2/2021	COPH internal award, University of South Florida, Tampa, FL.
1/2020	First Place Team, Data Science Hackathon, University of South Florida, Tampa, FL.

1/2019	First Place Team (Team leader, Data Visualization Team) NIH Data Science Hackathon, University of South Florida, Tampa, FL.
6/2018	Outstanding Poster Single Cell Genomics Symposium, University of South Florida, Tampa, FL.

SERVICE ACTIVITIES

I. Professional Service

2022-present	Editorial board in Computational Genomics, Frontier in Genetics
2022-present	Editorial board in Epigenomics and Epigenetics, Frontier in Genetics
2022-present	Editorial board in Epigenomics and Epigenetics, Frontiers in Cell and Developmental Biology
2022-2023	Guest Associate Editor in Human and Medical Genomics, Frontier in Genetics

II. Grant review

NIH Transmission of Vector-Borne and Zoonotic Diseases, Ad Hoc Reviewer, 2024

III. Committee Member

International Conference on Intelligent Biology and Medicine, FL, 2023. (Organizing Committee)
Chemgenomic Research Faculty Searching, FL, 2024. (Committee Member)
Bioinformatic Research Faculty Searching, FL, 2024. (Committee Member)
AI+X Symposium, FL, 2024. (Review Committee)

IV. Manuscript Reviewer

Briefings in Bioinformatics
eBioMedicine
Genomics Proteomics and Bioinformatics
Computers in Biology and Medicine
Computational and Structural Biotechnology Journal
Parasites & Vectors
BMC Genomics
BMC Supplements
Frontiers in Genetics
Scientific Reports
Journal of Cellular Physiology
Journal of Genetics and Genomic
IEEE/ACM Transactions on Computational Biology and Bioinformatics
Plos ONE
Current Pharmaceutical Design
Meta Gene
Journal of Bioinformatics and Computational Biology
Journal of Bioinformatics, Computational and Systems Biology
International Journal of Data Mining and Bioinformatics
Current Bioinformatics
Advances in Bioinformatics
Heliyon

TEACHING

1/2024, 1/2023 1/2022, 8/2020	**Director and Instructor**, Applied Computational Genomics (3 credit) Florida, Tampa, FL. Course Description: Hands-on training, along with an introduction to basic concepts in using popular tools and techniques for genome, transcriptome, epigenome, and microbiome.
8/2020	**Instructor,** Introduction to Biocomputing (3 credit) Florida, Tampa, FL. Course Description: Designed as a training of necessary computational and bioinformatical skills used in everyday analysis of biological data, especially DNA sequence and polymorphism data.
6/2021, 2/2021, 9/2020, 2/2020, 2/2019, 9/2018	**Director and Instructor**, Linux and R tutorials, RNA-seq Data Analysis Workshop. Genomics Program, University of South Florida, Tampa, FL. Course Description: Foundational Linux command and R programming, basic statistical concept, and data visualization.
6/2021, 6/2020, 3/2020	**Director and Instructor**, R tutorials, Microbiome Data Analysis Workshop. Genomics Program, University of South Florida, Tampa, FL. Course Description: R programming, basic statistical concept, and data visualization in microbiome 16S analysis.
1/2018	**Teaching Assistant**, Quantitative Genomics and Genetics. Genomics Program, University of South Florida, Tampa, FL.

PRESENTATIONS (last 5 years only)

1. **Wang C.** Using artificial intelligence to decipher genomic code in the deadliest malaria parasite. Keynote Oral Presentation, One Health Codeathon, FL. June 2023.

2. **Wang C.** MalariaSED: a deep learning framework to decipher the regulatory contributions of noncoding variants in malaria parasites. Oral Presentation, 2023 International Conference on Intelligent Biology and Medicine, FL. July 2023.

3. **Wang C.** MalariaSED: a deep learning framework to decipher the regulatory contributions of noncoding variants in malaria parasites. Invited Oral Presentation, 2023, AI+X symposium, FL. July 2023.

4. **Wang C**. Using artificial intelligence to decipher genomic code in the deadliest malaria parasite. Invited Oral Presentation, Johns Hopkins All Children's' Hospital, FL. Apr 2022.

5. **Wang C**. Unraveling the epigenome of the human malaria parasite *Plasmodium falciparum*. Oral Presentation, American Society of Tropical Medicine and Hygiene 68th Annual Meeting, MD. Nov 2019.

6. **Wang C**. From the first genome-sequences to the 4D nucleosome: Integrating fast-moving omics technologies to understand biology and human disease. Invited Oral Presentation, USF Genomics Forum, Genomic Program, University of South Florida, FL. Nov 2018.

GRANT SUPPORT

Ongoing and recently completed projects:

R01AI187153
NIH/NIAID
Role: Co-I (PI: Adams)
09/01/2024-08/31/2029
Phenotype-based Screens to Identify Genetic Factors Associated with Gametocyte Development in Plasmodium falciparum

U19AI181593
NIH/NIAID
Role: Co-I (PI: Cui)
05/01/2024 – 04/30/2029
Unraveling the Drivers of Persistent Malaria Transmission in Cameroon

R01AI175640
NIH/NIAID
Role: Co-I (PI: Suvorova)
04/12/2024 – 02/28/2029
Regulation of apicomplexan mitosis coupled to budding

R01MD011728
NIH/NIMHD
Role: Co-I (PI: Uddin)
08/16/17 – 05/31/26
Epigenomic Predictors of PTSD and Traumatic Stress in an African American Cohort

R01AI117017
NIH/NIAID
Role: Co-I (PI: Adams)
02/10/15 – 06/30/26
Chemogenomic Profiling of Plasmodium Falciparum Drug Responses and Resistance

R01AI141467
NIH/NIAID
Role: Co-I (PI: Survorova)
05/08/20 – 04/30/25
Cyclin-mediated Control of Toxoplasma Development

R21AI178797
Role: Co-I (PI: Survorova)
08/16/23 – 07/31/25
Deciphering the composite S-phase in Toxoplasma gondii

U19AI089672

NIH/NIAID
Role: Co-I (PI: Cui)
07/01/10 – 03/31/24
Southeast Asia Malaria Research Center

COPH internal award
Role: PI
03/2021-03/2022
Artificial Intelligence Model for Rapid Artemisinin Resistance Risk Prediction in the Malaria Parasite

PUBLICATIONS

A. Peer-reviewed Journal Paper

(#Cresponding author, *Co-first author)

1. Lucky BA*, **Wang C***, Li X, Liang X, Muneer A, Miao J. Transforming the CRISPR/dCas9-based gene regulation technique into a forward screening tool in *Plasmodium falciparum*. *iScience*. 2024; 27: 109602

2. Min H*, Liang X*, **Wang C***, Qin J, Boonhok R, Muneer A, Brashear AM, Li X, Minns AM, Adapa SR, Jiang RHY, Ning G, Cao Y, Lindner SE, Miao J, Cui L. The DEAD-box RNA helicase PfDOZI imposes opposing actions on RNA metabolism in *Plasmodium falciparum*. *Nat Commun*. 2024; 15: 3747

3. Malla P, Wang Z, Brashear A, Yang Z, Lo E, Baird K, **Wang C#**, Cui L#. Effectiveness of unsupervised primaquine regimen for preventing *Plasmodium vivax* malaria relapses in northeast Myanmar, a single-arm non-randomized observational study. *J Infect Dis.* 2024; 229: 1557-1564.

4. Kalamuddin M*, Shakri AR*, **Wang C***, Min H, Li X, Cui L. Miao J. MYST regulates DNA repair and forms a NuA4-like complex in the malaria parasite *Plasmodium falciparum*. *mSphere*. 2024; 9: e0014024.

5. Hawkins L, **Wang C**, Chaput D, Batra M, Marsilla C, Awshah D, Suvorova E. The Crk4-Cyc4 complex regulates G2/M transition in *Toxoplasma gondii*. *EMBO J*. 2024; 43: 2094-2126.

6. **Wang C#**, Dong Y, Li C, Oberstaller J, Zhang M, Gibbons J, Pires CV, Xiao M, Zhu L, Jiang RHY, Kim K, Miao J, Otto TD, Cui L, Adams JH, Liu X. MalariaSED: a deep learning framework to decipher the regulatory contributions of noncoding variants in malaria parasites. *Genome Biol.* 2023; 24: 31.

7. Lucky BA*, **Wang C***, Li X, Chim-Ong A, Adapa SR, Quinlivan E, Jiang RHY, Cui L, Miao J. Characterization of the dual role of Plasmodium falciparum DNA methyltransferase in regulating transcription and translation. *Nucleic Acids Res*. 2023; 51: 3918-3933.

8. Lucky BA*, **Wang C***, Liu M, Liang X, Min H, Fan Q, Siddiqui FA, Adapa SR, Li X, Jiang RHY, Chen X, Cui L, Miao J. A type II protein arginine methyltransferase regulates merozoite invasion in Plasmodium falciparum. *Commun Biol*. 2023; 6: 659.

9. Lucky BA*, **Wang C***, Shakri A*, Kalamuddin M, Chim-Ong A, Li X, Cui L, Miao J. Plasmodium falciparum GCN5 plays a key role in regulating artemisinin resistance-related stress responses. *Antimicrob Agents Chemother*. 2023; 67, e00577-23.

10. Zhang M*, **Wang C***, Oberstaller J*, Thomas P, Otto TD, Boyapalle S, Adapa SR, Button-Simons K, Mayho M, Rayner JC, Ferdig MT, Jiang RHY, Adams JH. The apicoplast link to fever-survival and artemisinin-resistance in the malaria parasite. *Nat Commun*. 2021; 12: 4563.

11. Zhang M*, **Wang C***, Otto TD, Oberstaller J, Liao X, Adapa SR, Udenze K, Bronner IF, Casandra D, Mayho M, Brown J, Li S, Swanson J, Rayner JC, Jiang RHY, Adams JH. Uncovering the essential genes of the human malaria parasite *Plasmodium falciparum* by saturation mutagenesis. *Science*. 2018; 360: eaap7847.

12. Brancucci NMB, Gerdt JP, **Wang C**, De Niz M, Philip N, Adapa SR, Zhang M, Hitz E, Niederwieser I, Boltryk SD, Laffitte MC, Clark MA, Grüring C, Ravel D, Blancke Soares A, Demas A, Bopp S, Rubio-Ruiz B, Conejo-Garcia A, Wirth DF, Gendaszewska-Darmach E, Duraisingh MT, Adams JH, Voss TS, Waters AP, Jiang RHY, Clardy J, Marti M. Lysophosphatidylcholine levels regulate stage differentiation in the human malaria parasite *Plasmodium falciparum*. *Cell*. 2017; 171: 1532.

13. **Wang C**, Gibbons J, Adapa DR, Oberstaller J, Liao X, Zhang M, Adams JH, Jiang RHY. The human malaria parasite genome is configured into thousands of co-expressed linear regulatory units. *Journal of genetics and Genomics*. 2020; 47: 513-521

14. **Wang C**, Adapa SR, Gibbons J, Sutton S, Jiang RHY. Punctuated chromatin states regulate *Plasmodium falciparum* antigenic variation at the intron and 2 kb upstream regions. *BMC Genomics*. 2016; 17: 652.

15. Fang R*, **Wang C***, Skogerbo G, Zhang Z. Functional diversity of CTCFs is encoded in their binding motifs. *BMC Genomics*. 2015; 16: 649.

16. **Wang C**, Zhang MQ, Zhang Z. Computational identification of active enhancers in model organisms. *Genomics Proteomics Bioinformatics*. 2013; 11: 142.

17. **Wang C**, Xi L, Li S, Liu H, Yao X. A sequence-based computational model for the prediction of the solvent accessible surface area for alpha-helix and beta-barrel transmembrane residues. *J Comput Chem.* 2012; 33: 11.

18. **Wang C**, Li S, Xi L, Liu H, Yao X. Accurate prediction of the burial status of transmembrane residues of α-helix membrane protein by incorporating the structural and physicochemical features. *Amino Acids.* 2011; 40: 991.

19. Marsilia C, Batra M, Pokrovskaya ID, **Wang C**, Chaput D, Naumova DA, Lupashin VV, Suvorova E. Essential role of the conserved oligomeric Golgi complex in *Toxoplasma gondii. mBio.* 2023; 14: e0251323.

20. Simmons C, Gibbons J, **Wang C**, Pires CV, Zhang M, Siddiqui F, Oberstaller J, Casandra D, Seyfang A, Cui L, Otto TD, Adams JH. A novel modulator of ring stage translation (MRST) gene alters artemisinin sensitivity in Plasmodium falciparum. *mSphere*. 2023; e0015223.

21. Pires CV, Oberstaller J, **Wang C**, Casandra D, Zhang M, Chawla J, Adapa SR, Otto TD, Ferdig MT, Rayner JC, Jiang RHY, Adams JH. Chemogenomic profiling of a Plasmodium falciparum transposon mutant library reveals shared effects of Dihydroartemisinin and Bortezomib on lipid metabolism and exported proteins. *Microbiol Spectr*. 2023; e0501422.

22. Chawla J, Goldowitz I, Oberstaller J, Zhang M, Pires CV, Navarro F, Sollelis L, **Wang C**, Seyfang A, Dvorin J, Otto TD, Rayner JC, Marti M, Adams JH. Phenotypic screens identify genetic factors associated with gametocyte development in the human malaria parasite Plasmodium falciparum. *Microbiol Spectr*. 2023; e0416422.

23. Simmons C, Gibbons J, Zhang M, Oberstaller J, Pires CV, Casandra D, **Wang C**, Seyfang A, Otto TD, Rayner JC, Adams JH. Protein KIC5 is a novel regulator of artemisinin stress response in the malaria parasite Plasmodium falciparum. *Sci Rep*. 2023; 13: 339.

24. Liu H, Zeng W, Mallavi P, **Wang C**, Lakshmi S, Kim K, Menezes L, Yang Z, Cui L. Risk of hemolysis in Plasmodium vivax malaria patients receiving standard primaquine treatment in a population with high prevalence of G6PD deficiency. *Infection*. 2023; 51: 213-222.

25. Yuan Y, Xu Q, Wani A, Dahrendorff J, **Wang C**, Donglasan J, Burgan S, Graham Z, Uddin M, Wildman D, Qu A. Differentially expressed heterogeneous overdispersion genes testing for count data. *bioRxiv*. 2023;

26. Zhu X, LiS, **Wang C**, Yu Y, Wang J, He L, Siddiqui FA, Chen L, Zhu L, Zhou D, Qin J, Miao J, Cui L, Cao Y. The Plasmodium falciparum nuclear protein Phosphatase NIF4 is required for efficient merozoite invasion and regulates Artemisinin sensitivity. *mBio*. 2022; 13: e0189722.

27. Hanson H, **Wang C**, Schrey A, Liebl A, Ravinet M, Jiang RHY, Martin L. Epigenetic potential and DNA methylation in an ongoing house sparrow (Passer domesticus) range expansion. *Am Nat.* 2022; 200: 5.

28. Naumov A, **Wang C**, Chaput D, Ting LM, Alvarez C, Keller T, Ramadan A, White M, Kim K, Suvorova E. Restriction checkpoint controls bradyzoite development in *Toxoplasma gondii*. *Microbiol Spectr*. 2022; 10: e00702-22.

29. Wang P, Jiang X, Zhu L, Zhou D, Hong M, He L, Chen L, Yao S, Zhao Y, Chen G, **Wang C**, Cui L, Cao Y, Zhu X. A G-Protein-Coupled receptor modulates gametogenesis via PKG-mediated signaling cascade in *Plasmodium berghei*. *Microbiol Spectr*. 2022; 10: e0015022

30. Hawkins L, Naumov A, Batra M, **Wang C**, Chaput D, Suvorova E. Novel CRK-Cyclin Complex controls spindle assembly checkpoint in Toxoplasma endodyogeny. *mBio*. 2022; 13: e0356121.

31. Miao J, **Wang C**, Lucky A, Liang X, Min H, Adapa SR, Jiang RHY, Kim K, Cui L. A unique GCN5 histone acetyltransferase complex controls erythrocyte invasion and virulence in the malaria parasite *Plasmodium falciparum*. *PLos Pathog.* 2021; 17: e1009351

32. Si Y, Zeng W, Li N, **Wang C**, Siddiqui F, Zhang J, Pi L, He X, Zhao L, Wang S, Zhao H, Li X, Yang Q, Miao J, Yang Z, Cui, L. In Vitro susceptibility of *Plasmodium falciparum* isolates from the China–Myanmar border area to piperaquine and association with candidate markers. *Antimicrob Agents Chemother*. 2021; 65: e02305-20

33. Gibbons J, Qin J, Malla P, Wang Z, Brashear A, **Wang C**, Miao J, Adams JH, Kim K, Jiang RHY, Cui L. Lineage-specific expansion of Plasmodium falciparum parasites with *pfhrp2* deletion in the Greater Mekong Subregion. *J Infect Dis*. 2020; 222: 1561-1569

34. Blomqvist K, Helmel M, **Wang C**, Absalon S, Labunska T, Rudlaff R, Adapa S, Jiang RHY, Steen H, Dvorin DJ. Influence of *Plasmodium falciparum* calcium-dependent protein kinase 5 (PfCDPK5) on the late schizont stage phosphoproteome. *mSphere.* 2020; 5, e00921-19

35. Yi H, Li H, Liang L, Wu Y, Zhang L, Qiu W, Jiang W, Yang F, Li Q, Yang Z, **Wang C**, Cui L, He Y. The glucose-6-phosphate dehydrogenase Mahidol variant protects against uncomplicated *Plasmodium vivax* infection and reduces disease severity in a Kachin population from northeast Myanmar. *Infect Genet Evol.* 2019; 75, e103980.

36. Li B, Liu R, **Wang C**, Ren C, Zhang S, Zhang F, Zhang J, Liu S, Wei Y, Liu W, Song B, Wu X. Impact of genetic and clinical factors on warfarin therapy in patients early after heart valve replacement surgery. *Eur J Clin Pharmacol.* 2019; 75, 1685-1693

37. Adapa SR, Taylor RA, **Wang C**, Thomson-Luque R, Johnson LR, Jiang RHY. *Plasmodium vivax* readiness to transmit: implication for malaria eradication. *BMC systems biology*. 2019; 13, 5.

38. Thomson-Luque R, **Wang C**, Ntumngia FB, Xu S, Szekeres K, Conway A, Adapa SR, Barnes SJ, Adams JH, Jiang RHY. In depth phenotypic characterization of reticulocyte maturation using mass cytometry. *Blood Cells Mol Dis.* 2018; 72, 22.

39. Thomas P, Sedillo J, Oberstaller J, Li S, Zhang M, Singh N, **Wang C**, Udenze K, Jiang RHY, Adams JH. Phenotypic screens identify parasite genetic factors associated with malarial fever response in *Plasmodium falciparum* piggyBac mutants. *mSphere*. 2016; 1, e00273.

40. Bronner IF, Otto TD, Zhang M, Udenze K, **Wang C**, Quail MA, Jiang RHY, Adams JH, Rayner JC. Quantitative Insertion-site Sequencing (QIseq) for high throughput phenotyping of transposon mutants. *Genome Res*. 2016; 26, 980.

41. Li B, **Wang C**, Xi L, Wei Y, Duan G, Wu X. Qualitative and quantitative analysis of Angelica sinensis using near infrared spectroscopy and chemometrics. *Anal. Methods*. 2014; 6, 9691.

42. Li S, Xi L, Li J, **Wang C**, Lei B, Shen Y, Liu H, Yao X, Li B. In silico Prediction of deleterious single amino acid polymorphisms from amino acid sequence. *J Comput Chem.* 2011; 32, 1211.

43. Liu H, Yao X, **Wang C**, Han J. In silico identification of the potential drug resistance sites over 2009 influenza A (H1N1) virus neuraminidase. *Mol Pharm*. 2010; 7, 894.

44. Li S, Xi L, **Wang C**, Li J, Lei B, Liu H, Yao X. A novel method for protein-ligand binding affinity prediction and the related descriptors exploration. *J Comput Chem*. 2009; 30, 900.

B. Abstracts and Proceedings

1. **Wang C**, Jahangiri S, Gibbons J, Adapa SR, Oberstaller J, Liao X, Zhang M, Jiang RHY, Adams JH. Unraveling the epigenome of the human malaria parasite *Plasmodim falciparum*. *American Journal of Tropical Medicine and Hygiene*. 2019; 101: 190.

2. Zhang M, **Wang C**, Otto TD, Oberstaller J, Bronner JF, Li S, Udenze K, Mayho M, Huckle E, Quail MA, Rayner JC, Jiang RHY, Adams JH. *Piggybac* mutagenesis screening of thousands of *Plasmodium falciparum* genes reveals what a malaria parasite can't live without. *American Journal of Tropical Medicine and Hygiene*. 2017; 95: 390.

3. Zhang M, **Wang C**, Thomas P, Oberstaller J, Otto TD, Liao X, Li S, Udenze K, Adapa RS, Button-Simons K, Ferdig MT, Rayner JC, Jiang RHY, Adams JH. A large-scale genetic screen of *Plasmodium falciparum* identifies genotypy-phenotype mutations affecting tolerance to febrile temperatures. *American Journal of Tropical Medicine and Hygiene*. 2017; 97, 323.

4. Zhang M, **Wang C**, Oberstaller J, Otto TD, Adapa SR, Liao X, Swanson J, Li S, Udenze K, Rayner JC, Jiang RHY, Adams JH. Saturation-level piggyback mutagenesis screen of the *Plasmodium falciparum* genome defines gene important for invitro asexual blood stage growth. *American Journal of Tropical Medicine and Hygiene*. 2017; 97, 19.

5. Oberstaller J, Zhang M, **Wang C**, Otto TD, Liao X, Swanson J, Adapa SR, Udenze K, Bronner IF, Li S, Haines H, Rayner JC, Jiang RHY, Adams JH. Essential aspects of RNA metabolism for *P. falciparum* blood stage survival. American Journal of Tropical Medicine and Hygiene. 2017; 97, 625.

6. **Wang C,** Adapa SR, Sutton S, Jiang RHY. Bridging epigenetic and genetic controls in malaria antigenic variation with evolutionarily conserved noncoding elements. *American Journal of Tropical Medicine and Hygiene.* 2015; 93, 177.

MENTORING:

2024	**PhD Dissertation Defense Chair,** Mianli Xiao, College of Public Health, Univeristy of South Florida, Tampa, FL
2024-Now	**PhD Dissertation Committee Member,** Olatunbosun Aringbangba, College of Public Health, University of South Florida, Tampa, FL
2023-Now	**PhD Dissertation Committee Member,** Jan Dahrendorff, College of Public Health, University of South Florida, Tampa, FL
2023-2024	**MS Dissertation Committee Member**, Mackenzie Maggio, College of Public Health, University of South Florida, Tampa, FL
2023-2024	**MS Dissertation Committee Member**, Lanie Mullins, College of Public Health, University of South Florida, Tampa, FL
2023-2024	**MS Dissertation Committee Member**, Isabella Correia, College of Public Health, University of South Florida, Tampa, FL
2021-2022	**MS Mentor**, Pranjal Tyagi, College of Public Health, University of South Florida, Tampa, FL
2020-2021	**MS Dissertation Committee Member**, Zoe Taylor, College of Public Health, University of South Florida, Tampa, FL

MS Mentor, Samira Jahangiri, College of Public Health, University of South Florida, Tampa, FL