Chengqi Wang, PhD

CONTACT INFORMATION

Genomics Program
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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 Sequencing Core **Research 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.
2007-2012	Doctoral Scholarship, Lanzhou University.

SERVICE ACTIVITIES

I. Professional Service

2025-present	Editorial board in BMC Infectious Diseases
2022-present	Editorial board in Computational Genomics, Frontiers in Genetics
2022-present	Editorial board in Epigenomics and Epigenetics, Frontiers 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, Frontiers in Genetics

II. Grant review

NIH Transmission of Vector-Borne and Zoonotic Diseases, Ad Hoc Reviewer,	2024
Medical Research Council, UK,	2024,2025

III. Committee Member

International Conference on Intelligent Biology and Medicine, Tampa, FL, 2023. (Organizing Committee)
Chemgenomic Research Faculty Searching, University of South Florida, FL, 2024. (Committee Member)
Bioinformatic Research Faculty Searching, University of South Florida, FL, 2024. (Committee Member)
AI+X Symposium, University of South Florida, FL, 2024. (Review Committee)
10x Genomics–USF Spatial Genomics Symposium, University of South Florida, 2025. (Co-Organizer)

IV. Manuscript Reviewer

Briefings in Bioinformatics
eBioMedicine
iScience
Life Sciences
Genomics Proteomics and Bioinformatics
Computers in Biology and Medicine
Computational and Structural Biotechnology Journal
Parasites & Vectors
Heliyon
BMC Biology
BMC Genomics
BMC Supplements

Frontiers in Cellular and Infection Microbiology
Frontiers in Genetics
Scientific Reports
Journal of Cellular Physiology
Journal of Genetics and Genomics
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

TEACHING

1/2026, 1/2025, 1/2024, 1/2023, 1/2022, 8/2020	**Director and Instructor**, Applied Computational Genomics (3 credit). Course Description: Hands-on training, along with an introduction to basic concepts in using popular tools and techniques for genome, transcriptome, epigenome, and microbiome.
1/2026, 1/2025, 1/2024, 1/2023,	**Director and Instructor**, Fundamentals of Genomics Data Science. Course Description: This is a micro-certificate course serving as an online lifelong learning course. It is designed to introduce genomic data science to biologists who do not have a background in bioinformatics.
5/2025	**Co-Director and Instructor**, Single Cell RNAseq Laboratory Workshop. Course Description: This workshop is designed for research and bench scientists seeking a comprehensive introduction and hands-on wet lab experience in single-cell RNA-seq.
9/2025	**Co-Director and Instructor**, Spatial Transcriptomic Laboratory Workshop. Course Description: This workshop is intended for research and bench scientists seeking a comprehensive introduction and hands-on wet lab experience with the 10X Visium HD Spatial platform.
10/2025	**Guest Instructor**, Fundamental Genomics (1 credit). Course Description: It is designed to introduce genomic data science to biologists who do not have a background in bioinformatics.
2/2025, 2/2024	**Guest Instructor**, Translational Biotechnology (2 credit), Morsani College of Medicine, University of South Florida, Tampa, FL. Course Description: An overview of biotechnology in molecular medicine, covering drug discovery, global health, and industry practices, with hands-on exposure through site visits to research centers and biotech organizations.
8/2020	**Guest Instructor,** Introduction to Biocomputing (3 credit)

	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. Course Description: Foundational Linux command and R programming, basic statistical concept, and data visualization.
3/2021, 12/2020, 6/2020	**Director and Instructor**, R tutorials, Microbiome Data Analysis Workshop. Course Description: R programming, basic statistical concept, and data visualization in microbiome 16S analysis.
1/2018	**Teaching Assistant**, Quantitative Genomics and Genetics.

GRANT SUPPORT

Ongoing and Recently Completed Projects:

USF Institution Research Core Facilities (IRCF)
Role: PI
07/01/2024-06/30/2025
Advancing Genomics Research and Education: Enhancing the Impact and Capacity of the USF Genomics Core Facility
$1,197,678.40

10X Single Cell Analysis Research Award
07/01/2024-06/30/2025
Role: Co-PI
Defining Correlates of Protection of Plasmodium vivax Duffy Binding Protein-based Nanoparticle Vaccine by Single Cell Immune Profiling
$25,000

USF Publications Council Subvention Award
06/2023
Role: PI
Support Publication in Genome Biology
Amount: $3,000

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

Amount: $25,000

1R01AI187187
NIH/NIAID
Role: Co-I (PI: Cui)
06/10/2025 – 05/31/2030
Functions of mRNPs in RNA metabolism in Plasmodium Falciparum
Effort: 10% FTE

The Advanced Research Projects Agency for Health (ARPA-H)
Role: Co-I (PI: Breslin)
08/01/2025-07/31/2027
Multi-Omics of Human Lymphatic Dysfunction in Obesity and Diabetes
$9,837,438.00
Effort: 10% FTE

R01MD011728
NIH/NIMHD
Role: Co-I (PI: Uddin)
08/16/2017 – 05/31/2026
Epigenomic Predictors of PTSD and Traumatic Stress in an African American Cohort
Effort: 25% FTE

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
Effort: 20% FTE

U19AI181593
NIH/NIAID
Role: Co-I (PI: Cui)
05/01/2024 – 04/30/2029
Unraveling the Drivers of Persistent Malaria Transmission in Cameroon
Effort: 6.5% FTE

R01AI175640
NIH/NIAID
Role: Co-I (PI: Suvorova)
04/12/2024 – 02/28/2029
Regulation of Apicomplexan Mitosis Coupled to Budding
Effort: 10% FTE

R01AI117017
NIH/NIAID
Role: Co-I (PI: Adams)
02/10/2015 – 06/30/2026
Chemogenomic Profiling of Plasmodium Falciparum Drug Responses and Resistance
Effort: 10% FTE

R01AI141467
NIH/NIAID
Role: Co-I (PI: Suvorova)
05/08/2020 – 04/30/2025
Cyclin-mediated Control of Toxoplasma Development
Effort: 10% FTE

R21AI178797
Role: Co-I (PI: Suvorova)
08/16/2023 – 07/31/2025
Deciphering the composite S-phase in Toxoplasma gondii
Effort: 3% FTE

U19AI089672
NIH/NIAID
Role: Co-I (PI: Cui)
07/01/2010 – 03/31/2024
Southeast Asia Malaria Research Center
Effort: 10% FTE

PUBLICATIONS

Key Contributions to the Field in High-Impact Journals (**#Corresponding authors, *Co-first authors**)

1. **Wang C**, Uddin M, Wani A, Graham Z, Dai Y, Peterson M, Aiello A, Koenen K, Galea S, Wildman D. The relationship between social adversity, micro-RNA expression and post-traumatic stress in a prospective, community-based cohort. *Nat Ment Health.* 2026; 4: 416-426.

2. 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.

3. Oberstaller J, Xu S, Naskar D, Zhang M, **Wang C**, Gibbons J, Pires CV, Mayho M, Otto TD, Rayner JC, Adams JH. Supersaturation mutagenesis reveals adaptive rewiring of essential genes among malaria parasites. *Science.* 2025; 387: eadp7347.

4. Lucky A, Shakri AR, Liang X, Min H, Li XL, Adapa SR, Jiang RHY, Cui L, **Wang C#**, Miao J#. GCN5 is a master regulator of gene expression in the malaria parasite Plasmodium falciparum. *Cells*. 2025; 14(12): 876.

5. 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

6. 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.

7. **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.

8. 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.

9. 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.

10. 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

11. 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.

12. 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.

13. 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.

First-Author and Corresponding-Author Publications ([#]Crresponding author, *Co-first author)

14. Zhu X*, Feng Y*, **Wang C***, Shi S, Zhou D, Sun L, Zhu L, Cui L, Cao Y. Loss of serine/threonine protein phosphatase 6 severely impairs sexual stage development in malaria parasite Plasmodium berghei. *PLoS Pathog*. 2025; 21: e1013318.

15. Wei X, Malla P, Wang Z, Yang Z, Cao Y, **Wang C**[#], Cui L[#]. Genetic diversity of Plasmodium vivax population in northeast Myanmar assessed by amplicon sequencing of PvMSP1 and PvMSP3α. *Acta Trop*. 2024; 260: 107461

16. 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.

17. 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.

18. **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

19. **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.

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

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

22. **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.

23. **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.

Additional Peer-Reviewed Publications

24. Miao J, Byaruhanga Lucky A, Ning G, Xia X, Liang X, Siddiqui F, Min H, **Wang C**, Li X, Zhou ZH, Cui L. Clathrins are involved in the endocytosis of host cytosol in the malaria parasite. Traffic. 2026; 27(1): e70025.

25. Pires CV, Oberstaller J, **Wang C**, Gibbons J, Micchelli C, Zhang M, Otto TD, Rayner JC, Taylor S, Adams JH. Phenotypic screens reveal Plasmodium falciparum genetic factors associated with infection of sickle-trait cells. *Blood Cells Mol Dis*. 2025; 102951.

26. Zeng W, Liu H, Malla P, Zhao Y, Menezes L, Cao Y, **Wang C**, Yang Z, Cui L. Efficacy of primaquine for the radical cure of Plasmodium vivax malaria in northeast Myanmar and the impact of cytochrome P450 2D6 genotypes. *Clin Infect Dis*. 2025; 81(2): 379–386.

27. Batra M, Marsilia C, Awshah D, Hawkins LM, **Wang C**, Chaput D, Naumova DA, Suvorova ES. Deciphering cell cycle organization of Toxoplasma endodyogeny. mBio. 2025; 16(8): e01119-25.

28. Siddiqui FA, Chim-Ong A, **Wang C**, Miao J, Cui L. The PfK13 G533S mutation confers artemisinin partial resistance in multiple genetic backgrounds of Plasmodium falciparum. *Antimicrob Agents Chemother*. 2025; 69(7): e00162-25.

29. Wei X, Brashear A, Siddiqui F, Agyekum G, Lucky A, Chim-Ong A, Afrane Y, Miao J, **Wang C**, Amoah L, Cui L. Plasmodium falciparum genetic diversity and multiplicity of infection in northern and southern Ghana assessed by amplicon sequencing. *Infect Genet Evol*. 2025; 131: 105754.

30. 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. *PloS One*. 2024; 19: e0300565.

31. 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.

32. 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.

33. 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.

34. 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.

35. 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.

36. 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.

37. 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.

38. 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.

39. 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.

40. 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

41. 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.

42. 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

43. 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

44. 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

45. 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

46. 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.

47. 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

48. 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.

49. 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.

50. 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.

51. 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.

52. 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.

53. 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.

54. 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.

55. 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.

A. 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 *Plasmodium 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:

2026-Now	**PhD Dissertation Committee Member,** Rebekah Tiller, College of Public Health, University of South Florida, Tampa, FL
2025-Now	**PhD Dissertation Committee Member,** Akua Obeng, College of Public Health, University of South Florida, Tampa, FL
2025-Now	**PhD Dissertation Committee Member,** Forouzandeh Farsaei, Morsani College of Medicine, University of South Florida, Tampa, FL
2025-Now	**PhD Dissertation Committee Member,** Brett Higgins, Morsani College of Medicine, University of South Florida, Tampa, FL
2024	**PhD Dissertation Defense Chair,** Mianli Xiao**,** College of Public Health, University of South Florida, Tampa, FL
2021-2024	**PhD Dissertation Committee Member,** Olatunbosun Aringbangba, College of Public Health, University of South Florida, Tampa, FL
2024-Now	**PhD Dissertation Committee Member,** Chiara Micchelli, Morsani College of Medicine, University of South Florida, Tampa, FL
2024-Now	**PhD Dissertation Committee Member,** Mary Avornyo, Morsani College of Medicine, University of South Florida, Tampa, FL
2024-Now	**PhD Dissertation Committee Member,** Kailey McCain, College of Public Health, University of South Florida, Tampa, FL
2023-2025	**PhD Dissertation Committee Member,** Jan Dahrendorff, College of Public Health, University of South Florida, Tampa, FL
2025-2026	**MS Dissertation Committee Member**, Mequela Bogle, 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
2023-2024	**MS Mentor**, Pranjal Tyagi, College of Public Health, University of South Florida, Tampa, FL
2021-2022	**MS Dissertation Committee Member**, Zoe Taylor, College of Public Health, University of South Florida, Tampa, FL
2020-2021	**MS Mentor**, Samira Jahangiri, College of Public Health, University of South Florida, Tampa, FL
2025-Now	**Undergraduate Dissertation Committee Member,** Shilen Abraham, College of Arts and Science, University of South Florida, Tampa, FL
2025 Summer	**Undergraduate Mentor,** Barbara Podgorski, College of Public Health, University of South Florida, Tampa, FL

2025 Summer	**Undergraduate Mentor,** Ishika Sonthalia, College of Public Health, University of South Florida, Tampa, FL
2025 Summer	**High School Mentor,** Isabella Porcelli, Tampa, FL

PRESENTATIONS (last 5 years only)

1. **Wang C.** From Social Stress to Malaria Drug Resistance: Multi-omics and AI Approaches in Translational Genomics. Invited Oral Presentation, Children's Hospital Los Angeles, University of South California, CA. September 2025.

2. **Wang C.** From Social Stress to Malaria Drug Resistance: Multi-omics and AI Approaches in Translational Genomics. Invited Oral Presentation, Integrative Biology Seminars, Department of Integrative Biology, University of South Florida, Tampa, FL. October 2025.

3. **Wang C.** Decoding Trauma: epigenetic signatures linking social adversity and PTSD in a community-based cohort. Plenary Lecture, Southeastern Association of Shared Resources (SEASR), FL. June 2025.

4. **Wang C.** Using artificial intelligence to decipher genomic code in the deadliest malaria parasite. Keynote Oral Presentation, One Health Codeathon, FL. June 2024.

5. **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.

6. **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.

7. **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.