

Jenna Oberstaller, Ph.D.
Curriculum Vitae

USF Genomics Program
Department of Global, Environmental & Genomic Health Sciences
College of Public Health
University of South Florida
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EDUCATION

- Ph.D. in Genetics** 2012
University of Georgia, Department of Genetics (Athens, GA)
Major Professor: Jessica C. Kissinger
Dissertation: *Strategic genomics: from improving malaria diagnostics to demystifying gene regulation in apicomplexan parasites*
- B.S. in Biological Sciences** 2007
University of South Carolina (Columbia, SC)
Magna cum laude with Honors from the South Carolina Honors College

EMPLOYMENT

- Research Associate** 2018-present
Laboratory of Prof. John H. Adams
Genomics Program, College of Public Health, University of South Florida
- NRSA F32 Postdoctoral Fellow** 2015-2018
Laboratory of Prof. John H. Adams
College of Public Health, University of South Florida
- Fellow** 2012-2015
Laboratory of Prof. John H. Adams
College of Public Health, University of South Florida (Tampa, Florida)
- Graduate Research Assistant** 2007-2012
Laboratory of Prof. Jessica C. Kissinger
Department of Genetics/Center for Tropical and Emerging Global Diseases
University of Georgia (Athens, Georgia)
- Undergraduate Research Assistant** 2006-2007
Laboratory of Prof. Bert Ely
Department of Biology
University of South Carolina (Columbia, SC)

PROFESSIONAL APPOINTMENTS

- Acting Director, Omics Hub computational consulting and training core** 2020-2022
Genomics Program, University of South Florida
⇒ Founded and led a computational consulting and training core supporting USF Genomics. Coordinated computational early-career faculty and postdocs to offer omics data analysis workshops for bench biologists. Designed virtual trainings; built supporting codebase and centralized resource platform. Organized interdisciplinary coding events and mentored researchers in computational and molecular biology.
- Genomics Program Interdisciplinary Sciences Liaison** 2018-2022

University of South Florida

- ⇒ Created and evolved a cross-functional role to support the launch and growth of the Genomics Program. Facilitated collaboration across labs and developed consulting services. Led infrastructure initiatives with Research Computing, streamlined data pipelines between sequencing and analysis teams, and organized events to build community and onboard new faculty.

PROFESSIONAL SERVICE AND MEMBERSHIPS

National

Member, American Society of Tropical Medicine and Hygiene 2012-present
Board member, American Committee for Molecular, Cellular and Immunoparasitology 2017-2019
Councilor for Trainees

- Represented basic-parasitology trainee-interests at annual ASTMH board meetings and ACMCIP executive committee-meetings, with a focus on exposing trainees with a basic-science research parasitology background to diverse career-opportunities in Academia and beyond.

Local

Co-chair/Co-organizer, USF Genomics Faculty Working Group 2018-2021
 Created to integrate new Genomics faculty, discuss computational/sequencing-core/infrastructure needs and long-term programmatic goals, and develop scalable systems to support those needs.

USF One Health Codeathon series 2019-2021
 Annual symposium and intensive, project-focused collaborative coding competition centered around tackling problems in public health. Established to encourage broad interdisciplinary collaboration across scientists of all fields and career-stages, with each year highlighting new local, national and global research partners.

Event organizer and Host, *Harnessing data sciences against pandemics* 2021
 In partnership with the Global Virus Network.

Organizing committee and Project Lead, *Host-microbiome interactions* 2020
 In partnership with the USF Microbiome Initiative and the USF Institute for the Advanced Study of Culture and the Environment.

Organizing committee and Project Lead, *IRONHACK: Rare, iron-based genetic diseases* 2019
 In partnership with NCBI, in honor of National Rare Disease Day.

HONORS AND AWARDS

NIH F32 NRSA Individual Postdoctoral Fellowship (NIAID) 2015-2018
 \$173,186 direct costs

American Committee of Molecular, Cellular and Immunoparasitology Best Talk award 2017
 28th Annual Molecular Parasitology Meeting (Woods Hole, MA)

Centers for Disease Control Shepard Award Nominee 2012 & 2013
P. falciparum and *P. vivax* diagnostic assays; Oberstaller et al. 2011
P. knowlesi diagnostic assays, Patel et al. 2012

NIH National Graduate Student Research Conference Travel Award 2012
 to present novel, multi-species PCR-based malaria diagnostics

ARCS Foundation Scholar 2011-2012
 National ARCS Foundation, Atlanta chapter (\$7500)

Ellison Medical Foundation Training in Parasitological Studies Scholar 2010 & 2011

2010: to fund field research in Tanzania (\$7200)

2011: to fund field research in Thailand (\$6800)

NIH Institutional Training Grant (T32) UGA Center for Global and Emerging Tropical Diseases (\$24000)	2011-2012
Kirby and Jan Alton Graduate Fellowship UGA Department of Genetics (\$24000)	2010-2011
NIH Institutional Training Grant (T32) UGA Department of Genetics (\$22000)	2009-2010
Graduate Student Research Award University of Georgia (\$11000)	2009-2010
Magellan Scholars Undergraduate Research Fellowship University of South Carolina (\$3000)	2007
Howard Hughes Undergraduate Research Fellowship Howard Hughes Medical Institute and USC (\$1500)	2006
National Merit Scholarship National Merit Foundation (\$1000/year)	2003-2007
Palmetto Fellows Scholarship State of South Carolina (\$6700/year)	2003-2007
Lieber Scholarship University of South Carolina Honors College (\$5500/year)	2003-2007
University Scholarship University of South Carolina (\$1500/year)	2003-2007

RESEARCH EXPERIENCE

University of South Florida, College of Public Health, Genomics Program 05/2022 – present
Tampa, FL

Genomics Program/COPH Research Associate

Mentor: Dr. John Adams

- Provided an entirely new level of gene annotation for any malaria parasite genome—defining essential functional domains within genes—through super-saturating transposon mutagenesis.
- Led high-throughput phenotypic screens identifying key malaria parasite pathways in fever and drug resistance, including isoprenoid biosynthesis.
- Contributed open-source tools for community use and spearheaded interdisciplinary collaborations across USF, Sanger, and University of Glasgow.
- Published in top-tier journals including *Science*, *Nature Communications*, *PNAS*, and *Genome Biology*

University of South Florida, College of Public Health, Genomics Program 11/2018 – 5/2022
Tampa, FL

Genomics Program Interdisciplinary Sciences Liaison

- Founded and established the USF Omics Hub to extend the expertise of our core group of early-career computational biologists to other USF researchers and trainees, facilitating collaborations across a vast array of experimental systems, biological questions and omics technologies.
- Both lead and worked collaboratively with a diverse team of researchers on several complex research projects culminating in publication or funded extramural grants.

University of South Florida, College of Public Health 11/2012 – 4/2018
Global Health and Infectious Diseases

Tampa, FL

Postdoctoral Researcher

Mentor: Dr. John Adams

- Advanced functional genomics in *Plasmodium falciparum* by scaling *piggyBac* mutagenesis to saturation, enabling characterization of ~95% of genes as essential or dispensable.
 - Published in *Science*, May 2018. (965+ citations)
- Dissected gene-regulatory mechanisms in the human malaria parasite *Plasmodium falciparum* using both laboratory-based and computational approaches.
 - NIAID F32 postdoctoral fellowship research

University of Georgia, Department of Genetics

8/2007 – 10/2012

Athens, GA

Ph.D. Graduate Research Assistant

Major Professor: Dr. Jessica C. Kissinger

- Developed molecular diagnostic targets for several human malaria-parasite species up to 1000 times more sensitive than existing assays, combining computational and laboratory approaches.
- Verified novel malaria diagnostic assays in field-labs in Tanzania and Thailand.
- Identified and characterized the ApiAP2 family of transcription factors and their putative regulatory target genes in an experimentally intractable parasite, *Cryptosporidium parvum*, through interdisciplinary approaches combining data mining and comparative genomics with bench validation.
- Extended findings in *C. parvum* to study evolution of the ApiAP2 TF network across apicomplexans, including malaria parasites.

University of South Carolina, Department of Biological Sciences

2/2006 – 5/2007

Columbia, SC

Honors Undergraduate Researcher

Research and Honors Thesis Advisor: Dr. Bert Ely

- Sequenced and analyzed human DNA samples from all over Africa to build a database of mitochondrial haplogroups as part of the African American DNA Roots Project.
- Genotyped African populations from three geographically separated countries to identify linkage groups of alleles commonly involved in aggressive prostate and breast cancers often found in African Americans.

PROFESSIONAL DEVELOPMENT**University of Glasgow: Visiting Scholar**

2018; 2023; 2024

Host lab: Prof. Thomas Otto

- Ongoing computational methods development for large-scale mutagenesis screens in malaria parasites
- single-cell RNAseq analysis training

University of Cambridge: Visiting Scholar

2018; 2023; 2024

Host lab: Prof. Julian C. Rayner

- *P. knowlesi* molecular genetics; comparative biology of malaria parasites

Managing a Bioinformatics Core Facility, EMBL-EBI Training

6/2020

- Topics: cost-models for sustaining an informatics core facility, identifying strengths and areas for growth; communicating services, establishing impact; tools for team project management

University of Georgia: Visiting Scholar

3/2018

Host lab: Prof. Jessica C. Kissinger

- Trained in computational methods for assessing orthology, phylogenetic inference
- Tools and strategies for bridging critical gaps between bench-biologists and data science with the team behind the VEuPath family of genomics databases

Pennsylvania State University: Visiting Scholar

3/2018

Host labs: Profs Manuel Llinas and Scott Lindner

- Intensive training in applying CRISPR and other mutagenesis techniques to malaria parasites

Field experience**Mahidol University, Vivax Research Center (Bangkok, Thailand)**

March - April, 2013

Host: Prof. Jetsumon Sattabongkot-Prachumsri

- *Plasmodium vivax* culture and maintenance (protocol development/exploration)
- Intensive microscopy training to distinguish multiple malaria parasite species from patient blood

Mahidol University, Vivax Research Center (Bangkok, Thailand)

Oct - Nov, 2011

Host Prof. Jetsumon Sattabongkot-Prachumsri

- Extracted DNA from patient samples collected from Thai malaria field stations.
- Field-tested patient samples using novel PCR-based malaria diagnostic assays for 3 different malaria parasites (developed in collaboration with the CDC).

Ifakara Health Institute (Bagamoyo, Tanzania)

March - May, 2010

- Extracted DNA from hundreds of patient blood samples collected all over Tanzania.
- Performed first field-tests of novel LAMP malaria diagnostic machine developed at CDC.

GRANT SUPPORT**ACTIVE**

12/1/24 - 11/30/29

Percentile: 2%

Co-Investigator (30% FTE)

NIH R01 (R01AI183599)

"Genomic surveillance for artemisinin resistance in Africa: a selection-based approach"

PI: Takala Harrison/Djimdé

11/12/24 - 10/31/29

Percentile: 7%

Co-Investigator (30% FTE)

NIH R01 (R01AI187153)

"Phenotype-based screens to identify genetic factors associated with gametocyte development in *Plasmodium falciparum*"

PI: Adams

07/29/24 - 06/30/26

Co-Investigator (30% FTE)

NIH R56 (R56AI130171)

"Discovering the essential genome of *Plasmodium falciparum*"

PI: Adams

02/10/15 – 06/30/26

Co-Investigator (10% FTE)

NIH R01 (R01AI117017)

"Chemogenomic profiling of *Plasmodium falciparum* drug responses and resistance"

PI: Adams

PENDING

Pending review

PI (50% FTE)

NIH R01

"High-resolution functional mapping of malaria parasite genes to unravel critical aspects of RNA metabolism"

PI: Oberstaller

SELECTED PREVIOUS

10/4/2015 – 9/4/2018

PI

NIH F32, NIAID (F32-AI112271)

Total direct costs: \$173,186

"Post-transcriptional regulation in the malaria parasite blood stage"

PI: Oberstaller

- The long-term objective of these studies is to understand *P. falciparum* post-transcriptional regulatory mechanisms to identify key players suitable as novel drug targets.

COLLABORATIONS

SELECTED ONGOING

Dr. Shannon Takala Harrison (University of Maryland)

- developing multi-locus genomic markers for surveillance of emerging artemisinin resistance in African malaria parasites

Dr. Julian Rayner (University of Cambridge)

- Identifying genetic factors driving chloroquine response in vivax-like malaria parasites; comparative essential biology between both human-infective malaria parasite lineages

Dr. Thomas Otto (University of Glasgow)

- comparative phylogenomics of essential genes across socially/economically important parasites; integrative multiomics methods-development

Dr. Mike Ferdig (University of Notre Dame)

- defining and interpreting parasite transcriptional regulatory networks underlying artemisinin resistance in malaria parasites

SELECTED PREVIOUS

- Dr. Shannon Takala Harrison (U. Maryland)
 - analyzing “historical” GWAS data generated since the emergence of artemisinin-resistant malaria parasites, harmonizing and re-interpreting it through the lens of recent mechanistic/functional data
- Dr. Sami Noujaim (USF Morsani College of Medicine, Molecular Pharmacology and Physiology)
 - assessing molecular basis of aging-mediated atrial fibrillation
- Dr. Christina Richards (USF and Tuebingen)
 - assessing ecological consequences of climate change through epigenetic analysis of marine grasses
- Developed international, national, local, and cross-disciplinary partnerships in establishing our annual USF One Health Codeathon series, including the Global Virus Network, NCBI, Tampa General Hospital, USF Initiative on Microbiomes, Departments of Engineering, Computer Science, Social Sciences, Integrative Biology, Molecular Medicine, and several research-concentrations within USF COPH.
 - We produce several publicly available GitHub repositories after each event, usually accompanied by a publication.
- Dr. Dennis Kyle (University of Georgia) and Dr. Isuare de Buron (University of South Carolina)
 - phylogenetics and speciation in economically important fish-parasites
- Dr. Lynn Martin (USF, Integrative Biology)
 - ecological impact of light-pollution on bird-reservoirs of West Nile Virus and consequences for transmission
- Dr. Scott Lindner (Pennsylvania State University)
 - regulatory mechanisms governing malaria-parasite transmission-stages
- Dr. Manuel Llinas (Princeton University, currently Penn State)
 - transcription-factor family evolution in apicomplexan parasites; defining transcription-factor binding sites in *Cryptosporidium parvum*
- Dr. Venkatachalam Udhayakumar and Dr. Naomi Lucci (Centers for Disease Control)
 - improved molecular and field-based malaria-diagnostic assays

MENTORING AND TEACHING EXPERIENCE**COURSES AND WORKSHOPS**

PHC_6934: Applied Computational Genomics (USF) 2020-2022

Co-developer/co-instructor, Fall 2020; guest lecturer, 2021-2022

- *Description:* A broad introduction to concepts in omics technologies and data-analysis at the command-line, targeted at MSPH and PhD students with limited computational experience. Includes applied modules on genome-sequencing, ChIP-seq and epigenomic data-analysis, using publicly available data repositories, functional enrichment analyses, and more.

USF Omics Hub Hands-on Data Analysis Workshops, virtual editions 2020-2021

Director and co-instructor

- Led the Hub in creating scalable methods for remote delivery of intensive, hands-on data-analysis workshops in **(1) RNAseq data-analysis** and **(2) Microbiome 16S data-analysis**, enabling us to continue offering these 3 to 4-day workshops 5x per year during the COVID pandemic.
- Created and developed the codebase enabling the Omics Hub to offer hands-on data-analysis workshops virtually.

Microbiome 16S Data Analysis Workshop (USF Genomics Program/Omics Hub) 2019-2021

Director and co-instructor

- *Description:* Intensive 3-day workshop targeted at USF researchers of all career-stages with limited computational experience planning to apply for research-funding and/or have an immediate need for analyzing microbiome sequencing data. Offered ~2x per year.

RNAseq Data Analysis Workshop (USF Genomics Program/Omics Hub) 2018-2021

Organizer and co-instructor

- *Description:* Intensive 4-day workshop targeted at USF researchers of all career-stages with limited computational experience and a need for analyzing RNAseq data.
- Offered ~3x per year.

RESOURCES AND TEACHING TOOLS

<https://usfomicshub.github.io> (Creator and developer) 2018-

- Infrastructure and instructional materials designed to provide a “gentle” introduction to computational analyses and programming for biologists, including key concepts in R, UNIX, and Python development-environments, as well as cluster-computing.
- Tutorials, wiki, tips and further resources, code, boilerplate for grant applications, and more.

omicshub user group on USF High-Performance Computing resources (Creator and Admin) 2018-

- Development-environment facilitating code- and pipeline-sharing amongst Hub developers.
- Platform through which I/the Hub provide a standardized resource for common omics workflows for all users with cluster accounts.

RESEARCH MENTEES**PhD students**

(Major advisor: John H. Adams)

Mary Avorny, USF College of Medicine 2024-present
 Olatunbosun Aringbangba, USF Genomics Program 2024-present
 Jyotsna Chawla, USF College of Public Health 2020-2023
 Caroline Simmons, USF College of Medicine 2020-2023

Master's students

Samira Jahangiri, USF Genomics Program Fellow 2020-2021

- Research project advisor, 3 semesters

Linda Zoungrana, USF College of Public Health MSPH 2020-2021

- Research project advisor, 3 semesters

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|-----------------------------------------------------------------|-----------|
| Justin Swanson , USF College of Public Health MSPH/staff | 2017-2018 |
| • Research advisor, 1.5 years | |
| Ian Padykula , USF College of Public Health MSPH | 2017 |
| • Research project advisor, 8 months | |
| Suzanne Li , USF College of Public Health MSPH/staff | 2015-2016 |
| • Research advisor, 1.5 years | |
| Emily Lucht , USF College of Public Health MSPH | 2014 |
| • Research project advisor, 1 semester | |

Undergraduates

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| Hannah Haines , USF College of Arts and Sciences, Biological Sciences | 2016-2018 |
| • Undergraduate Research Project advisor, 4 semesters | |
| Raaven Goffe , USF Honors College, Biomedical Sciences | 2016-2017 |
| • Undergraduate Research Project advisor, 2 semesters | |
| Amber Carey , USF Integrative Animal Biology | 2017 |
| • Undergraduate Research Volunteer supervisor, 3 months | |
| Neto Coulibaly , USF College of Arts and Sciences | 2017 |
| • Undergraduate Research Volunteer supervisor, 2 months | |

OTHER SKILLS AND EXPERIENCE**Computational***Coding languages*

- Extensive experience with scripting languages (BASH, AWK/SED, Lua), R, cypher, various markdown languages
- Moderate experience with Python, Cypher, HTML, CSS; some experience with SQL, Perl, Jekyll, Ruby

Developer tools for reproducible data-analysis, systems administration

- Containerization with Docker, Singularity
- Environment-management with Anaconda, Lua modules

Misc. software

- Extensive experience with many command-line tools for NGS data-processing and analysis, including differential expression, single-cell transcriptomics, genome-assembly, phylogenomics, variant-calling and population-genomics, motif-discovery, machine learning, etc.
- Bespoke pipeline and workflow development for analyzing quantitative insertion-site sequencing data (QIseq), tools for comparative tools for transposon-mutant phenotype screens.
- Graph-database creation and network exploration with Neo4J, GRAKN
- Extensive experience with Bioconductor R packages for omics data-analysis and functional annotation
- Data-visualization with R ggplot and extensions, plotly, base R
- R package-development, documentation and publishing with devtools, roxygen2; RShiny

Wet lab

- Illumina NGS library-prep and sequencing; RNA isolation/purification
- CRISPR targeted mutagenesis
- Molecular cloning/basic molecular biology techniques
- Protein expression and purification
- Antibody development and characterization
- Cell/tissue culture
- Fluorescence microscopy

Media and public relations

- Spokesperson for our high-impact *piggyBac* saturation mutagenesis-screen revealing all malaria parasite genes essential for survival in human blood (Science, 2018) and follow-up *super*-saturation screen pinpointing the essential functional regions within genes (Science, 2025), giving live and written interviews to several local, national and international media outlets to convey significance to lay-people.
- Spokesperson for the Genomics Program in addition to the USF Omics Hub, providing interviews and material for USF COPH Marketing.
- Designed logo, marketing materials for the Hub and events.

PEER-REVIEWED PUBLICATIONS

1. 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 Jul 25;115:102951. PMID: 40782493. doi: 10.1016/j.bcnd.2025.102951.
2. **Oberstaller J**[†], Xu S^{*}, Naskar S^{*}, 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 Feb 7;387(6734). PMID: PMC12131478. ***†Lead corresponding author**
 - ◆ **Highlighted in Research news (selected international media-coverage, interviews):**
 - ◇ Not just monkey business: Functional genomics in malaria unlocks comparative biology across the family tree. Rob W. Moon and Ellen S.C. Bushell. *Science*, Feb 2025
 - ◇ Detailed map reveals essential genes in malaria parasite. PNAS Journal Club, March 3 2025
3. Pires CV, Chawla J, Sollelis L, **Oberstaller J**, Zhang M, Wang C, Gibbons J, Rayner JC, Otto TD, Marti M, Adams JH. Genetic factors regulating *Plasmodium falciparum* gametocytogenesis identified by phenotypic screens. *Scientific Reports*. 2024 Dec 28;14(1):31010. doi: 10.1038/s41598-024-82133-z. PMID: 39730700; PMID: PMC11680961.
4. Zhang Z, Lyu M, Han X, Bandara S, Cui M, Istvan ES, Geng X, Tringides ML, Gregor WD, Miyagi M, **Oberstaller J**, Adams JH, Zhang Y, Nieman MT, von Lintig J, Goldberg DE, Yu EW. The *Plasmodium falciparum* NCR1 transporter is an antimalarial target that exports cholesterol from the parasite's plasma membrane. *Scientific Advances*. 2024 Dec 20;10(51):eadq6651. doi: 10.1126/sciadv.adq6651. Epub 2024 Dec 18. PMID: 39693420; PMID: PMC11654669.
5. Namasivayam S, Sun C, Bah AB, **Oberstaller J**, Pierre-Louis E, Etheridge RD, Feschotte C, Pritham EJ, Kissinger JC. Massive invasion of organellar DNA drives nuclear genome evolution in *Toxoplasma*. *Proc Natl Acad Sci*. 2023 Nov 7;120(45):e2308569120. doi: 10.1073/pnas.2308569120. Epub 2023 Nov 2. PMID: 37917792; PMID: PMC10636329.
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 Biology*. 2023 Oct 16;24(1):231. doi: 10.1186/s13059-023-03063-z. PMID: 37845769; PMID: PMC10577899.
7. 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 May 23:e0015223. doi: 10.1128/msphere.00152-23. PMID: 37219373. PMID: PMC10449512.
8. Chawla J, Goldowitz I, **Oberstaller J**, Zhang M, Pires CV, Navarro F, Sollelis L, Wang CCQ, 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 Jun 15;11(3):e0416422. doi: 10.1128/spectrum.04164-22. Epub 2023 May 8. PMID: 37154686; PMID: PMC10269797.

9. 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 Jun 15;11(3):e0501422. doi: 10.1128/spectrum.05014-22. Epub 2023 Apr 17. PMID: 37067430; PMCID: PMC10269874.
10. Simmons CF, 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 Jan 9;13(1):399. doi: 10.1038/s41598-023-27417-6. PMID: 36624300; PMCID: PMC9829687.
11. Chang M, Gada KD, Chidipi B, Tsalatsanis A, Gibbons J, Remily-Wood E, Logothetis D, **Oberstaller J**, Noujaim SF. IKACH is constitutively active via PKC epsilon in aging-mediated atrial fibrillation. *iScience*. 2022 Oct 25;25(11):105442. doi: 10.1016/j.isci.2022.105442. PMCID: PMC9650037.
12. Mounger JM, van Riemsdijk I, Boquete MT, Wagemaker CAM, Fatma S, Robertson MH, Voors SA, **Oberstaller J**, Gawehns F, Hanley TC, Grosse I, Verhoeven KJF, Sotka EE, Gehring CA, Hughes AR, Lewis DB, Schmid MW and Richards CL. Genetic and Epigenetic Differentiation Across Intertidal Gradients in the Foundation Plant *Spartina alterniflora*. *Frontiers in Ecology and Evolution* 2022; 10:868826. doi: 10.3389/fevo.2022.868826.
13. **Oberstaller J***, Zhang M*, Wang C*, Thomas P, Otto TD, Debora Casandra, Sandhya Boyapalle, Swamy R. Adapa, Xu S, Katrina Button-Simons, Mayho M, Rayner JC, Michael T. Ferdig, Jiang RHY, Adams JH. The apicoplast link to fever-survival and artemisinin-resistance in the malaria parasite. *Nat Commun*. 2021 Jul 27;12(1):4563. PMCID: PMC8316339. ***Co-first authors**
14. **Oberstaller J***, Zoungrana L, Bannerman CD, Jahangiri S, Dwivedi A, Silva JC, Adams JH, and Takala-Harrison S. Integration of population and functional genomics to understand mechanisms of artemisinin resistance in *Plasmodium falciparum*. *International Journal for Parasitology: Drugs and Drug Resistance*. Epub 2021 June 6. 16:119-128. doi: 10.1016/j.ijpddr.2021.05.006. ***Lead corresponding author**
15. Chawla J, **Oberstaller J**, Adams JH. Targeting Gametocytes of the Malaria Parasite *Plasmodium falciparum* in a Functional Genomics Era: Next Steps. *Pathogens*. 2021 Mar 16;10(3):346. doi: 10.3390/pathogens10030346. PMID: 33809464; PMCID: PMC7999360.
 ◆ **Pathogens Title Story, June 2021**
16. **Oberstaller J**, Otto TD, Rayner JC, Adams JH. Essential Genes of the Parasitic Apicomplexa. *Trends Parasitol*. 2021 Apr;37(4):304-316. doi: 10.1016/j.pt.2020.11.007. Epub 2021 Jan 5. PMID: 33419671; PMCID: PMC7954859.
 ◆ **Trends in Parasitology Featured Article, April 2021**
17. **Oberstaller J**, Adapa SR, Dayhoff II GW et al. Uncovering host-microbiome interactions in global systems with collaborative programming: a novel approach integrating social and data sciences. *F1000Res*. 2020, 9:1478. Doi: 10.12688/f1000research.26459.1.
18. Wang C, Gibbons J, Adapa SR, **Oberstaller J**, Liao X, Zhang M, Adams JH, Jiang RHY. The human malaria parasite genome is configured into thousands of coexpressed linear regulatory units. *J Genet Genomics*. 2020 Sep 20;47(9):513-521. doi: 10.1016/j.jgg.2020.08.005. Epub 2020 Oct 10. PMID: 33272860.
19. **Oberstaller J***, Ferreira GC*, Fonseca R, Keller TE, Adapa SR, Gibbons J, Wang C, Liu X, Li C, Pham M, Dayhoff II GW, Duong LM, Reyes LT, Laratelli LE, Franz D, Fatumo S, Bari AG, Freischel A, Fiedler L, Dokur O, Sharma K, Cragun D, Busby B, Jiang RHY. Iron Hack - A symposium/hackathon focused on porphyrias, Friedreich's ataxia, and other rare iron-related diseases. *F1000Res*. 2019 Jul 19;8:1135. doi: 10.12688/f1000research.19140.1. PMID: 31824661; PMCID: PMC6894363. ***Co-first author**
20. Kernbach ME, Newhouse DJ, Miller JM, Hall RJ, Gibbons J, **Oberstaller J**, Selechnik D, Jiang RHY, Unnasch TR, Balakrishnan CN, Martin LB. Light pollution increases West Nile virus competence of a ubiquitous

- passerine reservoir species. *Proc Biol Sci.* 2019 Jul 24;286(1907):20191051. doi: 10.1098/rspb.2019.1051. Epub 2019 Jul 24. PMID: 31337318; PMCID: PMC6661335.
21. Hart KJ, **Oberstaller J**, Walker MP, Minns AM, Kennedy MF, Padykula I, Adams JH, Lindner SE. *Plasmodium* male gametocyte development and transmission are critically regulated by the two putative deadenylases of the CAF1/CCR4/NOT complex. *PLoS Pathog.* 2019 Jan 31;15(1):e1007164. doi: 10.1371/journal.ppat.1007164. PMID: 30703164; PMCID: PMC6355032.
 22. de Buron I, Colon BL, Siegel SV, **Oberstaller J**, Rivero A, Kyle DE. First evidence of polychaete intermediate hosts for *Neosporichis* spp. marine turtle blood flukes (*Trematoda: Spirorchiidae*). *Int J Parasitol.* 2018 Dec;48(14):1097-1106. doi: 10.1016/j.ijpara.2018.08.002. Epub 2018 Oct 25. PMID: 30367866.
 23. 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 May 4;360(6388):eaap7847. doi: 10.1126/science.aap7847. PMID: 29724925; PMCID: PMC6360947.
 - ◆ **Highlighted in Research news (selected international media-coverage, interviews):**
 - ◇ Indispensable malaria genes. *Science*, May 2018
 - ◇ Tagging Essential Malaria Genes to Advance Drug Development. NIH Director's Blog by Dr. Francis Collins, 15 May 2018
 - ◇ New malarial gene findings could aid drug development. *BioWorld*, 14 May 2018
 - ◇ Deadliest human malaria parasite reveals the genomic chinks in its armor. Wellcome Trust Sanger Institute via AAAS EurekAlert!, 3 May 2018
 24. Siegel SV, Rivero AV, **Oberstaller J**, Colon BL, de Buron I, Kyle DE. Blood flukes *Cardicola parvus* and *C. laruei* (*Trematoda: Aporocotylidae*): life cycles and cryptic infection in spotted seatrout, *Cynoscion nebulosus* (*Teleost: Sciaenidae*). *Parasitol Int.* 2018 Apr;67(2):150-158. doi: 10.1016/j.parint.2017.10.012. Epub 2017 Oct 31. PMID: 29100926.
 25. **Oberstaller J***, Thomas P*, Sedillo J*, Li S, Zhang M, Singh N, Lopez-Rubio JJ, Wang C, Udenze K, Jiang RHY, Adams JH. Phenotypic screens identify parasite genetic factors associated with malarial fever response and cytoadherence in *Plasmodium falciparum* piggyBac mutants. *mSphere.* 2016 Sep-Oct; 1(5) e00273-16. PMID: 27830190. * Co-first author
 26. **Oberstaller J**, Pumpalova Y, Schieler A, Llinás M, Kissinger JC. Defining the *Cryptosporidium parvum* ApiAP2 gene family: Insights into the evolution of Apicomplexan AP2 regulatory systems. *Nucleic Acids Res.* 2014 Jul; 42(13):8271-84. PMID: 24957599.
 27. **Oberstaller J**, Joseph SJ, Mauzy M, Lancto C, Enomoto S, Abrahamsen M, Rutherford M and Kissinger JC. Genome-wide upstream motif analysis of *Cryptosporidium parvum* genes clustered by expression profile. 2013 Jul 29;14:516. PMID: 23895416.
 28. Patel J, **Oberstaller J**, Poorak M, Xayavong M, Narayanan J, DeBarry J, Srinivasamoorthy G, Villegas L, Escalante AA, DaSilva A, Peterson DS, Barnwel JI, Kissinger JC, Udhayakumar V, Lucchi NW. Real-time loop-mediated isothermal amplification (RealAmp) for the species-specific identification of *Plasmodium vivax*. *PLoS One.* 2013;8(1):e54986. PMID: 23349994.
 - ◆ **Highlighted publication, CDC Shepard Award**
 29. Lucchi NW, **Oberstaller J**, Kissinger JC, Udhayakumar V. Malaria diagnostics and surveillance in the post-genomic era. *Public Health Genomics.* 2013;16(1-2):37-43. PMID: 23548716.
 30. Lucchi NW, Poorak M, **Oberstaller J**, DeBarry J, Srinivasamoorthy G, Goldman I, Barnwell J, Kissinger JC, Udhayakumar V. A new single-step PCR target for the detection of the zoonotic malaria parasite *Plasmodium knowlesi*. *PLoS One.* 2012;7(2)e31848. PMID: 22363751.

31. Oberstaller J*, Demas A*, DeBarry J*, Lucchi NW, Srinivasamoorthy G, Sumari D, Kabanywany AM, Villegas L, Escalante AA, Kachur SP, Barnwell JW, Peterson DS, Udhayakumar V, and Kissinger JC. Applied genomics: Data mining reveals species-specific malaria diagnostic targets more sensitive than 18S rRNA. *J Clin Microbiol.* 2011 Jul;49(7):2411-8. PMID: 21525225. *Co-first author

◆ **Highlighted publication, CDC Shepard Award**

SOFTWARE

J Oberstaller (2021). pfGO: *P. falciparum* functional enrichment analysis tools. R package version 2.1. <https://github.com/oberstal/pfGO>.

SELECTED PRESENTATIONS

Selected Talks

1. Selected Talk, International Conference on *Plasmodium vivax* Research (ICPvR) 2025 in Puducherry, India: *P. knowlesi* supersaturation mutagenesis reveals adaptive rewiring of essential genes among malaria parasites.
2. Invited Talk, University of Glasgow (host: Thomas Otto), September 2024: Supersaturation mutagenesis reveals adaptive rewiring of essential genes among malaria parasites.
3. Selected Talk, Molecular Parasitology Meeting (MPM) 2023 in Woods Hole, MA: 'Super-saturation' transposon mutagenesis allows high-resolution mapping of essential functions of zoonotic malaria parasite *Plasmodium knowlesi* genes.
4. Invited Symposium Talk, American Society for Tropical Medicine and Hygiene 2020: Artemisinin resistance is enabled by plastid-derived survival mechanisms.
 - ◆ **Highlighted symposium, Malaria Eradication Scientific Alliance**
5. Invited Talk, American Society for Tropical Medicine and Hygiene 2017 in Baltimore, MD: Essential aspects of RNA metabolism for *P. falciparum* blood-stage survival.
 - ◆ **ACMCIP Travel-award sponsored talk**
6. Selected Talk, Molecular Parasitology Meeting (MPM) 2017 in Woods Hole, MA: Essential aspects of RNA metabolism for *P. falciparum* blood-stage survival.
 - ◆ **Awarded Best Talk**
7. Bill and Melinda Gates Foundation Malaria Culture Systems Consortium Meeting 2014, Madrid, Spain: Qualitative and quantitative analyses of *Plasmodium vivax* blood-stage parasites.
8. Selected Talk, Center for Tropical and Emerging Diseases Symposium 2012, Athens, GA: Defining the *Cryptosporidium parvum* ApiAP2 transcription factor network: Insights into evolution of the ApiAP2 regulatory system in the Apicomplexa.
9. Selected Talk, Molecular Parasitology Meeting (MPM) 2011 in Woods Hole, MA: Defining the *Cryptosporidium parvum* ApiAP2 transcription factor network: Insights into evolution of the ApiAP2 regulatory system in the Apicomplexa.
10. Selected Talk, Center for Tropical and Emerging Diseases Symposium 2011, Athens, GA: Title: Applied genomics: Data mining reveals species-specific malaria diagnostic targets more sensitive than the molecular gold standard.

Selected Posters

1. Molecular Parasitology Meeting (MPM) 2025, Woods Hole, MA (Teaser Talk): Deciphering the role of CCR4-Associated Factor 1 (CAF1) in regulating the *P. falciparum* blood stage.

Kolli SK (presenter), **Oberstaller J**, Xu S, Adams JH.

2. Gordon Research Conference for Host/Parasite Interactions 2024, Newport, RI:
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.
3. American Society of Tropical Medicine and Hygiene (ASTMH) 2016, Atlanta, GA:
Oberstaller J, Adapa S, Liao X, Komandosky C, Li S, Udenze K, Zhang M, Jiang RHY, Adams JH. Using comparative *Plasmodium falciparum piggyBac*-mutant transcriptomics to discern regulatory roles of the CCR4-NOT complex.
4. Molecular Parasitology Meeting (MPM) 2016, Woods Hole, MA:
Oberstaller J, Adapa S, Liao X, Komandosky C, Li S, Udenze K, Zhang M, Jiang RHY, Adams JH. Using comparative *Plasmodium falciparum piggyBac*-mutant transcriptomics to discern regulatory roles of the CCR4-NOT complex.
5. University of South Florida Research Day 2017, Tampa, FL:
Haines H (presenter), **Oberstaller J***, Adams JH. Designing a phenotypic screen to identify regulators of malaria parasite egress and invasion genes. ***As Undergraduate Research-mentor.**
6. University of South Florida Research Day 2016, Tampa, FL:
Goffe R (presenter), **Oberstaller J*** et al. Stage-specific RNAseq gene expression profiling of a malaria parasite CAF1 mutant: CAF1 is an important post-transcriptional regulator. ***As Undergraduate Research-mentor.**
◆ **Excellence in Undergraduate Research Award**
7. Bill and Melinda Gates Foundation Malaria Culture Systems Consortium Meeting 2014, Madrid, Spain:
Oberstaller J, Taylor-Conway AJ, Kamath SG, Roobsoong W, Barnes SJ, Naumov A, Singh N, Yimamnuaychok N, Kumpitak C, Rochanarutaiprida N, Bannister EC, Cuiffi JD, Thomas O, Prachumsri J, Saadi WM, Adams JH. Qualitative and quantitative analyses of *Plasmodium vivax* blood-stage parasites.
8. Society for Molecular Biology and Evolution Meeting 2014, San Juan, Puerto Rico:
Oberstaller J, Pumpalova Y, Schieler A, Llinas M, Kissinger JC. The *Cryptosporidium parvum* ApiAP2 gene family: Insights into the evolution of the Apicomplexan AP2 regulatory system.
9. National Graduate Student Research Conference 2012, Bethesda, MD:
Oberstaller J, DeBarry J, Lucchi NW, Srinivasamoorthy G, Demas A, Poorak M, Goldman I, Peterson DS, Udhayakumar V, and Kissinger JC. Applied genomics: Species-specific malaria diagnostic targets more sensitive than the molecular gold standard.
10. International Giardia and Cryptosporidium Conference 2012, Wellington, New Zealand:
Joseph SJ, **Oberstaller J**, Mauzy M, Enomoto S, Lancto C, Kissinger JC and Rutherford M. Gene expression analysis of *Cryptosporidium parvum*.
11. American Society of Tropical Medicine and Hygiene (ASTMH) 2011, Philadelphia, PA:
Patel J, **Oberstaller J**, Poorak M, Xayavong M, Narayanan J, DeBarry J, Srinivasamoorthy G, Villegas L, Escalante AA, DaSilva A, Barnwell J, Kissinger JC, Udhayakumar V, Lucchi NW. Real time loop-mediated isothermal amplification (RealAmp) for the species-specific identification of *Plasmodium vivax*.
12. ASTMH 2011, Philadelphia, PA:
Lucchi NW, Poorak M, **Oberstaller J**, DeBarry J, Srinivasamoorthy G, Goldman I, Barnwell J, Kissinger JC, Udhayakumar V. Novel PCR-based assays for the detection of *P. knowlesi*.
13. MPM 2010, Woods Hole, MA:
Oberstaller J, DeBarry J, Srinivasamoorthy G, Demas A, Lucchi NW, Udhayakumar V, Peterson DS, & Kissinger JC. Applied genomics to improve molecular malaria detection: *Plasmodium* subtelomeric regions harbor promising diagnostic targets.
14. CDC/UGA seed grant symposium 2010, Atlanta, GA:

Oberstaller J, Lucchi NW, Demas A, Kissinger JC, Udhayakumar V. Field-testing malaria diagnostics in Tanzania: Molecular detection using Loop-mediated Isothermal Amplification of DNA.

15. **American Society for Microbiology 2010, San Diego, CA:**
Cheng Sun, Barrie AB, **Oberstaller J**, Pace JK, Feschotte C, Kissinger JC, and Pritham EJ. Evolutionary and functional analysis of nuclear mitochondrial DNA in *Toxoplasma gondii*.
16. **MPM 2009, Woods Hole, MA:**
Oberstaller J, Kissinger JC. Phylogenetic analysis and distribution of the plant-like ApiAP2 family of transcription factors in the Alveolates.
17. **Genome Biology and Bioinformatics 2009, Atlanta, GA:**
Oberstaller J, Kissinger JC. Phylogenetic analysis and distribution of the AP2 family of transcription factors in the Chromalveolates: Rise of the domain in the Apicomplexa.