

Rays H.Y. Jiang

USF genomics, Global Health Infectious Disease Research Center (GHIDR), Global and Planetary Health, College of Public Health, University of South Florida, Tampa FL USA

Pioneering in genomics

As the first genomics lab in University of South Florida, Rays Jiang lab takes on a pioneer role in establishing a viable research program; as well as pushing the frontier of genomics science. She has published in high profile journals such as Cell, Nature, Science, Nature Communications and Genome Research, and secured diverse funding sources from NIH, NSF and Gates' foundations. Rays Jiang has been recognized as a globally Highly Cited Researcher by Clarivate, which recognizes researchers ranking in the top 1% by citations in the field by Web of Science.

Rays Jiang is one of the founding members of USF genomics program. She has been the lead PI of acquiring major genomics instruments of Next Generation Sequencing machines and single-cell biology instruments for initiation of USF genomics core.

Rays Jiang is the concentration director of the newly created Genomics Master's program (certified and approved).



Research interest

I have a PhD in genomics from Wageningen University, the Netherlands. I have been a computational biologist at the Broad Institute of MIT and Harvard and Harvard University. I came to USF with the vision to establish one of the first hybrid labs to synthesize computational biology and

experimental sciences. My lab bears the identity of **STEM_CORE (Single-cell, Translational, Evolution and Microbial, USF Central-lab for Omics Research and Engineering)**. STEM_CORE is supported multiple external funding sources and a strong track record of high profile publications.

More at www.RaysJiangLab.org

Education

Wageningen University, the Netherlands	Biotechnology	Ing	2000
Wageningen University, the Netherlands	Genomics	PhD	2006
Virginia Tech USA, Broad Institute USA, Wageningen University, the Netherlands, Visiting scholar (Funded by Dutch genomics initiative NGI#050-72-404) 2006-2007			

Appointments

Computational biologist 2008- 2013
Broad Institute of MIT/Harvard, MA, USA

Research associate 2012 - 2013
Department of Infectious Disease and Immunology, Harvard School of Public Health, Harvard University, MA, USA

Professor 2014 –
(Currently tenured associate professor rank)
Global and Planetary Research, College of Public Health, University of South Florida, FL, USA

Languages:

Human: Chinese, Dutch, English

Computational: Python, Perl, PHP, Java, Javascript, R, SQL, noSQL

Recent honors

Outstanding Faculty Award, University of South Florida, 2020

Dr. Moore Faculty Excellence Award, Women in Leadership and Philanthropy, 2023

Professional activities

Reading committee of PhD thesis 2013

Theoretic biology and Bioinformatics at Utrecht University, the Netherlands

Faculty recruiting committee 2015, 2016, 2017,2018,2019,2020,2021,2022

Public Health Genomics, College of Public Health, USF

Disease Biologist, College of Arts and Sciences, USF

USF Genomics clustering hiring, USF

International Malaria genomics research database advisory committee
2017-

Mentoring

Served on different PhD research committees in the field of public health, chemistry and engineering. Mentored Graduate students (30), research engineers (3), and Postdoc (2) with different and individually tailored genomics projects in the lab.

Teaching

Global Health – Principles and contemporary issues (Course director)

A data science driven course led by basic researchers, clinicians and global health professionals working in different continents

Anti-microbial drug discovery course (Course director)

An innovative course co-taught by chemistry department and global health

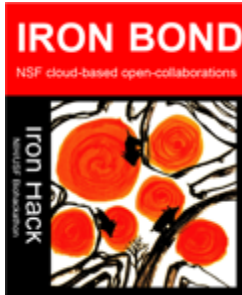
Quantitative Genomics and Genetics (Course director)

A newly created course teaches both classic genetics and new technologies of genomics

USF genomics master program (concentration director)

Initiated and responsible the first USF genomics/data science master program

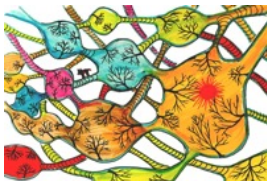
Organizing conferences and leadership in research programs



Iron hack and Iron bond (Feb-2019, USF)

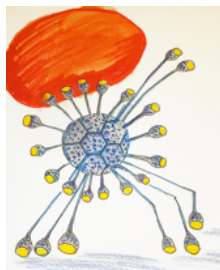
We organized **the first** NIH/NCBI/USF biohackathon, named Iron Hack, to creatively solve the human genetic disease problem by pulling together the effort of clinicians, researchers, genetic counselors and programmers. We aim to connect communities across fields, states, and continents for collaborative research with a program called Iron Bond. A paper reporting this effort has been accepted for publication; and several related proposals are in

planning.



Uncovering host-microbiome interactions in global systems with collaborative programming: a novel approach integrating social and data sciences (Feb-2020 USF)

Microbiomes data are undergoing exponential growth powered by rapid technological advancement. As the scope and depth of microbiome research increases, cross-disciplinary research is urgently needed for interpreting and harnessing the unprecedented data output. However, conventional research settings pose challenges to much-needed interdisciplinary research efforts due to barriers in scientific terminologies, methodology and research-culture. To breach these barriers, our University of South Florida OneHealth Codeathon was designed to be an interactive, hands-on event that solves real-world data problems.



Collaborative coding against pandemics. (Feb-2021 virtual, USF).

We organized the workshop during COVID-19 pandemic. The pandemics of COVID-19 has impacted global human health in nearly all aspects, including physical, emotional and mental health. Within 12 months of the official marking of pandemic by WHO, enormous amount of data have been generated to track pathogens, predict epidemics and manage outbreaks. Here, we utilized the codeathon format for collaborative, cross-disciplinary coding, to

harness the data generated by current technologies that have been actively applied in pandemics, such as Next Generation Sequencing and population genomics surveillance.

Symposium cell-to-cell communications underlying malarial life cycle transitions (Oct-2018, New Orleans)

I organized and chaired the symposium at the conference of American society of tropical medicine and hygiene, New Orleans, Louisiana USA. Established Speakers from 3 continents were invited to present their innovative research results.

Global Health and infectious disease symposium (March 2018, USF)

I organized this symposium centering around cutting-edge technologies of single cell biology, featuring speakers specializing in cancer biology, mathematics, infectious diseases from different institutions and countries.

American Microbiology Society Meeting (March 2018 St. Petersburg, FL, USA)

I organized a session on eukaryotic pathogenesis, with invited speakers in different domains of parasitology research.

Florida Malaria winter club (March 2018, March 2022 USF)

I co-organized the first malaria research network meeting at USF. Researchers from different institutions from Florida state actively participated and the club conference will continue on a yearly basis.

International Conference of Intelligent Biology and Medicine (July, 2023, Tampa, FL)



I co-organize this AI and biology conference, spanning field from computation, engineering and medicine. With invited speakers established in AI research and/or medical sciences.

Evolutionary System Biology group (Dec-2018 to current, USF)

I am one of the initiators and organizers of the EvoSysBio group at USF. We have participants from all colleges of USF system and MOFFIT, a partner cancer institute in Tampa. We aim at bringing evolutionary strength to systems biology with quantitative calculations of populations dynamics and evolutionary processes. And we strive to offer concrete biological insight to ecological and population research with mechanistic studies of cellular processes.

USF data science group

I have been taking initiatives to reach across the university system for collaborative data science work. I also gave an invited lecture on Artificial Intelligence and genomics in college of engineering and computer sciences.

Selected invited presentations

National Oceanographic and Atmospheric Administration (NOAA)|US department of Commerce “The need for a bold step in US marine mammal management” (webinar)
Feb-2023

Johns Hopkins all children hospital, st Petersburg FL, USA. “A double-edged sword: the role of heme in malaria infections”
March-2022

University of South Florida, USA (replanned from Venice Italy during COVID-19) “Track ancient epidemics with genomics and genetics” (Virtual)
Feb-2021

Texas Wesleyan University, USA. STEM research and career development workshop. (Virtual)
Sep-2020

Texas Tech, USA. NSF workshop of Machine Learning and life sciences
 Oct-2019

Wageningen University, the Netherlands, genomics seminar
July-2019

Nijmegen University, the Netherlands – medical center seminar
July-2019

Oban, Scotland, UK – oomycetes molecular genetics
July-2019

USF, USA - Artificial Intelligence and data science series
May-2019

Oakland, CA, USA – Gates foundation consortium meeting
 March-2019

New Orleans, USA – American society of tropical medicine and hygiene
 October-2018

Exeter, UK – University of Exeter, life sciences
 July - 2018

Osaka, Japan, - Research Institute for Microbial Diseases
 May-2018, Osaka University

Tsukuba, Japan - National Agriculture and Food Research Organization
 May-2018, NARO, Japan

Athens, GA, USA - Center for Tropical and Emerging Global Diseases,
 October-2017, University of Georgia

Manaus, Brazil - Gates Foundation liver stage malaria consortium meeting,
 June-2017

Bangkok, Thailand - Joint International Tropical Medicine Meeting, December-
 2016

New York, USA - Red Blood Cell club meeting, Feinstein Institute for Medical Research, October-2016

Quito, Ecuador - IV International meeting in infectious disease research and tropical medicine, June-2016

Kolkata, India - 17th All India Congress of Cytology and Genetics, December-2015

Publications

*co-first authorship, ^co-senior authorship

Featured publications

Zhang M*, Wang CQ*, Otto TD, Oberstaller J, Liao X, Adapa SR, Udenze K, Li S, Bronner IF, Casandra D, Mayho M, Brown J, Li S, Swanson J, Rayner JC, [Jiang RHY](#)[^] and Adams JH[^].

Uncovering the essential genome of the human malaria parasite *Plasmodium falciparum* by saturation mutagenesis

Science 2018 PMID: 29724925

This work is featured by [NIH Director Collins' post](#)

Brancucci NMB, Gerdt JP, Wang C, ... Waters AP, [Jiang RHY](#), Clardy J, Marti M. Lysophosphatidylcholine Regulates Sexual Stage Differentiation in the Human Malaria Parasite *Plasmodium falciparum*.

Cell 2017 PMID: 29129376

This work is featured by different research institutions across Europe and America

Cloud-based and community-based open source discoveries

Liu X, Cragun D, Pang J, Adapa SR, Fonseca R, [Jiang RHY](#).

False Alarms in Consumer Genomics Add to Public Fear and Potential Health Care Burden.

Journal of Personalized Medicine. 2020 PMID: 33113957

Iron hack consortium ... Busby B. and [Jiang RHY](#).

Iron Hack - A symposium/hackathon focused on porphyrias, Friedreich's ataxia, and other rare iron-related diseases

F1000 research, 2019

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 PMID: 30634978

Van Voorhis et al. Open Source Drug Discovery with the Malaria Box Compound
Collection for Neglected Diseases and Beyond.
PLoS Pathogen 2016 PMID: 27467575

Single-cell engineering, computation and biology

B.M. Stojanovski, G.A. Hunter, I. Na, V.N. Uversky, [Jiang RHY](#), and GC. Ferreira*
5-Aminolevulinate Synthase Catalysis: The Catcher in Heme Biosynthesis.
Molecular Genetics and Metabolism, 2019

Thomson-Luque R, Wang C, ..., 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 PMID: 30007855
This is the first single-cell human reticulocyte and erythroid study

Cheemalapati SV, Winkas J, Wang H, Konnaiyan K, Zhdanov A, Roth A, Adapa SR,
Deonaraine A, Noble M, Das T, Gatenby R, Westerheide SD, [Jiang RHY](#) and Pyayt A.
Subcellular and in-vivo Nano-Endoscopy.
Scientific Report 2016 Oct

Microbiome Research

Bonsack B, [Jiang RHY](#), Borlongan CV.
A gut feeling about stroke reveals gut-brain axis' active role in homeostasis and
dysbiosis.
J Cereb Blood Flow Metab. 2020 PMID:32063084

Obstaller et al... [Jiang RHY](#).
Uncovering host-microbiome interactions in global systems with collaborative
programming: a novel approach integrating social and data sciences
F1000 research, 2020

Marine biology and environmental health

Hanson HE, Wang C, Schrey AW, Liebl AL, Ravinet M, [Jiang RHY](#), Martin LB. Epigenetic Potential and DNA Methylation in an Ongoing House Sparrow (*Passer domesticus*) Range Expansion
Am Nat. 2022 PMID: 36260844

Kernbach ME, Martin LB, Unnasch TR, Hall RJ, [Jiang RHY](#), Francis CD. Light pollution affects West Nile virus exposure risk across Florida.
Proc Biol Sci. 2021 PMID: 33757351

Kernbach ME, Newhouse DJ, Miller JM, Hall RJ, Gibbons J, Oberstaller J, Selecknik 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 PMID: 31337318.

Bouchard C, Boudko DY, [Jiang RHY](#). A SLC6 transporter cloned from the lion's mane jellyfish (Cnidaria, Scyphozoa) is expressed in neurons.
PLoS One. 2019 PMID: 31233570

Novel computational methods and analysis

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 PMID: 33272860

Kazi A, Xiang S, Yang H, Delitto D, Trevino J, [Jiang RHY](#), Ayaz M, Lawrence HR, Kennedy P, Sebti SM. GSK3 suppression upregulates β -catenin and c-Myc to abrogate KRas-dependent tumors.
Nature Communication 2018 PMID: 30514931

Gibbons J, Button-Simons KA, Adapa SR, Li S, Pietsch M, Zhang M, Liao X, Adams JH, Ferdig MT, [Jiang RHY](#). Altered expression of K13 disrupts DNA replication and repair in *Plasmodium falciparum*.
BMC Genomics 2018 PMID: 30486796

Babatunde KA, Mbagwu S, Hernández-Castañeda MA, Adapa SR, Walch M, FigueiraL, Falquet L, [Jiang RHY](#), Ghiran I, Mantel PY. Malaria infected red blood cells release small regulatory RNAs through extracellular vesicles.
Scientific Report 2018 PMID: 29343745

Wang CQ, Adapa SR, Gibbons J, Sutton SG and Jiang RHY
 Punctuated chromatin states regulate Plasmodium falciparum antigenic variation at
 intron and 2kb upstream regions
BMC Genomics 2016 Aug

Tripathy S, Jiang RHY.
 Massively parallel sequencing technology in pathogenic microbes.
Methods Mol Biol. 2012 PMID: 22183660.

Large scale of novel forward mutagenesis

Zhang M, Wang C, Oberstaller J, Thomas P, Otto TD, Casandra D, Boyapalle S, Adapa
 SR, Xu S, 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 PMID: 34315897

Bronner IF, Otto TD, Zhang M, Udenze K, Wang CQ, Quail MA, Jiang RHY, Adams JH,
 Rayner JC.
 Quantitative Insertion-site Sequencing (QIseq) for high throughput phenotyping of
 transposon mutants.
Genome Research. 2016 May 10

Egan ES, Jiang RHY, Moechtar MA, Barteneva NS, Weekes MP, et al
 A forward genetic screen identifies erythrocyte CD55 as essential for Plasmodium
 falciparum invasion.
Science 2015 ; 348(6235):711-4

Host evolution in microbial interactions

Downs CJ, Schoenle LA, Goolsby EW, Oakey SJ, Ball R, Jiang RHY, Martin LB.
 Large Mammals Have More Powerful Antibacterial Defenses Than Expected from Their
 Metabolic Rates.
Am Nat. 2023 PMID: 36724463

Dankwa S, Lim C, Bei AK, Jiang RHY, Abshire JR, Patel SD, Goldberg JM, et al.
 Ancient human sialic acid variant restricts an emerging zoonotic malaria parasite.
Nature Communication 2016 Apr 4

Dankwa S, Chaand M, Kanjee U, Jiang RHY, Nobre LV, et al.
 Genetic Evidence for Erythrocyte Receptor Glycophorin B Expression Levels Defining a
 Dominant Plasmodium falciparum Invasion Pathway into Human Erythrocytes.
Infection & Immunity 2017 PMID: 28760933

Microbial evolution driven by hosts and environment

Sacco MD, Wang S, Adapa SR, Zhang X, Lewandowski EM, Gongora MV, Keramisanou D, Atlas ZD, Townsend JA, Gatlula JR, Morgan RT, Hammond LR, Marty MT, Wang J, Eswara PJ, Gelis I, Jiang RHY, Sun X, Chen Y.

A unique class of Zn²⁺-binding serine-based PBPs underlies cephalosporin resistance and sporogenesis in *Clostridioides difficile*.

Nature Communication. 2022 PMID: 35902581

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. PMID: 32386321

Blomqvist K, Helmel M, Wang C, Absalon S, Labunska T, Rudlaff RM, Adapa S, Jiang RHY, Steen H, Dvorin JD. Influence of *Plasmodium falciparum* Calcium-Dependent Protein Kinase 5 (PfCDPK5) on the Late Schizont Stage Phosphoproteome.

mSphere. 2020 PMID:31915223.

Jiang RHY, Stahelin RV, Bhattacharjee S, Haldar K. Eukaryotic virulence determinants utilize phosphoinositides at the ER and host cell surface.

Trends in Microbiology. 2013 Mar;21(3):145-56

Jiang RHY and Tyler BM

Mechanisms and evolution of virulence in oomycetes

Annu Rev Phytopathol 2012 Vol 50 Sep 8;50:295-318 PMID: 22920560

Neafsey DE, Galinsky K, Jiang RHY, Young L, Sykes SM et al.

The malaria parasite *Plasmodium vivax* exhibits greater genetic diversity than *Plasmodium falciparum*.

Nature Genetics 2012 Sep;44(9):1046-50.

Jiang RHY, Marti M.

A PIP Gets the plasmodium protein export pathway going.

Cell Host Microbe. 2012 PMID: 22341457.

Baxter L, Tripathy S, Ishaque N, Boot N, ...Jiang RHY... et al.

Signatures of adaptation to obligate biotrophy in the *Hyaloperonospora arabidopsidis* genome.

Science. 2010 PMID: 21148394

Raffaele S, Farrer RA, Cano LM, Studholme DJ, MacLean D, Thines M, Jiang RHY, Zody MC, Kunjeti SG, Donofrio NM, Meyers BC, Nusbaum C, Kamoun S.

Genome evolution following host jumps in the Irish potato famine pathogen lineage.

Science. 2010 PMID:21148391.

Lévesque CA, Brouwer H, ...Jiang RHY... et al
Genome sequence of the necrotrophic plant pathogen *Pythium ultimum* reveals original pathogenicity mechanisms and effector repertoire.
Genome Biology. 2010 PMID: 20626842

Haas BJ, Kamoun S, Zody MC, Jiang RHY, Handsaker RE et al,
Genome sequence and analysis of the Irish potato famine pathogen *Phytophthora infestans*.
Nature. 2009 PMID:19741609

Jiang RHY, Tripathy S, Govers F, Tyler BM. RXLR effector reservoir in two *Phytophthora* species is dominated by a single rapidly evolving superfamily with more than 700 members.
PNAS. 2008 PMID: 18344324

Mhashilkar AS, Adapa SR, Jiang RHY, Williams SA, Zaky W, Slatko BE, Luck AN, Moorhead AR, Unnasch TR.
Phenotypic and molecular analysis of the effect of 20-hydroxyecdysone on the human filarial parasite *Brugia malayi*.
Int J Parasitol. 2016 PMID: 26896576

Merrick CJ, Jiang RHY, Skillman KM, Samarakoon U, Moore RM, Dzikowski R, Ferdig MT, Duraisingh MT.
Functional analysis of sirtuin genes in multiple *Plasmodium falciparum* strains.
PLoS One. 2015 PMID: 25780929

Mechanisms of host-microbe interactions

Miao J, Wang C, Lucky AB, Liang X, Min H, Adapa SR, Jiang R, Kim K, Cui L.
A unique GCN5 histone acetyltransferase complex controls erythrocyte invasion and virulence in the malaria parasite *Plasmodium falciparum*.
PLoS Pathog. 2021 PMID: 34403450

Ganter M, Goldberg JM, Dvorin JD, Paulo JA, King JG, Tripathi AK, Paul AS, Yang J, Coppens I, Jiang RHY, Elsworth B, Baker DA, Dinglasan RR, Gygi SP, Duraisingh MT.
Plasmodium falciparum CRK4 directs continuous rounds of DNA replication during schizogony.
Nature Microbiology 2017 Feb

MohanKumar K, Namachivayam K, Cheng F, Jiang RHY, Flores-Torres J, Torres BA, Maheshwari A.
Trinitrobenzene sulfonic acid-induced intestinal injury in neonatal mice activates transcriptional networks similar to those seen in human necrotizing enterocolitis.
Pediatr Res. 2017 PMC5235988

Thomas P, Sedillo J, Oberstaller J, Li S, Zhang M, Singh N, Wang CC, Udenze K, Jiang RHY and Adams JH.
Phenotypic Screens Identify Parasite Genetic Factors Associated with Malarial Fever Response in Plasmodium falciparum piggyBac Mutants.
mSphere. 2016 PMID: 27830190

Pellé KG*, Jiang RHY*, Mantel PY, Xiao YP, Hjelmqvist D, Gallego-Lopez GM, Lau AO, Kang BH, Allred DR, Marti M.
Shared elements of host-targeting pathways among apicomplexan parasites of differing life styles.
Cell Microbiol 2015; May 21

Paul AS, Saha S, Engelberg K, Jiang RHY, Coleman BI, Kosber AL, et al
Parasite Calcineurin Regulates Host Cell Recognition and Attachment by Apicomplexans.
Cell Host Microbe 2015

Coleman BI, Skillman KM, Jiang RHY, Childs LM, Altenhofen LM, et al
A Plasmodium falciparum histone deacetylase regulates antigenic variation and gametocyte conversion.
Cell Host Microbe 2014; Aug 13

Jiang RHY, de Bruijn I, Haas BJ, et al.
Distinctive expansion of potential virulence genes in the genome of the oomycete fish pathogen Saprolegnia parasitica.
PLoS Genetics 2013 Jun;9(6)

***in vitro* human liver engineering and genomics**

Maher SP, ...Awuku NA, Conway AJ, Jiang RHY, Russell B, Bifani P, Campo B, Nosten F, Witkowski B, Kyle DE.
Probing the distinct chemosensitivity of Plasmodium vivax liver stage parasites and demonstration of 8-aminoquinoline radical cure activity in vitro.
Sci Rep. 2021 PMID: 34620901

Maher SP, Conway AJ, Roth A, Adapa SR, ... Saadi WM, Adams JH, Jiang RHY, Kyle DE.
An adaptable soft-mold embossing process for fabricating optically-accessible, microfeature-based culture systems and application toward liver stage antimalarial compound testing.
Lab-on-a-Chip. 2020 PMID: 32055808

Roth A*, Maher SP*, Conway A ...Lanar DE, Nosten F, Davidson S, Jiang RHY, Kyle DE, Adams JH.
A comprehensive model for assessment of liver stage therapies targeting Plasmodium

vivax and *Plasmodium falciparum*
Nature Communication 2018 PMID: 29743474

Roth A, Adapa SR, Zhang M, Liao X, Saxena V, Goffe R, Li S, Ubalee R, Saggi GS, Pala ZR, Garg S, Davidson S, Jiang RHY[^], Adams JH[^].
 Unraveling the *Plasmodium vivax* sporozoite transcriptional journey from mosquito vector to human host.
Scientific Report 2018 PMID:30111801

Funding support

Principal Investigator: John Adams, PhD
 Co-Investigators: Julian Rayner, PhD, Sanger Institute/Cambridge University; Rays H.Y. Jiang, PhD; Thomas Otto, PhD, University of Scotland
 Title: Chemogenomic Profiling of *Plasmodium Falciparum* Responses and Resistance
 Agency: National Institute of Allergy and Infectious Disease
 Grant/Contract #: R01AI130171
Total Amount Funded: \$736,437
 Award Dates: 07/21– 06/26

Principal Investigators: Said Sebti, PhD (Award is transferring from H. Lee Moffitt Cancer Center & Research Institute to Virginia Commonwealth University)
 Co-Investigators: Rays H.Y. Jiang, PhD
 Relative contribution made to the grant/contract:
 Title: Targeting Mutant KRAS for Cancer Therapy
 Agency: National Cancer Institute
 Grant/Contract #: R35CA197731
 Research Purpose: The overall goal of this project is to identify and validate novel targets and therapeutic agents for human cancers with mutant KRAs.
Total Amount Funded: \$3,706,347 (Funding to date: 03/01/16 – 02/29/20)
Candidate Share of Amount Funded: \$116,254 (Funding to date: 03/01/16 – 02/29/20)
 Award Dates: 03/01/16 – 02/28/23

Principal Investigator: Lynn Martin, PhD
 Co-PI: Rays H.Y. Jiang, PhD
 Title: IMAGINE: Epigenetic potential and range expansion in the house sparrow Agency: National Science Foundation
 Grant/Contract #: IOS-2027040
 Research Purpose: We are leveraging the near-global distribution of the house sparrow (*Passer domesticus*) to learn how a successfully invasive species quickly adapt to new environments, with new food sources, new diseases and new behaviors
Total Amount Funded: USF share \$772,004
 Award Dates: 9/1/20-8/31/24

Principal Investigators: Rays H.Y. Jiang, PhD (primary) and Gloria Ferreira, PhD
 Co-Investigators: Said Sebti, PhD, Virginia Commonwealth University; Gary Reuther, PhD, H. Lee Moffitt Cancer Center and Research Institute
 Relative contribution made to the grant/contract:

Title: Targeting Heme Dependency in Leukemia
 Agency: Florida Department of Health
 Grant/Contract #: 9BC14
 Research Purpose: This project uses a cross disciplinary approach to uncover and target cancer metabolic vulnerabilities.
Total Amount Funded: \$801,000
Candidate Share of Amount Funded: \$301,912
 Award Dates: 06/04/19 – 03/31/22

Principal Investigator: John Adams, PhD
 Co-Investigators: Julian Rayner, PhD, Sanger Institute/Cambridge University; Rays H.Y. Jiang, PhD; Thomas Otto, PhD, University of Scotland
 Relative contribution made to the grant/contract:
 Title: Discovering the essential genome of Plasmodium falciparum
 Agency: National Institute of Allergy and Infectious Disease
 Grant/Contract #: R01AI130171
 Research Purpose: This project, will identify genes essential for blood-stage growth and sexual development to prioritize therapeutic targets and provide a large collection of genetic mutant to the research community.
Total Amount Funded: \$1,474,760 through 5/31/20; Anticipated Total Funding: \$2,775,060
Candidate Share of Amount Funded: \$262,606 Anticipated Total Funding
 Award Dates: 06/15/18 – 05/31/22

Principal Investigator: Down Cynthia, PhD
 Co-PI: Rays H.Y. Jiang, PhD
 Relative contribution made to the grant/contract:
 Title: Collaborative Research: Constraints of Biomass on immunity across terrestrial mammals
 Agency: National Science Foundation
 Grant/Contract #: 165668
 Research Purpose: Using comparative immunogenomics to understand evolutionary pattern of immune system. Particularly, this project focus on the relationship between body mass in a wide range of terrestrial animals and their innate immune systems.
Total Amount Funded: \$384,543 (Funding to date: 05/15/17 – 04/30/20)
Candidate Share of Amount Funded: \$16,684 (Funding to date: 05/15/17 – 04/30/21)
 Award Dates: 05/15/17 – 04/30/22

Principal Investigator: Taylor-Clark, Thomas, PhD
 Co-Investigator: Rays H.Y. Jiang, PhD
 Agency: NIH/NIDDK
 Grant/Contract #: U01DK116311
 Title: Ionic and Structural Mechanisms for Sensory Neuromodulation of the Esophagus
 Major Goals: We hypothesize that conduction in esophageal afferent nerve types is mediated not only by Nav1.7, but also other tetrodotoxin (TTX)-sensitive channels, possibly distinct between the neural crest- and placodes-derived C-fibers (Nav1.1/1.6 vs. Nav1.2/1.3). This will be investigated in guinea pig and mouse innervated esophagus preparation using pharmacological tools and shRNA knockdown, and in human esophageal nerves.
Total Award Amount (including Indirect Costs): \$785,947
 Award Dates: 09/01/17 – 08/30/21

Principal Investigators: John Adams, PhD (contact); Michael Ferdig, PhD, University of Notre Dame
 Co-Investigators: Rays H.Y. Jiang, PhD
 Relative contribution made to the grant/contract:
 Title: Chemogenomic Profiling of *Plasmodium falciparum* Drug Responses and resistance
 Agency: National Institute of Allergy and Infectious Disease
 Grant/Contract #: R01AI117017
 Research Purpose: The project proposes to use a chemogenomic systems approach to define critical pathways linked to ART-R, understand mechanisms of action of ART and other antimalarial partner drugs, and predict drug combination therapies with optimal synergistic anti-parasite activity to minimize the emergence of resistance.
Total Amount Funded: \$3,541,531
Candidate Share of Amount Funded: \$220,035
 Award Dates: 02/10/15 – 01/31/20

Principal Investigator: Rays H.Y. Jiang, PhD
 Co-Investigators: Gloria Ferreira, PhD, Dept Molecular Medicine, MCOM and Elizabeth Sagatys, MD, H. Lee Moffitt Cancer Center & Research Institute
 Relative contribution made to the grant/contract:
 Title: Single-cell genomics and erythropoiesis: Their first high-resolution red blood cell developmental map to address iron-deficiency anemia
 Agency: Women's Health Collaborative, USF Health
 Research Purpose: This study will provide the first high-resolution red blood cell developmental map in anemic patients and an essential tool to search for pathological targets for future therapeutics.
Total Amount Funded: \$15,000
Candidate Share of Amount Funded: \$15,000
 Award Dates: 07/01/18 – 06/30/20

Principal Investigator: Rays H.Y. Jiang, PhD
 Co-Investigators: Derek Wildman, PhD, College of Public Health and Xingmin Sun, PhD, Dept Molecular Medicine, MCOM
 Relative contribution made to the grant/contract:
 Title: Decoding gut microbiome-host interactions at single-cell resolution during *Clostridium difficile* infection
 Agency: College of Public Health Interdisciplinary Team Award
 Research Purpose: We will use the well-accepted mouse model of *C. difficile* infection to analyze both microbiome community makeup and host gut responses at single-cell resolutions.
Total Amount Funded: \$100,000
Candidate Share of Amount Funded: \$54,237
 Award Dates: 01/01/19 - 05/31/20

Principal Investigator: Dennis Kyle, PhD, University of Georgia
 Current Co-Investigators: Rays H.Y. Jiang, PhD
 Relative contribution made to the grant/contract:
 Title: 3D Microfluidic Human Liver Models for Malaria Drugs
 Agency: Bill and Melinda Gates Foundation

Grant/Contract #: OPP1023601

Research Purpose: Establish an in vitro model for liver stage malaria parasites, based on 3D mimetic liver sinusoid, optimized to evaluate new drugs that kill liver stage malarial parasites.

Total Amount Funded: \$4,192,100 (Award to USF: 11/10/10 – 12/29/16) (Award transferred to University of Georgia – no data on total funding amount)

Candidate Share of Amount Funded: \$12,317 (Award to USF: 02/01/15 – 12/29/16); \$707,254 (Subaward to USF 12/30/16 – 12/31/19)

Award Dates: 11/10/10 – 12/29/16 (primary award to USF); 12/30/16 – 12/31/19 (subaward to USF)

Principal Investigator: Rays H.Y. Jiang, PhD

Co-Investigators: Gloria Ferreira, PhD, Dept Molecular Medicine, MCOM; Said Sebti, PhD and Elizabeth Sagatys, MD, H. Lee Moffitt Cancer Center & Research Institute

Relative contribution made to the grant/contract:

Title: Tracking the Cellular Origin of Malignant Erythropoiesis Using Single-Cell Genomics

Agency: American Cancer Society/H. Lee Moffitt Cancer Center & Research Institute

Grant/Contract #: IRG-14-189-19

Research Purpose: The project goals are to track down the origin of malignant erythroid lineages and identify potential diagnostic and therapeutic targets, including those responsible for heme overdrive.

Total Amount Funded: \$30,000

Candidate Share of Amount Funded: \$30,000

Award Dates: 08/01/17 – 7/31/18

Principal Investigator: Rays H.Y. Jiang, PhD

Co-Investigators: John Adams, PhD; Gloria Ferreira, PhD; Kami Kim, MD; Thomas McDonald, MD; Lindsey Shaw, PhD; Xingmin Sun, PhD; Michael White, PhD

Relative contribution made to the grant/contract:

Title: Single-cell Omics – the New Frontier of Life Sciences at USF

Agency: USF Research and Innovation (Equipment Acquisition and Improvement Grant)

Research Purpose: Obtaining a 10x genomics chromium controller will be an important step to establish USF's genomics capacity. The USF single-cell omics initiative will enable diverse single-cell omics such as genomics, epigenomics, immunogenomics, de novo genome assembly, in different advanced research fields at USF.

Total Amount Funded: \$122,385 (Awarded as a resource to all USF researchers)

Candidate Share of Amount Funded:

Award Dates: 04/01 – 06/30/18

Principal Investigator: Rays H.Y. Jiang, PhD

Co-Investigators: N/A

Relative contribution made to the grant/contract:

Title: Exploring third generation sequencing technology for malaria genomics

Agency: College of Public Health, USF (New Researcher Award)

Research Purpose: We propose to conduct proof-of-concept experiment with 3rd generation sequencer to understand malaria parasite transcript unit; and to pioneer computational protocol development to transform future infectious disease research.

Total Amount Funded: \$10,000

Candidate Share of Amount Funded: \$10,000

Award Dates: 04/01/16 – 03/31/17

Other

Created thousands of original art work; and wrote original computational code to digitally process these art pieces.

Personal website www.raysjiang.org