

Tongjun Gu, Ph.D.

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Profile

I am interested in developing and applying artificial intelligence algorithms and statistical models for understanding the complex biological systems and human diseases. My training and experience encompass: 1) build pipelines to process large scale raw sequencing data (>1000 samples per project); 2) develop machine learning, deep learning algorithms, and statistical models to identify functional elements; 3) familiar with almost all types of omics data and many public databases; 4) deep knowledge on genetics, genomics, RNA and cancer biology, and Alzheimer's disease; 5) collaborate with researchers from a wide range of biology fields and train students from diverse backgrounds.

Current Appointment

09/2023 – present Associate Investigator
Leader, Bioinformatics Core
Versiti Blood Research Institute

Education

09/2004 – 06/2009 Ph.D. in Bioinformatics
Institute of Biophysics, Chinese Academy of Sciences, China

09/2000 – 06/2004 B.S. in Biomedical Engineering
Huazhong University of Science and Technology, China

Prior Appointments

07/2023 – 09/2023 Associate Scientist (Faculty)

01/2016 – 06/2023 Assistant Scientist (Faculty)
Bioinformatics Group
Interdisciplinary Center for Biotechnology Research (ICBR)
University of Florida

02/2022 – present Courtesy faculty
Department of Biostatistics
University of Florida

01/2022 – present Member, Center For Genetic Epidemiology and Bioinformatics (GeneBio)
University of Florida

01/2019 – present Member, Biostatistics and Computational Biology
Division of Quantitative Sciences
University of Florida Health Cancer Center (UFHCC)

09/2014 – 01/2016 Research Professional
Institute for Genomics and Systems Biology (IGSB)
Department of Human Genetics
University of Chicago

Work/Training Experiences

09/2023 – present Associate Investigator; Leader, Bioinformatics Core, **Versiti Blood Research Institute**, Milwaukee, WI, USA

- 1) Research Lab: Pioneering advanced machine learning, deep learning, and statistical techniques to pinpoint personalized and generalized biomarkers for risk prediction, early detection, personalized treatment, and prognosis of leukemia, lung cancer, and kidney cancer. Furthermore, investigating individual and joint molecular level mechanisms driving cancer development.
- 2) Bioinformatics Core: Organizing and leading the core to offer state-of-the-art bioinformatics support to the Versiti Blood Research Institute and beyond, driving the progress in both basic and clinical research.

01/2016 – 09/2023 Associate and Assistant Scientist, **The University of Florida**, Gainesville, FL, USA

- 1) Research work: developed multiple advanced **Artificial Intelligence** methods since 2019 for **a.** Subtyping cancer patients to assist personalized treatment by directly integrating five types of **multi-omics** data using an unsupervised deep learning (DL) algorithm (**T Gu*** et al., 2019); **b.** **miRNA** target prediction using a supervised hybrid DL algorithm (**T Gu*** et al., 2021); **c.** Learning the intrinsic features/mechanisms in **miRNA:target** interactions using multiple deep learning interpretation methods (**T Gu*** et al., 2021); **d.** Identifying cancer specific **RNA editing** sites using an advanced pipeline (**T Gu*** et al., 2019); and **e.** Identifying cancer specific **RNA editing** regulators using a two-step logistic regression model (**T Gu*** et al., 2020).
- 2) Long term support from: Dr. Jinying Zhao (since 2020; 50% working time) and Dr. Ji-Hyun Lee (since 2019; 5% or 10% working time) from College of Public Health and Health Professions and College of Medicine. Three notable works with Dr. Jinying Zhao: **a.** Performed by far the largest genome wide association analysis between **5hmC** and Alzheimer's Disease (AD) starting from raw sequencing datasets (> 1,000 human brain samples) and about 200K 5hmC peaks were identified and thousands of 5hmC peaks were significantly associated with AD; **b.** Performed by far the largest association analysis between **circRNA** and AD across multiple brain tissues; **c.** Performed by far the largest association analysis between **m6A** and AD. Manuscripts are under preparation.
- 3) **Primary job responsibility:** Independently perform advanced fee-based data analysis and training; Independently supply free support on grant application and experimental design. Served more than 90 customer-based projects, more than 20 customer-based grant applications, numerous consultations, and more than 70 investigators since 2016.

09/2013 – 01/2016 Postdoc and Research Professional, **The University of Chicago**, Chicago, IL, USA

Supervisor: Dr. Kevin White, James and Karen Frank Family Professor of Human Genetics and Medicine, and Founding Director of the Institute for Genomics and Systems Biology

- 1) Led the analysis of Chicago Pancreatic Cancer Initiative project with collaboration of clinical groups, sequencing core and experimental groups: built many pipelines for systematically discovering somatic point variants, copy number alterations and RNA editing sites, and for quantifying gene, isoform and small RNA expression from fresh tumors, FFPE and Patient-derived tumor xenografts (PDX).
- 2) Analyzed thousands of cancer sequencing and clinical data from US national (TCGA) and international (ICGC) cancer projects: developed multiple statistical models to identify cancer specific RNA editing sites, and to study the interactions between RNA editing, gene expression and miRNA expression.

01/2010 - 09/2013 Postdoctoral Associate, **The Jackson Laboratory**, Bar Harbor, ME, USA

Mentors: Drs. Robert Braun (Primary) (Professor, Vice President for Research), Gary Churchill (Professor, Director of Center for Genome Dynamics) and Matthew Hibbs (Assistant Professor)

- 1) Identified the general problems in the analysis of next generation sequencing (NGS) data for variants discovery; and developed pipelines that integrate multiple algorithms to solve each problem and identified confident RNA editing sites. This led to multiple opportunities for give oral presentations at professional conferences both for the scientific work and the methods/pipelines used for analyzing NGS data.

- 2) Developed a quantitative genetic analysis model to identify the polymorphisms that control RNA editing process; identified a novel allelic series in the enzyme of APOBEC1 that control C-to-U editing efficiency while A-to-I editing efficiency is controlled by local polymorphisms. It is the first study that demonstrates the two types of RNA editing have distinct regulation pathways in mouse.

09/2004 - 07/2009 Ph.D. candidate, **Institute of Biophysics, Chinese Academy of Sciences**, Beijing, China

04/2005 – 07/2008 Visiting Ph.D. candidate, **Institute of Computing Technology, Chinese Academy of Sciences**, Beijing, China

Mentors: Drs. James Q. Yin (Primary), Yi Zhao and Zhen'ge Qiu

- 1) Developed multiple algorithms/pipelines to identify and characterize novel small RNAs from RNA-seq and genomic data: improved dynamic programming algorithm, secondary structure prediction, motif discovery, conservation and evolution analysis etc.
- 2) Developed multiple approaches for exploring the function, evolution, and transcription of different kinds of small RNAs; and first reported that miRNAs can be transcribed along with other elements by a read-through mechanism.
- 3) Discovered an endogenous small RNA that can convert *Flk1*⁺ stem cells into hematopoietic stem cells, supplying a potential alternate source of hematopoietic stem cells for transplantation.

Fellowships/Grants/Funds

- 1) UF Research (MPI Gu, Xie & Lee) 10/15/20 – 10/14/21 a high-rated proposal and obtained free computing time in UF server for one year
Title: OR-DRD-AI2020: deep learning algorithms for miRNA target prediction in kidney cancer research
- 2) UF Open Access Publishing Fund (Gu) 2019 Funded
Paper published: T Gu, X Zhao. (2019) Integrating multi-platform genomic datasets for kidney renal clear cell carcinoma subtyping using stacked denoising autoencoders. *Scientific reports* 9 (1), 1-11.
- 3) The Jackson Lab Postdoc Fellowship application (Gu) 01/2012 - 01/2014 Funded (Top 2)
Title: Identification of regulators of RNA editing using QTL mapping in Diversity Outbred Mice
- 4) Travel fellowship Application for the RNA Sciences in Cell and Developmental Biology II, The 22nd CDB Meeting, RIKEN CDB, Japan (Gu) 2012 Funded
Title: Canonical A-to-I and C-to-U RNA Editing is Abundant in Multiple Mouse Tissues
- 5) Research Scholarship, Chinese Academy of Sciences, China. (Gu) 2004 – 2009 Funded

Awards

- 2017 Reviewers' Choice Abstracts from American Society of Human Genetics (ASHG) meeting
- 2012 – 2014 The Jackson Lab Postdoc Fellowship (top 2; including one travel fellowship per year)
- 2012 Travel fellowship from RIKEN CDB, Japan
- 2007 - 2008 Outstanding student of Chinese Academy of Sciences
- 2000 - 2003 Outstanding student of School of Life Science and Technology, Huazhong University of Science and Technology

Invited/Selected Oral Research Presentations

- 07/2022 Invited talk at 13th Annual Rush Alzheimer's Disease Center ROSMAP Investigator's Meeting: Brain 5-hydroxymethylcytosine (5hmC) and Alzheimer's Disease.

- 12/2021 Invited talk at Scientific Retreat for PREDICTION MODEL DEVELOPMENTS with Statistical, AI, and Mathematical Approaches, Division of Quantitative Sciences at the University of Florida Health Cancer Center: An interpretable deep learning-based approach for miRNA target prediction.
- 09/2021 AI Day for Cancer Research, UF Health Cancer Center. Selected poster talk and poster presentation: miTAR: an interpretable deep learning-based approach for predicting miRNA targets.
- 04/2021 Invited talk at UF Health Cancer Center: Deep Learning-an emerging Machine Learning algorithm in Artificial Intelligence-advances cancer study.
- 11/2018 2018 Cold Spring Harbor Lab (CSHL) meeting on Biological Data Science. Selected poster talk and poster presentation: Integrating multi-platform genomic datasets for cancer subtype discovery using denoising autoencoders.
- 10/2017 American Society of Human Genetics (ASHG) meeting 2017. The abstract was selected as Reviewers' Choice Abstracts (top 10%). Selected poster talk and poster presentation: Clinical relevance of non-coding A-to-I RNA editing in multiple human cancers.
- 07/2016 Intelligent Systems for Molecular Biology (ISMB) 2016, Invited oral presentation at Highlight Track; and poster talk and poster presentation at TransMed Special Interest Group Meetings: Genetic Architectures of Quantitative Variation in RNA Editing Pathways.
- 03/2013 Invited talk at Institute for Genomics & Systems Biology, University of Chicago
- 06/2012 RNA Sciences in Cell and Developmental Biology II, The 22nd CDB Meeting, RIKEN CDB, Japan. Invited talk and a poster presentation
- 05/2012 2nd generation sequencing, GTC. Invited talk
- 11/2011 2011 CSHL meeting on Genome Informatics. Invited talk
- 04/2011 Maine Biological and Medical Sciences Symposium. Invited talk
- 06/2011 Invited talk at The Jackson Laboratory

Poster Research Presentations

- 06/2022 Advances in Genome Biology and Technology (AGBT)
- 07/2021 ISMB (online)
- 10/2020 ASHG (online)
- 05/2020 2020 CSHL meeting on The Biology of Genomes (online)
- 10/2019 ASHG
- 05/2014 TCGA Third Annual Scientific Symposium, NIH
- 01/2013 2013 Gordon Research Conferences (GRC)
- 05/2013 2013 CSHL meeting on The Biology of Genomes
- 09/2011 JAX-MDIBL Joint Scientific Symposium
- 08/2011 Mammalian Gametogenesis & Embryogenesis, Gordon Research Conference

Editorships/Memberships/Journal Reviews

- 2018 – present Review Editor in Bioinformatics and Computational Biology, part of the journal(s) *Frontiers in Genetics*, *Plant Science* and *Bioengineering and Biotechnology*

- 2018 – present Reviewer for Briefings In Bioinformatics, Cell Reports Methods, Bioinformatics, International Journal of Molecular Sciences, IEEE, PLOS Genetics, JCO Clinical Cancer Informatics, Cellular and Molecular Life Sciences, Scientific Reports, Frontiers, Current Bioinformatics...
- 2017 – 2022 Member of the American Society of Human Genetics
- 2010-2011/2016-2022 Member of the International Society for Computational Biology

Services at VRBI and UF

- 2023 Member of the faculty search committee of the Stem Cell and Hematopoiesis Program at VBRI
- 2023 Serve as the reviewer of AI Supplement Grant applications at UF
- 2022 Serve as the reviewer of AI Supplement Grant applications at UF
- 2022 Serve as the reviewer of a Special Pilot Grant on utilizing Oxford Nanopore Technology at UF
- 2022 Member of the search committee for the director of NextGen DNA Sequencing core at UF
- 2020 – present Member of UF AI Collaborative
- 2020 – present Member of UFHCC AI Working Group
- 2020 Member of UF Health Cancer Center AI initiative committee: draft the proposal about the application of AI on genomics/genetics research for UF Health Cancer Center AI initiative committee, and help the committee determine the direction of AI development in UFHCC

Pedagogy

- 2016-2021 Performed numerous trainings to a small group of researchers from undergraduate students, graduate students, Postdocs to junior faculties for NGS data analysis or developing pipelines or statistical analysis.
- 2020 Taught for the short course of Bioinformatics 101: about 50 students with/without computational background; include three classes of hands-on practice on High Performance Computing Cluster.
- 2014 UChicago two-day program to visit Chicago-Area Institutions (teaching focus): classroom visit; conversation with faculty; roundtable. Visited Dominican University, Saint Xavier, Lake Forest College, and Northwestern University.
- 05/2013 Introduction to Biology, Teaching practice with mock university students from The Jackson Laboratory.
- 03/2013 Introduction to RNA-seq Data and Analysis Methods, Teaching practice with mock university students from University of Maine.
- 03/2008 - 06/2008 Independently mentored three senior undergraduate students for graduation thesis research.
- 03/2006 - 06/2006 Independently mentored a senior undergraduate student for graduation thesis research.

Selected Publications (*corresponding author)

H Tao, D Chen, C Yang, DT Nguyen, R Liu, T Liu, AY Hou, NA Petit, M Abbas, CV Roemeling, L Jin, **T Gu**, A Pepe, DI Pedro, M Gbadamosi, A Chakraborty, S Yu, G Abboud, H Mendez-Gomez, A Karachi, F Weidert, D Jin, K Long-James, EK Molchan, PC Castillo, JA Ligon, A Ghiaseddin, EJ Sayour, M Rahman, LP Deleyrolle, BYS Kim, DA Mitchell, WG Sawyer, J Huang. Disrupting the LAIR1-FXIIIa-collagen Loop by LAIR1 blockade enhances antitumor immunity. Submitted.

C Yang[#], V Trivedi[#], K Dyson, **T Gu**, KM Candelario, DA Mitchell. Identification of tumor rejection antigens and the immunologic landscape of medulloblastoma. Submitted.

C Gobin, S Inkabi, CC Lattimore, **T Gu**, JN Menefee, M Rodriguez, H Kates, C Fields, T Bian, C Xing, N Silver, C Yates, R Renne, M Xie, K Fredenburg. Investigating miR-9 as mediator in laryngeal cancer health disparities. Accepted.

PM Duarte, BC V Gurgel, J Sardenberg, R Hauer, **T Gu**, TS Miranda, I Aukhil. Whole-transcriptome sequencing identifies important genes and pathways associated with type 2 diabetes-related periodontitis. Submitted.

H Ghayee, Y Xu, H Hatch, R Brockway, AS Multani, **T Gu**, W Bollag, A Turcu, W Rainey, J Rege, K Namba, VJ Bhagwandin, F Nwakiaku, V Stastny, A Gazdar, J Shay, R Auchus, S Tevosian. (2022) Development of Human Adrenocortical Adenoma (HAA1) cell line from Zona Reticularis. *Int. J. Mol. Sci.* 24(1), 584.

H Palma-Gudiel, L Yu, Z Huo, J Yang, Y Wang, **T Gu**, C Gao, PL De Jager, P Jin, DA Bennett, J Zhao. (2022) Fine-mapping and replication of EWAS loci harboring putative epigenetic alterations associated with AD neuropathology in a large collection of human brain tissue samples. *Alzheimer's & Dementia*, <https://doi.org/10.1002/alz.12761>.

Y Chang, Y Ahlawat, **T Gu**, A Sarkhosh, T Liu. (2022) Transcriptional profiling of two muscadine grape cultivars 'Carlos' and 'Noble' to reveal new genes, gene regulatory networks, and pathways that involved in grape berry ripening. *Frontier in Plant Science*, <https://doi.org/10.3389/fpls.2022.949383>.

T Gu*, M Xie, WB Barbazuk, JH Lee*. (2021) Biological features between miRNA and their targets are unveiled from deep learning models. *Scientific Reports*, 11 (1), 1-10.

T Gu*, X Zhao, WB Barbazuk, JH Lee. (2021) miTAR: a hybrid deep learning-based approach for predicting miRNA targets. *BMC bioinformatics*, 22 (1), 1-16.

K Yu, M Rodriguez, Z Paul, E Gordon, **T Gu**, K Rice, EW Triplett, M Keller-Wood, CE Wood. (2021) Transfer of oral bacteria to the fetus during late gestation. *Scientific Reports*, 11 (1), 1-13.

CJ Fields, Lu Li, NM Hiers, T Li, P Sheng, T Huda, J Shan, L Gay, **T Gu**, J Bian, MS Kilberg, R Renne, M Xie. (2021) Sequencing of Argonaute-bound microRNA/mRNA hybrids reveals regulation of the unfolded protein response by microRNA-320a. *PLoS Genetics*, 17 (12), e1009934.

LA Elsadek, JH Matthews, S Nishimura, T Nakatani, A Ito, **T Gu**, D Luo, LA Salvador-Reyes, VJ Paul, H Kakeya, H Luesch. (2021) Genomic and targeted approaches unveil the cell membrane as a major target of the antifungal cytotoxin amantelide A. *ChemBioChem*, 22 (10), 1790-1799.

T Gu*, AQ Fu, MJ Bolt, X Zhao. (2020) Systematic identification of A-to-I editing associated regulators from multiple human cancers. *Computers in Biology and Medicine*, 119, 103690.

T Gu*, X Zhao*. (2019) Integrating multi-platform genomic datasets for kidney renal clear cell carcinoma subtyping using stacked denoising autoencoders. *Scientific reports*, 9 (1), 1-11.

T Gu*, AQ Fu, MJ Bolt, KP White. (2019) Clinical Relevance of Noncoding Adenosine-to-Inosine RNA Editing in Multiple Human Cancers. *JCO clinical cancer informatics*, 3, 1-8.

LR Reznikov, YSJ Liao, **T Gu**, KM Davis, SP Kuan, KR Atanasova, JS Dadural, EN Collins, MV Guevara, K Vogt. (2019) Sex-specific airway hyperreactivity and sex-specific transcriptome remodeling in neonatal piglets challenged with intra-airway acid. *American Journal of Physiology-Lung Cellular and Molecular Physiology*, 316 (1), L131–L143.

A Riva, JL Boatwright, **T Gu**, F Yu, WB Barbazuk. (2019) Streamlining DNA Sequencing and Bioinformatics Analysis Using Software Containers. *Journal of Biomolecular Techniques: JBT*, 30 (Suppl), S38.

- P Sheng, C Fields, K Aadland, T Wei, O Kolaczkowski, **T Gu**, B Kolaczkowski, M Xie. (2018) Dicer cleaves 5'-extended microRNA precursors originating from RNA Polymerase II transcription start sites. *Nucleic acids research*, 46 (11), 5737-5752.
- L Reznikov, Y Liao, K Davis, **T Gu**, S Kuan, K Atanasova, J Dadural, E Collins, M Guevara, K Vogt. (2018) Airway-nervous system mediators for airway protection. *Pediatric Pulmonology*, 53, 200-200.
- SJ Ahn, **T Gu**, J Koh, KC Rice. (2017) Remodeling of the *Streptococcus mutans* proteome in response to LrgAB and external stresses. *Scientific Reports*, 7 (1), 1-13.
- C Han, MJ Kim, D Ding, HJ Park, K White, L Walker, **T Gu**, M Tanokura, T Yamasoba, P Linser, R Salvi, S Someya. (2017) GSR is not essential for the maintenance of antioxidant defenses in mouse cochlea: Possible role of the thioredoxin system as a functional backup for GSR. *PLoS One*, 12(7), e0180817.
- Y Qi, R Goel, AS Mandloi, R Vohra, G Walter, YF Joshua, **T Gu**, MJ Katovich, JM Aranda, M Maden, MK Raizada, CJ Pepine. (2017) Spiny mouse is protected from ischemia induced cardiac injury: leading role of microRNAs. *The FASEB Journal*, 31 (1), 721.4-721.4.
- KC Rice, ME Turner, OV Carney, **T Gu**, SJ Ahn. (2017) Modification of the *Streptococcus mutans* transcriptome by LrgAB and environmental stressor. *Microbial Genomics*, 3 (2), e000104.
- IR Calvo, A Akki, A Ugolkov, MM Buschmann, SM Sparrow, T Barry, M Eber, **T Gu**, SQ Zhang, H Kindler, W Dale, K Roggin, AP Mazar, KP White, CR Weber. (2016) Organoids and patient-derived tumor xenograft of pancreatic adenocarcinoma share morphological and genetic feature with the primary tumor. *Cancer Research*, 76 (14_Supplement), 4272-4272.
- T Gu**, DM Gatti, A Srivastava, EM Snyder, N Raghupathy, P Simecek, KL Svenson, I Dotu, JH Chuang, MP Keller, AD Attie, RE Braun, GA Churchill. (2016) Genetic Architectures of Quantitative Variation in RNA Editing Pathways. *Genetics*, 202 (2), 787-798.
- T Gu**, FW Buaas, AK Simons, CL Ackert-Bicknell, RE Braun, MA Hibbs. (2012) Canonical A-to-I and C-to-U RNA Editing Is Enriched at 3'UTRs and microRNA Target Sites in Multiple Mouse Tissues. *PLoS ONE*, 7 (3).
- A Aljakna, S Choi, H Savage, R Hageman Blair, **T Gu**, KL Svenson, GA Churchill, M Hibbs, R Korstanje. (2012) Pla2g12b and Hpn Are Genes Identified by Mouse ENU Mutagenesis That Affect HDL Cholesterol. *PLoS ONE*, 7 (3), e33720.
- AR Greenlee, MS Shiao, E Snyder, FW Buaas, **T Gu**, TM Stearns, M Sharma, EP Murchison, GC Puente, RE Braun. (2012) Deregulated Sex Chromosome Gene Expression with Male Germ Cell-Specific Loss of Dicer1. *PLoS ONE*, 7 (10), e46359.
- TJ Gu**, X Yi, XW Zhao, Y Zhao, JQ Yin. (2009) Alu-directed transcriptional regulation of some novel miRNAs. *BMC Genomics*, 10 (1), 1-13.
- T Gu**, J Yin, Y Xu, ZH Dai, Z Qiu, S Feng, X Yi, L Jiang, H Zhang. (2008) A novel class of endogenous shRNAs in human cells. *Nature Proceedings*, 1-1.
- D Xu, H Li, **T Gu**. (2008) Shape Representation and Invariant Description of Protein Tertiary Structure in Applications to Shape Retrieval and Classification. *Geometric Modeling and Processing. Lecture Notes in Computer Science*, 4975, 556-562.
- D Xu, H Li, **T Gu**. (2007) Protein Structure Superposition by Curve Moment Invariants and Iterative Closest Point. 1st International Conference on Bioinformatics and Biomedical Engineering (ICBBE'07), 1, 25-28.

D Xu, H Li, T Gu. (2007) Common Substructure Extraction of Proteins by Geometric Invariants. 10th International Conference on Computer-Aided Design and Computer Graphics (CAD/Graphics'07), 86-91.

Selected Acknowledged Publications

N Khodayari, R Oshins, AM Aranyos, S Duarte, S Mostofizadeh, Y Lu, M Brantly. Comprehensive characterization of hepatic inflammatory changes in a mouse model of alpha-1 antitrypsin deficiency. Submitted.

AL Paul, SM Elardo, R Ferl. (2022) Plants grown in Apollo lunar regolith present stress-associated transcriptomes that inform prospects for lunar exploration. *Communications biology*, 5 (1), 1-9.

L David, J Kang, J Nicklay, C Dufresne, S Chen. (2021) Identification of DIR1-Dependant Cellular Responses in Guard Cell Systemic Acquired Resistance. *Frontiers in Molecular Biosciences* 8,746523.

N Khodayari, RL Wang, R Oshins, Y Lu, M Millett, AM Aranyos, S Mostofizadeh, Y Scindia, TO Flagg, M Brantly. (2021) The mechanism of mitochondrial injury in alpha-1 antitrypsin deficiency mediated liver disease. *International Journal of Molecular Sciences*, 22 (24), 13255.

N Khodayari, R Oshins, LS Holliday, V Clark, Q Xiao, G Marek, B Mehrad, M Brantly. (2020) Alpha-1 antitrypsin deficient individuals have circulating extracellular vesicles with profibrogenic cargo. *Cell Communication and Signaling*, 18, 140.

T Yang, H Li, AC Oliveira, R Goel, EM Richards, CJ Pepine, MK Raizada. (2020) Transcriptomic signature of gut microbiome-contacting cells in colon of spontaneously hypertensive rats. *Physiol Genomics*, 52(3):121-132.

Supported Grant Applications

2023

- 1) Title: A rapid CRISPR-based self-testing platform for early detection of HIV
PI: Piyush Jain from University of Florida (UF)
Role: Key personnel

2022

- 2) Title: Florida Consortium of Small Cell Lung Cancer (SCLC)
PI: Mehdi Mirsaeidi and Dejana Braithwaite (co-PI) from UF
Role: Proposal writing and key personnel

2021

- 3) Title: A rapid CRISPR-based self-testing platform for early detection of HIV
PI: Piyush Jain from UF
Role: Key personnel
- 4) Title: Development of a CRISPR Chain Reaction for an equipment-free detection of SARS-CoV-2 RNA
PI: Piyush Jain from UF
Role: Key personnel
- 5) Title: Discovery and engineering of CRISPR/Cas systems
PI: Piyush Jain from UF
Role: Key personnel
- 6) Title: Detecting lethal prostate cancer at an early stage in the high-risk population using CRISPR-based detection system in the urine
PI: Piyush Jain from UF
Role: Key personnel

2020

- 7) Title: Rapid detection of Hepatitis C virus using CRISPR/Cas

PI: Piyush Jain from UF
Role: Key personnel

- 8) Title: Early detection of breast cancer in the urine using CRISPR
PI: Piyush Jain from UF
Role: Key personnel
- 9) Title: Muscle and Bone Growth in Aging
PI: Joshua Yarrow from UF
Role: Key personnel
- 10) Title: Site-specific integration of DNA sequences using Cas-integrase fusion proteins
PI: Piyush Jain from UF
Role: Key personnel

2019

- 11) Title: Interrogating the role of chemical exposures and the microbiome on preterm birth
PI: John Bowden from UF
Role: Key personnel and proposal writing
- 12) Title: Development of Genomic Breeding Tools through Transcriptome Analysis
PI: Huiping Yang from UF
Role: consultations and proposal writing

2018

- 13) Title: Probing the effect of simulated microgravity on the pathogenic potential of cariogenic *Streptococcus mutans*
PI: Kelly Rice from UF
Role: Key personnel
- 14) Title: Genes Editing in Human Cancers
PI: K.C. Balaji from UF
Role: Key personnel
- 15) Title: Soluble OSCAR Isoforms and Endothelial Function
PI: Ikramuddin Aukhil from UF
Role: Key personnel
- 16) Title: Investigating mRNAs Targets of Differentially Expressed microRNAs from Black Laryngeal Cancers
PI: Kristianna Fredenburg from UF
Role: Key personnel
- 17) Title: Novel DNA modifications from Pacbio platform
PI: Wioletta Czaja from University of Georgia
Role: consultations, and prepare preliminary data

2017

- 18) Title: Pancreas Islets heterogeneity discovery from RNA-seq
PI: Martha Campbell-Thompson from UF
Role: consultations, and proposal writing
- 19) Title: Probing the druggable genome in African-American patients with pancreatic cancer
PI: Chris Vulpe from UF
Role: consultations, and proposal writing
- 20) Title: Delineating the effect of simulated microgravity on host-pathogen interactions
PI: Kelly Rice from UF
Role: Key personnel

- 21) Title: Periodontal bacterial Colonization, Proliferation and Transcriptional Profiling
PI: Kesavalu Lakshmyya from UF
Role: consultations and proposal writing
- 22) Title: Systems biology assessment of marijuana use on immunity in HIV-infected youth
PI: Maureen Goodenow from UF
Role: consultations, and proposal writing
- 23) Title: The marine pinfish, *Lagodon rhomboides*, as a novel model species for understanding developmental neurogenesis in the retina
PI: Scott M. Taylor from University of West Florida
Role: Key personnel

2016

- 24) Title: Transcriptome Analyses of Two Hard Clam Species for Genomic Tool Revealing for Clam Breeding and Aquaculture
PI: Huiping Yang from UF
Role: Key personnel
- 25) Title: Understanding the molecular basis of TRIM29 mammary tumor suppression
PI: Kevin D. Brown from UF
Role: consultations, proposal writing, and prepare preliminary data

Professional Courses/Meetings

2021	RECOMB 2021 and two Satellite meetings: Computational Methods in Genetics; and RECOMN-Seq
04/2020; 06/2020	American Association for Cancer Research meeting, online
2020	Joint Statistical Meetings
08/2013	22 nd Annual Short Course on Experimental Models of Human Cancer, The Jackson Laboratory, Bar Harbor, ME
05/2013	Short Course of The Whole Scientists, The Jackson Laboratory, Bar Harbor, ME
08/2011	Short Course on Genetics, The Jackson Laboratory, Bar Harbor, ME
09/2010; 06/2011	Grant Writing Short Course, The Jackson Laboratory, Bar Harbor, ME
28/10-04/11, 2012	Short Course on Systems Genetics, The Jackson Laboratory, Bar Harbor, ME
07/2010	51 st Annual Short Course on Medical and Experimental Mammalian Genetics, The Jackson Laboratory and Johns Hopkins University