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, particularly Acute Myeloid Leukemia. 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 Director, Bioinformatics Core Versiti Blood Research Institute
09/2024 – present	Adjunct Assistant Professor Data Science Institute Medical College of Wisconsin
02/2022 – present	Courtesy faculty Department of Biostatistics University of Florida

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
01/2016 – 06/2023	Assistant Scientist Bioinformatics Group Interdisciplinary Center for Biotechnology Research (ICBR) University of Florida
01/2022 – present	Member, Center For Genetic Epidemiology and Bioinformatics (GeneBio) University of Florida
01/2019 – 09/2023	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; Director, 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 Alzhermer'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.

Funded Grants/ Fellowships as PI or PPG Core Lead

1) American Cancer Society – MCW Cancer Center Institutional Research Grant (ACS-IRG) Pilot Awards (Gu) 04/01/2025 – 03/31/2026
   Title: Enhancing Acute Myeloid Leukemia Subtyping through Integrated Epigenetic Analysis
2) 2025 Pilot Award to Advance Translational Science from Clinical and Translational Science Institute of Southeast Wisconsin (Gu) 08/01/2025 – 07/31/2026
   Title: Enhancing Precision Detection of Cancer-Specific and Cell-Type-Specific RNA Editing Sites and DNA Mutations via a Novel Computational Pipeline from Single-Cell RNA Sequencing Data
3) NIH/NHLBI (PPG) (P01HL151333) (Gu: Core B Lead; PI: Hoffmeister) 03/01/2025 – 12/2025
   Title: Molecular and Clinical Glycobiology of the Bone Marrow Environment
4) 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
5) UF Open Access Publishing Fund (Gu) 2019
   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.
6) The Jackson Lab Postdoc Fellowship application (Gu) 01/2012 - 01/2014 Top 2
   Title: Identification of regulators of RNA editing using QTL mapping in Diversity Outbred Mice
7) Travel fellowship Application for the RNA Sciences in Cell and Developmental Biology II, The 22nd CDB Meeting, RIKEN CDB, Japan (Gu) 2012
   Title: Canonical A-to-I and C-to-U RNA Editing is Abundant in Multiple Mouse Tissues

8) Research Scholarship, Chinese Academy of Sciences, China. (Gu) 2004 – 2009

Submitted LOI/Full Grant Applications as PI

1) Title: Enhancing Acute Myeloid Leukemia Subtyping through Integrated Epigenetic Analysis
PI: Tongjun Gu
Submitted time: March 16, 2025
Funding agency: National Cancer Institute (R21)

2) Title: Molecular and Clinical Glycobiology of the Bone Marrow Environment
Core B Lead: Tongjun Gu (PI: Karin Hoffmeister)
Submitted time: Feb. 4, 2025
Funding agency: NIH/NHLBI

3) Title: Global Profiling and Unveiling the Essential Role of Single-Cell RNA Editing in Pediatric Acute Myeloid Leukemia and Pediatric Acute Lymphoblastic Leukemia
PI: Tongjun Gu
Submitted time: Feb. 16, 2024 (not funded)
Funding agency: CURE

4) Title: Global Profiling and Unveiling the Essential Role of Single-Cell RNA Editing in Acute Myeloid Leukemia: Insight from Diagnosis through Post-Treatment Phases
PI: Tongjun Gu
Submitted time: Feb. 15, 2024 (not funded)
Funding agency: Leukemia Research Foundation

5) Title: Investigating Ensemble Effects of Multi-Epigenetic Profiles in Acute Myeloid Leukemia Through Advanced Deep Learning Models
PI: Tongjun Gu
Submitted time: Aug. 26th, 2024 (not funded)
Funding agency: Department of Defense

Funded/Submitted grants as a Co-Investigator or Computational Biologist

1) Title: Mechanisms of Lung Endothelial Cell Homeostasis: The role of Rap1B
PI: Chrzanowska
Funding agency: NIH/NHLBI (R01)
%efforts: 7 (01/2026 -12/2029) (funded); Computational Biologist

2) Title: Targeting chromatin deregulation in CEBPA mutant acute myeloid leukemia
PI: Pulikkan
Funding agency: NIH/NCI (R01)
%efforts: 5 (04/2025 - 03/2030) (funded); Computational Biologist

3) Title: Immunologic and Molecular Determinants of Myeloid Sarcoma
PI: Drobyski and Rao (MPI)
%efforts: 1 (01/2025 – 12/2025) (funded); Co-I

4) Title: B cell IgD low (BDL) B cell biology and therapeutic potential
PI: Dittel
%efforts: 7 (submitted on 02/2025); Co-I

5) Title: Genetic and Epigenetic Mechanisms of Blood Pressure Regulation
PI: Rao (PPG Project)
%effort: 5 (submitted on 01/2025); Co-I in Project 1

6) Title: Mapping public and private B cell receptor clonotypes in activated memory B cells in multiple sclerosis
PI: Dittel

%efforts: 5 (submitted in 02/2025); Co-I

7) Title: Artificial Intelligence Approaches to Engineer Neoantigen-Targeted CAR-T Therapies with de novo Designed Protein Binders
   PI: Sun
   %efforts: 5 (submitted in 03/2025); Co-I

8) Title: Computational Identification and Validation of Small Molecule Drugs Targeting Integrins in Cardiovascular Diseases
   PI: Heng Zhang
   %efforts: 5 (submitted in 04/2025); Co-I

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

04/2025	Invited talk at VBRI seminar: single cell RNA editing in leukemia.
02/2025	Invited talk at VBRI seminar: Introduction to Artificial Intelligence and Its Applications in Biological Research.
12/2024	Lecture presentation at MCW Advanced Immunology class: Bioinformatics and Resources
10/2024	Presentation at Immunology Research Roundtable: VBRI Bioinformatics Core
05/2023	Invited talk at VBRI annual retreat: Deep Learning---an advanced machine learning algorithm in Artificial Intelligence--- advances biological research.
02/2023	Invited talks at The University of Texas at San Antonio: Deep Learning advances omics data analysis for precision medicine.
07/2022	Invited talk at 13th Annual Rush Alzheimer's Disease Center ROSMAP Investigator's Meeting: Brain 5-hydroxymethylcytosine (5hmC) and Alzhermer'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 Haematologica; Blood Vessels, Thrombosis & Hemostasis; 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

2025	Member of the endowed chair search committee of the Hematopoiesis and Immunology Program at VBRI Co-chair, Director of Shared Resources Search Committee at VBRI Co-chair, Hematopoiesis Program Annual Symposium

2024	Member of the endowed chair search committee of the Stem Cell and Hematopoiesis Program at VBRI
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
	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

Mentoring/Pedagogy

2025	Lecturer at Advanced Immunology class at MCW
2024	PhD student, Chris Hansen’s Dissertation committee member
	PhD student, Kimani Njoya’s thesis committee member
01/2024	NRMN Entering Mentoring Training, Faculty and Staff Mentoring Dialogues.
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; [a]Second senior author; [#]equal contribution; Full List (34; not include submitted or accepted): https://www.ncbi.nlm.nih.gov/myncbi/1pYrDcULXZ2Ai/bibliography/public/)

HG Zhao, KC Johnson, AD Pomicter, B Bates, B Bateman, T Haferlach, **T Gu**, N Cruz-Rodriguez, J Ahmann, D Yan, GS Lee, W Zhu, J Bishop, SJ Odelberg, MW Deininger. Submitted.

A Roisman, L Rivadeneyra, L Conroy, MM Lee-Sundlov, N Weich, S Glabere, S Zheng, AJ Veltri, JT Lau, **T Gu**, H Weiler, RC Sun, K Hoffmeister. Complex N-glycans regulate megakaryocyte-biased hematopoietic 1 stem cell subsets. Submitted.

T Wong, K Rosenbalm, M Nemeth, **T Gu**, K Hoffmeister, JTY Lau. Platelet glycan profiles from MDS patients are distinct from healthy individuals. Submitted.

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.

F Yu, S Zheng, C Yu, S Gao, Z Shen, R Nar, S Huang, L Wu, **T Gu**[a], Z Qian. (2025) KRAS Mutants Confer Platinum Resistance by Hijacking ALKBH5 Post-translational Modifications–mediated DNA Damage Response in Lung Cancer. **The Journal of Clinical Investigation**, 135 (6).

J Zhao, **T Gu**[#], C Gao[#], G Miao[#], H Palma-Gudiel, L Yu, J Yang, Y Wang, Y Li, J Lim, R Li, B Yao, H Wu, JA Schneider, F Grodstein, PL. De Jager, P Jin, DA Bennett. (2025) Brain 5-hydroxymethylcytosine alterations are associated with Alzheimer's disease neuropathology. **Nature Communications**, 16(1), 2842.

W Zhu, Y Zheng, M Yu, N Witman, L Zhou, J Wei, Y Zhang, P Topchyan, C Nguyen, R Janecke, A Padmanabhan, LB Kreuziger, GC White, P Hari, **T Gu**, AT Fields, L Kornblith, RH Aster, J Zhu, W Cui, SM Jobe, MB Graham, D Wang, D Wang, R Wen. (2024) Prothrombotic Antibodies Targeting the Spike Protein's Receptor-Binding Domain in Severe COVID-19. **Blood**, 145(6):635-647.

C Yang[#], V Trivedi[#], K Dyson, **T Gu**, KM Candelario, DA Mitchell. (2024) Identification of tumor rejection antigens and the immunologic landscape of medulloblastoma. **Genome Med**., 16, 102.

N Mohammad, R Oshins, **T Gu**, V Clark, J Lascano, N Assarzadegan, G Marek, M Brantly, and N Khodayari. (2024) Transcriptomics reveal an association between lung inflammation and liver disease in patients with alpha-1 antitrypsin deficiency. Journal of Clinical and Translational Hepatology, 12 (10), 845.

PM Duarte, BC V Gurgel, TS Miranda, J Sardenberg, **T Gu**, I Aukhil. (2024) Distinctive genes and signaling pathways associated with type 2 diabetes-related periodontitis: Preliminary study. Plos one, 19 (1), e0296925.

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. (2023) Investigating miR-9 as mediator in laryngeal cancer health disparities. Frontiers in Oncology, 13, 1096882.

H Palma-Gudiel, L Yu, Z Huo, J Yang, Y Wang, **T Gu**, C Gao, PL De Jager, P Jin, DA Bennett, J Zhao. (2023) 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.

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.

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. (2022) Comprehensive characterization of hepatic inflammatory changes in a mouse model of alpha-1 antitrypsin deficiency. J Physiol Gastrointest Liver Physiol, 323(6):G594-G608.

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.

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Supported Grant/Fellowship Applications

2025

1) Title: Understanding cellular variation in fetal hemoglobin distribution

PI: Phil Doerfler
Role: Consultant

2) Title: Assessing the functional and molecular glycoregulatory role of B4galt1 in hematopoietic stem cell function and its contribution to the pathogenesis of myeloid malignancies
PI: Alejandro Roisman
Role: Mentor support on Bioinformatics
3) Title: MS4A3 as a Tumor Promoter and Therapy Target in Chronic Myelomonocytic Leukemia
PI: Micheal Deininger
Role: Consultant
4) Title: Platelet dependent thrombosis in severe flu
PI: Prithu Sundd
Role: Support on bioinformatics
5) Role of neuronal chemokine receptors in spinal cord injury
PI: Antje Kroner-Milsch
Role: Support on bioinformatics
6) Title: Thermo Orbitrap Ascend Tribrid Mass Spectrometer system for a multidimensional proteomics workflow
PI: Kazuhiro Aoki
Role: Support on bioinformatics

2024

1) Title: Assessing the functional and molecular glycoregulatory role of B4galt1 in hematopoietic stem cell function and its contribution to the pathogenesis of myeloid malignancies
PI: Alejandro Roisman
Role: Mentor support on Bioinformatics
2) Title: Targeting SF3b complex in Acute Myeloid Leukemia with N-terminal CEBPA mutations
PI: John A. Pulikkan
Role: Support on bioinformatics
3) Title: Circulating Extracellular Vesicles Promote IFN-Dependent Lung Injury in Sickle Cell Disease
PI: Ayyanar Sivanantham
Role: Consultant on bioinformatics
4) Title: Therapeutic targeting of an oncogenic translational program in AML
PI: John A. Pulikkan
Role: Support on bioinformatics
5) Title: Platelet dependent mechanism of cigarette smoking induced severe flu
PI: Prithu Sundd
Role: Support on bioinformatics
6) Title: Targeting chromatin deregulation in CEBPA mutant acute myeloid leukemia
PI: John A. Pulikkan
Role: Support on bioinformatics
7) Title: Research Supplements to Promote Diversity in Health-Related Research
PI: Karin Hoffmeister
Role: Support on bioinformatics
8) Title: Cohesin Haploinsufficiency Disrupts Polycomb Targeting in Hematopoiesis and Myeloid Leukemogenesis
PI: Josiah Murray
Role: Mentor support on Bioinformatics
9) Title: Cohesin’s role in the epigenetic identity of hematopoietic stem cells

PI: Josiah Murray
Role: Mentor support on Bioinformatics

10) Title: Targeting advanced chronic myeloid leukemia with a potent and selective BCR::ABL1 degrader
PI: Nataly Cruz Rodriguez
Role: Mentor support on Bioinformatics

11) Title: Endothelial glycans in bone marrow vasculature and hematopoiesis
PI: Karin Hoffmeister
Role: Support on Bioinformatics

2023

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

13) Title: Targeting Chronic Myeloid Leukemia with Potent and Specific BCR::ABL1 Degraders
Project Period
PI: Michael W. Deininger
Role: Support on bioinformatics

14) Title: Is IL17A a driver of disease progression in chronic myelomonocytic leukemia?
Project Period
PI: Michael W. Deininger
Role: Support on bioinformatics

2022

15) 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

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

17) 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

18) Title: Discovery and engineering of CRISPR/Cas systems
PI: Piyush Jain from UF
Role: Key personnel

19) 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

20) Title: Rapid detection of Hepatitis C virus using CRISPR/Cas
PI: Piyush Jain from UF
Role: Key personnel

21) Title: Early detection of breast cancer in the urine using CRISPR
PI: Piyush Jain from UF
Role: Key personnel

22) Title: Muscle and Bone Growth in Aging
PI: Joshua Yarrow from UF

Role: Key personnel

23) Title: Site-specific integration of DNA sequences using Cas-integrase fusion proteins
PI: Piyush Jain from UF
Role: Key personnel

2019

24) Title: Interrogating the role of chemical exposures and the microbiome on preterm birth
PI: John Bowden from UF
Role: Key personnel and proposal writing

25) Title: Development of Genomic Breeding Tools through Transcriptome Analysis
PI: Huiping Yang from UF
Role: consultations and proposal writing

2018

26) Title: Probing the effect of simulated microgravity on the pathogenic potential of cariogenic Streptococcus mutans
PI: Kelly Rice from UF
Role: Key personnel

27) Title: Genes Editing in Human Cancers
PI: K.C. Balaji from UF
Role: Key personnel

28) Title: Soluble OSCAR Isoforms and Endothelial Function
PI: Ikramuddin Aukhil from UF
Role: Key personnel

29) Title: Investigating mRNAs Targets of Differentially Expressed microRNAs from Black Laryngeal Cancers
PI: Kristianna Fredenburg from UF
Role: Key personnel

30) Title: Novel DNA modifications from Pacbio platform
PI: Wioletta Czaja from University of Georgia
Role: consultations, and prepare preliminary data

2017

31) Title: Pancreas Islets heterogeneity discovery from RNA-seq
PI: Martha Campbell-Thompson from UF
Role: consultations, and proposal writing

32) Title: Probing the druggable genome in African-American patients with pancreatic cancer
PI: Chris Vulpe from UF
Role: consultations, and proposal writing

33) Title: Delineating the effect of simulated microgravity on host-pathogen interactions
PI: Kelly Rice from UF
Role: Key personnel

34) Title: Periodontal bacterial Colonization, Proliferation and Transcriptional Profiling
PI: Kesavalu Lakshmyya from UF
Role: consultations and proposal writing

35) Title: Systems biology assessment of marijuana use on immunity in HIV-infected youth
PI: Maureen Goodenow from UF
Role: consultations, and proposal writing

36) 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

37) 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

38) 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

10/24	21st annual meeting of the Complex Trait Community in collaboration with the Rat Genomics Community (CTC-RG)
07/24	ISMB
05/24	FOURTEENTH INTERNATIONAL WORKSHOP ON MOLECULAR ASPECTS OF MYELOID STEM CELL DEVELOPMENT AND LEUKEMIA
12/23	American Society of Hematology (ASH)
01/24-03/24	Methods in Grant Preparation from Clinical and Translational Science Institute of Southeast Wisconsin
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	22nd 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	51st Annual Short Course on Medical and Experimental Mammalian Genetics, The Jackson Laboratory and Johns Hopkins University