

# Justin Gibbons, PhD

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## Research Summary

Dr. Justin Gibbons is a computational biologist specializing in multiomics integration, microbiome research, and high-throughput sequencing analysis. His work explores how microbial communities and host biology intersect in contexts such as preterm infant health, malaria parasite genetics, and environmental disease ecology. He collaborates extensively across medicine, engineering, genomics, and environmental sciences and is experienced in developing computational pipelines, performing large-scale data analyses, and supporting interdisciplinary research teams.

## Education

PhD, Medical Sciences — University of South Florida (2019)

MSc, Bioinformatics & Computational Biology — University of South Florida (2013), GPA 3.84

BSc, Biology — University of Central Florida (2011), GPA 3.7

## Professional Experience

### Research Associate

College of Public Health, University of South Florida (2024–present)

- Conduct multiomics research focused on the gut microbiome, anemia, and growth outcomes in preterm infants.
- Apply whole metagenome sequencing, metabolomics, and proteomics to study host–microbe interactions.
- Collaborate with the Adams Lab to develop methodologies for pooled piggyBac transposon mutant analysis in *Plasmodium falciparum*.
- Provide bioinformatics consulting, experimental design guidance, power analyses, and data interpretation to interdisciplinary clinical and research teams.
- Generate publication-quality figures, pipelines, and methods sections for manuscripts and grant applications.

Teaching contributions:

- Guest lecturer for Applied Computational Genomics (PHC7736): RNA-seq QC, 16S analysis
- Guest lecturer for Fundamental Genomics (PHC6739): microbiome multiomics
- Instructor for single-cell RNA-seq and spatial genomics workshops

### **Postdoctoral Scholar**

USF Genomics Program (2019–2024)

- Led or supported projects involving RNA-seq, WGS, metagenomics, machine learning, and multiomics integration.
- Developed and improved sequencing pipelines (RNA-seq, metagenomics, long-read 18S, proteomics workflows).
- Mentored graduate students and trainees in computational methods and high-performance computing.

Major collaborations include:

- Thao Ho, DO: Multiomics of anemia and microbiome composition in preterm infants.
- John Adams, PhD: RNA-seq guidance for malaria genetics; drug mechanism prediction using mutant screens.
- Greg O’Corry-Crowe, PhD: Nanopore-based HAB monitoring in Indian River Lagoon.
- Liwang Cui, PhD: Genomic variants and gene-expression changes in drug-resistant *P. falciparum*.
- Moffitt Cancer Center & USF collaborators: RNA-seq and microbiome analyses for cancer and cardiac research.

### **Selected Earlier Research Experience**

#### **PhD Researcher, Jiang Laboratory — University of South Florida (2015–2019)**

- Developed pipelines for Hi-C, ChIP-seq, and RNA-seq analysis in *Plasmodium falciparum*.
- Identified drug resistance-associated genes and assessed chemical diversity of antimalarial compounds.

#### **Research Internships — USF, Moffitt Cancer Center, and Florida Hospital (2013–2015)**

- Conducted bioinformatics analyses for gene expression, differential expression filtering, GO prediction, and clinical datasets.
- Created visualizations (e.g., Circos plots) for publications and presentations.

## Teaching Experience

- Microbiome Workshop Instructor (2019–2022): R-based microbiome analysis, diversity metrics, statistics.
- RNA-seq Workshop Instructor (2019–2022): HPC workflows, HISAT2 pipeline.
- Python Programming for Bioinformatics Instructor (Spring 2018): Introductory Python for MS students.
- Applied Bioinformatics Lab Instructor (Spring 2014): R and Bioconductor for microarray analysis.

## Student Mentorship

- Yikun Zhou (2024–2025): Undergraduate Honors Thesis — In silico docking of *P. falciparum* StAR-related proteins.
- Max Pietsch (2016–2017): Developed optimized Tuxedo Suite pipeline; now employed at Google.

## Invited Talks & Conference Presentations

- 2025 ASBMB Student Chapter: Multiomics of anemia and the preterm infant gut microbiome.
- 2018 & 2016 ASTMH Annual Meetings: Genomic and chemogenomic analyses of malaria parasites.
- 2016 Frontiers of Drug Discovery: Chemoinformatics for malaria drug screening.

## Awards

- 2016 Frontiers of Drug Discovery Outstanding Presentation
- 2014 University Graduate Fellowship
- 2010 McCurry Endowed Scholarship
- 2006 Regional OTM Award

## Current Research Funding

- R01 AI117017 — Adams (PI) — Chemogenomic Profiling of *Plasmodium falciparum* Responses and Resistance (2015–2026)
- R56 AI130171-05A1 — Adams (PI) — Discovering the Essential Genome of *P. falciparum* (2018–2026)

## Past Funding

- R21 HD112776 — Ho (PI) — Gut dysbiosis and anemia in preterm infants (2023–2025)

- HBOIF 6408115300 — O’Corry-Crowe (PI) — Environmental impacts on wild Florida dolphins (2023)

## **Selected First-Author Publications**

- Gibbons J. et al. Severe anemia in preterm infants increases bacterial virulence potential. *Pediatric Research* (2025).
- Gibbons J. et al. In vitro model of premature intestinal epithelium and microbiota interactions. *mSphere* (2021).
- Gibbons J. et al. Lineage-specific expansion of pfhrp2-deleted *P. falciparum* parasites. *Journal of Infectious Diseases* (2020).
- Gibbons J. et al. Altered K13 expression disrupts DNA replication in *P. falciparum*. *BMC Genomics* (2018).

## **Technical Skills**

**Computational:** Python, R, PERL, MySQL, Linux/Ubuntu, HPC/SLURM systems

**Sequencing & Multiomics:** RNA-seq, whole-genome sequencing, metagenomics, 16S rRNA, proteomics, metabolomics, scRNA-seq, spatial genomics

**Bioinformatics Tools:** HISAT2, STAR, bwa, bowtie2, Samtools, CellRanger, Bedtools, scikit-learn, Circos, OpenMS, custom Python/R pipelines

**Domains:** Microbiome ecology, malaria genetics, machine learning, multiomics integration, drug resistance mechanisms