



National Institute of Allergy and Infectious Diseases



# Molecular Basis of Infectious Diseases (MBID)

Funded by the National Institute of Allergy and Infectious Diseases (NIAID), T32AI055449

Program Director: **Michael Lorenz**, PhD, Professor, Microbiology and Molecular Genetics, The University of Texas Health Science Center at Houston

Program Co-Director: **Theresa Koehler**, PhD, Professor and Chair, Microbiology and Molecular Genetics, The University of Texas Health Science Center at Houston

<https://www.gulfcoastconsortia.org/home/training/molecular-basis-of-infectious-diseases-mbid/>

## Meet the Trainees 2022-2023



**Lois Armendariz**, Biosciences, Rice University  
Appointment: September 1, 2022 – August 31, 2023

**Mentor:** Dr. Natasha Kirienko, Biosciences, Rice University

**Project Title:** *Elucidating the Role of Host Lipid Metabolism in Pathogenic Infection of *Caenorhabditis elegans**

The dramatic increase in development and spread of antimicrobial resistance has rendered current methods to combat it ineffective. Among innovative solutions proposed is the idea that we can modulate host and bacterial pathways to push the host-pathogen interaction in favor of the host. Preliminary data has shown lipid metabolism to be involved in response to liquid-based pathogenesis by the opportunistic pathogen *Pseudomonas aeruginosa*. By conducting host-pathogen interaction studies using *Caenorhabditis elegans*, I will characterize the changes in host lipid metabolism in response to *P. aeruginosa* as well as the virulence mechanisms employed by this pathogen to kill its host in a liquid setting.



**Jason Pizzini**, Immunology and Microbiology, Baylor College of Medicine  
Appointment: September 1, 2022 – August 31, 2023

**Mentor:** Dr. Robert Britton PhD, Molecular Virology and Microbiology, Baylor College of Medicine

**Project Title:** *Microbial therapeutics to prevent ExPEC colonization and disease*

*Escherichia coli* (*E. coli*) is a diverse species encompassing nonpathogenic beneficial gut microbes and microbes capable of causing human disease. Disease causing strains of *E. coli* are divided into categories based upon the site of infection. Extraintestinal pathogenic *Escherichia coli* (ExPEC) encompasses strains which cause infection outside of the gastrointestinal tract, such as urinary tract infection, meningitis, and bacteremia. The emergence of hyper-virulent and antibiotic resistance strain has exacerbated the morbidity and mortality associated with this pathogen. Despite current research in vaccination against ExPEC they have meet with little success, and there is currently no vaccine or prophylactic strategy to combat this deadly pathogen. It is known that ExPEC requires colonization of the gastrointestinal tract (GIT) in order to cause infection. Once colonized, ExPEC can persist as a normal member of the GIT until the conditions for dissemination are met. There are currently no known ways to de-colonize ExPEC from the GIT. However, our GIT microbiome provides natural defense against several pathogens through what it known as colonization resistance. Our project seeks to leverage this natural defense by identifying a small number of indigenous

microbes found in the GIT which provide natural resistance to ExPEC colonization. These simplified communities would serve as a prophylactic treatment, given to those at high risk of ExPEC disease, and would prevent the establishment of ExPEC into the GIT thus preventing infection and transmission.



**Jacob Rutherford**, Institute of Biosciences and Technology, Texas A&M University  
Appointment: October 1, 2021 – July 31, 2022

**Mentor:** Julian Hurdle, PhD, Center for Infectious and Inflammatory Diseases, Institute of Biosciences and Technology, Texas A&M University

**Project Title: *Study of Fusobacterium nucleatum FAS-II Using Molecular and Chemical Genetics***

*F. nucleatum* has been classified as a carcinogen that promotes the formation of colorectal cancer, and I am investigating the *fabK* gene as a possible drug target. We have compounds that specifically inhibit FabK and are planning to use these to determine if FabK inhibition *in vitro* and *in vivo* leads to a decrease in *F. nucleatum* associated cancer pathologies. Additionally, these compounds will be used alongside molecular genetic tools to increase our understanding of *F. nucleatum* lipid biology, an area that has not previously been studied.



**Hannah Wilson**, University of Texas Health Science Center at Houston

Appointment: October 1, 2021 – July 31, 2022

**Mentor:** Michael Lorenz, PhD, Department of Microbiology and Molecular Genetics, The University of Texas Health Science Center at Houston

**Project Title: *Determining the contributions of C. albicans metabolism and morphogenesis to phagosomal alkalization***

My project focuses on the dynamic interaction between host macrophages and the opportunistic fungus, *Candida albicans*. Specifically, I am studying the molecular mechanisms by which *C. albicans* neutralizes the acidifying phagosome and escapes from the phagocyte via filamentous growth. By characterizing this process, I will identify the elements that are central to the ability of *C. albicans* to disseminate and cause systemic infections.

The MBID program is administered by the:



[www.gulfcoastconsortia.org](http://www.gulfcoastconsortia.org)

The GCC is a collaboration of:

Rice University

Baylor College of Medicine

University of Houston

University of Texas Health Science Center at Houston

University of Texas Medical Branch at Galveston

University of Texas MD Anderson Cancer Center

Institute of Biosciences & Technology at Texas A&M Health Science Center

Houston Methodist Research Institute