THE UNIVERSITY OF NEW MEXICO

U-RISE
Summer Research Symposium

August 26th, 2022
3:00 - 6:30 pm

Schedule

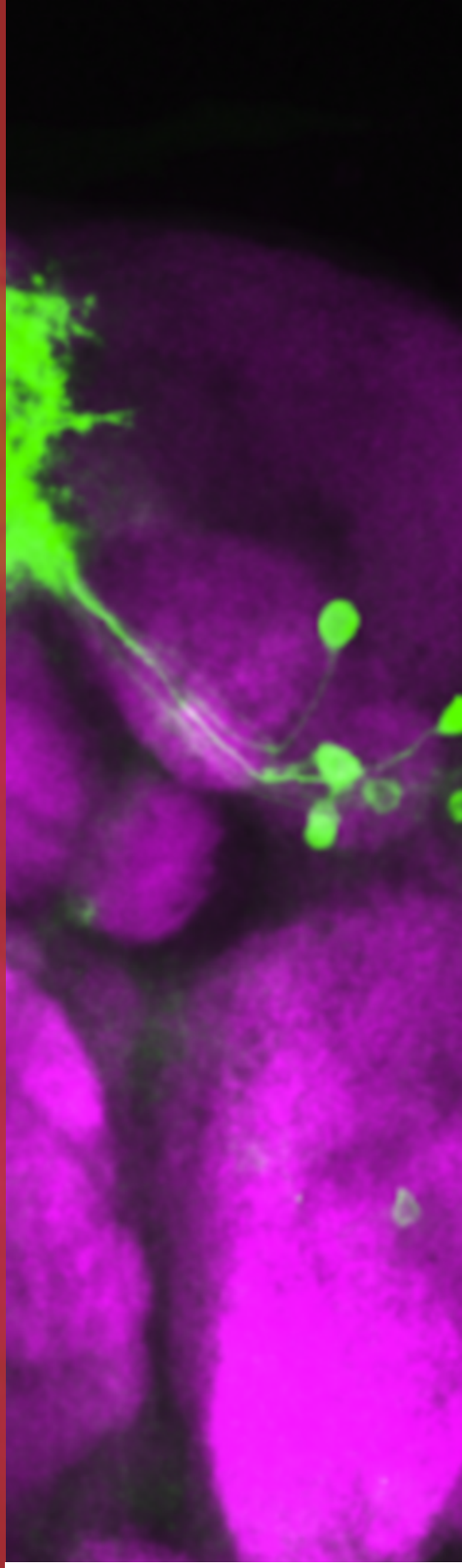
3:00 PM	Opening Remarks
3:15 PM	Julian Rojo
3:30 PM	Marelessis Palomino
3:45 PM	Alexa Gonzalez
4:00 PM	Daisy Belmares-Ortega
4:15 PM	Brendan Sanders
4:30 PM	Courtyard Reception
5:15 PM	Diego DeMmon
5:30 PM	Brandi Hess
5:45 PM	Brenda Ramos Villanueva
6:00 PM	Adina Abudushalamu

About U-RISE

Our program offers a two-year research experience with the mentorship of a UNM faculty member. With additional support, our scholars develop skills to enter a field in the biomedical sciences.

This experience is essential to preparing a successful application to the top Ph.D. programs in the country.

Program Director -
Dr. Cristina Takacs-Vesbach



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U-RISE
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Our Scholars

Julian Rojo

Julian Rojo is a senior majoring in chemical engineering with minors in mathematics and chemistry. His research revolves around better understanding the adaptive immune system. At UNM, he is working to elucidate further how PD-1, a potent target for cancer immunotherapies, regulates the signaling pathways of CD28 and the TCR complex, ultimately impacting the T cell response. At MIT, he worked on sampling microneedles that enable the collection of tissue-residing immune cells in a minimally invasive manner, with implications for vaccine monitoring and treating autoimmune diseases. He will pursue a Ph.D. in biological engineering, particularly in the field of immune engineering to treat cancer. He enjoys reading, working out, and hanging out with friends and family in his free time.

Using pain-free microneedle skin patches to sample tissue-residing leukocytes

Julian Rojo[1], Ryan Hosn[2], Sasan Jalili[2], and Darrell Irvine[2]

[1]Department of Chemical and Biological Engineering, University of New Mexico, Albuquerque, NM
[2]Koch Institute for Integrative Cancer Research, Massachusetts Institute of Technology, Cambridge, MA

Blood draws are used to analyze a plethora of metabolites. However, they require a trained professional, increase the risk of blood-borne pathogen spreading, and trypanophobia can deter some patients from seeking medical attention. Interstitial fluid (ISF), which is accessible through the skin, has the potential to address these shortcomings. Additionally, ISF has a large and unique leukocyte population absent in the blood, which can give insight into autoimmune skin diseases, vaccine responses, and organ transplants. Current methods of sampling ISF are invasive, cause discomfort, and lead to scarring. To address this, we fabricated microneedle skin patches (MNs), which allow for the pain-free sampling of ISF. Our MNs are made of a polymeric backbone and coated with a hydrogel layer that absorbs the ISF. To test our sampling capacity in vivo, we vaccinated mice with ovalbumin, administering a prime, booster, intradermal challenge, and applying MNs a week after the challenge. These samples were analyzed via immunophenotyping using flow cytometry. Our MNs collected a diverse pool of leukocytes, including ovalbumin-specific T cells and innate immune cells. Ultimately, these MNs are a safe and minimally invasive sampling tool with the ability to help communities with a lack of medical infrastructure.

Marelessis Palomino

My name is Marelessis Palomino, and I am majoring in Chemical Engineering. My family is from Chihuahua Mexico, but I was raised in Santa Fe, NM. In my free time I enjoy building Legos, meditating, and spending time with my family and friends. This summer I had the opportunity to participate in a biomedical research program at West Virginia University, where I worked in Dr. Ivan Martinez's lab. During my time in the Martinez lab my research interests included creating cell lines that will be used to visualize and understand the role that Linc-SPRY3 RNAs has on radiation sensitivity in lung cancer.

Introducing Y Chromosome Long Non-coding RNAs in Mouse Lung Cancer Cells to Induce Radiation Sensitivity

Marelessis Palomino[1], Emily S. Rice[2], Travis Rawson[2], Michael T. Winters[2], Ivan Martinez[2]

[1]Department of Chemical and Biological Engineering, University Of New Mexico, Albuquerque, NM
[2]Department of Microbiology, Immunology & Cell Biology, West Virginia University Cancer Institute, School of Medicine, West Virginia University, Morgantown, WV

Lung cancer is the leading cause of cancer related deaths. Radiation therapy is the most common treatment for lung cancers, unfortunately radiation resistance continues to be a problem. The discovery of new molecular pathways related to radiation resistance are essential to develop better treatments. In the last decade, the field of noncoding RNAs has given us new information about radiation resistance. Recently, our lab discovered a group of long non-coding RNAs (lncRNAs) known as Linc-SPRY3 RNAs that give radiation sensitivity to human lung cancer cells. Interestingly, these lncRNAs are expressed from the human Y chromosome, and are only present in primates. To develop an animal model of these lncRNAs, we will artificially introduce linc-SPRY3 RNAs into two different mouse lung cancer cell lines. Our hypothesis is the introduction of these human lncRNAS to mouse lung cancer cells will sensitize them against radiation because of the conserved molecular pathways shared between mammals. We will artificially introduce these lncRNAs into these mouse cell lines by using retroviral vectors containing the linc-SPRY3 RNAs. After antibiotic selection, we will radiate these cells and measure radiation sensitivity using flow cytometry. Our preliminary results will show the creation of radiosensitive mouse lung cancer cell lines expressing the human linc-SPRY3 RNAs, giving us an essential tool to investigate the conserved molecular pathways affected by these non-coding RNAs. Furthermore, we will be able to use these new mouse cell lines to study syngeneic in vivo mouse model systems to understand the importance of the tumor microenvironment.

Alexa Gonzalez

Hello! I am a junior pursuing a Biology and Spanish degree. I am a first-generation student of an immigrant family from Mexico. My research journey began in the Syed Lab where I became fascinated with understanding the mechanisms regulating and maintaining neural identity and where my love for neuroscience in general began. I have focused on studying the fruit fly central nervous circuit, specifically the areas that are responsible for olfaction and navigation. This summer, I investigated genetic factors associated with tumor formation through *Drosophila* neural stem cells at the University of Michigan. I plan to resume my studies in biomedical research to eventually earn a Ph.D. Along with my other interests, I always look forward to spending time with loved ones, trying new dishes, art viewing, and occasionally exploring nature!

RNA Modifications Play a Role in Exit from Stem Cell State in the *Drosophila* Larval Brain

Alexa Gonzalez[1], Hideyuki Komori[2], Cheng-Yu Lee[2], and Mubarak H. Syed[1]

[1]University of New Mexico, Biology Department, Albuquerque, NM
[2]University of Michigan, Life Sciences Institute, Ann Arbor, MI

Stem cells undergo stages of division to produce specialized progeny along with more stem cells for growth and development. This system is dependent on RNA as a master regulator of gene activity to generate all cell types. Changes in these regulating mechanisms may lead to diseases such as cancer. In *Drosophila* larval neural stem cells, Brain Tumor (Brat); an RNA binding protein, is essential for the exit from the stem cell state by down-regulating stem cell state promoting transcription factors. The mechanism in which Brat represses these factors and recognizes its targets is not fully understood. We suspected internal RNA modifications as a factor in Brat function. RNA modifications account for post-transcriptional regulation to sustain cellular processes. We generated a Brat mutant fly susceptible to a change in stem cell numbers when factors that contribute to the stem cell state are removed. We crossed this Brat sensitized line with many individual fly lines that lacked specific modifiers through RNA interference (RNAi) and quantified stem cells of interest. A loss of adenosine methylation at position 6 in mRNA (m^6a) resulted in a significant increase in stem cell numbers, inducing tumors in the fly brain. Our results suggested that RNA modifications contribute to the Brat protein function in stem cell regulation and, therefore, asymmetric cell division. Understanding the relationship between RNA modifications and stem cell regulation allows us to understand the mechanisms underlying tumor genesis, applicable for the comprehension and treatment of cancer.

Daisy Belmares-Ortega

Daisy Belmares-Ortega is a Senior studying Mechanical Engineering with a minor in Chemistry and Mathematics. Daisy a first-generation college student from Albuquerque, New Mexico. Her research interests include hydrogel spheroid modeling for liver toxicology. Daisy completed her summer research experience at the University of New Mexico: Health Science Center's Undergraduate Pipeline Network (UPN). As an aspiring physician-scientist, Daisy is interested in exploring research in pathology, neuroscience, and toxicology. In her free time, Daisy enjoys dancing, writing poetry, and training for her private pilot license.

Enabling a Hepatoxicity Assay Platform Using HepG2 and HUH-7 Cells Through A Centrifugal Hydrogel Synthesis Method

Daisy Belmares-Ortega[1], Rahul Kumar[2 3] M.S., Valeria Rojas[4], Rama Gullapalli M.D., Ph.D.[2 3]

[1]Department of Mechanical Engineering, [2]Pathology, [3]Chemical and Biological Engineering, University of New Mexico, Albuquerque, NM
[4]Department of Biomedical Engineering, Columbia University, New York, NY

Drug development processes depend on hepatoxic assays. Novel platforms and assays are key to investigate hepatoxic effects of drug and environmental xenobiotics. Existing cell scaffolding techniques are two-dimensional and lack physiologically relevant environments necessary for hepatoxicity assessment. The centrifuge-based method was optimized to synthesize hydrogel microdroplets for the embedding of model cell lines: HepG2 and HUH-7. The central hypothesis indicates model liver cells cultured in hydrogel spheroids parallels in-vivo hepatoxic outcomes compared to 2-D cell growth modes in chronic exposures of heavy metals such as Cadmium. Microdroplets were synthesized using calcium-alginate hydrogels from sodium alginic salt. Optimal centrifugal rotation speeds ranged from 250-1,500 rpm across 1, 2, and 3 % weight by volume (w/v) viscosities of sodium alginate into 0.1 M calcium chloride catch solution. Model rotation speeds increase linearly as alginate solution viscosity increases (3% > 2% / 1%). Hydrogel solutions were discharged through a glass microcapillary in a 3-D printed insert. Ideal glass capillary diameters ranged from 10-25 micrometers at a drop height of 3-6 millimeters. HepG2 and HUH-7 cells were encapsulated at 2,500-5,00 cells per microliter of sodium alginate and DMEM media composite. HepG2 and HUH-7 spheroids were cultured in a 3-D Rotary Cell Culture System (RCCS). Samples were taken at days 1, 3, 7, and 14 of culture to determine cell viability. Viability from cultured spheroids using the RCCS was compared to 3-D spheroids cultured in a standard 2-D well plate. Preliminary findings indicate the spheroid platform is a viable approach to synthesize 3-D hydrogel spheroids.

Brendan Sanders

Hi! I am a rising 4th year undergraduate majoring in biochemistry. This summer, I conducted research with Dr. Laura Gonzalez Bosc and PhD student Benjamin Lantz of the Cell Biology and Physiology department at the UNM School of Medicine. I worked with the protein Collagen V (col V) and its contribution to pulmonary arterial remodeling and changes in pulmonary vasculature as a result of chronic hypoxia, as well as its contribution to pulmonary hypertension. Specifically, my lab is currently researching the mechanisms of how col V exposure intranasally prior to chronic hypoxic conditions attenuates right ventricular systolic pressure, hopefully finding a connection between col V and pulmonary arterial remodeling. In my free time, I enjoy mountain and road biking, hiking, and reading.

Collagen V Exposure Prior to Chronic Hypoxia and Alters Inflammation and Pulmonary Arterial Remodeling

Brendan Sanders, David T. Jones, Benjamin Lantz, Laura Gonzalez Bosc

University of New Mexico Health Sciences Center, Cell Biology and Physiology Department, Albuquerque, NM

Pulmonary hypertension (PH) is a well-known and slowly progressing disease in which elevated pulmonary pressure, usually due to several different mechanisms, but effective treatments for pulmonary hypertension are yet to be found. This can lead to noticeable, yet untreated progression of PH with disastrous implications, from elevated pulmonary pressure, to right ventricular hypertrophy, heart failure, and death. One such category of PH arises from chronic hypoxia. One major mechanism of CH-induced PH is the proinflammatory immune response. Our lab has shown collagen V (Col V)-specific proinflammatory cells exist under normal conditions, chronic hypoxia increases Col V within the lungs, and proinflammatory cells traffic to the lungs following CH exposure. We have also shown that exposure to Col V prior to CH exposure attenuates PH. Whether or not prior exposure to Col V affects the pulmonary vasculature is unknown. Based on our preliminary right ventricular systolic pressure data, we hypothesize that Col V exposure prior to CH exposure will attenuate pulmonary arterial remodeling. To measure this, I will be analyzing lung sections from mice that received vehicle or Col V exposure, followed by normoxia or CH exposure stained with a smooth muscle marker to examine arterial wall thickness. Completion of this study will further elucidate how Col V reactive cells affect the pulmonary vasculature in CH-induced PH, laying the groundwork for possible targeted therapies in the future.

Diego DeMmon

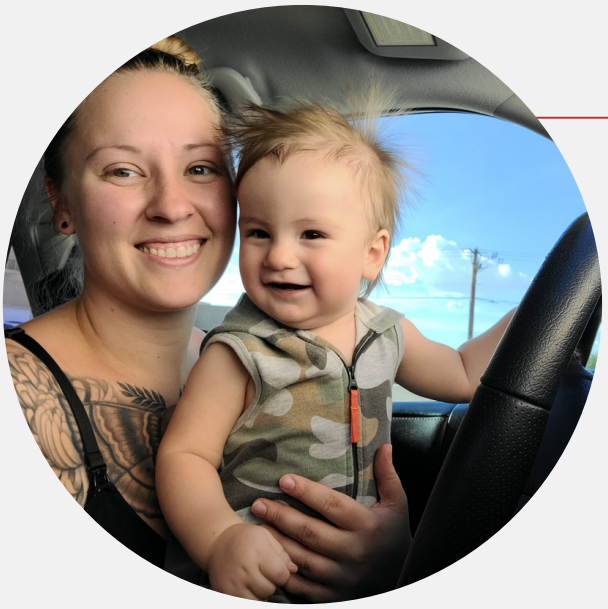
I am a senior at UNM pursuing dual degrees in Chemistry and Biology. I'm originally from Belen, NM and started my education at UNM-Valencia after obtaining my GED. I was first exposed to research when my chemistry professor, Dr. Tracy Terry, invited me to conduct research with her. Now on main campus, I'm working with Dr. Irene Salinas on the characterization of T-cell receptors within the skin and prepyloric spleen tissues of African lungfish. This summer, I worked with Dr. Sarah Ewald at the University of Virginia, where we worked to develop a cyst-deficient strain of the parasite *Toxoplasma gondii* by editing genes that the parasite requires for survival. This year, I'm excited to complete my project with Dr. Salinas and apply to graduate programs that relate to my passions in molecular biology and immunology!

Development of novel cyst-deficient strains of *Toxoplasma gondii*

Diego DeMmon[1 2], Jamison Smiley[3], Sarah Ewald[3]

[1]Department of Chemistry, [2]Department of Biology, University of New Mexico, Albuquerque, NM
[3]University of Virginia, Bernie B. Carter Center for Immunology Research, Charlottesville, VA

Toxoplasma gondii is an obligate intracellular parasite that causes chronic infection in warm-blooded hosts. Infection begins with the ingestion of oocysts shed by definitive feline hosts or by the consumption of meat harboring tissue cysts. Once *T. gondii* has been ingested and passes through the small intestine, the parasite differentiates into tachyzoites, a fast-replicating form of the parasite that infects a variety of host cell types. This eventually causes a host immune response that forces the tachyzoites to transition into the long-lived, cyst-forming bradyzoites, predominantly found in neural and muscle tissue. Currently, there is no treatment for chronic infection with *T. gondii*, which is thought to last the life of the host. The goal of this study is to develop self-sterilizing strains of *T. gondii* that have normal acute infection biology and selectively expire at the onset of tachyzoite to bradyzoite transition. To develop these novel strains, we will selectively remove essential genes in *T. gondii* by driving expression of Cre-recombinase under control of the bradyzoite-specific gene enolase-1. The essential genes, ribosomal protein L28, proteolipid protein 1, and mitogen-activated protein kinase 1, are engineered to contain LoxP sites flanking the essential exon(s). In this way, the normal expression of enolase-1 will cause a deletion in LoxP flanked (floxed) regions and remove expression of essential metabolic genes. Additionally, we are generating two control strains. In one, the non-essential gene toxofillin will be floxed to ensure that the altered enolase-1 does not compromise the viability of the parasites. In a second, a nonfunctional Cre-recombinase will be expressed by enolase-1, ensuring that the essential metabolic gene of interest is not removed and controlling for off-target effects of the floxing process. We anticipate that these novel strains will serve as an experimental tool to separate the effects of chronic infection from the long-term consequences of acute inflammation and may be a novel immunotherapy or vaccination tool to recruit a robust and safe host immune response.



Brandi Hess

Hello! My name is Brandi Hess, I am currently working on my B.S. in Biochemistry at UNM, and I am interested in conducting research related to neuroscience. I became interested in neuroscience after discovering my love of psychology and paring that passion with my love of biology and chemistry. During the summer of 2022 I spent time in a neuroscience lab working on a genetic screen to track gene expression related to Alzheimer's research.

Outside of the lab I am the mother of a beautiful baby boy whom I work diligently for. I love spending time with him outside, as well as having the chance to guide him through new experiences so he may learn more about the world while developing a healthy curiosity.

Gene Disruption Project

Brandi Hess[1], Mubarak Syed[2]

[1]Department of Biochemistry, University of New Mexico, Albuquerque, NM
[2]Department of Biology, University of New Mexico, Albuquerque, NM

A large number of genes have been identified related to various neurodegenerative disease in humans and, because of the similarities in flies, Bellen Lab was able to identify the orthologs in Drosophila Melanogaster. As genetic testing becomes more common in humans researchers are able to identify a huge variety of mutated genes that cause diseases such as Alzheimer's, Parkinson's, Amyotrophic Lateral Sclerosis, and Friedreich Ataxia. In order to create a vast database for all to be able to study targeted genes this lab is creating hundreds of fly lines to better assist researchers. After finding these genes CRIMIC insertions were made under a UAS promoter to induce transcription of GAL-4 so neuropeptides and neurotransmitters may be seen when conducting experiments.

The next step is to identify where and when these neural developmental signals are expressed. Once each fly line is developed and balanced they need to be screened to identify where the gene is active and during what critical developmental period. During a large genetic screen flies are dissected at the L3 larval stage and the adult fly stage to determine expression during early neural population during early and adult stages. Brains are dissected and scanned to see if signals are expressed in glia, neurons, or stem cells to help catalog their function. Further research can then be done to determine the function of the targeted gene and how loss of function might affect overall neurodevelopment of the fly. We can use this type of information to determine the significance of these genes in relation to neurodegenerative diseases as well.

Brenda Ramos Villanueva

My name is Brenda, and I am from Oaxaca, Mexico from the community of the Ñuu Savi. I am a first-generation college student majoring in Biology and conducting avian malaria research in Witt's lab. This past summer I had the opportunity to participate in the IDEAL SUIP program at the University of Pennsylvania conducting research on genome compartmentalization at the Joyce Lab. I have had amazing research experiences that have reinforced my goals towards continuing my education. Upon graduation, I am hoping to participate in the PREP Program and eventually apply to PhD programs. In my free time I enjoy sewing, painting, outdoor activities and spending time with my friends.

Understanding the role of Condensin II in genome compartmentalization

Brenda Ramos Villanueva[1], Randi Isenhart[2], Son Nguyen[2], Leah Rosin[2], Olivia Crocker[2], Eric Joyce[2]

[1]Department of Biology, University of New Mexico, Albuquerque, NM
[2]Department of Genetics, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA

Understanding 3D genome organization is crucial to the understanding of how our genomes function in normal development and in disease. One widespread feature higher-order chromatin organization in the nucleus is the compartmentalization and spatial separation of transcriptionally active (A) and silent (B) regions of the genome. However, it remains unclear how this level of organization is achieved. Previous studies in our lab and others have found that the protein Cap-H2, a component of the Condensin II complex, is essential for the regulation of large-scale chromatin folding. We aim to determine whether this involves the disruption of A/B compartments. First, we will be using custom chromosome paints to image A/B compartments in *Drosophila* nuclei after Cap-H2 knockdown to determine how the size, shape and behavior of different chromatin types are being disrupted in individual cells. In addition, to test a compartment interaction directly, we will use the *Drosophila* bw^D mutation, which is a position effect variegation (PEV) assay that requires a long-range B-B compartment interaction for its transcriptional silencing. We will test whether Condensin II depletion disrupts this interaction and the silencing of the bw gene in the developing fly eye. Together, these experiments will determine if Condensin II is a critical component of genome compartmentalization, which would represent one of the only complexes implicated in this level of organization.

Adina Abudushalamu

Hi! I'm Adina Abudushalamu, and I am currently a junior. I was raised in Las Cruces, New Mexico and moved up to Albuquerque to study Biochemistry and Computer Science here at UNM. This summer, I was able to do research at the University of Colorado Anschutz Medical Campus on translation elongation and how it regulates gene expression. In my free time, I like spending time with friends and family as well as listening to music or practicing calligraphy.

MetAP2 expression is regulated by translation elongation

Adina Abudushalamu[1 2], Evan J. Morrison[3], Olivia S. Rissland[3]

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[3]University of Colorado Anschutz Medical Campus, Department of Biochemistry and Molecular Biology, Aurora, CO

The primary structure of a protein dictates its secondary and tertiary structures, as well as its function and localization. However, emerging evidence from our lab and others suggests that the primary structure is also critical to controlling the levels and dynamics of gene expression. In particular, poly-basic tracks exert substantial control over protein synthesis and translational efficiency due to ribosome stalling, which activates ribosome quality control pathways (RQC). However, there is still minimal understanding of the mechanisms governing the connections between primary structure and gene expression. I hypothesize that the biochemical properties of positively charged protein sequences and not necessarily poly-A tracks of the mRNA sequence control gene expression through RQC. To test this model, I will use reporter constructs with variable upstream peptide sequences to control gene expression. Specifically, I will create constructs with long sequences of positive charges upstream of a *Renilla* Luciferase, and measure translational efficiency compared to a non-positively charged control. I will use *in vitro* translation systems, as well as live cells, to determine the difference in expression due to ribosome stalling. This project will elucidate further the mechanisms underlying gene regulation. Since misregulation of gene expression contributes to several disease phenotypes, our results will enhance our understanding of how gene expression is regulated in these contexts.

Ellie Larence

Ellie Larence is a returning student majoring in computer science after receiving a degree in biology in 2018. Previously, she was a research assistant in Dr. Joseph Cook's lab, completing a senior thesis using geometric morphometric techniques to characterize unique marten species (Martes spp.). After working as a molecular biologist at the New Mexico Department of Health, she became interested in the intersection of computer science and biology, leading her make the decision to return to UNM to study computational biology. Upon graduation she intends to attend a graduate program focusing on machine learning applications in molecular biology. In her free time, she enjoys re-watching the Harry Potter and Star Wars movies, undertaking time consuming baking recipes, and traveling to new places.

UNM Faculty Mentors

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Mubarak H. Syed, Ph.D
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Christopher Witt, Ph.D.
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