3rd Annual CSU Summer Symposium at UCLA

August 14, 2018
1:00 - 3:00 p.m.
Geffen Hall Learning Studio
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Graduate Programs in Bioscience

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# CSU SUMMER SYMPOSIUM AT UCLA

## Abstract Book

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Welcome to the third annual CSU Summer Symposium and Graduate Program Fair at UCLA!

We are happy to have you join us for an afternoon featuring research presentations by students from neighboring CSU campuses, and information sessions on graduate training opportunities in STEM at UCLA. The aim of the Symposium and Fair is to promote scientific exchange and provide information on graduate educational opportunities as a way to strengthen interactions between CSU capstone research programs and UCLA graduate programs.

UCLA offers a wide variety of exceptional graduate programs in STEM. The college, with Divisions of Life and Physical Sciences, is located on a single campus with the School of Medicine and hospital. This proximity provides a wealth of research training opportunities and promotes a collaborative and collegial culture of discovery and innovation that crosses traditional academic boundaries and spans disciplines, departments and schools. Our UCLA STEM community is built on core values of openness, inclusion, and respect that foster creativity and excellence by embracing a diversity of backgrounds, experience, ideas, and approaches.

We welcome CSU participants and extend thanks to our UCLA graduate program representatives.

Gregory S. Payne, Ph.D.
Director, Graduate Programs in Bioscience
Associate Dean of Bioscience Graduate Education, David Geffen School of Medicine
Associate Dean of Graduate Education, College of Life Sciences
CSU SUMMER SYMPOSIUM AT UCLA
Schedule of the Day

1:00 – 1:20  Welcome

1:20 – 3:00  Graduate Program Tabling

2:00 – 3:00  Tabling continued with concurrent CSU Poster Session

Poster session will highlight CSU students planning to apply to UCLA who are participating in broadening participation capstone research programs such as MARC, IMSD, MBRS Rise, HMMI and others.

Light refreshments will be served.
Stress has been shown to impair maternal behavior, which can significantly impede the development of offspring and disrupt the mother-infant bond. Hypocretin (HCRT) may attenuate the effects of stress on maternal behavior. HCRT is a modulatory neuropeptide important for arousal and reward-seeking behavior, both essential elements for successful maternal care. At high levels, along with corticotropin-releasing factor (CRF), HCRT is associated with stress and impaired maternal behavior. Moderate doses of HCRT, both intracerebroventricular and site-specific medial-preoptic area administration, support maternal behavior in lactating dams. The dose-dependent involvement of HCRT in stress and postpartum behavior suggests HCRT imbalances might be a factor in disorders of dysregulated maternal care and depression. In the present study, lactating dams were administered a HCRT receptor 1 antagonist (HCRTR1A; SB-334867, 30 mg/kg; I.P., n=9) or a vehicle control (n=13) on postpartum day 3 before undergoing 15-minute restraint stress. Dams were then tested for depressive-like behavior on the tail suspension test (TST) preceding observation in a 15-minute pup-retrieval maternal behavior task. No significant differences were found between the HCRTR1A group and control on time immobile (t(20)= -0.276, p=0.785) or latency to retrieve the first pup (t(20)= -0.854, p=0.403). Dams receiving the HCRTR1A spent more time nursing (t(20)= -2.662, p=0.039) and showed increased latency to self-groom (t(20)= 2.193, p=0.048) than vehicle treated dams. Results suggest blocking HCRTR1 neurotransmission buffers adverse effects of stress on maternal behavior.
Post-transcriptional modification of mRNA is a common feature among eukaryotic cells. In the chloroplasts and mitochondria of most land plants and some protists, one such modification involves the deamination of cytidine (C) nucleotides to uracil (U). The DYW subclass of pentatricopeptide repeat (PPR) proteins along with other protein editing factors form an active complex called an editosome that facilitates the C-to-U deamination. PPR proteins contain a N-terminal long and short repeat (PLS) region that selectively binds to RNA, and a C-terminal Aspartate-Tyrosine-Tryptophan (DYW) domain that is hypothesized to catalyze the deamination reaction. Other studies have also implicated the DYW domain in RNA endoribonuclease cleavage, an observation that confounds the biochemical role of the DYW domain, since RNA cleavage is theoretically not required for this type of RNA editing nor is the hydrolysis of the sugar-phosphate backbone required during RNA editing in vitro. We have shown that the protein DYW1 from Arabidopsis thaliana acts as an endoribonuclease in vitro, and that nuclease activity is dependent on bound Zn2+. Previous studies have also shown that DYW1 is necessary for RNA editing in vivo. Considering these results, we hypothesize that a single DYW domain is capable of catalyzing both RNA cleavage and RNA editing. To determine the biochemical mechanism that regulates endonuclease or deaminase activity, we will investigate the role of oligomerization and the effect of other editing factors on the DYW domain’s activity.
The development of reprogramming technology for the generation of induced pluripotent stem cells (iPSCs) has catalyzed powerful possibilities in the field of stem cells and regenerative medicine. For these applications, one of the enabling methods that is critical is the ability to scale up while reducing variability between users. Initial steps in the iPSC workflow typically requiring clonal selection and manipulation can be further streamlined to develop a robust process for iPSC establishment. This study explores the use of novel solutions for clonal versus bulk iPSC generation. Clonal isolation of single colonies is the traditional method for establishment of iPSCs. Sendai virus based reprogramming has shown to be consistent and robust thus allowing for pooling of the clones. iPSCs established through bulk expansion should therefore be comparable to clonally expanded iPSCs. A critical factor for a pooled iPSC generation and scale up was the need for mild cell harvesting methods. We identified a novel solution that facilitates gentle passaging across a broader window of manipulation. To confirm the comparability between iPSCs generated using clonal and bulk methods, the cells were monitored for growth rates and morphology. The resulting iPSCs were subjected to rigorous characterization using transcriptome analysis, in vitro differentiation potential, and genomic stability. Further, iPSCs generated using the two different methods were expanded in large scale cell culture system such as Nunc Cell Factories. The combination of these workflow improvements, with tools that allow for elimination of partially reprogrammed and Sendai virus-containing cells provides a consistent, streamlined protocol.
According to the Center for Disease Control and Prevention 25% of all deaths are relating to coronary artery disease. To treat these disease polymer-based drug eluting stent coatings have been used and showed great advantages over bare metal stents alone. However, clinical studies have been shown the polymer coating has been linked to a numerous amount of cases of hypersensitivity reactions and inflammatory responses. Our goal is to use an iron-based metal organic framework (Fe-MOF) as an alternative for the polymer coating for its non-toxic, high porosity, and biodegradable characteristics. Our research involves a three-step method starting first with the successful synthesis of the (Fe-MOF), next obtaining a uniform thin film of the MOF, and lastly testing for its drug loading and eluting capabilities. We intend to see high drug loading capabilities and for time control release of the drug of choice.
The federally endangered Smith’s blue butterfly (Euphilotes enoptes smithi) and its buckwheat hostplant species (Eriogonum latifolium and E. parvifolium) are threatened in their historic range by invasive species and habitat destruction, amplifying the importance of identifying and conserving their remaining populations. The diverse landscape of the Santa Lucia Preserve, a 20,000-acre conservation development in the Santa Lucia Mountains, supports Smith’s and E. parvifolium as well as four other sensitive buckwheat species, many of which grow in chaparral environments. The inland range of these species tends to cliffs and steep slopes, which presents challenges in detecting and quantifying these populations. To better document these species on the Preserve, we used physical and climatic variables such as rainfall, vegetation type, and aspect to create a habitat suitability model using ArcGIS and Maximum Entropy (MaxEnt). Initial model parameters were determined based on literature, and an updated model was created based on observations in 2017. Habitat predictions were tested in the field using a hand-held Trimble GPS and DJI drone with an on-board GPS tracker (accuracy sub-1 m), with initial results indicating successful predictions of buckwheat outside of known populations. Model predictions will be updated with ground-truthed data to increase MaxEnt model fit, and accuracy will be evaluated in fall after the 2018 blooming season. An effective and accurate buckwheat habitat suitability model will improve our understanding of these species on the Preserve, and will be applicable to habitat monitoring and conservation activities for Smith’s blue butterfly and buckwheat throughout their range.
Brine shrimp (Artemia franciscana) are aquatic crustaceans that are commercially harvested and inhabit inland and coastal aquatic environments with high salinity (10-20%). These organisms are often used in testing the toxicity of a chemical due to their availability and low cost. In this study, we observe how bacterial virulence of Escherichia coli (E. coli) at both high and low concentrations effect the growth in mass weight of brine shrimp hatchlings. We predict that the lower concentration of E. coli will allow more survival of nauplii in comparison to the high concentration E. coli. To begin, E. coli (Microbiologics™ Kwik-Stik ATCC 8739) was cultured in LB broth at a concentration of 1,000 CFU and incubated for 24 hours at 37°C. Post-incubation, 4 solutions (with 3 replicates of each) were made to a total of 2mL per dilution. The undiluted solution composed of 2 mL of undiluted E. coli, the following two dilutions were diluted to 1: 10 and 1:100 and one control solution comprised of 2mL of 20% saline solution. Half a milliliter of brine shrimp eggs (Harvested from the Great Salt Lake) were allowed to grow in 20% saline solution (1,000mL) for 24 hours until hatchlings were apparent. Once hatchlings were produced, 1 mL of nauplii were transferred to each of the 4 solutions and incubated at room temperature for 24 hours. After incubation 0.5 mL of nauplii were observed under a microscope and living individuals were accounted for along with the deceased individuals. All data was placed in Prism and a survival analysis was ran to determine if there were significant differences in survival rates between the control, diluted factors and undiluted E. coli. Results have not been gathered however data will be generated within the coming days*. This study can be furthered in biomedical research since it is believed that brine shrimp bioassays can be used as a guide to detect antitumor and pesticidal compounds. It also perceived that brine shrimp bioassays can also be correlated to human solid tumor cells.
Developing an R Package for Bioconductor based on the Ribolog method for ribosome profiling data analysis

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CSU Fullerton, NIH MARC

Eukaryotes experience extensive post-transcriptional regulation, alluding to the need of techniques that directly measure protein synthesis. It is crucial to accurately measure protein expression to elucidate differential translation and determine how genes are regulated in specific diseases or traits. Ribosome profiling was developed by combining ribosomal footprinting and deep RNA sequencing to provide an accurate depiction of the translating ribosome on corresponding mRNA strands. Ribosome profiling has the ability to identify translational start sites, determine the speed of translating ribosomes as well as identify translated mRNA regions of specific genes. A number of statistical software has been developed such as Xtail, which assumes a negative binomial distribution when determining differential translation from ribosome profiling data. An R package called Ribolog is currently in development to perform statistical analyses on these data. Ribolog does not assume any distribution of sequencing reads, thus generating a more flexible logistic regression to estimate the translational efficiency based on the ratio of RNA reads and ribosome protected fragments, and examine the significance of its difference among samples. Ribolog uses individual reads as units of observation, rather than genes or transcripts, which increases statistical power significantly. Unique to Ribolog, a local non-uniformity correction is performed to generate codon counts and it has the ability to calculate bias coefficients, normalize library reads and generate quality control reports. Ribolog will provide users with a comprehensive software that has the ability to perform the statistical analysis needed to determine differential translation of specific genes from ribosome profiling data.
We report sensitive detection of carbohydrate antigen 19-9 (CA 19-9) and carbohydrate antigen 242 (CA 242), the biomarkers of pancreatic cancer, using laser wave-mixing spectroscopy. Current detection methods require more time-consuming and complicated labeling steps. Our patented nonlinear laser wave-mixing methods offer significant advantages including label-free native detection, excellent sensitivity, small sample requirements, short optical path length, high spatial resolution and portable detector designs. The wave-mixing signal is generated when the two input beams are mixed inside the analyte and it can be collected with virtually 100% efficiency and maximum signal-to-noise ratio. The signal has a quadratic dependence on analyte concentration, and hence, small changes can be monitored more effectively. Since wave-mixing probe volume is small (nanoliter to picoliter), it is intrinsically suitable for microfluidics or capillary-based electrophoresis systems (e.g., 75 μm i.d. fused silica capillary). Different biomarkers can be immobilized on a custom 3D printed slide. Since wave mixing is an absorption-based method, both fluorophore and chromophore labels could be used, if desired. Excellent sensitivity levels for CA 19-9 are demonstrated using a Chromeo P503 tag and a 473 nm solid-state excitation laser. One can run a standard protein ladder to estimate capillary electrophoresis retention time for CA 19-9. The glass slides and microarrays used in these detection methods for early diagnosis of pancreatic cancer are custom 3D printed in our research lab.
Heavy metal contamination of drinking water and food sources is becoming an increasing concern in the United States, with arsenic and cadmium being amongst the top 10 toxins of most concern. These toxins enter the environment via a plethora of anthropogenic activities such as industry, pesticide spraying, and mining, and are threatening many potable water sources throughout the world. Arabidopsis Thaliana is a weed that can be seen thriving around the world in different kinds of environment including high levels of heavy metal. More than 100 strains of natural Arabidopsis Thaliana accessions from around the world were gathered. Seeds from these samples were harvested, sterilized, and placed in 1/2 Murashige and Skoog medium (MS media) to test for their viability to germinate. After 7 days, seeds that germinate will be transferred to their minimal media treatment medium and allowed to grow in the presence of arsenic, or cadmium. After 5-7 days, plant root growth will be measured via J-imaging to determine which strains of Arabidopsis Thaliana flourished the most in their heavy metal environment. These seeds can then be selected for and compared to one another to find the fittest strain. The goal is to use these plants to absorb heavy metals in the soil and prevent them from reaching water supplies.
Hermes Copper butterfly (Lycaena hermes) is endemic to Northern Baja California, Mexico through southern San Diego, CA, and very minimal research has been done on their biology and habitat. Thus, we would like to know more about this rare and endangered insect. It is known why the hermes population is limited to San Diego county and surrounding areas. Interestingly, Hermes are dependent on spiny redberry (Rhamnus crocea) shrubs as their host plant to lay their larvae. Spiny redberry are native to California, Arizona, and Baja California, expanding into larger areas than Hermes ranges. This research was focused on chemical composition of spiny redberry leaf extracts, to determine the significance of certain chemicals in the spiny redberry leaves and how it correlates to where the butterfly will lay their larvae. The non-polar leaf extracts were examined using gas chromatography-mass spectrometry (GCMS), revealing a single major component with the molecular weight of 430 g/mol and a partial structural match to tocopherol (vitamin E). Continuation of this project will consist of developing a method for liquid chromatography-mass spectrometer (LCMS) to analyze polar extracts and use of GCMS to quantify the tocopherol derivative.
ESTEBAN DELGADO III, Erik Paulson, Arnold L. Rheingold, and Douglas B. Grotjahn

San Diego State University, NIH IMSD

The Grotjahn lab has developed two catalysts that are highly selective in the production of (E)-alkenes from terminal alkenes. The cyclopentadienyl (Cp)-catalyst produces a mixture of internal (E) isomers, while the pentamethylcyclopentadienyl (Cp*)-catalyst selectively produces (E)-2 alkenes in up to ca. 95% yield. Currently, there are several alkene isomerization catalysts that convert terminal alkenes to internal (E)-alkenes relatively selectively, but fewer that select for (Z)-alkenes. As a result, an unmet need is to have a catalyst that makes (Z)-alkenes which tolerate polar functional groups, including alcohol and acid OH groups. We hypothesize that the high (E)-selectivity originates from the bifunctionality of the phosphine ligand. A potential approach to reversing selectivity is to further modify the Cp ligand to incorporate even bulkier R groups and change the position of the nitrogen base. The synthesis and characterization of functionalized cyclopentadienyl ligands, their respective ruthenium complexes, as well as their efficacy toward selective alkene isomerization, will be presented.
Let $H$ be a normed space. We explore the Pythagorean complement of a vector $v$ in $H$ on different norms. For norms that stem from an inner product on $\mathbb{R}^n$, we find that the Pythagorean complement is always a linear subspace. We are interested in exploring the outcomes for the Pythagorean complement on norms that do not stem from an inner product such as the taxi-cab norm and the uniform norm. Is the Pythagorean complement always a linear subspace of $H$? Is the Pythagorean complement always a connected set? Is it always a convex set? To answer these questions, we deduce all possible cases and find the image of the Pythagorean complement of a vector $v$ under different norms. Some of our results turned out to be predictable. Other results are surprising.
The use of Kratom has grown increasingly popular in the United States, it can be found in many local stores and is relatively inexpensive. It has been historically used to treat diarrhea and pain (Riverso) as well as for its psychoactive effects (Hamid). However, there are reports that claim Kratom can cause liver damage (Riverso) as well as lead to seizures and even to a coma state (Singh). Kratom’s active ingredient, Mitragynine, is important to understand and regulate by government agencies such as the FDA due to its increasing popularity. There are many strains of Kratom and strains can vary in Mitragynine concentration.

This study focuses on 4 strains of Mitragynine, Bali, Maeng Da, Borneo, and Indo. We extracted Mitragynine from Kratom leaves using liquid-liquid extraction to compare the concentration of Mitragynine in each strain. This study also compared soaking periods of two-day soaking period in methanol to seven day soaking periods. Results suggested that a two-day soaking period is not enough to completely transfer Mitragynine to methanol and showed that a seven-day soaking period gives a larger overall yield at the end of the extraction. When comparing the Mytragynine concentration of the four strains, results suggested that the order from least concentrated to most concentrated was Indo, Borneo, Bali, and Maeng Da. Results were obtained using a Shimadzu HPLC system consisting of a UV/VIS.
Rickettsia parkeri, a causative agent of tick-borne rickettsiosis, is an obligate intracellular bacterial pathogen that inhabits the host cell cytosol. Upon infection of host cells, R. parkeri undergoes actin-based motility to enable intercellular spread of the bacteria. R. parkeri has two phases of actin-based motility that require separate bacterial proteins: RickA acts early post-infection to assemble short, curved actin comet tails, and Sca2 acts later to assemble longer, straight actin tails. In response to rickettsial infections, the host innate immune system produces type I interferon, which upregulates antimicrobial genes such as guanylate binding protein 2 (GBP2). Although it is known that GBP2 functions in protecting against infection, the specific molecular mechanisms are not well understood. Previous studies have shown GBPs impair actin assembly by other bacterial pathogens, suggesting the hypothesis that GBP2 may also disrupt R. parkeri actin-based motility. As an initial assessment, immunofluorescence microscopy was used to visualize GBP2 localization in R. parkeri-infected cells. We determined that GBP2 localizes to the surface of stationary R. parkeri but not motile bacteria that have actin tails. In future studies we will assess GBP2 localization on wild-type versus rickA/sca2 mutant bacteria, and actin-based motility in wild-type versus mutant macrophages lacking GBP2 and other GBPs. From these experiments, we will determine if GBP2 acts to inhibit R. parkeri actin-based motility. These studies aim to elucidate for the first time an important aspect of innate immunity against microbial infection and establish whether and how GBP2 protects against infection by obligate cytosolic bacteria.
Alzheimer’s disease affects more than 44 million people and is the 7th leading cause of death worldwide. Large genome wide association studies have identified ABCA7 as a late-onset Alzheimer’s disease risk variant. This study aims to unravel the cellular processes that may be altered in variant ABCA7 cell types and how they play a contributing role in LOAD. We used CRISPR/CAS9 technology to generate an ABCA7 knockout human iPSC line, as a means to further model and investigate LOAD. Single stranded guide RNAs were selected to target exon 4 of the ABCA7 gene. The targeting oligomers were annealed and inserted into a pSpCas9 plasmid, with a GFP reporter. The plasmid was nucleofected into cells and transfected. GFP+ cells were FACS sorted. Individual cells were plated at a single cell density to allow for the creation of isogenic colonies. The colonies were picked and placed in a 96 well plate. Cell lines were expanded, DNA was isolated, PCR amplified, and sent for sequencing. Sequence analysis identified multiple cell lines that appeared to have a genome edit that would cause an early stop codon. Currently, we have 18 clones with edits in ABCA7 that we are interested in and we are validating the lines to confirm the genotype. Future studies will differentiate the generated ABCA7 knockout iPSC line into neuronal cell types. Due to the impending number of AD reported cases and deaths worldwide, it is of urgency to take advantage of a human model system to advance our knowledge of LOAD.
Different Types of Negative Emotion May Impact Memory for Associations

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Forming a coherent memory of a specific event involves binding together and encoding individual elements of the event. For example, during a bank robbery, encoding the robber’s face, his outfit, and his getaway car may be critical to later providing accurate eyewitness testimony. Prior research has shown that emotional arousal can produce vivid memories for an individual item that elicits emotion, but may weaken memory for information associated with that item. Previous work has not specified whether this effect generalizes across different negative emotions, like fear and anger. Fear and anger present an interesting comparison because a face showing an angry expression may be perceived as a direct threat to the viewer, thus enhancing processing of that face. A face with a fearful expression may indicate a threat elsewhere in the environment, directing attention to its surrounding context. The present study tested whether memory for face-object associations differed for when associations contained an angry versus a fearful face. Participants viewed triads consisting of an emotional face (neutral, angry, or fearful) and two neutral objects. We tested participants’ memories for all triad event associations and recognition of individual objects. Compared to neutral facial expressions, we expect both the fearful and angry facial expressions to impair memory for associations between elements. However, between fearful and angry expressions we expect to see better performance in the fearful condition. This study will contribute to understanding how negative events are encoded and produce findings relevant to eyewitness testimony.
TAR DNA binding protein 43 (TDP-43) is a nuclear protein that contains two RNA recognition motifs (RRMs) and a Glycine-rich region in its C-terminal domain. The function of TDP-43 is unclear, but it has been found to aggregate in deposits observed in patients with Amniotic Lateral Sclerosis (ALS) and Frontotem- poral Dementia (FTD). Recently it has been demonstrated that TDP-43 colocalizes with Stress Granules (SG), RNP granules that form during stress conditions by the aggregation of proteins and RNAs. Our research group is interested in understanding the aggregation behavior of TDP-43 by varying protein concentration, as well as altering environmental conditions. To understand the aggregation of TDP-43 we used yeast as a model: wild type hu- man TDP-43 protein attached to the mRuby2 fluorescent protein marker is driven by the Tet-On promoter which is dependent on doxycycline concentration. Based on the results obtained from concentration dependency of TDP-43, we determined that the optimal concentration is 40 ng/μL of doxycycline. Based on the optimal concentration test, we followed TDP-43 over time and observed that the expression of TDP-43 increased over time and predominantly localized to the nucleus. Surprisingly we found that when our cultures were infected with another fungus this caused caused TDP-43 to translocate from the nucleus to the cytoplasm and form cytoplasmic aggregates. To determine the colocalization of the aggregates in our yeast model we will use nuclear fluorescent markers as well as other RNP granule markers. Overall, we hope to learn more about the factors that control TDP-43 aggregation.
The issue of plastic packaging has become a pressing matter in recent years, as plastic waste is known to be detrimental to the environment. This research aimed to synthesize various aliphatic and aromatic polyesters that could potentially serve as solidifying agents. Such compounds could further be incorporated into liquid cosmetics, such as shampoos, soaps, and detergents, effectively eliminating the need for plastic packaging. Special attention was placed on esters containing linear carbon chains due to their affinity to form strong intermolecular interactions and display of hydrophobic behavior. A family of esters was prepared through well-established esterification methods, purified through extractions, Prep TLC, and column chromatography, and characterized by TLC, IR, and H NMR. Synthetic procedures of the aliphatic esters were generally more successful in formation of the products in moderate yields compared to the aromatic esters. However, purification proved difficult in most cases. On-going research is being conducted to further improve methods of synthesis and purification in order to obtain these products in higher yields.
Kazhdan constants relative to groups who yield isomorphic Cayley graphs are computed. The Kazhdan constant is dependent on the non-trivial irreducible representations of the respective group and the generating set. We focus on two distinct pairs of isomorphic Cayley graphs and compute the Kazhdan constant relating to the group and subset that generate the cayely graph. The question we are investigating is as follows: If two Cayley graphs are isomorphic, does this imply that their corresponding Kazhdan constants are equal? Our research began with investigating the dihedral groups and we will demonstrate to that this is not always the case. Our research continues with cyclic groups and will show that for specific generating cyclic groups and generating sets that the equality of Kazhdan constants holds.
Classical mathematical models are useful in modeling biological processes such as tumor volume growth. However, fitting these models to small data sets makes developing new treatment plans for cancer patients difficult. Regular and long-term measures of growth are not dependable and collecting sufficient data to confidently estimate the model parameters is challenging. Furthermore, fitting prediction models to small data sets can result in larger margins of error. We explore the minimum number of observations and time periods for these observations to confidently fit the logistic, generalized logistic, and the dynamic carrying capacity models for the prediction of tumor growth via computer simulations in R. These models were fit to data sets from Lewis lung and human breast carcinomas using Nonlinear Least Squares and other methods for fitting ordinary differential equations to small data sets. The results of this research may help identify the sufficient amount of information needed to select the appropriate mathematical model and confidently estimate the model parameters. Furthermore, this would allow for the development of new treatment methods for humans using minimal amounts of data while reducing costs of in vivo experiments by keeping the use of living test subjects to a minimum.
Formation of inorganic salts (i.e., scale deposits) is a problem in industrial and domestic setting. To control scale deposits, chemical scale inhibitors are commonly used. Thus, it is imperative to identify highly efficient polymeric inhibitors to replace phosphonate inhibitors due to their environmental risks. Antifreeze proteins (AFPs) from cold-adapted organisms can bind to specific ice surfaces, thereby inhibiting the nucleation and crystallization of ice. They also control the crystallization of some non-ice like compounds by interacting with their crystalline surface. We correlate the charge and molecular properties of the polyelectrolytes with their efficiencies in inhibiting the scale crystal formation. A beetle AFP from Tenebrio molitor (TmAFP) having regular spaced charged residues on its surfaces is prepared and studied here. Calcium carbonate (CaCO3) is a scalent of interest in this study. We investigate the effects of TmAFP and their mutants on the formation of CaCO3. One TmAFP mutant (D4) was modified with aspartate residues interspersed at equidistance apart from each other. The second TmAFP mutant (N5) was modified by removing all negatively charged residues, aspartate and glutamate, and replacing them with asparagine. Results show that the presence of TmAFP inhibits the formation of CaCO3, resulting much fewer CaCO3 crystals. The effect is more pronounced in the mutants. By analyzing the charged residues on the surfaces of TmAFP and calcite surfaces, we propose that TmAFP may affect the formation of calcite via adsorption to the crystalline surfaces of CaCO3.
The increased usage of pesticides in conventional cropping systems are impacting businesses, communities, and ecosystems by the unintended dispersal of the excess additives that can contaminate groundwater or promote eutrophication. A proposed solution to mitigate the effects are the use of naturally-occurring microbes in the environment to remediate the excess pesticides. Bioreactors are an innovative, closed-system strategy designed and used to understand the efficacy of these microbes in their ability to remediate pesticides; however, there is a lack of understanding in the genetic mechanisms that actually allow bacteria to metabolize pesticides. In this study, we use 10 bacterial strains that have been sampled from three different sites located at Molera Constructed Treatment Wetland and are known to possess the ability to metabolize the organophosphate-based pesticide, Diazinon. We will extract the DNA of these bacterial strains and genome sequence the results with a MinION sequencer to identify, compare, and analyze the particular genes associated with remediation. In addition to generating novel genome sequences for these strains of bacteria, the results from the bacteria that metabolize Diazinon will be used as a “proof-of-concept” of methodology for examining other bacteria that are able to remediate other pesticides that are less-studied, but widely used (e.g. Imidacloprid, a neonicotinoid-based pesticide). This increased accessibility to genome sequencing will allow us to more easily investigate bacterial mechanisms, apply more strategic techniques to bioreactor design, and increase the effectiveness of bioreactors in mitigating damages caused by excess pesticide usage in agriculture.
Changes in the extracellular matrix (ECM) of tissues are observed in a wide array of acute and chronic diseases. These changes result in differences in the tissue biomechanics recorded during compressive testing, which would enable the development of a novel method for classifying and diagnosing disease. However, understanding how structural changes in the ECM occur and change with disease development is a challenge due to the complex viscoelastic behavior of biological samples and the limitations of current biomechanical models. To overcome these challenges, novel physical and computational models were developed for specific tissue types and disease pathology. By taking experimental compressive testing measurements with Optical Fiber Polarimetric Elastography (OFPE), models were developed to understand how specific structural changes in the ECM affect the complex viscoelastic behavior of biological samples. Based on physiological parameters, determined from testing and imaging of cardiac, cartilage, and pancreatic tissues, we designed simple geometric structures in SolidWorks. The structures were imported to Abaqus, a finite element analysis (FEA) software, to model how geometric changes impact the viscoelastic behavior observed during compressive testing. Geometric changes in the structure were systematically conducted to simulate the damage that occurs during disease development. After FEA modeling, structures are 3D printed using projection microstereolithography and compressively tested. The results from the computational and physical modeling demonstrate how these novel models can be used to study the complex role of the ECM in dynamic tissue biomechanics.
We present a study on the usage of piezoelectric disks within synthetic jet actuators. Synthetic Jet actuators are frequently used in various cases when flow separation occurs. Whether an airplane is in flight or a turbine blade rotates flow separation can occur. This separation occurs over an airfoil or when turbomachinery is used off design. The phenomena of flow separation increases the drag, making vehicles less efficient by an increase in fuel usage and decreased runtime. Studies show that flow can be controlled though an active or passive form. Active form would include an apparatus that reacts to changing conditions in the flow. Passive form devices have a constant state. The past two years Synthetic Jet actuators (synjets) have been studied at the San Diego State University. The focus is flow over an airfoil using separation control. The synjet is a piezoelectric diaphragm encased by a 3D printed cavity. A sinusoidal voltage applied to the piezoelectric disk oscillates it, creating a jet of air used to control the suction side of the airfoil. Over the past decade piezoelectric actuator studies have concentrated on actuation performance and on enhancing actuation displacement, but little has been done to ensure the integrity and reliability of these disks. We present the introduction to recent research conducted using piezoelectric disks and what changes can be made to increase the lifespan of the piezoelectric diaphragms. This will be done by testing the strength of the disk by cyclic loading, as well as testing within a NACA airfoil. Our goal is to give the audience a basic understanding of both the material properties and the new techniques that can be applied to this new research project.
HUGO A. MORA and Howard Xu

CSU Los Angeles, NSF LSAMP Bridge to the Doctorate

With the rapid increase of antimicrobial resistance to current antibiotics, a need to discover and develop novel antibiotics is a priority. High throughput screening (HTS) coupled with exploring chemical diversity have made it easier to identify antibacterial compounds. However, linking antibacterial inhibitors to their cellular targets remains a bottleneck in developing new antibiotics. In this research project, our goal is to identify novel antibacterial inhibitors by screening synthetic and natural compound libraries, followed by testing hit compounds in our disk diffusion assay (Target Identification Platform for Antibacterials 2; TIPA II) to identify potential drug targets. HTS will be achieved using our Beckman Coulter Biomek FX\textsuperscript{\textregistered} Liquid Handling Automation Workstation for the preparation of test compound assay plates and FilterMax F5 for reading the 96-well plate assay cell turbidity. The TIPA II platform leverages a collection of Escherichia coli clones in AS19 host cells, which has a more permeable membrane rendering it more sensitive to identify cellular target of compounds. So far 10,080 synthetic compounds and 419 natural compounds have been screened resulting in 20 hits from the synthetic compounds 49 hits from natural compounds giving a hit rate of .2% hit rate 11.6% respectively. These hit compounds will be ordered in their pure form to perform TIPA 2 to determine potential cellular targets. Significance of these findings will allow us to facilitate the discovery of antibacterial compounds along with their putative targets for future development.
Energy limits are one of the toughest problems that humanity faces. Methane is a common byproduct from oil companies that is generally flared off. Converting methane to methanol would provide an energy-dense fuel source that is easier to transport. The direct oxidation of methane is currently not used industrially, because there is no viable and efficient method. Methane monooxygenases (MMOs) are bacterial enzymes that can effectively and selectively catalyze the oxidation reaction that converts methane to methanol. The bacteria that use this enzyme are difficult to cultivate and a synthetic system that mimics the enzyme would be a useful alternative. Our research focuses on fabricating both diiron and tri-copper complexes that will be inserted into a polymer in order to effectively mimic the coordination sphere of the MMO active site. We have successfully reproduced ligand syntheses for both diiron and tri-copper complexes. Metallation of these species produced two known complexes we can use as benchmarks for alkane oxidation catalysis. Currently, we are modifying the ligand syntheses to add alkenes onto the ligand framework as an easy connection to a polymer. Our next step is to covalently connect our modified metal complexes (via thiol-ene click chemistry) to synthetic polymers which will serve as scaffolds for the desired reactivity, hopefully enhancing the catalytic activity and selectivity of the two complexes.
As antibiotic resistance increases, there is a pressing need to develop new antimicrobials. Although initial discovery is done in vitro, in vivo assays are essential to provide additional information. The purpose of this project is to develop an in vivo protocol that will use lobster cockroaches (Nauphoeta cinerea) to test the antimicrobial activity of essential oils when roaches are challenged with an entomopathogen. Essentially, we want to incorporate this project into ethnopharmacology studies where traditional herbal medicine antibiotic properties may be examined in invertebrate models instead of vertebrates. Initially, cockroach bacterial pathogens will be exposed to a series of essential oils suspected to inhibit their growth and tested via Kirby Bauer assays. This step will confirm which essential oils do inhibit the available strains of the cockroach bacterial pathogens. Next, will be to determine the minimal inhibition concentration (MIC) of the essential oils on the cockroach pathogens. After the MIC is determined for each essential oil, these will be injected into cockroach groups along with the bacterial pathogens to determine if antimicrobial activity inhibits pathogen growth and prevents death. Developing a cheap and simple in vivo model using cockroaches will be invaluable in assessing antimicrobial activity of ethnopharmacological compounds.
Metal-Organic Frameworks (MOFs), as the most porous family of materials, are being synthesized and studied for various green chemistry applications. Hydrogen can be employed as a fuel source with a carbon-neutral energy cycle. In our work, we report five new porous MOFs based on a tetratopic ligand. Through the variation of the metal salts and solvents in the solvothermal reaction, these MOFs exhibit varying structural features. All of the MOFs analyzed showed impressive hydrogen storage capacities, especially the ionic Co-MOF, which reaches 2.64 wt% uptake at 77K and 1 bar. Based on the hydrogen uptake data, a list of structural properties including catenation, metal nodes, charge, topology and pore size are reported and evaluated for hydrogen storage application. These structure-property studies are effective in guiding the future rational design of MOFs for hydrogen storage. Future work will focus on the incorporation of new metal clusters and hybrid (MOFs/GO) iterations of the MOFs described in this work.
Abstract rescinded
Dark field microscopy (DFM) has various advantages in studying nanoparticles but can also be applied to a wide range of other applications in biology and particle tracking. It can provide an alternative to fluorescence super resolution localization. DFM has scattering that is label-free and does not photobleach or blink, therefore eliminates common complications. This microscope was built so all the optics are located on one side of an optical table. Having the other side available to be easily integrated with other illumination techniques like broadband infrared (BBIR). This work involved the development of a dark field microscope that has the capability of obtaining high resolution images with high sensitivity. The method used for scanning is a modification of interferometric scattering microscopy (iSCAT), where only the scattered light is detected. This is accomplished by focusing the laser light to a fixed point and raster scanning the sample, while collecting the scattered light on a single channel photodiode. The dark field microscope was used to obtain high resolution images of 1-micron gold nanoshell particles and E coli. tagged with red fluorescent protein. The future focus will be on enhancing the scanning speed for single particle tracking using the method and microscope described above.
Protection of wetlands is crucial to the maintenance of worldwide biodiversity, and conservation and management of wetlands require measures of biodiversity. The aim of this study was to examine seasonal variation in avian biodiversity. I examined the seasonal changes to biodiversity (Species Richness \([R]\) and Shannon Diversity index \([H']\)) in the San Elijo Lagoon wetland over a 15 year period. The influence of seasons on biodiversity was examined to assess which seasons expressed the highest levels of biodiversity. I found that both Species Richness and Shannon Diversity vary temporally. Fall and Winter \(H'\) increased positively across years with high levels of correlation (\(R^2 =0.6773, p<0.0001\) Fall linear regression; \(R^2 =0.5771, p=0.001\); Winter linear regression). Furthermore, Species richness and Shannon Diversity index were higher in Spring. Wetland use varies greatly from season to season indicating temporal variation in wetland use, and indicating a need for further protection of wetlands during critical periods in use. Overall, Shannon Diversity values above 3.5 for the 15 years indicate consistently high levels of species diversity and evenness throughout the San Elijo Lagoon wetland.
Mucolipidosis type IV (MLIV) is caused by a dysfunctional Mucolipin-1 (TRPML1) ion channel. We previously reported elevated levels of zinc within lysosomes of MLIV cells and identified Transmembrane (TMEM)-163 protein, a putative zinc transporter, as an interaction partner for TRPML1. To further study its zinc transport function and connection to certain human diseases like MLIV, we used the single nucleotide polymorphism (SNP) database from the National Center for Biotechnology Information website to study sequence variations within the TMEM163 gene. We identified non-synonymous SNPs located in areas of the protein that could affect post-translational modification. We hypothesize that these SNPs could disrupt the zinc transport function of TMEM163 in cultured cells. Site-directed mutagenesis using In-Fusion homologous recombination cloning was used to systematically replace specific nucleotides corresponding to the SNPs located within or in proximity of N- and C-termini, as well as Transmembrane domain (TMD)-1 to TMD-6. Upon sequence verification, the effect of each SNP-associated mutant was transfected into cultured HEK-293 cells. Twenty-four hours post transfection, the cells were exposed to zinc chloride (10 μM) and zinc pyrithione (1 μM), and assayed for zinc flux using the zinc specific, membrane impermeable FluoZin-3 AM dye. We found that TMEM163 is an effluxer, and clones with non-synonymous SNP showed markedly lower zinc efflux relative to the wild-type control. Thus, this study confirmed that TMEM163 is a zinc efflux transporter and showed for the first time that certain non-synonymous SNPs could disrupt the function of the protein. Future investigation will focus on other SNPs.
Selective recognition and complexation between two or molecules is a critically valuable in biological as well as in synthetic processes. We seek to exploit non-covalent recognition processes by synthesizing a conformationally switchable capsule that will controllably complex and release molecules. Resorcin[4]arenes have the capacity to be synthetically transformed to a structure with a cavity, including a capsule shape. We propose that by using quinoxaline and ethylene linker groups we will be able to synthesize a capsule that has more flexibility than previously synthesized capsules in our lab. The goal of this project is to study the proposed capsule through different solvents, pH, and temperatures to observe the conformational switching under mild conditions. Analysis of the studies will provide an understanding of capsule rigidity and design optimization of the capsule for the next generation. The analysis and characterization of the capsule will be done through Variable Temperature (VT) NMR, 1HNMR, 13CNMR, infrared spectroscopy, and high-resolution mass spectrometry. Advances in the design of this capsule will allow for future development of its applications in selective binding, quantitative separation, and detection techniques.
Thermochemical water splitting is an attractive method for hydrogen production due to its lack of greenhouse gas emissions. Efficacious catalysts for this reaction are oxygen-rich; they exchange their own oxygens with those in gaseous water, leaving behind hydrogen fuel as a byproduct. Previous studies on metal oxides have determined ceria (CeO$_2$) to be an effective catalyst. To identify new viable catalysts, we computationally model 4 cerium-based perovskite oxide crystals (CeBO$_x$, B=La, Mn, Co, Fe) using ab initio methods. Structures of each compound of interest are constructed by the evolutionary crystallography structure prediction software USPEX and density functional theory (DFT) methods. The ground state energy of each crystal is then calculated via DFT and compared to its counterparts containing oxygen defects. The structures found to have these “vacancy formation energies” between 2.5-5eV are viable catalysts for water splitting- and therefore hydrogen production.
We report sensitive detection of carbohydrate antigen 19-9 (CA 19-9) and carbohydrate antigen 242 (CA 242), the biomarkers of pancreatic cancer, using laser wave-mixing spectroscopy. Current detection methods require more time-consuming and complicated labeling steps. Our patented nonlinear laser wave-mixing methods offer significant advantages including label-free native detection, excellent sensitivity, small sample requirements, short optical path length, high spatial resolution and portable detector designs. The wave-mixing signal is generated when the two input beams are mixed inside the analyte and it can be collected with virtually 100% efficiency and maximum signal-to-noise ratio. The signal has a quadratic dependence on analyte concentration, and hence, small changes can be monitored more effectively. Since wave-mixing probe volume is small (nanoliter to picoliter), it is intrinsically suitable for microfluidics or capillary-based electrophoresis systems (e.g., 75 μm i.d. fused silica capillary). Different biomarkers can be immobilized on a custom 3D printed slide. Since wave mixing is an absorption-based method, both fluorophore and chromophore labels could be used, if desired. Excellent sensitivity levels for CA 19-9 are demonstrated using a Chromeo P503 tag and a 473 nm solid-state excitation laser. One can run a standard protein ladder to estimate capillary electrophoresis retention time for CA 19-9. The glass slides and microarrays used in these detection methods for early diagnosis of pancreatic cancer are custom 3D printed in our research lab.
The human intestinal mucosa is defined by its epithelium where nutrient absorption occurs. The intestinal epithelium contains two regions, the villi and the crypts. The cells in both regions adhere together via tight junction proteins such as zonula occludens 1, or ZO-1. Various cell types constitute the intestinal epithelium, with the crypts containing intestinal stem cells (ISCs) that differentiate into five other cell types. These cell types include transit-amplifying, enteroendocrine, goblet, enterocytes, and Paneth cells (PCs). The Paneth cells provide defense to the intestines in the form of secreted antimicrobial peptides. However, they have also been recently known to help regulate environmental niche for these stem cells to grow by providing growth signals to their predecessor, the Lgr5+ ISC (Sato 2011). Both Lgr5+ ISCs and Paneth cells are important for several gut related diseases. Lgr5+ ISCs are associated with intestinal cancers, specifically colorectal (Uchida 2010). Paneth cells with their defensive nature are involved in combatting intestinal infections such as Salmonella, but also with inflammatory bowel disease (Porter 2001). Due to both cell population’s major contributions to the intestinal epithelium, their localization in the gut need to be investigated. Our objective is to highlight these cells and other homeostatic characteristics related to them, as well as establish protocols. We have opted to use immunohistochemistry and immunofluorescence as a means to achieve this objective. We have set protocols for PC staining using antibodies against human defensin 5, tight junctions via antibodies against ZO-1, and ISCs via antibodies against Lgr5.
Reward processes related to pups in lactating dams support maternal behavior, but the underlying neural mechanisms of this pathway in the postpartum period are not well understood. Conditioned place preference (CPP) is a behavioral test that measures a preference to an area after pairing it with a rewarding stimulus. Past studies have used food or drugs to elicit a reward response in a chamber even if they weren’t present because the subjects learned to associate the chamber with them. Our goal was to alter CPP so it would be relevant for postpartum dams using pups as a reinforcer, as pups are a rewarding stimulus for dams. In this study, 13 postpartum mice underwent CPP. The apparatus consisted of three chambers. The two side chambers having horizontal or vertical black and white stripes on the walls as visual stimuli and either corn cob or wood chip shavings as tactile cues. Dams were deprived of her pups for 90 minutes before conditioning. During conditioning, dams were placed in one chamber per day for one hour with or without her pups alternating chambers each day for four days. The dam was allowed access to every chamber to test for preference. The results showed seven of the 13 dams showed an increase in preference to the pup-associated chamber compared to baseline. This means that manipulating pup deprivation and exposure can elicit a place preference in dams and CPP may be a useful measure to study the underlying neuromechanisms of reward in the postpartum period.
The goal of this project is to create a Metal-Organic Frameworks (MOF) catalytic converter that can effectively reduce the waste production of harmful gases, and particles produced during the operation of internal combustion engines. The waste produced from combustion includes: nitrogen oxides (NOx), carbon monoxide (CO), volatile organic compounds (VOCs), and particulate matter (PM). The ability of MOFs to capture small particles and gases as well as catalyze heterogeneous reactions suggest their advantage in this application. The MOF catalytic converter has the potential to capture PM, operate optimally at all temperatures, and use cost effective materials to perform its function, all of which are limitations of current catalytic converter systems. The project requires the development of a model, composed of a MOF catalytic chamber for catalysis of gases and multiple MOF membranes for PM capturing. The initial step of the project, the one discussed in this work, is the development of the catalytic chamber. The first target reaction will be the conversion of NOx into N2 and O2 gas. The proposed catalysts for the conversion of NOx are two Ti (IV) containing MOFs: MOF-74(Zn)-Ti and PCN-222-Ti.
The purpose of the current study is to examine the relationship between gender, parental closeness, and risky behaviors, such as substance use, motivation to engage in sexual behaviors, and delinquency in Latinx adolescents. We hypothesized that those who reported greater closeness with their parents would report lower levels of risky behavior. This study uses data from the National Longitudinal Study of Adolescent and Adult Health (ADD Health) and the sample consisted of 743 Latinx adolescents in middle and high school around the United States. Pearson’s r correlations found that greater closeness to mothers and fathers was associated with less substance use, lower internal motivations to engage in sexual behaviors, and less delinquency. Independent samples t-test found that adolescent males reported greater internal reasons to engage in risky sexual behavior, delinquency, and substance use than adolescent females. After controlling for gender, multiple linear regression analyses found that greater maternal closeness was associated with less delinquency and less alcohol use in the past twelve months and greater paternal closeness was associated with less delinquency and internal and external motivations to engage in risky sexual behaviors. This study also explores these associations in Latinx adolescents, an understudied group in psychological research. These findings may be reflective of Latinx cultural values and have broader implications for treatment of substance use disorders. Latinx adolescents may benefit the most from a multicultural, family-based therapy.
Pseudomonas aeruginosa is a gram negative, opportunistic pathogen that has been listed by the World Health Organization as a “priority pathogen” for its threat to human health, which is worsened by increasing antibiotic resistance. Cationic antimicrobial peptides (CAPs), like polymyxin B, are used as a last resort treatment against multidrug resistant strains of P. aeruginosa. CAP-resistant strains of the bacterium possess less negatively charged outer membranes due to lipid A modification directed by the arnBCADTEF operon. This change in charge lessens the driving force of the electrostatic interactions with the positively charged CAPs, hindering entry of the antibiotic. Each enzyme in the pathway is required for modification, making them all candidates for inhibition to block the resistance pathway. We targeted ArnA for further biochemical study. ArnA is the first committed step in the lipid modification pathway, catalyzing an oxidative decarboxylation of UDP-glucuronic acid as well as a N-formylation after modification by ArnB. Recombinant expression of ArnA was achieved by cloning the arnA gene into the pET28b vector, followed by transformation into the Escherichia coli expression strain BL21(DE3). The addition of a hexa-histidine tag will allow for nickel column purification. After purification, future research will include kinetics and binding studies. The information gathered from this study will help in the development of inhibitors to block the resistance pathway and restore the efficacy of CAPs.
Candida albicans is part of the normal microbiota of the human body and causes opportunistic infections in immunocompromised individuals. During infection Candida albicans is exposed to oxidative and osmotic stress, which is deadly to the fungus. Thus Candida albicans responds to these stresses by activating compensatory mechanisms that up regulate cell wall chitin production. The high osmolarity glycerol pathway (Hog1p) and the cell wall integrity pathway (Mkc1p) are known to regulate the oxidative and osmotic stress responses in C. albicans. Previous research in our lab demonstrated that removing yeast casein kinase 2 (Yck2p), a fungal homolog of the casein kinase 1 family, caused an increased susceptibility to cell wall and cell membrane stressors and an increase in chitin synthesis and expression. These results suggest that Yck2p is required to manage cell wall integrity and stress response. To determine the role of Yck2p in the stress response of Candida albicans the yck2 mutant strain was grown under osmotic and oxidative stress. The yck2Δ/yck2Δ mutant strain displayed hypersensitivity to osmotic stressors (1.2 M Sorbitol, 0.6M KCl, 2M glycerol, and 1M NaCl) and oxidative stressors (0.03125 mM and 0.0625mM menadione, 0.005M H2O2, and 0.01M Caffeine) as compared to the wild type strain. These results led us to hypothesize that Yck2p participates in the stress response by activating the Hog1p and Mkc1p in C. albicans. Future work will determine if Yck2p governs osmotic stress and oxidative stress by phosphorylating and activating the Hog1p and Mkc1p mediated MAPK pathways.
Presenter Program Interest

Biochemistry, Biophysics & Structural Biology

2  Robert Boyd III
4  Angela Bui
6  Carmen Camarena
11 Esteban Delgado III
13 Daniel Flores
15 Salena Gallardo
17 Magaly Guzman Sosa
18 Elizabeth Tadevosyan
21 Audrey Kishishita
29 Mario Pizarro Rojas
30 Rosa Romero
40 Cassandra Villicana

Bioinformatics

6  Carmen Camarena
7  Christina Chavez
9  Salvador Cruz Matus
20 Maria Teresa Hernandez

Cell & Developmental Biology

3  Amy Briggs
6  Carmen Camarena
9  Salvador Cruz Matus
14 Joshua Fonbuena
15 Salena Gallardo
17 Magaly Guzman Sosa
32 Vanessa Sanchez
35 Nino Shatirishvili
36 Elvia Silva
18 Elizabeth Tadevosyan
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**Genetics & Genomics**

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**Immunity, Microbes & Molecular Pathogenesis**

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21 Audrey Kishishita  
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27 Valeria Navarro  
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35 Nino Shatirishvili  
36 Elvia Silva  
41 Cipriano Zuluaga
## Presenter Program Interest

### Molecular, Cellular & Integrative Physiology

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### Molecular Pharmacology

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### Neuroscience

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Presenter Program Interest

Physics & Biology in Medicine

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23 Juan Leal Doblado
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40 Cassandra Villicana

Chemistry

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California State University, Los Angeles

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25 Hugo Mora
28 Yessica Nelson
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39 Rachel Verhagen
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22 Mercedez Lam

California State University, San Marcos

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3  Amy Briggs
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9  Salvador Cruz Matus
10 Jessica Dang
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17 Magaly Guzman Sosa
30 Rosa Romero
31 Adrian Ruiz
37 Jhair Torres

San Diego State University

8  Samantha Crawford
11 Esteban Delgado III
24 Jennifer Martin Velazquez
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San Jose State University

26 David Navarro
40 Cassandra Villicana

Glendale Community College

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18 Elizabeth Tadevosyan