College of Natural Sciences & Mathematics

LONG BEACH STATE UNIVERSITY

ABSTRACT BOOK

CNSM Student Research Symposium

Friday, September 20, 2019

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California State University, Long Beach

Student Research Symposium

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Without their support throughout the year, this event would not be possible.

Symposium Booklet and Event

The Student Research Symposium is held in the University Student Union (USU) Friday, September 20th, 2019. This event, held by CSULB, College of Natural Sciences and Mathematics is open to undergraduate and graduate participation. The research being presented at this event is from on-campus research and/or from summer research experiences performed at other universities.

The symposium provides an opportunity for students to write abstracts, produce posters, and present research findings thereby bringing scientific and non-scientific communities together to share in ideas and discoveries. Students, staff, faculty, administrators, and community members attend this event and enrich the experience of all participants. If this is your first time attending a symposium, feel free to walk around and ask the students questions about their research experience. We encourage any questions you may have about the research presented today. Thank you for attending our event.

The abstracts provided in this booklet are original works of students in our programs. Each abstract is included alphabetically by first author's first name.

Symposium Program

10:00-10:10am:	**Dean's Welcome** Dr. Curtis Bennett *Richard D. Green Dean of CNSM*
10:10-10:30am:	**Keynote** Dr. Benjamin Hagedorn *Assistant Professor in the Department of Geological Sciences*
10:30-10:50am:	**Getting Started in Research** Cynthia Alarcón *Program Coordinator*
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11:55-12:05pm:	Poster Session 2 Set Up
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Pizza will be served in the Alamitos Bay Room at 11:30am.

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1. The Role of Lysine 52 and 54 in the Stability of Apolipophorin III

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Apolipophorin III (apoLp-III) is an 18 kDa exchangeable protein found in insects and it is similar to human apolipoprotein in structure and function. Due to the availability of its three-dimensional structure it is used as a model protein to study lipid transport processes and innate immunity. ApoLp-III from *Locusta migratoria* contains eight lysine residues which reside on the protein surface and it is hypothesized that these residues form salt bridges with neighboring acidic residues to stabilize the protein. Denaturation studies with guanidine-HCl demonstrated a reduction in stability when lysine residues at position 52 and 54 were replaced with glutamine, indicating disruption of a salt bridge. In order to identify which lysine residue forms a salt bridge formation, site-directed mutagenesis was employed to create two single lysine to glutamine mutants, K52Q- and K54Q-apoLp-III. The mutants were created with the Quick-change site-directed mutagenesis kit and the mutation was confirmed with DNA sequencing. The proteins were expressed in *E. coli* and purified by size exclusion chromatography and HPLC. Measurement of the secondary structure content by circular dichroism showed an increase in helical content from 67% in wild-type apoLp-III to 73% for K52Q-apoLp-III and 83% in K54Q-apoLp-III. The protein was incubated with increasing concentration of guanidine-HCl to determine its resistance to the denaturant. The midpoint of denaturation was calculated as a measure for protein stability. The midpoint decreased from 0.50 ± 0.01 M for wild-type apoLp-III to 0.42 ± 0.06 M for K52Q-apoLp-III. The midpoint of denaturation did not change significantly for K54Q-apoLp-III (0.48 ± 0.02 M). The decrease in midpoint for K52Q-apoLp-III indicates that this residue participates in an interhelical salt-bridge, potentially with aspartate 90, to stabilize the protein structure of apoLp-III. Solubilization of anionic and zwitterionic phospholipid vesicles were used to investigate the effect of the mutation on the apoLp-III lipid binding properties. No difference in lipid binding between wild-type-apoLp-III and the mutants were observed. Changes in tertiary structure were measured with anilinonapthalene-8-sulfonic acid (ANS) and tryptophan fluorescence. A decrease in the tryptophan quantum yield was noted for the two mutant proteins indicating changes in the microenvironment of the tryptophan residues. However, no differences in the ANS fluorescence were observed suggesting no major changes in the tertiary structure of the protein.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers GM089564, 8UL1GM118979-02, 8TL4GM118980-02, and 8RL5GM118978-02.

2. Complex Oxides for Oxygen Evolution Reaction

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Electrochemical water splitting is important in sustainable production and storage of energy. This process involves two half reaction of hydrogen evolution reaction (HER) and oxygen evolution reaction (OER). Both reactions are slow and require a catalyst. Electrochemical water splitting uses electrocatalysts in the anode (for HER) and cathode (for OER) of electrolyzers to perform this reaction. OER is the more difficult reaction and requires substantially higher overpotential. Hence, we are focused on using complex oxides of iron as stable, cost-effective, and nontoxic alternative to the noble metal-based catalysts, *i.e.* RuO_2 and IrO_2 often used for this reaction. Complex oxides are attractive due to their high tunability and stability. In our work, we explore the catalytic properties of perovskites, brownmillerites, and pyrochlores type structures for OER. Solid state synthesis is employed to rationally design compounds with varying compositions. Electrochemical and physical characterization methods are used to analyze materials properties and electrocatalysis of these compounds. We will present our results related to the interplay of structure, activity and stability in aqueous media.

This research was partly supported by NSF-DMR-RUI Award #1601811.

3. Deterring the Aggregative Growth of Zeolitic Imidazolate Framework-8 Nanoparticles for Gas Adsorption

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Zeolitic imidazolate framework-8 (ZIF-8) is a type of metal-organic framework (MOF) composed of tetrahedrally coordinated zinc ions connected with 2-methylimidazolate (mIm) ligands. Due to its large surface area and high porosity, ZIF-8 is widely used for gas adsorption to capture greenhouse gases such as carbon dioxide. Consequently, the available surface area is crucial for the efficiency of the gas adsorption. By altering the molar ratio of mIm to Zinc ions, the size of the synthesized ZIF-8 particles could be controlled in the nanoscale. However, the aggregation of particles at high mIm to Zinc rations compromise the effective surface area of the particles, hampering their gas adsorption effectivity. In this work, various approaches were attempted at mitigating the aggregation of the ZIF-8 particles to maintain the nanoparticle size as well as retaining the maximum gas sensing effectivity. By introducing a cationic surfactant into the synthesis solution, the electrostatic interactions between the ZIF-8 particles were disrupted, lowering the amount of aggregation among the particles. The biochemical buffer Tris(hydroxymethyl) aminomethane (THAM) was added in hopes of amine functionalizing the ZIF-8, but instead resulted in the formation of ZIF-8 that retained moisture with a gel-like consistency. Further experiments will be conducted to assess the nature of ZIF-8 synthesized with surfactants applications of the gel-like ZIF-8.

This project is supported in part by the Environmental Research and Education Foundation (EREF), the American Chemical Society Petroleum Research Foundation (ACS PRF), and the CSULB ORSP grant.

4. Investigating the Role of Stereochemistry in the Development of Cholinesterase Inhibitors to Treat Alzheimer's Disease

Michael Lam[1] and Jason Schwans[2]
[1]Department of Biological Sciences, California State University Long Beach, Long Beach 90804 and [2]Department of Chemistry and Biochemistry, California State University Long Beach, Long Beach 90804

In persons afflicted with Alzheimer's and other neurodegenerative diseases, previous literature has implicated the role of cholinesterases, a group of enzymes, involved in neuronal signal transduction. Previous studies have shown butyrylcholinesterase (BChE) activity increases in patients with Alzheimer's Disease (AD), leading to the depletion of an neurotransmitter, acetylcholine. To alleviate the symptoms of AD, cholinesterase inhibitors have been used as pharmaceuticals. We recently identified amino acid analogs bearing the 9-fluorenylmethyloxycarbonyl (Fmoc) group as potent and selective BChE inhibitors. As the Fmoc amino acids contain a chiral center and stereochemistry often has a substantial on inhibitor potency, we are currently testing both enantiomeric forms of Fmoc Leu, Fmoc Lys, and Fmoc Trp. The inhibition constant (KI value) will be determined using enzymatic assays followed by UV-vis spectroscopy. The KI values of our study were used to evaluate the effectiveness of the respective compound's enantiomeric form as an effective inhibitor. Altogether, this study's purpose is to analyze the significance, if any, of stereochemistry on inhibition.

This research was supported by the Undergraduate Research Opportunity Program (UROP).

5. Antimicrobial Activity of Apolipoprotein on Gram-negative Bacteria

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Antimicrobial peptides (AMPs) are an organism's innate defense against pathogenic bacteria, fungi, and enveloped viruses and parasites through targeting cellular membranes, specifically the outer surface lipids and membrane proteins. Multiple AMPs can be released to work synergistically against gram-positive and gram-negative bacteria. Gram-negative bacteria, such as *Escherichia coli*, consists of two membranes, the outer membrane and inner membrane, which is separated by a periplasmic space that includes a peptidoglycan layer. Both membranes contain proteins, while the outer membrane also is embedded with a lipopolysaccharide (LPS), that is a strong endotoxin. Human apolipoprotein A-I (apoA-I), the main protein of high-density lipoprotein, has been identified as a potential AMP. Previous studies have shown that apoA-I binds to LPS and phosphatidylglycerol (PG), an abundant negatively charged phospholipid that

may attract cationic AMPS. The focus of this project is to study the antimicrobial activity of apoA-I, in concert with the antimicrobial enzyme lysozyme. This enzyme catalyzes the hydrolysis of the peptidoglycan layer in gram-negative bacteria, compromising the structure of the bacteria cell wall. To effectively ascertain the level of activity of apoA-I and lysozyme, Cecropin B will be used as a positive peptide control. Cecropin B is an insect AMP originally isolated from *Hyalophora cecropia* and is known for lysing bacterial membranes by binding to the LPS layer of the bacterial outer membrane. The effect of Cecropin B on *E. coli* was tested using LIVE/DEAD® BacLight Bacterial Viability Assay. This assay uses two nucleic acid stains: SYTO 9, a green fluorescent membrane-permeable stain, and Propidium Iodide, a red fluorescent membrane-impermeable stain. Only if the membrane is compromised will the cells fluoresce red, due to the Propidium Iodide being unable to reach DNA through an intact membrane. Fluorescent emission spectral measurements, from 490 to 670 nm, showed *E. coli* cells incubated with Cecropin B for one hour to have similar fluorescent levels of that of *E. coli c*ells incubated with 70% ethanol, which serves as a negative cell control. Once the minimum inhibitory concentration has been determined for Cecropin B, apoA-I will be tested on *E. coli,* both in the presence or absence of lysozyme.

Research is supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number GM089564.

6. Tyrosine hydroxylase neurons project to β-endorphin neurons regulated by progesterone

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In ovariectomized (OVX) rats, a priming dose of 2μg of estradiol benzoate (EB) induces the release of β-endorphin (β-END) from neurons of the arcuate nucleus of the hypothalamus (ARH) that project to the μ-opioid neuron in the medial preoptic nucleus (MPN). The β-END neurotransmitters activate and internalize the μ-opioid receptors (MOR) to inhibit sexual receptivity (lordosis). Lordosis can be rapidly induced 48 hours after the EB initial injection, progesterone by infusion into the ARH, which also reduce the internalization of MOR. Concurrently, this EB treatment increases associated progesterone receptors (PGR) expression in the ARH. In the ARH, progesterone activates PGR that complex with and signal through Src family kinase (Src) on the plasma membrane. This PGR-Src complex also interacts with dopamine D1 receptor. This PGR-Src-D1 interdependent signaling has been localized to a subpopulation of the ARH β-END neurons, suggesting that a progesterone responsive dopamine dependent input to ARH β-END neurons should exist. In this experiment, we tested the hypothesis that progesterone signals through a dopaminergic neuron which projects to β-END neuron in the ARH to rapidly facilitate lordosis. OVX Long Evans rats were treated with 2μg EB or oil, and rats were perfused 48 hours later. Brain sections through the ARH were processed for doubled labeled immunohistochemistry for PGR-tyrosine hydroxylase (TH; marker for potential dopamine neurons), Src-TH, and β-END-TH. A set of potential dopamine neurons were

immunopositive for TH and PGR, and EB treatment increased the number of TH-PGR positive ARH neurons. ARH neurons were also immunopositive for both Src and TH indicating that a similar PGR-Src complex could rapidly regulate the activity of these neurons. Lastly, we observed very little co-localization of β-END-TH immunoreactivity. However, TH immunopositive fibers were in close proximity to immunopositive β-END cell bodies and processes. These results support our hypothesis that progesterone may signal through PGR-Src signaling complexes to activate a subpopulation of potential dopaminergic neurons that project to ARH β-END neurons to reduce their neurotransmission and facilitate lordosis.

This project is supported by Research Initiative for Scientific Enhancement Grant G181515100.

7. Computer Simulations of Previtamin D Dynamics in a Lipid Bilayer

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We employ computational chemistry methods to simulate the dynamics of Vitamin D photoisomers (DPI) in a cell membrane. We do this by embedding DPI in a lipid bilayer composed of water/dipalmitoylphosphatidylcholine and propagating the system by molecular dynamics (MD) based on classical force fields and density functional theory base MD. Interest in DPI photochemistry originated from clinical research of Vitamin D deficiencies in mammals.[1] An atomistic resolution of the reversible photo reactions of DPI in a cell membrane is missing. We investigate the effects of a lipid bilayer on regulating Vitamin D photosynthesis and on DPI dynamics. Gas phase simulations of Pre show molecular conformations that are dependent on the steric effects of two rings that rotate relative to one another.[2] In a cell membrane these rings are likely restricted by interactions with neighboring lipid molecules and hydrogen bonding with water. We evaluate the effects of lipids on the conformational space of Pre by observing the ensemble of structures achieved during dynamics simulations.

Research reported in this presentation was supported by National Institute of General Medical Sciences of the National Institutes of Health (NIH) under award numbers R15GM126524, UL1GM118979-02, TL4GM118980, and RL5GM118978. The content is solely the responsibility of the authors and does not necessarily represent the official views of the NIH. We acknowledge technical support from the Division of Information Technology of CSULB.

8. Examining Preservation Bias and Depositional Setting with Grain Size at La Brea Tarpits Fossil Bed, California

Karin Rice[1], Lora Stevens[2], Matthew Hong[2], Lorenzo Cebreros[2], Karissa Hansen[2], Alexis Mychajliw[1], and Emily Lindsey[1]
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Rancho La Brea of Los Angeles, California, is an iconic North American fossil locality representing a diverse record of plant, insect, and vertebrates spanning the last 50,000 years. Despite the exceptional fossil yield of these asphaltic sands and gravels resulting from over 100 years of excavation, there has been no systematic description of variation in grain size and asphalt concentration across the numerous deposits, and nearly all taphonomic interpretations have been drawn from studies of megafaunal mammal remains, rather than the sediments preserving them. A lack of radiocarbon stratigraphy on bones coupled with disarticulated skeletons and apparent abrasion or "pit wear", have been taken to imply movement or churning of liquid asphalt or the activity of mammalian carnivores. We conducted a preliminary quantitative study of grain-size analysis to test three questions: 1) are visual descriptions of the matrix sufficient for understanding the depositional environment and related taphonomy of the site, 2) does grain size relate to variations in preservational quality of fossil material, 3) can paleoenvironments be reconstructed, or are depositional settings "churned" by asphalt and natural gas movement? Twenty-nine samples from five distinct deposits ("boxes" of Project 23) collected during a construction project adjacent to Hancock Park were selected for this project. Preliminary results suggest that mean grain size is overestimated in purely visual descriptions as fine silts and clays are mixed in with the asphalt. The amount of asphalt increases in a linear fashion with a greater percentage of fine material (< 63 microns) indicating that fines are underestimated in visual descriptions. There is no correlation between mean grain size and asphalt concentration. In contrast, some of the more delicate fossils, including birds and reptiles, are found in samples with a high percentage of coarse material. Plant fossils are found in samples with minimal coarse material. Insufficient samples have been processed to determine if there is sorting/stratigraphy in the deposits however, the initial data suggest that there is valuable information in a more quantitative matrix analysis.

9. Ionic Residues in Helix 10 of the C-terminal Domain of Human Apolipoprotein A-I Regulate Self-association

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Cardiovascular disease is currently the leading cause of death in the modern world. High-density lipoprotein (HDL), or "good cholesterol", remains a key component in research seeking to development treatments for such diseases. Apolipoprotein A-I (apoA-I) is the central protein of HDL. Sequestration of lipids by lipid-free apoA-I results in formation of discoidal HDL. No

high-resolution structure of the protein is currently available, but biophysical characterizations indicate apoA-I is comprised of two domains; a highly ordered N-terminal domain and a less structured C-terminal domain. The C-terminal domain initiates lipid binding and formation of discoidal HDL. Lipid-free apoA-I exists in an oligomeric state, which is also facilitated by the C-terminal domain. Six lysines reside in this domain at positions 195, 206, and 208 in helix 8 (H8) and 226, 238, and 239 in helix 10 (H10). Substitution of all six lysine residues with glutamine resulted in a monomeric form of the protein, indicating that ionic bonds play a role in self-association. To identify the lysines critical for self-association, site-directed mutagenesis was implemented to engineer seven single and two triple mutants. Upon expression in *E. coli* and purification by N-affinity and gel filtration chromatography, circular dichroism and fluorescence spectroscopy revealed all mutants retained their structural integrity. Dimethyl suberimidate crosslinking analysis demonstrated a strongly reduced amount of self-association for the H10 triple mutant, while the H8 triple mutant was much less affected by the mutations. FPLC elution profiles of the H10 triple mutant suggests that the protein is primarily monomeric, and may be amenable for studies to obtain the high-resolution structure. All H10 single mutants displayed increased elution times, however, not to the extent of the triple mutant, suggesting the H10 lysines work collectively to contribute to self-association. The K226Q mutation produced the largest increase in elution volume of all single mutants, and when nearby glutamate 223 was substituted with glutamine the elution profile this E223Q mutant matched that of K226Q-apoA-I. This suggests an ionic bond between these two residues. The results of this study indicate that intrahelical salt bridges in H10 facilitate apoA-I oligomerization through stabilization of amphipathic α-helices. Assembly of the H10 helices into a small helix bundle then results in an oligomeric state of the protein.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; SC3GM089564 [Weers]; and 5UL1GM118979, 5TL4GM118980, 5RL5GM118978 [BUILD scholarship Basi].

10*. Clinopodium chandleri* Pollination*: Honey Bees Versus Native Pollinators

Gregory Cruz and Dessie Underwood Ph.D
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There are many rare plants around the world that are in need of conservation. However, in order to conserve them, they must first be researched to understand important aspects of their biology, such as reproduction. Plants in the family Lamiaceae, for example, rely on pollinators for successful reproduction. One such plant is *Clinopodium chandleri*, more commonly known as San Miguel Savory. It is a rare, Southern California native found in sparse populations in montane chaparrals in Orange, Riverside, and San Diego counties. No research has been done on the pollination of *C. chandleri*, putting this plant at risk if its populations were to decline. Furthermore, studies have shown that rare plants are highly reliant on their native pollinators and decline in parallel with the loss native pollinators. I sought to find out what animals visit *C. chandleri* flowers and act as pollinators. I observed insect visitation rates to *C. chandleri* flowers

at Cleveland National Forest, Trabuco District and the Santa Rosa Plateau Ecological Reserve. I observed 476 visits over28 days. I found there are 15 species of bees, flies, a wasp, and a skipper butterfly visiting the flowers. Four species of bees account for 80% of all observations. Among the native pollinators pollinating *C. chandleri* in Southern California, is the ever-present and abundant non-native honey bee (*Apis mellifera*). Though frequent visitors, honeybees may not be optimal pollinators of *C. chandleri* if their visitation rates are insufficient in spreading pollen to flowers of other *C. chandleri* individuals. Pollinators that have evolved alongside their native plants may have morphological adaptations to the shape of the flowers. Tongue length and head shape, for example, may affect how a pollinator acquires nectar resources and makes contact with the reproductive organs of the flowers. For this research, I hypothesize that native pollinators are more effective at spreading pollen between *C. chandleri* individuals than non-native bees. In the future, I will compare tongue lengths of native pollinators and non-native honey bees to the length of *C. chandleri* corolla tubes. These studies will give valuable insight into the reproduction of *C. chandleri* that can, in turn, be used for its conservation.

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11. Anti-Woodward-Hoffmann [1,5]-Sigmatropic Hydrogen Shifts in Cis,cis-1,3-cyclooctadiene

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The Woodward-Hoffmann rules have been used successfully to predict the stereochemistry of the products formed from a pericyclic reaction. In some cases, however, these rules are violated and the reaction products show a different stereochemistry than expected. One such case is the excited state intramolecular hydrogen-transfer reaction of cis,cis-1,3-cyclooctadiene (COD) forming cis,cis-1,3-cyclooctadiene, cis,trans-1,3-cyclooctadiene, and trans,cis-1,3-cyclooctadiene (Fig. 1). The Woodward-Hoffmann expected product for this reaction is formed through a [1,5]-suprafacial shift while our study finds a [1,5]-antarafacial shift to occur instead. In order to understand the mechanisms of the different reaction pathways the molecule can undergo, we simulate the photodynamics of COD using time-dependent density functional theory. We find that 26.38% of the simulations form the anti-Woodward-Hoffmann intramolecular hydrogen-transfer product. Besides undergoing a [1,5]-sigmatropic hydrogen-transfer, we find COD to undergo an isomerization reaction and an electrocyclic ring-closing reaction. After excitation, the isomerization mechanism leads to a geometrical change from cis,cis-1,3-cyclooctadiene to cis,trans-1,3-cyclooctadiene (6.78%) and trans,cis-1,3-cyclooctadiene (17.84%), while the ring-closing mechanism leads to the formation of bicyclo[4.2.0]oct-7-ene (2.01%), both of which are products accurately predicted by Woodward-Hoffmann. To verify our results, we simulate time-resolved photoelectron spectra to compare to experimental data.

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12. Abscission Zone Anatomy of Grasses Changes Rapidly Through Evolutionary Time

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Seed shattering is an economically important agricultural trait. It is the process by which the fruit or seed falls off the plant. Excess or non-uniform shattering reduces crop yield, which makes it the driving force for crop domestication and thousands of years of breeding. Shattering occurs in the abscission zone (AZ) of the plant, which is often described as one or a few layers of small, cytoplasmic dense and non-lignified cells located at the junction of plant organs. So far, a few genes that are attributed to the loss of shattering of domesticated rice, wheat, barley, and maize have been identified. However, whether a common genetic pathway underlies AZ development in different grass species is unclear. Our previous study showed that the anatomy and gene network of the AZ is different in distantly related grass species, including rice, *Brachypodium,* and *Setaria*. To further look for conservation and divergence of AZ development across the grass family (Poaceae), we performed extensive histological analyses of the AZ, using a total of fourteen different species from seven different subfamilies of Poaceae. We hypothesized that the AZ of grass species within the same tribe and/or subfamily would have similar patterns of cell morphology, cell wall composition, and location. Safranin O and fast green staining showed that most species exhibited at least one of the typical AZ characteristics, including small cell size and differential lignification, with a few exceptions. However, we found no correlation between histological characteristics and the phylogenetic relationship of the species. These results suggest that the anatomy of AZ is subject to rapid change during evolution.

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13. Towards a Better Model of Vitamin D in Skin Membrane

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We are developing a molecular mechanics force field for Previtamin D for use in molecular dynamics simulations. We intend to use these simulations to test our hypothesis that human skin membrane holds Previtamin D in an advantageous configuration to facilitate its efficient conversion to Vitamin D.

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14. The Role of Androgen Receptor in Regulation of Sexual Dimorphism in Hippocampal Morphology of Juvenile Mice

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The hippocampus, in particular, is highly involved in spatial memory and processing navigational information, which has been long found to be sexually dimorphic in mice. Sex differences in spatial navigation, correlating with hippocampal morphology, have been attributed to organizational effects of perinatal testosterone. Since the hippocampus is reported to contain substantial levels of androgen receptor (AR) during early development, it is possible that AR activation might mediate hippocampal masculinization, leading to sex differences in spatial ability and hippocampal morphology. To test this hypothesis, we collected the whole brains of wild-type male (WTM) and female (WTF) mouse pups as well as testicular-feminized mutant (Tfm) males, lacking functional AR, at postnatal days 21-24 (n=4 for WTM, n=5 for WTF and n=6 for Tfm). The brains were post-fixed in 4% paraformaldehyde, sectioned, and stained with cresyl violet. After cover-slipping, area size of pyramidal cell layers in the CA1, CA2, and CA3, and granular cell layer in the dentate gyrus (DG) of the hippocampus were measured under a light microscope using ImageJ. Among the four hippocampal sub-regions, the CA1 pyramidal cell layer and DG granule cell layer showed an increase in area size from rostral to caudal regardless of sex or genotype. WTM juveniles had larger area sizes in the CA1, CA3, and DG than WTF. Interestingly, the differences in area size of those hippocampal subregions appear to be present more rostrally. While the effect of genotypes on the area sizes in the CA1, CA3, and DG was not significant, there seemed to be a trend of female-like reduction in Tfm mice compared to their wild-type littermates. Based on these findings, we conclude that AR might be essential for the masculinization of hippocampal morphology in a region- and level-specific manner.

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15. Synthesis and Characterization of Luminescent Metal-Organic Frameworks for Explosives Detection

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Metal-organic frameworks (MOFs) have emerged as a class of crystalline structures with an incredible range of environmental and biomedical uses due to their highly modifiable organic and inorganic components. Several studies have been conducted on the creation of luminescent MOFs that are able to detect explosive compounds. However, most of this detection occurs via fluorescence quenching, or a reduction in fluorescence, rather than a more efficient increase in fluorescence. Our current study focuses on the use of a type of luminescent MOF, organic dye-doped zeolitic imidazolate framework-8 (ZIF-8), in order to detect explosive compounds via a fluorescence increase. Fluorescein dye molecules were incorporated into ZIF-8 nanoparticles to synthesize a luminescent MOF. Infrared spectroscopy (IR), X-ray powder diffraction (XRD), and UV/Vis spectroscopy were then utilized to study the chemical composition, crystal structure, and optical absorbance of the luminescent MOF. Results suggested that the fluorescein was encapsulated by the ZIF-8, rather than being adsorbed on the surface or in the pores of the crystal cells. Additionally, the solid luminescent ZIF-8 retained the fluorescent quality of fluorescein dye that is typically only present in liquid phase. Fluorometer measurements were then used to quantify the fluorescence increase of the luminescent ZIF-8 upon the addition of pyridine, a chemical that models nitramine explosives. We noticed a 47.86% increase in fluorescence of fluorescein-doped ZIF-8 after exposure to 10% v/v pyridine. These results provide a promising precursor for the synthesis of an efficient explosive-detecting luminescent MOF.

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16. Using Metal Organic Frameworks as a Drug Delivery Method in Stents

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The leading cause of death in the United States is cardiovascular disease, and one very common treatment to this problem is stent implantation. One concern when implanting stents is thrombosis, which can be caused by a polymer that remains on drug eluting stents (DES) after all the drug molecules have eluted. To eliminate this risk, the polymer can be replaced by an iron-based metal organic framework (MOF). Not only is the MOF non-toxic, but it is also

biodegradable, meaning as soon as the drug molecules have been released, the MOF will break down and leave behind the bare metal stent (BMS). Our research focuses on utilizing MIL-88B as our MOF because of its large pores and 3D channels which make loading and unloading drug molecules more efficient. To study the kinetics behind the drug loading and eluting process, MIL-88B is added on top of a self-assembled monolayer (SAM) with a carboxylate terminal group all on a gold plate. Using surface plasmon resonance (SPR), the association and dissociation of the drug to the MOF can be tracked. With these results, we hope to one day be able to eliminate the risk of thrombosis and minimize the risk of blood clots that result from the implantation of stents.

17. Probing the Lipid Binding and Self-Association Properties of N-terminal and C-terminal Helices of Apolipoprotein A-I using Chimera Proteins

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Human apolipoprotein A-I (apoA-I) is a major component in high-density lipoprotein and plays a critical role in reverse cholesterol transport. The 28 kDa protein (243 residues) is composed of an N-terminal (NT) helix bundle domain and a less structured C-terminal (CT) domain. The CT domain contains helices responsible for high-affinity binding to phospholipids which initiates apoA-I lipidation and also mediates self-association. Previous studies have suggested that the NT domain may also initiate lipid binding. To better understand the role of NT and CT helices of apoA-I in lipid binding and self-association, four chimera proteins were designed. A chimera system has been developed in which monomeric insect apolipophorin III (apoLp-III) is used as a scaffold to present segments of apoA-I. Lipid binding of apoLp-III has been disabled by introducing two cysteine residues locking the protein in a closed inactive conformation. The apoLp-III/ apoA-I chimera can thus adopt affinity for lipids and acquire self-association properties. Thus, the chimera protein approach allows for determination of the functional properties of NT and CT helices of apoA-I. In the present study, residues 1-43 or 44-65 of apoA-I were attached to the NT of apoLp-III to assess the role of apoA-I NT helices. In addition, CT domain residues 209-243 or residues 220-243 of apoA-I were attached to the CT of apoLp-III. Circular dichroism showed that the chimeras displayed an α-helical content of ~60%, which is similar to apoLp-III, indicating that the structural integrity of apoLp-III was not affected by addition of apoA-I segments. Lipid binding was analyzed by phospholipid vesicles solubilization. Phospholipid solubilization rates for apoA-I(1-43)/apoLp-III (16.8×10^{-3} s^{-1}), apoA-I(44-65)/apoLp-III (8.6×10^{-3} s^{-1}), apoLp-III/apoA-I(209-243) (9.1×10^{-3} s^{-1}), apoLp-III/$(G_4S)_2$/apoA-I(220-243) (6.4×10^{-3} s^{-1}) presented a 6 to 17 fold increase in comparison to apoLp-III (1.0×10^{-3} s^{-1}). To analyze the self-association state of the chimeras, proteins were crosslinked with dimethylsuberimidate. This showed that only apoLp-III/apoA-I(209-243) formed oligomers, while the NT segments of apoA-I and CT segment 220-243 were not able to induce self-association. Thus, the NT and CT helices of apoA-I have high-affinity for phospholipids,

indicating the potential to initiate lipid binding. However, only specific CT residues of apoA-I can mediate self-association.

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18. Proton Gradient Regulation Across Cell Membrane Mimics

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Proton transport across cell membranes is an essential component in the production of adenosine triphosphate (ATP). ATP, which is produced in the mitochondria, provides the energy needed by all living organisms. The electron transport chain in cell membranes is responsible for controlling the proton gradient and the production of ATP. In relation to the electron transport chain, our tests were conducted to mimic a cell membrane where the proton regulation was studied using a bi-phasic system of 1,2 - Dichloroethane (DCE) and Milli-Q water.

The focus of this study is on 2,4-Dinitrophenol (DNP), Coenzyme Q0 (CoQ0), and Coenzyme Q10 (CoQ10). CoQ's are naturally part of the electron transport chain in cell membranes and DNP has been used as a synthetic drug for proton gradient regulation. Ferrocene based molecules are added to control the oxidation state of the CoQ's, and tetrabutylammonium tetraphenylborate (TBATPB) and phosphate buffers are used to facilitate ion transfer measurements. UV-Visible spectroscopy was then employed to examine detailed molecular changes that occurred in regard to absorbance. Since the CoQ's are a component already known to control the proton gradient, the UV-Vis spectrum results were expected. The signals showed a slight, insignificant decrease of CoQ's over set periods of time, which implies that the proton transfer occurred at a steady, slow rate. Unlike the CoQ's, DNP is a synthetic drug known to disrupt membrane proton gradients. The UV-Vis spectrums showed a significant change in signal when DNP had pH 1 and pH 7. When present in pH 1, the DNP peak absorbance increased because the DNP had no effect on the proton gradient, so the concentration remained the same. However, when present in pH 7, the peak absorbance decreased significantly because DNP disrupted the gradient. Using a bi-phasic system to mimic a cell membrane, along with UV-Visible spectroscopy, allows us to test other biomolecules and the positive or negative effects they may have on the proton gradient of cell membranes.

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19. U1A – U1hpII: A model for establishing the DRX^2 Biosensor as a new technology for studying RNA-Protein interaction

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Lung cancer is the leading cause of cancer death among men and women in the United States, resulting in around 220,000 cases and 140,000 deaths in 2018. To minimize side effects of treatment, many new therapies target specific mutations found in patients' tumors. Once these mutations are identified, drugs are screened to identify specific inhibitors. The accurate characterization of the interactions between drugs and targets is a crucial step in therapeutic drug development. Of key importance is the intermolecular binding affinity, expressed in kinetic data. The DRX^2 Biosensor utilizes nanotechnology to provide this kinetic data for numerous biophysical (DNA-protein, RNA-protein, protein-protein) interactions with extremely high sensitivity (nm-pm range). It does so by the switchSENSE® principle – a methodology that utilizes fluorescent DNA tethers bound to a gold surface that receives alternating positive and negative voltages, causing the DNA molecules to be attracted (quenched) or repelled (fluoresce). To analyze an interaction, a complimentary sequence containing the ligand of interest is annealed to the DNA nanolevers and the analyte of interest is introduced in a solution that flows through a channel in the biochip. My research is aimed at establishing the use of the DRX2 to study RNA/protein interactions. The first goal was to accurately replicate the published kinetics data (k_{ON}, k_{OFF}, K_D) for the U1A spliceosomal protein-U1 hairpin II snRNA interaction. The ligand, U1 hairpin II snRNA (U1hpII) construct, was synthesized *in vitro* and quantified using spectrophotometric methods. The U1A protein was expressed in *E. coli*, Ni-NTA purified and quantitated on SDS-PAGE gels relative to a known standard. Several experiments were performed using the DRX^2 biosensor to analyze the reaction kinetics and provided rates of $k_{ON} = 2.14 \times 10^6\ M^{-1}s^{-1}$, $k_{OFF} = 6.73 \times 10^{-4}\ s^{-1}$, and $K_D = 4.28 \times 10^{-10}$M. The measured rate was about 5-fold slower than previously established by surface plasmon resonance (SPR), which may be related to technical differences between the conditions/instruments used. It will be of interest to study other RNA/protein interactions for comparison. The DRX^2 biosensor, which unlike SPR offers the ability to detect conformational changes, promises to be a powerful tool to investigate future unknown biophysical interactions. The Offringa lab hopes to apply it to the development of new therapies for lung cancer.

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20. Introducing Substrate Features to Fmoc-Based Compounds Increases the Potency of Butyrylcholinesterase Inhibitors

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Cholinesterases such as Butyrylcholinesterase (BChE) and Acetylcholinesterase (AChE) are enzymes prevalent in the human brain and are responsible for hydrolyzing acetylcholine—a molecule necessary for neuronal signal transduction. Low levels of acetylcholine (ACh) in the brain have been correlated to the reduction of cognitive function in individuals suffering from neurodegenerative disorders such as Alzheimer's Disease (AD). Relative to healthy individuals, those suffering from AD exhibit a significant increase in BChE activity, and no change or a slight decrease in AChE activity. Therefore, 9-fluorenylmethoxycarbonyl (Fmoc) amino acid-based inhibitors have been synthesized to downregulate BChE. To increase the potency and specificity of these amino acid-based inhibitors, substrate features such as a cholinyl group has been introduced. A cholinyl group was first introduced via esterification of the carboxylic acid of the Fmoc-amino acid. The inhibitors were purified by silica gel chromatography and characterized by NMR. Enzyme assays monitored by UV-Vis spectrometry suggested the compounds were potent inhibitors with inhibition constants (K_I values) in the μM range. However, HPLC (high-performance liquid chromatography) experiments indicated that the Fmoc-cholinyl-ester compounds acted as substrates for BChE, complicating analysis and minimizing their potential to act as inhibitors. To combat this limitation, a stable amide was substituted in place of the ester. Initial HPLC results of these Fmoc-cholinyl-amide compounds indicate this substitution prevents hydrolysis of the molecule. Initial biochemical results for the Fmoc-amides suggest the compounds inhibit BChE with K_I values in the 0.06-10.0 μM range, with the amide of Fmoc-Lys being the most potent inhibitor with a K_I value of 0.06 μM. Overall, the results suggest that introduction of substrate-like characteristics within the Fmoc-amino acid-based background intensify their potency and may help guide the generation of future inhibitors.

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21. Including a linker segment in the apolipophorin III/apolipoprotein A-I (220-243) chimera protein greatly improved the expression in *Escherichia coli*

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Human apolipoprotein (apoA-1) plays a critical role in reverse cholesterol transport. The protein consists of two domains: the N-Terminal (NT) helix bundle and the C-Terminal (CT), less structured helix bundle. The CT domain of apoA-1 has great affinity for lipids and is responsible

for the initiation of lipid biding. Chimeric protein containing residues 220-243 of the CT domain of apoA-1 were attached to insect apolipophorin III (apoLp-III). In order to prevent lipid binding of apoLp-III, two cysteines were introduced at position 20 and 149, creating disulfide bonds; therefore, any observed binding properties are due to the CT- domain of apoA-1. SDS-PAGE showed that recombinant protein expression of apoLp-III/apoA-1(220-243) was unsuccessful. Linker segments are flexible polypeptides of glycine and serine that promote expression of multidomain proteins. SDS-PAGE verified that after the addition of a $(G4S)_2$ linker segment between apoLp-III and CT apoA-1, protein expression was restored. Circular dichroism analysis showed that chimeras contain similar α-helical content to apoLp-III, indicating that adding the CT-domain of apoA-1 and the $(G4S)_2$ linker segment did not compromise the integrity of apoLp-III. Phospholipid solubilization rates of all chimeras increased compared to apoLp-III and were similar to those of apoA-1. The chimeras showed greater affinity to lipids in comparison to apoLp-III.

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22. Expanding the Use of Tyrosine Phenol Lyase in the Enzymatic Synthesis of Naphthol Unnatural Amino Acids

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The use of enzymes in the synthesis of pharmaceuticals and biochemical tools offers an attractive approach to generating complex structures, as enzymatic reactions often lead to the formation of specific products in high yields. Tyrosine phenol lyase (TPL), an enzyme biologically involved in the degradation of tyrosine, has been used to synthesize a variety of substituted tyrosines including fluorotyrosines for biochemical studies. In addition to fluorotyrosines, expanding the scope of substrates to naphthol-based compounds offers an attractive target for enzymatic synthesis of complex molecules, as substituted naphthols can be used as biochemical probes and as building blocks in potential pharmaceuticals. Using *Citrobacter freundii* TPL we enzymatically synthesized the naphthol-analog of tyrosine, but the unnatural amino acid was generated in low yield. The simplest model for the low conversion is that the larger substrate is poorly accommodated by the enzyme active site and this poor binding leads to the low yield in the enzymatic reaction. To test this hypothesis, we mutated several bulky residues near the substrate-binding site (M288, M397, F448) to open space for substrate binding and facilitate synthesis of the unnatural amino acid. A series of mutant plasmids were generated using site-directed mutagenesis and sequenced to confirm the mutation. The wild type and mutant

enzymes were recombinantly expressed in *E. coli*, purified by affinity and ion-exchange chromatography, and purity was analyzed by gel electrophoresis. Enzyme activity with tyrosine in an NADH-dependent coupled enzyme was first used to determine that the wild type and mutants are active, and initial results for the first mutants generated (M228S and M379A) indicate that the mutants are active. We are currently surveying reaction conditions using high-performance liquid chromatography (HPLC) to evaluate the reactions of the TPL mutants with naphthols as substrates. HPLC is being used to determine the generation of product to calculate yields and provides a method to test if additional products are formed. While a goal of this study is aimed at the more efficient production of tyrosine derivatives, a larger goal is to better understand the features important for substrate binding in enzymatic reactions. This understanding may aid in the development of enzymes with a broad range of substrates efficiently converted to products in the biochemical generation of complex molecules.

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23. Characterization of the microbial community in a recently discovered digestive organ in the heart urchin *Brisaster townsendi*

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Heart urchins (Echinoidea: Spatangoida) of the genus *Brisaster* are often abundant in deep water soft-sediment marine communities. They are deposit feeders and important bioturbators, but little is known of how these mud-dwellers process and digest food. Recently, a novel organ, the intestinal caecum, has been found in several spatangoid genera, but its physiological role is presently unknown. In *B. townsendi* (Agassiz, 1898), a heart urchin common in southern California, this organ is distinct from the rest of the gut in that it contains no sediment, but instead is filled with a dense microbial mass. We used next-generation sequencing to compare microbial communities in the stomach, intestine, intestinal caecum, and rectum of *B. townsendi* with the goal of understanding the caecum's role in the echinoid's biology. We collected *B. townsendi* from ~300 m depth off Long Beach, CA, and sampled the contents of each of the four gut regions from two specimens; in addition, the contents of the caecum were analyzed from an additional eight specimens. We extracted genomic DNA and amplified 16S rRNA genes using Illumina MiSeq. The results show that the caecum harbors a diverse community of anaerobic bacteria with large contributions from sulfate-reducing bacteria of Desulfobacterales averaging approximately 15.97% of the microbial community, as well as Spirochaetales (9.17%) and Bacteroidales (34.64%); this community is distinct from that of the rest of the gut. Using the relative abundance of microbial taxa within the different gut regions as well as additional data, a model for the role of the intestinal caecum in the digestive process of *B. townsendi* is presented.

24. Break-down of *myo*-inositol via *Drosophila melanogaster myo*-inositol Oxygenase; Establishing an Assay and Mutant Phenotypes.

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myo-inositol oxygenase (MIOXp) is an enzyme involved in the only known pathway for the catabolism of *myo*-inositol in higher eukaryotes including the model organism *Drosophila melanogaster* and humans. *myo*-inositol (MI) is important for many cellular functions such as growth, signal transduction, osmoregulation, and thermoregulation. MI is a precursor of the phospholipid phosphatidylinositol, and has been implicated in diseases such as diabetes, Alzheimer's, and bipolar disorder. MIOXp catalyzes the first step of *myo*-inositol catabolism, cleaving MI and converting it to glucuronic acid (GA), which can ultimately enter the pentose phosphate pathway to generate NADPH and pentose sugars needed for nucleotide synthesis. To elucidate the role of MIOXp in development and survival, we are studying the effects of MIOXp disruption in *Drosophila melanogaster*. Studies using two RNAi strains (iMIOX2 and iMIOX3), each integrated into a different noncoding site in chromosomes 2 and 3, show that RNAi flies reared on food with inositol as the sole carbon/energy source have approximately one-third the lifespan of wildtype flies (CS). Preliminary qPCR data reveal that steady-state *MIOX* RNA levels in iMIOX2 larvae are lower than wildtype larvae (CS). Furthermore, preliminary MIOX protein activity assay data confirm decreased activity in iMIOX2 larvae in comparison to wildtype larvae (CS). Attempts to generate a homozygous strain with a P-element inserted into the *MIOX* gene did not yield sufficient progeny to examine RNA and protein activity levels. So, developmental studies were initiated, and preliminary results have demonstrated that most P-MIOX/P-MIOX homozygotes are not transitioning from the pupal to the adult stage. These data give us a better understanding of the role of MIOXp and *myo*-inositol in development, growth, and survival, and will help elucidate the mechanisms of important cellular processes.

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25. Antibiotic Resistance among Fecal Coliform Bacteria Isolated from Madrona Marsh, Torrance, CA.

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Antimicrobial resistance is a serious threat to human health. Urban runoff increases the emergence and dissemination of antibiotic-resistant bacteria. Madrona Marsh is a preserved freshwater wetland located in the city of Torrance, CA and is subject to urban runoff from the surrounding city including a carwash that drain directly into the marsh. Fecal coliform bacteria

(FIB) are commonly found in urban runoff and include potential pathogens, further increasing the threat to human health. The goal of this project is to determine whether antibiotic resistance is found among fecal coliform bacteria isolated from Madrona Marsh. Water samples were collected from four different sites. The water was vacuum filtered onto a membrane and transferred onto selective mEndo plates. After a 24-hour incubation, FIB colonies were streak plated three times to obtain a pure isolate. A Kirby-Bauer test using nine different antibiotic disks was performed on ten pure isolates from each site. Preliminary data indicate there is site-to-site variation in the numbers of FIB; the carwash drain had the highest numbers of coliforms. Our findings also indicate common antibiotic resistance to ampicillin compared to other antibiotics for which little resistance was observed. These preliminary findings suggest that there are variable levels of coliform bacteria and that ampicillin resistance is of greatest concern. Future studies will continue to observe coliform levels and antibiotic resistance across different seasons and will use PCR to confirm identification of coliform species.

This project is supported in part by the National Institute of General Medical Sciences of the National Institute of Health under Award Number R25GM071638. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health. A special thanks to the Madrona Marsh Preserve City of Torrance Community Services Department and staff: Melissa Loebl, Miriam D. Taeubel, and Steve Ash.

26. Trans Regulating Expression of *myo*-Inositol Synthase in *Drosophila melanogaster* Larvae

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Myo-inositol is a six-carbon sugar alcohol that is a precursor of phosphatidylinositol (PI), a cell membrane phospholipid. PI is involved in the phosphoinositide-signaling pathway, which is essential for the regulation of cellular functions. Abnormalities in *myo*-inositol metabolism have been implicated in diseases and complications such as polycystic ovary syndrome, cancer, and Type 2 diabetes. Inositol-3 phosphate is synthesized from glucose-6-phosphate by *myo*-inositol phosphate synthase (MIPSp). In *Drosophila melanogaster*, the *Inos* gene is located on chromosome 2 and encodes MIPSp. This study focuses on the effects of dysregulation of *Inos* gene through the use of an actin promoter driving GAL4 production (ActGAL4-3). The GAL4 protein turns on *Inos* gene transcription via a UAS_{GAL4} inserted upstream of the 5' end of the *Inos* UTR (D element). Other concurrent studies in the lab have shown that this dysregulation results in developmental abnormalities. This study examines the *Inos* transcript and MIPS protein expression levels across three strains: D element with ActGAL4-3, D element homozygotes (no ActGAL4-3), and wild type (Canton S, CS). It is hypothesized that heterozygotes with the D element and ActGAL4-3 will have high levels of *Inos* transcript and MIPS protein, compared to D element homozygotes (with no ActGAL4) and wild type strains. Real time qPCR experiments demonstrated that indeed heterozygous larvae with a D element and ActGAL4-3 have high levels of *Inos* transcript and D element homozygotes have

intermediate levels of expression compared to the control (CS), which have the lowest level. Western blot experiments showed that MIPS protein levels in the different strains had a similar trend. A thorough understanding of inositol metabolism may be essential to the causes of aforementioned diseases and developmental defects.

This project is supported in part by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number R25GM071638.

27. The Effects of Larval Culturing Density on Development and Physiology of the Echinoid Echinoderm, Dendraster excentricus

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Echinoderm larvae are model organisms used in many areas of research. Interpretations of experimental results can be confounded by culture conditions used to rear larvae. The objective of this study was to quantify effects of culture density on larval development and physiology. Larvae of the Pacific sand dollar, Dendraster excentricus, were reared at densities of 0.1, 0.25, 0.5, 1.0 and 5.0 larvae mL-1 and fed Rhodomonas sp. at 10,000 cells mL-1. Morphological measurements and determinations of total protein growth were made at 11 days post-fertilization (DPF), and the percentage of competent larvae was subsequently assessed daily. Larvae grown at densities ≤1.0 mL-1 exhibited no significant differences in larval arm growth and had protein biomass of ~ 2,300 ng ind-1. Larvae grown at 5 mL-1 had similar arm length but significantly lower protein biomass and less rudiment development. Importantly, larvae reared at ≤1.0 mL-1 were metamorphically competent at 14-16 DPF while those in the 5 mL-1 treatment did not reach competency until at least 26 DPF. Our data support the use of culture densities no higher than 1 mL-1 when testing hypotheses regarding the influence of experimental variables on larval biology. Higher densities will increase the possibility of experimental artifacts and erroneous conclusions. Given the usefulness of the echinoderm larval system in a wide range of studies, the information presented here is critical for ensuring appropriate experimental design so as to make sound biological interpretations.

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28. iNPC Therapy for Canavan Disease in CD Mouse Model

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Canavan Disease (CD) is an autosomal recessive leukodystrophy resulting in spongy degeneration of CNS myelin affecting infants within the first few years of life. The disease is caused by a mutation in the ASPA gene, coding for the enzyme aspartoacylase, responsible for the metabolism of neuron derived N-acetyl-L-aspartic acid (NAA) to acetate and aspartic acid after transport to oligodendrocytes. CD patients are seen to have elevated NAA believed to be attributed to disease pathology, and decreased NAA-derived acetate used for myelin lipid

synthesis. As time progresses, a loss of oligodendrocytes and demyelination in dense white matter regions of the brain is witnessed, resulting in delayed development, weakness, and poor motor skills. The nur-7 mouse with the nonsense mutation, Q193X, has served as a common laboratory model for the disease. $ASPA^{nur7-/nur7-}$ mice like CD patients are seen to have extensive vacuolation in the white matter of the CNS. With the rise in popularity and potential of stem cells, cellular therapies have become increasingly widespread. Neural progenitor cells (NPC's) derived from iPSC's are of particular interest to us for their potential for regeneration in the CNS and potency for differentiation into various lineages, including oligodendrocytes. Here we take a cellular approach to treatment in our CD model through the lentiviral introduction of the wild type ASPA gene into CD patient iPSC derived iNPC's. The ASPA-NPC's were transplanted into different sites of the CD mouse brains, and rescue of the CD phenotype is monitored through time. A reduction in vacuolation throughout the brain can be seen.

This project was supported by funding from CIRM Grant EDUC2-08383

29. Nest Site Characteristics of the California Least Tern (*Sternula antillarum browni*)

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The California Least Tern (*Sternula antillarum browni*; CLT) is a subspecies of migratory sea bird whose breeding range is along the coast of California and Baja California, between April and September. The (CLT) is a state and federally protected bird, that is threatened by predation, habitat loss, and human disturbance. Since receiving its protected status in 1970, CLT's number of breeding pairs and fledglings have recovered, but have started to experience a steady decline in recent years. Successful nesting locations are a vital factor when developing recovery strategies for avian species. This study focuses on factors affecting nesting success including inter-colony dispersal of nests and nest location relative to percent cover of vegetation at a colony within the Seal Beach National Wildlife Refuge (SBNWR). A nearest neighbor analysis of the nest location suggests a trend toward random dispersion, indicating exterritorial social behavior within the colony. Vegetation data at transect and quadrant level shows nonsignificant correlation, while data at the grid cell level was only weakly coordinated, but data at nest level does suggest an influence of vegetation on nest location. I hypothesize that increased sample size, revision of methods and implementation of more complex data analyses will produce more significant results. By examining the factors that dictate the CLT preferred nesting conditions, this study can inform resource managers on the best strategies for nest site preparation and management.

OC Water District funded the second and third author, The Department of Fish and Wildlife allowed us site access and provided GPS data.

30. Functional Validation of Choroid Plexus Epithelial Cells Derived from Human Embryonic Stem Cells

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Choroid plexus epithelial cells (CPECs), which make up the blood-cerebrospinal fluid barrier, have been found to maintain homeostasis in the brain by contributing to immune surveillance, removal of toxins, and the secretion of cerebral spinal fluid. In Alzheimer's disease and various other neurological disorders, CPECs are thought to be dysfunctional and/or morphologically abnormal. Despite these abnormalities, very little research has been done on the human choroid plexus and human CPECs. As a result, our lab has created a unique protocol to derive CPECs from human embryonic stem cells for disease modeling and other regenerative medicine applications. In the brain, CPECs exclusively synthesize Transthyretin (TTR), a carrier protein, which is secreted via the classical secretory pathway and is used to determine CPEC identity. We have detected abundant TTR in the cell conditioned media of the human derived CPEC (hdCPEC) cultures; however, one of the concerns is whether the detected TTR is due to active secretion or release by dying cells. Brefeldin A (BFA) is a fungal metabolite that inhibits the classical secretory pathway by blocking protein transport from the endoplasmic reticulum to the Golgi apparatus. If TTR is actively being secreted by hdCPECs, then after treatment with BFA, there should be low levels of TTR expression detected in cell-conditioned media. For this study, active secretion of TTR was measured by collecting cell conditioned media at different timepoints. When the cells were treated with 0.1, 1, or 10 ug/ml BFA, TTR secretion dramatically decreased at the lowest concentration, demonstrating a high sensitivity to the blocker. An established feature of BFA on the classical secretory pathway is immediate reversibility, so cultures were either continuously exposed to 0.1 ug/ml BFA or the BFA was withdrawn after an hour of incubation. Exposure to BFA inhibited TTR secretion compared to the non-treated control, but TTR levels quickly recovered upon removal of the drug, while TTR levels remained low in the continued presence of BFA. This study establishes that Brefeldin A quickly affects secretion, and that those effects are rapidly reversible. Therefore, the human stem cell derived CPECs clearly function as TTR secretory cells.

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31. Growth rates of Dendraster excentricus when fed Rhodomonas sp. vs. Dunaliella tertiolecta

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In order to understand the developmental physiology of marine invertebrates it is necessary to culture them under controlled laboratory conditions. This allows the researcher to control the critical environmental conditions and understand their influence on larval growth and development. Larvae of the sand dollar, Dendraster excentricus, are commonly used for such studies. In the present study, we sought to determine the effect of algal food type on growth and development of D. excentricus. We fed independent cultures of larvae the same algal concentration (5,000 cells/ml) of either Dunaliella tertiolecta or Rhodomonas sp. These two types of algae are commonly used as a food source for many types of echinoderm larvae and are capable of supporting growth to metamorphic competency. Larvae were reared in 180 L vessels at a density of 1 larva/ml and water changed and larvae refed 3-times per week. Larval development was assessed through microscopic observations noting time required to achieve key developmental milestones. Larval growth was determined by quantifying the change in larval protein biomass over the course of development. Protein biomass was determined using a Bicinchoninic Assay (BCA). Our results clearly showed that larvae fed Rhodomonas sp. developed and grew faster than the larvae grown on Dunaliella tertiolecta. Larvae fed Rhodomonas sp. grew three times larger than the larvae fed Dunaliella tertiolecta. These results demonstrate that the choice of algal food for studying larvae in lab-based cultures is an important consideration. Further research understanding how lab-based cultures compared to field-based larval growth rates are necessary for furthering our knowledge of larval growth and development.

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32. Development of Human Induced Pluripotent Stem Cell Reporter Lines for Directed Differentiation to Specialized Lung Endodermal Progenitors.

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Idiopathic pulmonary fibrosis (IPF) is a progressive lung disease characterized by epithelial progenitor cell dysfunction, scarring and declining lung function. Treatment options are extremely limited and at best only slow disease progression; the only curative option is lung transplantation. Stem cells have huge potential as tools to study mechanisms of tissue maintenance, remodeling and for the development of novel therapies. By mimicking cell signaling that occurs in vivo during development and applying it to cell culture, directed

differentiation can be used to induce specific lung cell fates. The differentiation of the human induced pluripotent stem cell (hiPSC) line, 83iCTR-33n (83i), was directed towards multipotent lung endoderm in vitro. This was achieved through the addition of stage-specific extrinsic transcription factors to basal medium each day to direct 83i's through the three main developmental stages of lung progenitor differentiation: definitive endoderm, anterior foregut endoderm, and lung endoderm. At each stage of differentiation, cells were fixed and immunostained for stage-specific molecular markers to confirm cell identity. CRISPR/Cas9 gene editing of the 83i cell line was used to introduce a YFP tag onto SOX2, an important pluripotency marker. As a result, the engineering and generation of this 83i SOX2-YFP reporter cell line allows for the real-time monitoring of cell phenotype during regulated differentiation towards lung endoderm and serves as an additional diagnostic tool to confirm cell fate at each developmental stage during differentiation towards lung endoderm.

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33. Geometric Magnetic Frustration in a New Structural Modification of (S = 3/2) $Li_3Mg_2RuO_6$

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Compounds with triangular cationic sublattices with nearest neighbor antiferromagnetic (AFM) exchange cannot satisfy spin constraints simultaneously and exhibit a phenomenon known as geometric magnetic frustration (GMF). GMF is quantitatively measured using the frustration index, $f = |\theta_W| / T_N$, were θ_W represents the Weiss constant and T_N is the transition temperature. Non-frustrated lattices have values between 2 and 4 while highly frustrated lattices are 10 or higher. We report on the synthesis and magnetic properties of a new modification of the previously studied ruthenate, $Li_3Mg_2RuO_6$. The former orthorhombic phase with space group Fddd was found in the ordered NaCl structure type and here we report the synthesis, characterization and magnetism of the monoclinic version, C2/m, with the same chemical composition. The orthorhombic phase underwent a long-range antiferromagnetic (AFM) transition at ~17 K and exhibited moderate geometric magnetic frustration (GMF) with frustration index, (f)≈6. The monoclinic phase of $Li_3Mg_2RuO_6$ was synthesized at different temperature and undergoes a short-range AFM transition at ~17 K and also exhibits a frustration index, (f)≈6. In addition, the novel S=1 system comprising Ru^{6+} magnetic ions, Li_4MgRuO_6, was successfully synthesized in the monoclinic structure. This was followed by the synthesis of a series of intermediate compounds between the two title compositions namely $Li_{3+x}Mg_{2-x}RuO_6$ (x=0.25, 0.50, and 0.75). By varying Li^+/Mg^{2+} ratio, a systematic study is ongoing,

which will further enable in the understanding of the role of spin quantum number on resulting magnetism.

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34. Structural Variations and Magnetism in Ca_2ScRuO_6 and Ca_2FeRuO_6

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Here we report on synthesis, crystal structures and magnetic properties of two novel ruthenium-based double perovskites, namely Ca_2FeRuO_6 and Ca_2ScRuO_6. These oxides were synthesized employing high temperature solid state method. The crystal structures were determined by refining powder x-ray diffraction data. Magnetic properties were measured using Physical Property Measurement System (PPMS). Structural refinements reveal that while the Ca_2ScRuO_6 crystallize in B-site ordered double perovskite structure (Sc^{3+} and Ru^{5+} reside in their own specific crystallographic positions) there exist a site mixing between Fe^{3+} and Ru^{5+} in Ca_2FeRuO_6. The differences between the crystal structures and magnetic properties of the two title compounds will be presented.

This research was supported by the NSF-DMR-RUI Award #1601811.

35. Examining the Physico-Chemical Properties of an Extreme Halophilic Virus, GNϕ2

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Extreme halophiles, known to withstand high salinity concentrations ~20%-30%, have been manipulated for use in the environmental, medicinal, and agricultural industries. Examples of applications are alternative biofuel production, degradation of toxic compounds, and synthesis of bioplastics. Halophilic viruses may potentially be exploited in this way as well. Our current research aim is to characterize the physico-chemical properties of an extreme hypersaline virus, GNϕ2, that infects a Halorubrum haloarchaeal host. We determined the virus' tolerance to different salinities, temperatures, and pHs through measuring its infectious capability with a top agar plaque assay. We discovered that GNϕ2 is still infectious between 4°C and 60°C; between 5% and 35% salinity; and from pH 4-11. For future directions, we will perform adsorption and desiccation experiments, sequence its genome, and complete the analysis of the GNϕ2 life cycle, modifying current experimental design.

This project is supported in part by the National Institute of Health Grant 5R25GM071638-13, in affiliation with the Research Initiative for Scientific Enhancement (RISE) program.

36. Injectable Nanocomposite Hydrogel Scaffold Incorporated with Two-Dimensional Materials for Bone Tissue Engineering

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An estimated 55% of Americans over the age of 50 have either low bone mineral density or osteoporosis, putting them at high risk for bony defects such as fractures and lesions. Recent advances in bone tissue engineering have helped to develop synthetic hydrogels that enhance the natural regenerative capabilities of the human body. Biodegradable hydrogel scaffolds could be injected into bony defects, fill the void space, and provide structural integrity to the damaged area. Furthermore, various materials or factors could be added into the hydrogel formulation to guide cellular differentiation and proliferation. In this study, carbon nanotubes functionalized with poly(ethylene glycol)acrylate (CNTPega) and two dimensional (2D) black phosphate nano sheets (BPNS) are incorporated into oligo(polyethylene fumarate) (OPF) hydrogels to stimulate proliferation and differentiation of pre-osteoblast cells (MC3T3-E1) *in vitro*. Our hypothesis was that the OPF hydrogel containing CNTs and BPNS will have a synergistic effect, increasing MC3T3-E1 cell proliferation and differentiation at a faster rate than OPF containing CNTs or BNPS alone. Creation of the injectable hydrogel was performed by adding CNT and BPNS components into the OPF base. The base was then crosslinked upon the addition of ammonium persulfate and L-ascorbic acid. The gelation time was measured via rheology testing for future *in vivo* applications. *In vitro* live/dead cell studies with MC3T3-E1 cells show increased cellular proliferation of OPF containing CNTPega and BPNS when compared to all controls. This suggests a synergistic effect of CNTPega on MC3T3-E1 cells, supporting our overall hypothesis.

37. Monochloramine Reactivity with Amino Acids in Wastewater: Kinetic and Temperature Dependence

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The Orange County Water District (OCWD) California specializes in wastewater treatment by augmenting the standard primary and secondary treatments with a series of filtration steps (microfiltration, and reverse osmosis) prior to using an Advanced Oxidation Process (AOP). In order to minimize biofouling OCWD generates chloramines through the addition of 12.5% sodium hypochlorite into the treatment train just before the microfiltration step. This bleach

reacts with the ammonia present in the wastewater to produce a mixture of monochloramine (NH_2Cl), dichloramine ($NHCl_2$) and trichloramine (NCl_3) which passes through the membrane filters and into the AOP. In addition, chloramines can also react with organic matter present in the wastewater to create unwanted chlorinated disinfection byproducts (DBP's): toxic and hazardous chemicals that are highly regulated. As such, understanding this byproduct formation chemistry is essential. The focus of this project was to determine the temperature-dependent rate constants for NH_2Cl reacting with a suite of amino acids at a neutral pH of 7, mimicking the wastewater treatment conditions. Simple amino acids were selected as prototypical organic matter. Solutions were made in borate buffers to keep the pH constant throughout the reaction. NH_2Cl was made using a 1:1 ratio of bleach to ammonium prior to mixing with the acids. These reactions were monitored through the decay of the NH_2Cl absorbance peak at 243 nm in a stopped-flow spectrophotometer. Typical results of these pH-dependent reactions with Alanine indicate that at a high basic pH, NH_2Cl decay is slower than at a neutral pH. From the overall changes in the decay rate of NH_2Cl at different amino acid concentrations, pseudo-first-order rate constants for the kinetics were obtained over a range of temperatures. The reactivity-structure relationships and the corresponding Arrhenius parameters were measured to provide insight into this chemistry.

This project is supported in part by the National Institutes of Health Grant 5R25GM071638-13.

38. Hybrid Peptide-Drug Conjugate Heterotrimer for Combinational Chemotherapy

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There is a great interest and need to improve treatment options in cancer, including metastatic cancer. General treatment of cancer can include: surgery, radiation, immunotherapy, and chemotherapy. In severe cases where surgery is not feasible, combinational chemotherapy has been found to be effective in treatment of various cancers, where multiple agents has been used either subsequently, or simultaneously. In order to administer multiple agent simultaneously that vary in chemical properties and potency, the use of a carrier system has been studied. Here we present the development of a hybrid peptide heterotrimer to effectively administer a combinational therapy for three agents commonly used in breast cancer treatment (Paclitaxel, Doxorubicin, and 5-Fluorouracil). Paclitaxel and Doxorubicin were modified with succinyl linker and cis-aconityl linker respectively, in order to produce 2'-O-succinyl-paclitaxel and cis-aconityl-doxorubicin (CAD). The formation of products were confirmed with Nuclear Magnetic Resonance Spectroscopy (NMR) and Electrospray Ionization-Mass Spectrometry (ESI-MS). We are continue working on 5- Fluorouracil modification with a succinyl linker and conjugation of all three modified agents to the hybrid peptide carriers. The final peptide carrier modified with three agents will be characterized with circular dichroism (CD) spectroscopy and biological activity will be evaluated *in vitro* with MCF-7 breast cancer cells.

This project is supported in part by the National Institute of Health via RISE program.

39. Study of the Effect of Acid Functionality in the Organo-Photoinitiator on the Hydroacylation of Diethyl Maleate

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Photochemistry concerns the initiation or catalysis of chemical reactions using electromagnetic radiation in the UV-visible or near infrared region of the spectrum. Developing organic photo-initiators is of interest owing to their potential to be greener and cost-effective alternatives to more traditional metal-based photochemical initiators. Prior reports by the Papadopolous group have looked at the photoinitiated hydroacylation of diethyl maleate by aldehydes using benzophenone derivative initiators. Of those tested, phenylglyoxylic acid produced both faster reactions and gave high product selectivity than initiators lacking the acid functionality. To determine the nature of the influence of the acid functionality on the reaction, we replaced the phenylglyoxylic acid with its ester, methyl benzoylformate. We compared the reaction rates via comparing conversion ratios at set reaction times via GC/MS analysis. The preliminary results shown no little or no effect in rate or reaction selectivity when using the ester photoinitiator, except that the rate of initiator decomposition is lower. This suggests that the presence of the 1,2-dicarbonyl, rather than the acid, may be the critical factor influencing the improved reaction rate and selectivity. Future studies will investigate this hypothesis.

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40. Dysregulation of *myo*-inositol Synthase Causes Developmental and Birth Defects in *Drosophila melanogaster.*

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Myo-inositol is a six-carbon sugar alcohol that is a precursor of phosphatidylinositol (PI), a cell membrane phospholipid. It is also involved in the phosphoinositide signaling pathway, which is essential for the regulation of cellular functions. *Myo*-inositol has been implicated in diseases and medical complications such as hyperglycemia, diabetes, and obesity – all of which are major threats, especially within the United States. The hypothesis of this study was that inositol would reduce obesity and hyperglycemia. En route, we discovered that inositol has a role in birth defects. This study directs attention to the effects of transcriptional dysregulation the *Inos* gene using various drivers (promoters) on Chromosome 2 and 3 of the model organism *Drosophila melanogaster*. Increased nearly constant (dysregulated) synthesis of inositol yields individuals with growth and developmental defects. With near constitutive provision of GAL4

protein using an actin, ubiquitin, or tubulin promoter driving *Inos* expression (via a UAS_{GAL4}), the heterozygotes were developmentally stunted. Few progeny developed beyond the pupal stage. Across all these drivers, ActGAL4-3 yielded only female adult progeny, a noticeable number having morphological defects in the mouth, wing, and leg regions. These studies should contribute to a better understanding of inositol's role in birth defects and developmental disabilities.

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41. Synthesis and Crystal Structure of Novel Nickel Ruthenates: Li_4NiRuO_6 and $Li_3Ni_2RuO_6$

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Antiferromagnetic interactions in ordered NaCl structure type (composed of triangular sub-lattice) could potentially cause geometric magnetic frustration (GMF). Our group has studied several members of this family with Os ions as magnetic centers; Li_5OsO_6, Li_4MgOsO_6, Li_3MgOsO_6. Recently, the efforts have been extended to systems where collaborative effects among *3d* and *5d* metals are in place. Previous work was done by our group on synthesizing and characterizing Li_4NiOsO_6 and $Li_3Ni_2OsO_6$ where the magnetic exchange interactions among Ni^{2+} ($3d^8$) and Os ions result in ferrimagnetic transitions. In an effort to understand the role of principal quantum number on resultant magnetism, the 5*d* Os ions were replaced by isoelectronic 4*d* Ru ions. The direct adaptations resulted in the successful synthesis of Li_4NiRuO_6 and $Li_3Ni_2RuO_6$ which were obtained by annealing stoichiometric mixtures of Li_2CO_3, NiO, and RuO_2 at high temperatures using a solid state synthesis approach. Powder x-ray diffraction analyses confirm monoclinic crystal structure with a *C2/m* space group for both Li_4NiRuO_6 and $Li_3Ni_2RuO_6$. Preliminary crystal structure refinements suggest mixed occupancy in the cation position, so future work utilizing neutron diffraction measurements will be performed to fully understand chemical compositions in various crystallographic positions. To further evaluate the crystal structure and its effects on magnetic susceptibility, temperature dependent magnetic susceptibility and magnetic field dependent magnetization will be conducted.

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42. Development of a Glioblastoma Organoid Model for the Study of Antigen Escape Following IL13Rα2-targeting CAR T Cell Therapy

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Poor prognosis for patients with glioblastoma has prompted development of innovative therapies, including immunotherapy using chimeric antigen receptor (CAR) T cells targeting tumor antigens. However, extensive tumor cell heterogeneity is thought to underlie antigen escape and tumor recurrence due to incomplete eradication and subsequent emergence of an antigen loss variant population that is deficient in the targeted antigen. Combination immunotherapy is proposed as a way to limit antigen escape by targeting multiple tumor antigens, and may be an efficacious approach to combat this limitation of immunotherapy. Here we present data on the use of organoid cultures to study glioblastoma (GBM) tumor cell growth and differentiation within a 3-dimensional matrix, and their responses to IL13Rα2-targeting CAR T cells. The patient-derived glioblastoma (GBM) cell lines used to establish the GBM organoids differ in their expression of the target antigens IL13Rα2, HER2 and EGFR, as do the tumors from which they were derived. We will present data for tumor organoids derived from GBM cell lines PBT030 and PBT106 over the first 30 days in culture illustrating heterogeneity of IL13Rα2, EGFR and Her2 expression, and responses of PBT030 organoids to IL13Rα2-CAR T cell infiltration based on Immunofluorescence and Flow Cytometry. This model allows for reproducible tumor growth and controlled exposure to CAR T cells targeting multiple antigens, and will facilitate devising optimal strategies for administration of combination CAR T cell immunotherapy.

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43. Effects of Sediment Augmentation on a Coastal California Wetland

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Coastal wetlands are ecosystems which transition between the land and ocean. Wetlands provide a range of ecosystem services, including water filtration, habitat provision, and water quality improvement. Despite this recognized importance to humans, wetlands have been and will continue to be impacted by sea level rise (SLR) as a result of climate change. In order to continue the water quality function of these habitats, ecologists have implemented strategies

to help wetlands keep pace with SLR including sediment augmentation. In 2015, a team of scientists and managers used sediment augmentation at the Seal Beach National Wildlife Refuge (SBNWR) in response to sea level rise threats. Our goal is to examine the impact of sediment augmentation at the SBNWR by analyzing the restoration trajectory of the invertebrate community. Sediment samples from a control site and an experimental site were collected in fall from 2015 to 2018 to compare infauna within California cordgrass (*Spartina foliosa*) plant communities. The samples were washed, sieved, and sorted to identify the invertebrates down to the lowest taxonomic level. Analyses of species richness, abundance, and diversity of the infauna community within the *Spartina foliosa* habitats across treatments and years provided insight on restoration trajectory. Although the experimental site has lower diversity, species richness and abundance than the control site post-augmentation, the experimental site is starting to show some evidence of recovery in fall of 2018 with slightly higher abundances and more similar community composition to the control. Understanding how the invertebrate communities and overall marsh recovers following augmentation will assist in proper maintenance and improve protection to crucial ecosystems that protect coastal cities from sea level rise.

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44. Minimally-Invasive Intravenous Delivery of PLG Nanoparticles Modulates Chronic Pathology in Repeat-Mild Traumatic Brain Injury

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There are approximately 2.8 million Americans that sustain a traumatic brain injury (TBI) annually. While the majority of these cases are mild (mTBI) and managed early on without lasting structural damage; repeat mild events (rmTBI) can cause chronic pathology. There are currently no available treatments for rmTBI. Using our novel mouse model of rmTBI, we intravenously delivered five doses of an FDA-approved Poly(Lactic-co-glycolic acid) (PLG) nanoparticle (NP) treatment into 5-hit rmTBI animals. PLG NPs are known to modulate circulating neutrophils and inflammatory monocytes, which are key players in the early inflammatory response and thereby pathology following injury. Locomotor function (Catwalk) was assessed at 3, 6, and 8 weeks post injury, while anxious-like behavior (Elevated Plus Maze; EPM) was assessed at 4 and 8 weeks post injury. Spatial learning (Morris Water Maze) and depressive-like behavior (Forced Swim Test) were tested only at 8 weeks post injury. Histological readouts, including corpus callosum volume, will be evaluated at the study endpoint. Our preliminary results suggest that injured mice exhibit unsteady gait relative to uninjured controls (Catwalk - Base of Support) at 3, 6, and 8 weeks post injury, which is rescued

in NP-treated mice at the same time points. Although we expected to see a decrease in the time in open arms on the EPM task with NP treated injury group, there was no significant difference. Interestingly, changes in animal gait and mobility may be confounders in this task. Analysis of other behavioral tasks is in progress. Finally, since it is well known that brain trauma alters neurogenesis, and that there is a link between inflammation and neurogenesis, we will be measuring doublecortin positive immature neurons in the hippocampus across groups. We predict that NP treatment will reduce brain inflammation and restore normal neurogenesis. Taken together, we have early evidence to suggest that PLG NPs may be able to reduce locomotor deficits in rmTBI. Further experimentation is necessary to understand the mechanisms at play and optimize the approach for potential clinical deployment.

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45. Identification of Binding Modes in Molecular Recognition Processes via Non-Heuristic Clustering of Computational Data

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All-atom molecular dynamics (MD) simulations of butyrylcholinesterase in complex with two previously studied alkyl aryl phosphate inhibitors were conducted to develop a methodology to consistently identify and characterize inhibitor binding modes. For each inhibitor, 1000 independent simulations were run for 100 ns or longer, yielding a total sampling time of over 100 □s per inhibitor in explicit ionic solvent.To capture the inherent flexibility of the protein-ligand complex, each simulated structure was then summarized as a descriptor vector (DV), each component of which consisted of the number of atoms in a neighboring amino acid within 5.0 Angstroms of each specific functional group in the inhibitor. This treatment ensures that the resulting high-dimensional DV is defined by connectivity, such that binding modes are defined by highly similar intermolecular contact schemes, as identified via k-means clustering of the resulting DV's. The k-means algorithm, however, requires knowledge of the number of clusters present within the data *a priori* and is also known to suffer from heuristic tendencies when incorrect cluster numbers are employed. To overcome these problems, we report herein a protocol to determine the optimal cluster number that will yield accurate and reproducible clustering. The results of our binding mode analysis for the full data set of 1000-simulations were then compared to those for smaller sampling sizes of 1, 10, and 100 randomly chosen simulations. Though the 1- and 10-simulation data sets captured the most populated binding modes observed when using massive sampling, many binding modes were absent from or incompletely characterized by the smaller data sets. In contrast, the 100-simulation data set captured all binding modes observed in, and reflected few differences from, the full 1000-simulation mass sample. Although our method of overcoming the heuristic nature of clustering

was demonstrated using massive MD simulations, we expect it is generalizable to other types of structural data.

46. Determining the Role of C9orf72 in Immune Function and Amyotrophic Lateral Sclerosis

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Amyotrophic Lateral Sclerosis (ALS) is a neurodegenerative disease characterized by the progressive loss of motor neurons. This leads to deficits in motor function, speech, and breathing, eventually leading to death within 3-5 years of disease onset. Mutations in several genes have been identified as the cause of both familial and sporadic ALS, however, a hexanucleotide repeat (GGGGCC)n in the intronic region of the gene C9orf72 is the leading genetic cause. The repeat expansion seems to effect a dual-mechanism: a toxic accumulation of RNA foci and RAN dipeptides, as well as a loss-of-function phenotype resulting from a 50% decrease in the wild type protein. The C9orf72 protein has been shown to play key roles in autophagy and membrane trafficking, however, the entire scope of its function is yet to be characterized. Importantly, the expression of the protein has been found to be highest in myeloid cells and microglia, a cell type supportive to neurons. O'Rourke et al generated a C9orf72 KO model in which mice did not develop ALS symptomatology, however, did present with splenomegaly and lymphadenopathy, suggesting that C9orf72 may have another role in immune function. The aim of this study is to elucidate the role of C9orf72 in immune function by using C9orf72 KO, heterozygotes, and wild type murine bone marrow derived macrophages (BMDMs) as a model. Specifically of interest is the measurement of downstream markers of the type 1 interferon response upon activation of the cGAS-STING pathway to determine if there is a connection between ALS pathology and the role of C9orf72 in these immune cells. The goal is to progress to in vitro human patient models using a differentiation protocol that derives macrophages from peripheral blood mononuclear cells (PBMCs). The PBMCs will provide more relevant insight to the mechanism underlying the C9orf72 mutation and its role in ALS pathology.

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47. Evaluating Di-n-butyl 2-chlorophenyl Phosphate (DB2CIPP) as Potential Alzheimer's Disease Drug in Mice Studies

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Alzheimer's disease is a neurodegenerative, progressive brain disease responsible for degraded memory, thinking, and behavior. One of the most common early symptoms involves difficulty remembering newly learned information. Alzheimer's affects those above the age of sixty-five

and is more prevalent in women than in men. One of the hallmarks of this neurodegenerative disease involves a dramatic increase in butyl cholinesterase activity. Butyl cholinesterase is an enzyme responsible for the hydrolysis (breakdown) of acetylcholine, a major neurotransmitter in the brain. Due to the decrease in acetocholine activity, there is an overall loss of cognitive function. The rise in butyl cholinesterase (BuChE) activity and decrease in acetylcholine activity drives a dramatic increase in beta amyloid (β-amyloid) peptide levels. Beta amyloid (β-amyloid) peptide forms neurotoxic plaques in the hippocampal region of the brain, where the formation of memories takes place. Aryl Dialkyl phosphates, specifically Di-n-butyl 2-chorophenyl phosphate (DB2CIPP), is known to be a selective irreversible inhibitor of butyl cholinesterase. Butyl cholinesterase inhibition may be helpful in the treatment of this neurodegenerative disease by eliminating, reducing, or preventing the formation of beta amyloid plaques. The purpose of these experiments is to test the hypothesis that inhibiting butyl cholinesterase activity reduces beta amyloid plaque formation in the hippocampus and maintains cognitive function. Preliminary studies showed that DB2CIPP can cross the blood brain barrier of rodents and block BuChE activity. We are proposing to test this hypothesis in Adult C57BL/6J male mice that have premature β-amyloid formation and cognitive deficits. Starting at 9 months of age mice will be subcutaneously injected twice weekly with either 10mg/ml or 20mg/ml of DB2CIPP or DMSO control. Animals will be tested for cognitive deficits in a Y-maze and brains will be collected at 9 months, 11 months, and 13 months of age. Levels of β-amyloid formation in the hippocampus will be measured by immunohistochemistry. We expect that control treated animals will have cognitive deficits and increased β-amyloid formation in the hippocampus compared to DB2CIPP treated mice. These results would indicate that DB2CIPP treatments prevent the induction of Alzheimer-like deficits in mice by blocking BuChE activity.

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48. Epigenetic Modification of Chromatin Insulators Directs Transgene Expression Heterogeneity

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The emergence of cellular and genomic engineering tools has sparked the discovery of novel and innovative cell-based therapies. Both basic biomedical research and cell-based therapies will rely on the expression of multiple genes under the control of multiple promoters. Currently, the rapid development of these complex therapeutics has been hindered by expression heterogeneity in multigene transcripts. Even with the use of chromatin insulators expression heterogeneity still occurs with the cause largely unknown. Hence, there is a need to elucidate and circumvent the mechanisms behind this. Chromatin insulators have become a ubiquitous solution towards combating a cell's propensity to regulate genes and ensuring reliable and

robust expression of integrated constructs. These insulators are nucleotide sequences which interact with endogenous CCCTC-binding factor (CTCF) proteins to form stable DNA loops and are thought to prevent the epigenetic silencing of integrated transgenes. We show that the inclusion of current chromatin insulators is not sufficient for safeguarding transgene expression. Utilizing a multi-transcript unit construct, we demonstrate that despite the presence of chromatin insulators transfected cells exhibit heterogeneous expression following several rounds of selection. We hypothesized that chromatin insulators are susceptible to *de novo* methylation for a short period of time after integration, which abrogates their protective effects. Sequential methylation of exposed transcript promoters further facilitates permanent silencing of integrated genes. Herein we investigated the role of methylation in expression heterogeneity by modifying chromatin insulators to resist epigenetic silencing and exhibit stable, long term expression of complex multigene constructs.

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49. Spectroscopic Characterization of Iron Oxides

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We report on the spectroscopic analysis of iron oxides as a (photo)anode for water oxidation. We are particularly interested in α-hematite type iron oxides and iron perovskite from $Ca_xSr_{2-x}Fe_2O_{6-\delta}$ series. These materials are particularly attractive as a clean and inexpensive alternative for (photo)electrochemical water oxidation, an important process in natural and artificial energy cycles. However, application of these materials in (photo)electrochemical devices is challenging, mainly due to their poor electrical conductivity and sluggish oxygen evolution kinetics. Improvements to electrocatalytic activity for oxygen evolution often address the low hole mobility in these materials which may contribute to their low electrical conductivity and slow kinetics. Light can be harnessed to drive water oxidation on iron oxides, and dopants can be introduced to create oxygen deficiencies. We seek to elucidate the interplay between dopants, optical properties, electrical conductivity, and activity of low-dimensional iron oxides. Raman spectroscopy is used to identify the vibrational modes characteristic of oxygen deficiency dependence in these structures.

This project is supported in part by the Stern Foundation

50. Synthesis of Hematite Microwires for Photoelectrochemical Water Splitting

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The goal of this work is to develop a controlled synthesis method for making well-defined hematite structures for photoelectrochemical water splitting, which is important in a sustainable energy cycle. The emphasis is on changing the morphology of α-hematite to achieve scales optimum for photoelectrochemical activity. We use a potassium hydroxide and ferric nitrate [KOH + $Fe(NO_3)_3$] solution with controlled pH. The resulting solution is drop casted onto an FTO (Fluorine-doped Tin Oxide) sonicated glass slide prior high temperature synthesis. We place our slides into a glass tube, then place the glass tube into a chemical vapor deposition (CVD) furnace where we heat, then cool the substrate, while running the synthesis under Argon gas flow. We use optical microscopy for assessing the morphology of the films. Lastly, Raman spectroscopy analysis confirms the presence of α-hematite and shows interesting properties related to the oxygen deficiency of the films.

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51. Characterizing the Molecular Components that Couple Bolting Time to Age-Dependent Leaf Senescence in *Arabidopsis thaliana*

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In plants, the vegetative to reproductive growth phase transition (bolting) precedes age-dependent leaf senescence (LS). Understanding the timing of bolting and its molecular connection to LS is agriculturally important. During LS, nitrogen and other macromolecules are recycled from dying leaves and relocated to reproductive organs (fruits/seeds), which in many species are then harvested for human consumption. Understanding the molecular causes of coupling may allow for the development of crops that can overcome stress-related early-bolting-induced early LS. Homozygous *Arabidopsis trithorax* (*ATX)* triple T-DNA insertion mutants (*atx1 atx3 atx4*) display significantly early bolting coupled to significantly early LS, thus we used this line as a model to study the coupling of these developmental stages. We completed an RNA-seq time-course experiment that revealed 121 genes with differential expression (DEGs) in early bolting *atx* triple mutants relative to vegetative wildtype plants of the same age. Gene Ontology Analysis of these DEGs showed enrichment of many defense (response to oxygen-containing compound, glutathione metabolic process) and stress response (response to water deprivation, detoxification) pathways, which are often enriched in LS-related DEG lists. Response to salicylic acid (SA) and ethylene were both enriched in these DEGs, and both are endogenous hormones that positively regulate LS. We hypothesize that some of these DEGs, which change expression during bolting, are signaling the onset of LS. If a gene is responsible for coupling, then a plant carrying a null mutant copy of that gene should display an uncoupled phenotype. Twenty-one genes from this list contain predicted regulatory

domains, likely having a role in some type of signaling. To test our hypothesis, T-DNA insertion mutants for 17 of the 21 potential regulatory genes were isolated to screen for mutations that uncouple bolting and LS. Bolting time and above-ground fresh weight, along with *NIT2* expression (a gene up-regulated during LS) and Leaf 3 chlorophyll concentration were analyzed in a time course experiment to characterize LS phenotypes in single mutants. Preliminary data from the candidate screen show four mutants that display uncoupled bolting and LS phenotypes. Three mutants display weak but significant stay green phenotypes relative to WT. One mutant, *erf054*, displays significantly delayed bolting and a net stay green type phenotype. However, *erf054* displays more rapid chlorophyll degradation than WT after bolting. Currently, data support the hypothesis that there are bolting-time specific expression changes of senescence-regulating genes. Further study of the four regulatory gene candidate mutants may elucidate the molecular connection between bolting and age-dependent leaf senescence.

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52. Biophysical and Functional Analysis of Apolipoprotein E3 and E4 Modification by 4-Hydroxynonenal, A Lipid Peroxidation Product

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Background: Post mortem tissues from brains of Alzheimer's disease (AD) patients show higher levels of 4-hydroxynonenal (4-HNE)-modified proteins, with 4-HNE arising as a result of oxidative stress and lipid peroxidation. The overall goal of our study is to understand the effect of 4-HNE modification on the structure and function of apolipoprotein E3 (apoE3) and apoE4, which are 34 kDa exchangeable apolipoprotein isoforms that play a critical role in brain cholesterol homeostasis. Individuals carrying the *APOE* ε4 allele are at a higher risk of developing AD in a gene-dose dependent manner. In the present study, we report the biophysical and functional analyses of 4-HNE modification of apoE3 and apoE4 in terms of protein fold and conformation. **Methods:** Recombinant apoE3 and apoE4 were modified by 4-HNE at concentrations typically found in pathological tissues (~20 □M), followed by Western blot and MALDI TOF mass spectrometric analyses to confirm modification. The modified samples were then subjected to circular dichroism (CD), fluorescence (intrinsic and 1-anilinonaphthalene-8-sulfonic acid (ANS) fluorescence) spectroscopic, guanidine hydrochloride (GdnHCl)-induced unfolding analyses, and lipid binding assessment. Results: Western blot with 4-HNE specific antibody confirmed modification of apoE3 and apoE4, with a major band at ~36 kDa, while mass spectrometric data revealed modification of K72 and K75. 4-HNE-modified apoE3 and apoE4 were highly helical (~60%) comparable to that of unmodified proteins (~58%) as revealed by far UV CD spectroscopy. A significant decrease in the intrinsic fluorescence emission was noted for both 4-HNE-apoE3 and 4-HNE-apoE4, compared to the corresponding unmodified proteins. GdnHCl-induced denaturation monitored by changes in intrinsic fluorescence revealed a notable difference in terms of increased susceptibility to unfolding for

4-HNE-apoE4, but not 4-HNE-apoE3. 4-HNE modification significantly impaired the ability of apoE to transform DMPC vesicles to small discoidal protein/lipid complexes. The calculated t½ (time required for initial absorbance to decrease by 50%) for apoE3 was 165.6 mins, while that for 4-HNE-apoE3 was 516.8 mins. Similarly, the t½ for apoE4 was 4.95 min, while that for 4-HNE-apoE4 was 16.3 mins. Further, ANS fluorescence emission spectra revealed a 10 nm red shift in the wavelength of maximal fluorescence emission for 4-HNE-apoE4 (but not for 4-HNE-apoE3) compared to unmodified protein. **Conclusions:** Taken together, our data indicate that there are isoform-specific differences in protein conformation, tertiary fold and functional ability as a consequence of modification of apoE by 4-HNE. Assessing the differences in the susceptibility to age-related oxidative modifications aid in understanding the molecular basis for the role of apoE4 as a risk factor for AD and amyloid pathology.

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53. Mechanism of Sex-Specific Sleep Disruption by Ovarian Hormones

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Women are twice as likely as men to experience sleep disruptions and insomnia compared to men. Despite this striking health disparity, our understanding of how female sex hormones (e.g. estrogens, progesterone) influence the brain to change sleep is limited. One potential target of ovarian hormones are neurons of the lateral hypothalamus that express the neuropeptide hypocretin (hcrt, otherwise known as orexin). These neurons promote wakefulness and play a critical role in stabilizing sleep and wakefulness, and previous literature has indicated hcrt production is increased by ovarian hormones. Thus, we hypothesized that ovarian hormones impact hcrt neurons to promote wakefulness. The objective of this project was to test whether estrogen and progesterone also regulate hcrt neural projections to its major sleep/wake-regulating target regions. Specifically, we used a cre-dependent fluorescently-tagged synaptophysin construct to specifically label hcrt presynaptic terminals in targeted regions in hcrt-cre mice, as a proxy for the strength of hcrt communication to these regions. The number of hcrt presynaptic terminals was then compared between control and hormone-treated animals within each region. These data reveal how ovarian hormones can regulate connectivity within the neural sleep/wake circuit and support the continued and ongoing work investigating how sex differences in physiology can produce important health disparities.

54. Incorporation of Antioxidant Luteolin into ApoE3NT and ApoAI containing HDL Nanodiscs

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High-density lipoprotein (HDL) is a large spherical protein-lipid complex that is composed of proteins such as apolipoprotein (apo) AI and apoE3, several molecules of lipids, and cholesterol. Amongst these apolipoproteins, only apoE3 has the ability to bind low density lipoprotein receptor family of proteins that facilitate cellular uptake of lipoproteins via receptor-mediated endocytosis. Other ways of cellular entry for lipoproteins involves scavenger receptor B1, (SR-B1), which recognizes apoAI, apoE3 and other apolipoproteins. We propose to capitalize these features of apolipoproteins to deliver the antioxidant luteolin (3',4',5,7-tetrahydroxyflavone) into breast cancer cells (MDA-MB-231). The overall goal is to incorporate luteolin into reconstituted high-density lipoproteins (rHDL). The objectives of the current study are to: (i) overexpress, and purify recombinant human apoE3 encompassing residues 1-191 of the N-terminal domain (apoE3NT) and apoAI both bearing a His-tag; (ii) reconstitute HDL in the presence of synthetic phospholipids, apoE3NT or apoAI, and luteolin; (iii) perform biophysical and biochemical characterization of the rHDL. Overexpression of apoE3NT and apoAI was accomplished using *E. coli* BL21-Gold (DE3) pLysS cells and the proteins purified by affinity chromatography using a Nickel Hi-Trap chelating column. SDS-PAGE analysis revealed that the proteins were ~ 95% pure. The proteins were mixed with one of the following phospholipids: POPC, DMPC, 1DMPE, or DMPG in the absence or presence of luteolin and sodium deoxy cholate, and dialyzed to obtain rHDL. The samples were subjected to density gradient ultracentrifugation, fractionated and protein-containing fractions pooled. Non-denaturing polyacrylamide gel electrophoresis (PAGE) confirmed formation of high molecular mass complexes (~ 600 kDa). Future studies will include utilizing HPLC to determine the efficiency of incorporation of luteolin into rHDL, and assessing the effect of phospholipid head group variation on the incorporation. Subsequently, the rHDL particles will be examined by electron microscopy and the effect of the presence of luteolin on cellular uptake of rHDL, and the antioxidant activity against cellular oxidative stress assessed in MDA-MB-231 cells. Successful completion of this study will aid in developing nanodiscs as a viable drug delivery vehicle of other hydrophobic drugs such as chemotherapeutic agents.

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55. Tracking the Genomic Position of Cellulases to Determine Their Participation in the *BCS* Operon

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Cellulose synthesis and subsequent degradation is an essential part of carbon cycling across many ecosystems. Beside plants, some bacteria produce cellulose as part of their biofilm. The bacterial cellulose synthesis (bcs) operon encodes the enzymes involved in this process. However to date, the detailed enzymatic mechanisms of cellulose production remain unclear. However research suggests that a cellulase is required for efficient synthesis (i.e., bcsZ). Here, we investigated the distribution and architecture of the bcs operon in sequenced bacterial genomes. First, most bcs operons are identified in Proteobacteria, and few in Firmicutes and Spirochaetes. Next, strains with bcsABC generally contained less cellulases than other bacteria. Finally, regarding the bcsABC strains but no identified bcsZ gene, we investigated the genomic context of distantly located cellulases to determine whether they can still participate in cellulose synthesis or be involved in cellulose degradation. We identified both cellulases in potential hydrolytic and biosynthetic clusters. In the future, the sequence of the potential biosynthetic cellulases will be aligned in order to build custom HMM-profiles to differentiate the biosynthetic from hydrolytic enzymes.

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56. Ferrocene Electrochemistry in Ionic Liquid and Aqueous Mixtures.

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We report on electron and proton transfer properties of room temperature imidazolium based ionic liquids (IL), such as 1-Butyl-3-methylimidazolium tetrafluoroborate ($BMIMBF_4$) and 1-Ethyl-3-methylimidazolium tetrafluoroborate ($EMIMBF_4$) as they interact with aqueous media. One of the main challenges in using ionic liquids is property changes as they interact with water and air containing media. Here, we study the water/ionic liquid miscibility and compositional changes during water/IL interactions. Ionic liquids are attractive for their high ionic conductivity and interesting electrochemical properties. We use ferrocene, as an electrochemical probe to study the ionic liquid/water interaction. For this analysis, we use cyclic voltammetry (CV) to study ferrocene under different conditions. Miscibility of IL/water is a function of the gas environment and water concentration. Interestingly, pH of the aqueous phase has an influence on the redox potential of ferrocene. The redox potential can be tuned from 0.0 V (vs. Fc/Fc^+ in dry conditions) to as low as -0.4 V (vs. Fc/Fc^+). Ferrocene voltammetry shows progressively higher currents at lower pHs. We will explain these effects using electrochemical analysis. Such

interactions are especially important in understanding the possible reaction pathways of proton couplet electron transfer (PCET) reactions in ionic liquids.

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57. Does High-Fat Diet-Induced Obesity Increase Resilience Against Gram-Negative Bacterial Infection in *Drosophila* Larvae?

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Obesity is a global epidemic but its molecular mechanisms are yet to be thoroughly understood. It is necessary to study the less understood pathways in order to alleviate the health risks associated with the disease through pharmaceutical drugs and other treatments. The primary objective of this research is to explore the effect of a high-fat diet on the inflammatory response within the immune system using the model organism Drosophila melanogaster and relate it back to the human body. Drosophila melanogaster were raised on control or high-fat content food. The high-fat flies were raised in the same conditions for several generations. Triglyceride assays (TAG) confirmed that these larvae have an overall higher triglyceride levels than the control counterparts. To visualize the innate antibacterial response within high-fat flies, third instar larvae are carefully injected with a sample of gram-negative bacteria Serratia marcescens, a natural pathogen, that has been transformed with a plasmid that confers Carbenicillin resistance (BSKS), and a bacterial colony assay is performed. Infected and control larvae are homogenized immediately after infection and four hours later, diluted to a 1:100 ratio in LB broth, and the homogenate is streaked on LB Carbenicillin plates. Based on preliminary data (Huynhle, MS Thesis, 2017), we hypothesize that high-fat flies will have fewer colonies than the control flies. These results will establish whether or not high-fat larvae exhibit higher immunity to the Serratia bacterial load than control larvae. This could be due to a more rapid antimicrobial response, or could reflect constitutive activation of the antimicrobial response.

58. Macrophage Production of Innate Immune Proteins C1q, C1r and C1s

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The classical complement pathway of the innate immune response is triggered by the detection of targets by recognition molecules. Pattern Recognition Receptors, such as complement component C1, are essential for the recognition of damage-associated molecular patterns, pathogen-associated molecular patterns, or apoptotic cell-associated molecular patterns. C1 subunit C1q has previously been found to play a dual role in vivo: triggering inflammation via the classical complement pathway as well as the anti-inflammatory role of directly opsonizing

targets including apoptotic cells and other damaged-self molecules. We hypothesize that macrophages encountering foreign targets (e.g. bacteria) will synthesize higher levels of all subunits of C1 (C1q, C1r, and C1s) to form an active C1 complex and mount an inflammatory response. However, we predict that macrophages encountering damaged-self targets will not alter production of C1r or C1s but may increase C1q production to promote anti-inflammatory responses and clearance by phagocytosis. Therefore, we investigated macrophage production of C1 subunits after M1 (inflammatory) or M2 (anti-inflammatory) macrophage polarization and when exposed to foreign or damaged-self targets. Human monocyte derived macrophages (HMDMs) were subjected to treatments including incubation with lipopolysaccharide (LPS), *E.coli* bioparticles, oxLDL, or apoptotic cells for 24 hours or polarization towards M1 or M2 phenotypes. RNA was isolated from treated HMDMs for qPCR analysis and supernatant for protein analysis by Luminex, ELISA, and C1 hemolytic titer. Data show that M1 HMDMs increase C1r and C1s mRNA but decrease C1s protein levels. In contrast, there is no significant change in gene or protein expression of C1q, C1r, and C1s in M2 HMDMs. Preliminary C1 hemolytic titer data suggests that M1 HMDMs produce significant levels of active C1 complexes. Interestingly, C1 activity was not detected in response to the remaining HMDM treatments. HMDMs incubated with foreign targets (LPS or *E.coli* bioparticles) revealed a trend of increased C1r and C1s mRNA, and decreased C1q mRNA. However, these trends were not reflected at the protein or functional level. HMDMs treated with damaged-self targets show varying results. While C1q gene and protein expression increases in response to apoptotic cells, there are no substantial changes in C1q, C1r, or C1s levels in HMDMs treated with oxLDL. These preliminary data support the hypothesis that macrophages modulate C1q, C1r and C1s production in response to different types of targets. While the link between sub-component production and inflammatory responses is still unclear, our data suggest that C1q is produced in the absence of C1r and C1s in response to apoptotic targets which may be important in resolving inflammation during clearance of damaged-self targets, thus preventing autoimmune diseases.

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59. Investigation on the Effect of Aspirin on the PI3K-Akt Pathway and the Unfolded Protein Response during Endoplasmic Reticulum Stress

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Acetylsalicylic acid (ASA), more commonly known as aspirin, is a non-steroidal anti-inflammatory drug (NSAID). According to an epidemiological study, a daily dose of aspirin acts

as a chemo-preventative agent against colorectal cancer and increases the rate of survival. However, the mechanism behind it remains abstract. Therefore, we aim to investigate the effects of aspirin during endoplasmic reticulum stress on the Unfolded Protein Response (UPR) and phosphatidylinositol 3-kinase (PI3K-Akt) pathways. The endoplasmic reticulum is a eukaryotic organelle which is responsible during protein synthesis, folding, modification, and transport. Cells become compromised when the ER is burdened with aggregates of misfolded and unfolded proteins – this is the cause of ER stress. Upon stress the cell will activate the UPR, which is composed of three transmembrane sensors: Activating transcription factor 6 (ATF6), Inositol-requiring enzyme 1 (IRE1), and Protein Kinase R-like ER kinase (PERK). These sensors are activated in order to restore homeostasis of the cell by halting protein synthesis, selectively enhancing the cells protein folding capacity and averting from apoptosis. Aside from activating the UPR, the cell can also upregulate the PI3K-Akt pathway, which is embedded in the cell membrane. Akt is a serine/threonine kinase that, when phosphorylated, initiates kinase activity, promotes cell survival, proliferation, and metabolism.

HeLa (cervical cancer) and HEK 293 (human embryonic kidney) cells were treated with aspirin an hour prior to induction of ER stress by tunicamycin. The cell lysate was electrophoretically separated by molecular weight on SDS-PAGE gel, transferred to a PVDF membrane, blocked with milk and probed with primary and fluorescent secondary antibodies. The protein biomarkers for the UPR and PI3K-Akt pathway from the cell lysate was detected and analyzed. Our preliminary data suggests that at the concentration tested and time of treatment used in this study, aspirin activates the Akt pathway in HeLa cells. Our current and future experiments are directed towards testing higher concentrations of aspirin and longer time of treatment on UPR induction in these two cell lines as well as a colorectal cancer cell line. By understanding the mechanism by which aspirin acts as a chemo-preventive agent can most likely lead to a coherent drug for cancer treatment.

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60. Muscle Fiber-Types in Mice Selected for Wheel Running Behavior

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Mammalian skeletal muscle fibers contain varying amounts of myosin isoforms for slow and fast myosin-heavy chains, (Types 1, 2A, 2X, 2B,). Muscle fibers containing different isoform profiles typically correlate with variable force, speed, and fatigue resistance. We investigated the isoform profiles of various hindlimb muscles in two types of mice, from lines that have been undergoing laboratory selection for high wheel-running behavior for over 80 generations. We hypothesized that mice from the selected lines would typically have the most type 1 or type 2a myosin. This isoform is most often expressed in muscle with higher oxidative capacity and

therefore greater fatigue resistance. We collected lower leg muscles including the quadriceps, soleus, medial and lateral gastrocnemius, and plantaris from the breeding pairs of generation 84 from selected and control lines.

Some data were previously reported from generations collected one and two decades ago, but many muscles were not included, and we wished to see if further changes to the isoform profiles have arisen. SDS PAGE and densitometry were used to quantify the myosin isoforms. Preliminary analysis using densitometry shows that some leg muscles of high-running mice had a higher concentration of type 1 myosin, or in other cases, a shift towards slower type 2 fibers (i.e. 2x to 2a). The findings were highly muscle-specific and indicate shifts in muscle protein expression are continuing under selection.

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61. Do AAT1, DUR3, and PTR3 Nitrogen Transporters Contribute to N Mobilization During Leaf Senescence?

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The final stage of leaf development is leaf senescence, a recycling event in which nitrogen and other nutrients are reallocated to developing tissues to promote growth. In *Arabidopsis thaliana*, transporters such PTR3, AAT1, and DUR3 which respectively function in transporting dipeptides, amino acids, and urea, have shown a parallel increase in mRNA abundance and H3K4me3 histone marks during leaf senescence. The aim of this study is to determine whether PTR3, AAT1, and DUR3 transporters function in the mobilization of nitrogen during leaf senescence in *Arabidopsis.* To address this aim, T-DNA insertion mutants of the three transporters will be studied. Single mutants have been used to construct double and triple mutant plant lines, and these higher order mutants will be tested to determine if there is a decrease in nitrogen mobilization to the seeds and an increase in Rubisco retention in the leaves during senescence. Rubisco is a highly-abundant leaf protein that is the major source of mobilized nitrogen. Western blot analysis will be conducted to quantify Rubisco levels during senescence in double and triple mutants. Nitrogen elemental analysis will be conducted to determine the nitrogen content WT and triple mutant seeds. Rubisco decrease will be evaluated in three senescence systems that function in different time frames. From slowest to fastest, these are age-related, dark-induced-attached leaves and dark-induced-detached leaves. Upon completion, I expect higher order mutant lines with non-functional transporters to experience lower levels of nitrogen mobilization and higher levels of rubisco retention, thus

supporting the role of AAT1, PTR3, and DUR3 transporters during leaf senescence. Currently, dark-induced senescence protocols using attached and detached leaves are being conducted on double mutants. Western blot and chlorophyll analysis results for double mutant lines will be presented.

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62. Addressing the impact of polychlorinated biphenyl environmental mixtures on ryanodine receptor organismal pathways

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Polychlorinated biphenyls (PCBs) are halogenated aromatic hydrocarbons with 209 congeners. They were commonly used in commercial and industrial products until their ban in 1979 due to the rising concerns over their adverse effect on humans and the environment. Despite the ban, PCB congeners are still found in the air, in environmental water, on sediment, and in organismal and human samples. Some PCB congeners can alter the activity of ryanodine receptors (RyR), a Ca^{2+} channel important for neuronal and muscle cell Ca^{2+} homeostasis. Most studies focus on the effect of individual PCBs on RyR activity, but PCBs are found in mixtures in the environment. We aim to address the additivity of environmental mixtures of PCBs on RyR activity using radio-ligand binding assays. Currently, I have validated the binding assay in a crude protein preparation and have confirmed that the highly active PCB 95 causes a 700% increase in activity at the ryanodine receptor in fish. I am currently developing a sucrose gradient to further purify the crude protein in order to isolate the target ryanodine receptor to aid in activity measurements. Based on previous research, we hypothesize that PCBs will act additively towards RyRs, providing more insight into the influence of environmental mixtures on RyR based cellular pathways and organismal physiology.

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63. *Drosophila melanogaster* X-Chromosome Deficiencies Interacting with *18-Wheeler* Cause Defects in Salivary Gland Development.

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Drosophila melanogaster salivary glands are an excellent model for mammalian organ development because epithelial organ development is evolutionarily conserved. The *Drosophila 18-wheeler* gene directs epithelial cell migration during embryonic development and contributes to salivary gland morphogenesis. Previous work has demonstrated that homozygous *18-wheeler* mutant embryos have abnormal salivary glands. To identify genes that interact with *18-wheeler* during epithelial organ development we take advantage of the observation that an embryo heterozygous both for *18-wheeler* and for a gene that interacts with*18-wheeler* has defective salivary glands. We are systematically searching the X-chromosome for interacting genes using a collection of 93 X-chromosome-linked deficiencies (*Df(1)*). Together these deficiencies delete 2,288 of the 2,331 euchromatic genes on the X-chromosome (98.1%). To obtain embryos that are heterozygous for *18-wheeler* and an X-linked deficiency, males carrying an *18-wheeler* mutation and a green fluorescent protein (GFP) reporter expressed in salivary glands (stock 84-1) are crossed with females heterozygous for an X-linked deficiency. Their other X-chromosome is a GFP-expressing “balancer”. Control embryos are obtained using males that are wild type at the *18-wheeler* locus, but carry the GFP salivary gland reporter (stock 15-1). Embryos are collected, fixed, and subjected to immunocytochemistry to detect GFP. If the mutations interact, salivary gland morphogenesis will be abnormal. Defects include, but are not limited to, glands lengthening, shortening, or migrating asymmetrically. We have identified two deficiencies on the X chromosome that interact with *18-wheeler*. Embryos produced by crossing *Df(1)BSC755* (stock 26853) to the *18-wheeler* mutant, show abnormal glands, likely in male progeny, which have only the deficiency bearing X-chromosome. Glands are asymmetric, smaller in size, and do not elongate. When crossed to wild type males, fewer embryos show the defect, suggesting that the presence of two copies of the wild type *18-wheeler* gene lessens the frequency of defects in males. The second stock, *Df(1)ED7170* (stock 8898), also shows a genetic interaction. Embryos heterozygous or homozygous for the deficiency and heterozygous for the *18-wheeler* mutation show a high frequency of defects in migration and morphology. Two copies of wild type *18-*wheeler rescues embryos heterozygous for the deficiency, while embryos homozygous for the deficiency still show defective gland morphology. From these results we can conclude that within these deficiencies there genes gene(s) that interact with *18-wheeler*. Smaller deficiencies located within the large deficiencies will be used to narrow down the location of genes causing defects in salivary gland morphogenesis.

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64. The Effects of Ezh2 Mutation on Kras-Driven Adenocarcinoma.

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Lung cancer is the deadliest form of cancer worldwide. Non-small cell lung cancer (NSCLC) is the most common type of lung cancer, constituting an estimated 84% of diagnoses. Conducting research regarding the metastasis of lung adenocarcinomas is especially pertinent, as the 5-year survival rate for localized NSCLC is an estimated 50% versus 6% in metastatic lung cancer. Here we investigate the activation effects of Polycomb Repressive Complex 2 (PRC2), an epigenetic regulator commonly found to be dysregulated in human lung cancer, as a driver of metastasis. We employed genetically engineered mouse models harboring activating point mutations in Kras and inactivating mutations in the p53 pathway (KP model) which develop lung adenocarcinomas but exhibit low penetrance and long latency for metastasis. As a resolution, our lab has generated a KPE mouse model which carries a mutation that induces Ezh2 activation, a core component of PRC2. We hypothesize that effectively establishing a robust metastatic model that displays a shorter latency period in order to further study lung adenocarcinomas. In this project we plan to use a histological approach to characterize morphological properties of primary tumors as well as distinct lymph node metastases in KPE mouse models. By visualizing cellular phenotypes through Hematoxylin & Eosin staining, we intend to quantify tumor area and composition of lymphatic micrometastases.

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65. Functional potential for Sulfur metabolism across sequenced bacterial and archaeal genomes from KEGG

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Intro: Microbial sulfur oxidation and reduction impacts global biogeochemical cycling of sulfur, one of the six essential elements for life. Public access databases such as the Kyoto Encyclopedia for Genes and Genomes (KEGG) are a wellspring of hundreds of thousands high quality structurally and functionally annotated genomes. Objective: This study aimed to mine the KEGG database to determine the presence of sulfur metabolism traits within sequenced bacterial and archaeal genomes (n=5,571). This study also aimed to code the many combinations of genes that can achieve sulfur metabolism into modules either described by KEGG or by literature review, then summarize the presence/absence of potential activity at each level of phylogeny. Methods: A custom BASH shell language program was designed and implemented to return KEGG genomes with the potential for sulfur metabolism. In R, complex modules for sulfur metabolism activity were coded and tested on each genome to determine presence or absence of complete pathways for sulfur oxidation or reduction. The coded modules were summarized by mean, standard deviation, and coefficient of variation (CoV) by

ascending orders of phylogeny. Results: Of 4,253 microbial KEGG genomes 1,723 were positive for at least one of the four categories of: Assimilatory, Dissimilatory, Sox, and Dissimilatory Oxidative. There were 1,453 Assimilatory positive genomes, 50 Dissimilatory genomes, 187 Sox genomes, and 33 Dissimilatory Oxidative genomes. There were 23 genomes positive for both Sox and Dissimilatory, and two organisms that had the genomic potential to perform all four module functions. For Assimilatory Proteobacteria, Firmicutes, Actinobacteria, and Chloroflexi had a CoV>2. For Dissimilatory, Proteobacteria, Firmicutes, Crenarchaeota and Euryarchaeota have a CoV>2. For Sox, Proteobacteria had the highest CoV (>2). For Dissimilatory Oxidative, Proteobacteria, Firmicutes, and Euryarchaeota had a CoV>2. Conclusion: The overlap between Sox and Dissimilatory positive genomes is interesting and may indicate those Dissimilatory positive genomes are performing an oxidative process using reductive genes, but in reverse. A CoV>2 indicates high variability of potential sulfur metabolism activity. It was expected that Proteobacteria would have the largest variation among pathways across levels of phylogeny, however, it is interesting to note that archaeal phyla are highly variable as well. The previously published algorithm consen-Trait will be applied to determine trait depth, the Fritz and Purvis test will determine phylogenetic dispersion. The results of this work will elucidate the phylogenetic distribution and conservatism of sulfur metabolism traits across bacteria and how molecular complexity of trait affects both distribution and conservatism.

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66. The Effect of Lovastatin on Processing of Activating Transcription Factor 6

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The Endoplasmic Reticulum (ER) is the largest eukaryotic organelle known to mediate multiple integral cellular processes such as protein folding and trafficking. Perturbation of these processes leads to a type of cellular stress known as ER stress, which activates the Unfolded Protein Response (UPR), an evolutionarily conserved transcriptional program that works to restore ER homeostasis. The UPR is primarily regulated by three ER transmembrane proteins, including Activating Transcription factor 6 (ATF6), which is translocated to the Golgi and undergoes proteolytic cleavage by Golgi-resident proteases to release its N-terminal fragment in response to ER stress. The same proteases are known to cleave Sterol Regulatory Element Binding Proteins (SREBPs) in a manner similar to ATF6 in order to regulate lipid homeostasis. Previous studies have shown that the cleavage of SREBPs is promoted by Lovastatin, a common drug prescribed to lower blood cholesterol levels. We hypothesized that Lovastatin should also induce cleavage of ATF6 in a manner similar to SREBPs, thus triggering the UPR. To test our hypothesis, we treated HeLa cells, a cervical cancer cell line, with either Lovastatin or induced ER stress with tunicamycin as the control. The cells were then lysed and the levels of known

UPR proteins were tested by immunoblotting. Our preliminary data suggest that Lovastatin treatment induces ER stress as determined by enhanced level of a key chaperone that is known to be upregulated under ER stress conditions. Our results also demonstrate that HeLa cells upregulate the cytoprotective Akt signaling when treated with lovastatin. Collectively, our results suggest that lovastatin indeed induces ER stress like conditions in cells triggering the UPR. Our current and future experiments are focused on determining the effect of lovastatin on cell viability.

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67. Effect of Cyclin-Dependent Kinase 5 inhibition on Epidermal Growth Factor Receptor Signaling in DU-145 Prostate Cancer Cells

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Cyclin-dependent kinase 5 (CDK5), a member of the CDK family, is ubiquitously expressed and plays a crucial role in embryonic development. Dysregulation of CDK5 has been implicated in several diseases including cancer, neurodegeneration, and type II diabetes. In prostate cancer, CDK5 promotes cell migration and invasion through both androgen receptor (AR)-dependent and -independent mechanisms. The AR-independent effects of CDK5 have been shown to be mediated via the Akt pathway using AR deficient prostate cancer cell line, PC3. We hypothesized that either depletion or inhibition of CDK5 in another AR-deficient prostate cancer cell line, DU-145, should also downregulate the Akt pathway. To test our hypothesis, we treated DU-145 cells with roscovitine, an ATP competitive inhibitor of CDK5, prior to lysing the cells and analyzing the lysates using immunoblotting. Our results indicated that roscovitine treated cells show marginally higher level of activated Akt than the control treated cells. To further study the effect of CDK5 inhibition on DU-145 cells, we then determined Akt activation downstream of stimulated epidermal growth factor receptor (EGFR). Serum-starved cells were treated with epidermal growth factor for 0, 5, and 15 minutes followed by cell lysis and immunoblotting. Our results showed that roscovitine treated cells showed significantly higher levels of not only Akt but also extracellular-signal-regulated kinase (ERK) activation upon EGFR stimulation. Together, our results indicate that as opposed to the reported CDK5-dependent Akt activation in PC-3 cells, DU-145 cells show an opposite trend. Our current and future experiments are aimed at studying the effect of CDK5 depletion on the Akt and ERK pathway in DU-145 cells.

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68. Comparison of leaf anatomy from PCK and NAD-ME C_4 chloridoid grasses

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Photosynthesis is the process that plants use to extract carbon from CO_2 to convert to glucose. Approximately 3% of plant species use C_4 photosynthesis, in contrast to the more prevalent C_3 photosynthesis. In species with C_4 photosynthesis, the leaves have rings of cells around each vein, called a bundle sheath and this pattern is called 'kranz anatomy.' This anatomy reduces exposure of RuBisCO to oxygen (photorespiration), which wastes energy. Instead, C_4 plants capture CO_2 using phosphoenolpyruvate carboxylation, convert it into malate, and then concentrate the CO_2 in the bundle sheath cells. C_4 photosynthesis requires more energy than C_3 photosynthesis, but reduces the risk of photorespiration. Plants that use C_4 photosynthesis can differ in the enzyme that converts malate to CO_2 in the bundle sheath. In NAD-ME C_4 the bundle sheath cells are approximately the same size and chloroplasts are centripetal, whereas in PCK C_4 the bundle sheath cells alternate in size and chloroplasts are peripheral. As far as is known, all species in the chloridoid subfamily of grasses use NAD-ME or PCK C_4 photosynthesis. Although C_4 photosynthesis is an important physiological adaptation, few anatomical studies have been done to compare the leaf anatomy of plants with different C_4 subtypes. Columbus collected leaf tissue from 63 species of chloridoid grasses that are representative of the evolutionary diversity in the subfamily. Fisher determined the C_4 type based on the position of the chloroplasts within the bundle sheath. Columbus prepared and stained leaf sections. Nguyen imaged sections at 4x, 10x, and 25x using a Zeiss or Motic light microscope and a Nikon D750 camera with a microscope attachment. For each species, Nguyen used ImageJ to measure leaf thickness, the distance between bundle sheaths, and distance between veins for 1-6 replicate sections per species. Distances were compared using ANOVA and t-tests in R. We sampled 31 PCK, 29 NAD-ME, and 3 C_3 (non-chloridoid) species. The ANOVA found that C_3 leaves are significantly different from both C_4 subtypes in terms of the inter-veinal distance, but are not significantly different for leaf thickness and bundle sheath distance. The t-test results showed no significant difference between NAD-ME and PCK C_4 subtypes for any of the measurements. This suggests that leaf thickness and distance between veins do not need to change when lineages transition to a new C_4 subtype. Future work will include comparisons of the areas of the mesophyll, the outer sheath, and the inner sheath and mapping evolutionary transitions onto a phylogeny to further understand the difference between PCK and NAD-ME and their evolution in the chloridoid grasses.

69. Behavioral Mechanisms Involved in Oviposition Preference in *Drosophila melanogaster*

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To reveal the behavioral mechanisms involved in food preference in fruit fly *Drosophila melanogaster*, oviposition choices were compared for pairs of food flavorings. Although it is known that the *Drosophila* relies on the presence of the yeast *Saccharomyces cerevisae* and acetic acid as oviposition guides, food flavor preferences are largely unknown. Furthermore, the degree to which preferences may be influenced by individual history or even via epigenetic mechanisms is unknown. We mated isogenic and identical parental generation flies and allowed them to oviposit in food flavored with various extracts and observed subsequent oviposition preferences in their offspring (individuals exposed to the flavors) and F1 generation flies (which were exposed to control food lacking the flavors). Our data showed that exposure in earlier stages of development, and even in parents' larval environments, may modify *Drosophila* food preferences. These results have implications for insect population control and sympatric speciation.

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70. Evaluating a Series of Fmoc-Leucine Based Amino Acids to Identify Potent Butyrylcholinesterase Inhibitors as Potential Therapeutics to Alzheimer's Disease

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Alzheimer's Disease (AD) is characterized as a neurodegenerative disease which over time causes increasing impairment of brain function. It effects 44 million people worldwide and is the 6th highest cause of death in the United States. A target of interest in pharmacology and biochemistry is the development of enzyme inhibitors to act as drugs to mitigate the effect of AD. Activity of the enzyme butyrylcholinesterase (BChE) increases in Alzheimer's patients, and this increase is suggested to lead to a depletion of the neurotransmitter, acetylcholine. Based on these findings, BChE specific inhibitors have been designed to counteract the increasing activity of BChE and reduce or cease the progression of AD. We previously identified that 9-fluorenylmethyloxycarbonyl (Fmoc) amino acids could provide a new class of BChE specific inhibitors, as the compounds contain similar features to BChE inhibitors publicly available in pharmacology. From the initial Fmoc-amino acids tested, Fmoc-Leu-O$^-$ was found as the most effective inhibitor with an inhibition constant (K_I) value of 115 mM. Building on this result, we hypothesized that introducing groups to increase van der Waal's interactions with the enzyme active site will lead to better inhibitors, as previous studies in a different structural context showed that adding alkyl groups generated more effective inhibitors. A series of nine

compounds were evaluated including four compounds that required synthesis from the corresponding amino acid. The K_I value for each inhibitor was determined using kinetics assays monitored via UV-absorbance spectroscopy. Of the compounds tested, Fmoc-neopentylglycine-O^-, which contains an additional methyl group compared to Leu, and Fmoc-*tert*-Leucine, a constitutional isomer of Fmoc-Leu was shown to inhibit BChE at high efficiency with K_I values of 36 mM and 38 mM, respectively. However, Fmoc-Norleucine, a constitutional isomer of Leucine with a predicted great van der Waals surface area was a less effective inhibitor with a K_I value of 320 mM. Additional experiments showed the inhibitors were reversible and that the compounds specifically inhibit BChE over the related cholinesterase, acetylcholinesterase (AChE) and another serine protease, chymotrypsin. The results identified two Fmoc-amino acids that are more potent BChE inhibitors compared to the original series and highlighted the challenges in identifying the features important for inhibition. Computational studies are current underway to evaluate the physical basis for difference in BChE inhibitor for the series. Together, the results may aid in the incorporation of important features in future generation of inhibitors to provide more potent cholinesterase inhibitors.

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71. Effects of *cyp81F2xcyp81F1* Double Mutants on Senescence in *Arabidopsis thaliana*

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Senescence is an integral part of plant growth that helps relocate nutrients from older leaves to growing organs. *Arabidopsis thaliana* is a model plant species used in many genetics studies. Senescence processes are studied mainly for agricultural purposes that would help to increase crop yield as well as reduce fertilizer costs. Senescence is an observable process as older leaves are seen to turn from green to yellow. Our lab has shown that the indole glucosinolate (IG; a compound thought to be involved as a plant's defense against biotic stress) pathway may be a negative regulator of leaf senescence, slowing down the process to maximize nitrogen export. Within this pathway, the four genes of the CYP81F family (CYP81F1, CYP81F2, CYP81F3, CYP81F4) are involved in the catalysis of certain steps toward the formation of IGs. The CYP81F1 and CYP81F2 genes catalyze the addition of hydroxy groups of indol-3-ylmethylglucosinolate (I3G) into 1OH-I3G and 4OH-I3G, respectively, both of which eventually lead to the formation of indole glucosinolates. Of the 4 family members, CYP81F2 is unlinked on chromosome 5, whereas the remaining three are linked, all found along chromosome 4. It was previously found that single mutants (*cyp81F1* and *cyp81F2*) did not show earlier senescence than wildtype (WT). This then led us to hypothesize that double mutants for these genes will show earlier senescence than WT due to redundancies in this gene family. Isolating double

mutants first began with isolating DNA from leaves, then amplifying that DNA through PCR, and finally running the samples on a gel to determine the plant's genotype (homozygous or heterozygous) in the F_1 generation (all heterozygotes). Confirmed heterozygotes were allowed to self-fertilize to give the F_2 generation, which can be a mix of homozygotes and heterozygotes. Repeats of the genotyping process have confirmed the presence of a double mutant in the F_2 generation. Further steps require quantifying chlorophyll catabolism and quantifying NIT2 gene expression using real-time qPCR to determine any phenotypic changes in the double mutant versus the wildtype. NIT2 is a senescence-associated gene (SAG) that increases in presence during senescence encoding a nitrilase involved in the catabolism of nitrile compounds. Results from phenotyping will be analyzed via a t-test. Upon disruption of two of the four gene family members, we propose that double mutants for this gene family will senesce at a slower rate than WT specimens.

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72. Development of Apolipoprotein AI Chimera for Targeted Drug Delivery to Breast Cancer Cells via MMP14

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A current challenge in drug delivery for cancer treatment is the ability to effectively target specific diseased cell types; several promising treatments suffer the limitation that they are non-selective and have toxic off target effects on neighboring healthy cells. Our overall objective is to generate a platform for targeted drug delivery employing self-assembling nanodiscs comprised of phospholipids and apolipoprotein AI (apoAI). ApoAI is an exchangeable apolipoprotein located on high density lipoproteins (HDL), which promotes cholesterol efflux from macrophages and facilitates selective uptake of cholesterol by binding scavenger receptor, class B type 1 (SR-B1), also known as the HDL receptor. We hypothesize that a chimeric protein of apoAI with MT1-AF7p (apoAI-MT1), a peptide ligand that binds membrane metalloproteinase 14 (MMP14), will enhance the targeting capability of the nanodiscs to tumor cells. MMP14 is a cell surface protein that is overexpressed in many types of cancers responsible for metastasis and linked to poor prognosis in patients. We designed a construct bearing the coding sequence for human apoAI with a hexa-His-tag at the N-terminal end to facilitate protein purification by affinity chromatography, and MT1-AF7p (HWKHLHNTKTFL) at the C-terminal end with an intervening linker segment ($[G_4S]_3$). The construct was designed and custom-generated with optimized codon sequence commercially in pCR2.1 vector. Subsequently, we successfully sub-cloned the chimeric insert into a pET20b(+) expression vector employing standard molecular biology protocols and verified the resulting plasmid through Sanger sequencing. Recombinant wild type (WT) apoAI and apoAI-MT1 proteins were over-expressed in *E. coli*, harvested and purified by immobilized metal affinity chromatography using a nickel affinity chromatography. The purified proteins were visualized by 15% acrylamide SDS-PAGE, which revealed major

bands ~ 24 kDa band for apoAI and 27 kDa band for apoAI-MT1. We obtained ~ 10 mg purified protein/L culture medium, which is sufficient to carry out structural and functional characterization. The chimeric apoAI-MT1 nanodiscs bear tremendous potential not only for targeting MDA cells, but also for drug delivery since these cells are reported to have high expression levels of both SR-B1 and MMP14 which mediates homing and selective uptake of the hydrophobic core of HDL, respectively. Preliminary immunofluorescence data indicate the presence of both these proteins as well as the LDLr in MDA-MB-231 cells. Our next steps are to further characterize the expression of MMP14, SR-B1, and LDLr on MDA-MB-231 cells via FACS, qPCR and immunoblotting as well prepare reconstituted HDL (rHDL) nanodiscs with the chimera. Subsequently, upon confirming particle formation and cellular expression of MMP14, SR-B1, and LDLr , the cells will be treated with nanodiscs bearing the chimeric apoAI_MT1 and the and targeting and uptake assessed. The chimeric apoAI-MT1 nanodiscs bear tremendous potential not only for targeting MDA cells, but also for drug delivery since MDA-MB-231 are reported to have high expression levels of SRB1, which would serve as a point of entry for drug delivery into the cells.

This project is supported by the National Institutes of Health (NIH) under the award numbers: GM105561 (VN); R25GM071638 (DK), and T34GM008074 (RM).

73. Optimizing Copper Phthalocyanine Thin Films By Altering Spin Coating Parameters

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Copper phthalocyanine (CuPc) is an important molecule forming crystals in thin films. This material can be used in cost-effective electronic devices and its numerous applications include gas sensors, thin-film transistors, and photovoltaic cells. Spin coating is a faster and more cost-effective method for creating thin film CuPc samples as compared to thermal evaporation. Spin coating can produce samples in less than ten minutes; however, the crystal quality may be inferior. Copper phthalocyanine tetrasulfonic acid was spin coated onto silicon (100) and glass substrates, resulting in 21 samples. Altering certain parameters on the spin coater program, including rate per minute (RPM) and time, affected the quality of each thin film. X-Ray diffraction (XRD) data with Bragg-Brentano focusing) is graphed to observe the crystalline properties for each sample. Additionally, the XRD data of a spin coated sample and thermally evaporated sample is compared to understand the advantages of each method. The aim of this project is to optimize the spin coater parameters to obtain high-quality samples of copper phthalocyanine thin films.

CSULB LSAMP Program & National Science Foundation (NSF) Grant #HRD-1826490).

74. Structural Characterization of Spin-Coated Soluble Copper Phthalocyanine on Silicon Thin Films

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Phthalocyanine coated thin films are utilized as gas sensors and photovoltaic cells. The specific traits of these thin films often depend on structural properties that were entrained during sample deposition. Spin-coated copper phthalocyanine-3,4',4'',4'''-tetrasulfonic acid tetrasodium salt (CuPcTs) on silicon wafers are characterized by atomic force microscopy (AFM.) The surface roughness is determined using standard WSxM software to graph the relationship between position versus height. Two samples deposited at varied spin speeds are compared using AFM snapshots each 2 micrometers on the side. The surface sample at 2k revolutions per minute (rpm) shows long filaments crisscrossing the surface, while the 3k rpm sample shows a more dense and smoother surface filament network.

75. Do *pub22pub23pub24* triple mutants in *Arabidopsis* show early leaf senescence?

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The Plant U-box (PUB) gene family of *Arabidopsis thaliana* functions in ubiquitination signaling and immune responses involving pathogen-associated molecular patterns (PAMPs). *PUB22, PUB23*, and *PUB24* are highly-related and code for U-box ubiquitin ligases that may contribute to the negative regulation of PAMP responses, a process that may be related to leaf senescence. In previously conducted studies, *PUB22* and *PUB23* have been shown to be up-regulated during leaf senescence. We elucidate that the defensive responses of these two genes along with *PUB24*, a structurally and functionally related gene, somehow negatively regulate progression of leaf senescence. Chlorophyll and gene expression levels were measured in the leaves of isolated *pub22pub23pub24* triple mutants and wildtype plants at twelve days apart to determine differential levels of leaf senescence. Preliminary phenotypic analyses hold that there are no significant differences in onset of senescence between wildtype and triple mutant lines. Further examination into senescence patterns of *pub22pub23pub24* will be conducted and may involve extension of the second time point upon which data are collected.

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76. The Effect of Microplastics on Innate Immune Responses

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Microplastics (MP) are small pieces of plastic materials that range from 1 - 1000 µm in size that result from the fragmentation of plastic waste. These particles are now found in environmental samples across the globe including outdoor and indoor air, aquatic environments, organism and human food items such as seafood and honey. As such, risks presented due to ingestion or inhalation have become a major concern in human health assessments. However, there is currently a lack of information regarding the potential impacts of microplastic exposure in mammals, especially humans. Since some of the first interactions of ingested or inhaled microplastics after MP tissue absorption through lung or gut epithelia will be with cells and proteins of the innate immune system, complement activation assays (C4-depletion assays) and macrophage phagocytosis assays were conducted. Two types of plastic beads, polyethylene and polystyrene, in varying sizes were utilized for this study. For complement assays, beads were incubated with normal human serum (NHS), a source of complement immune proteins, and incubated to allow activation (depletion of C4 protein). The complement depleted sera were then incubated with antibody opsonized erythrocyte targets in C4-deficient serum to determine the amount of C4 remaining to activate the complement cascade. Preliminary data show that roughly half of the C4 was depleted for all samples, suggesting some complement activation, though there were no significant differences between types of plastic or size of bead. We then incubated the beads with human monocyte-derived macrophages (HMDM) to determine if they can be phagocytosed. Each bead type was either treated with NHS (as a source of complement opsonization) or left untreated. This assay concluded that HMDMs phagocytose more beads in the presence of NHS, further suggesting an interaction between microplastics and the innate immune system. Further studies will determine whether ingestion of these particles are immunosuppressive or immunostimulatory. Understanding more about the interactions of microplastics with the innate immune system may provide important insight into the impact of these particles on human health.

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77. Comparison of Skull Morphology Between Urban and Rural Coyote Populations Via Bite Force

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Urbanization is increasing across the globe and it is recognized as a major factor impacting species, populations and assemblages (Turner et al. 2004; Grimm et al. 2008). Urbanization is a

new selective force that is changing the composition of animal communities by affecting their behavior and morphology. This research will focus on the comparison of skull morphology between urban (Los Angeles, California) and rural (Fresno, California) coyotes. Urban coyotes subsidize their food up to 50% with anthropogenic food and the cranial form is associated with dietary category hardness and handling. A gross dissection of mastication muscles, chemical digestion, and measurement of the skull was conducted during this research project. The analysis will include a comparison of mean for canine bite force, molar bite force, length:width ratio, and skull length.

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78. Comparison of Bite Force and Skull Dimensions Between Urban and Rural Coyotes (*Canis latrans*)

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Humans are capable of drastically altering their environment within a relatively short time frame, turning vast natural landscapes into bustling cities. Few organisms can adapt quickly enough to survive these changes; those who do often subsidize their diet with anthropogenic food since an animal's natural food source may not be readily available. A species with populations living in both urban and rural environments may, therefore, experience musculoskeletal changes in response to different selective pressures stemming from food diversity, availability, and acquisition difficulty. Here, we compare the skull dimensions and bite force of coyotes (*Canis latrans*) from an urban population (Greater Los Angeles) with those from a rural population (Fresno County). Upper jaw length and width, mastication muscle masses, lower jaw lever length, and skull length measurements were recorded for each specimen; and upper jaw length/width ratio and bite force at the carnassial molar and lower canine were calculated. Current findings indicate urban coyotes have wider skulls than rural coyotes, as well as statistically nonsignificant trends towards longer skulls and stronger molar bite force in urban coyotes. While more data is needed, trends suggest that urban environments favor the development or evolution of powerful bites to allow for feeding on domestic pets.

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79. Effects of Oxidation on Saturation Magnetization in Iron Phthalocyanine Thin Films over 45 days

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Iron phthalocyanine (FePc) is a square-planar molecule with many interesting magnetic properties. Its current applications include gas sensors, photovoltaics, and dyes, but could potentially be used in novel spintronics devices. As a metallo-organic semiconductor, FePc is advantageous in these applications because it is flexible, chemically tunable, and inexpensive compared to metal semiconductors. However, it is important to understand how oxidation will affect the magnetic properties of FePc thin films over time. Thin films of FePc were deposited onto heated silicone substrates by thermal evaporation in a high vacuum chamber. In order to get samples of different structural morphologies, the substrate temperature during growth was 100°C or 190°C, respectively. Magnetic properties were measured using a vibrating sample magnetometer to obtain field-dependent magnetization sweeps in the temperature range from 3.5K – 300K. Below 4.5 K, magnetic hysteresis is observed in both thin films and the saturation magnetization was recorded over a time period from 12 hours to 45 days after deposition.

With the financial support from the Gredig Research Stimulus Fund.

80. Investigating the role of innate immune protein C1q in cholesterol metabolism in macrophages

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Heart disease is a major concern today due to it being the leading cause of death in the United States. There are many factors that contribute to heart disease, one of the most common being atherosclerosis. Atherosclerosis is a disease characterized by chronic inflammation and the accumulation of fatty deposits and cholesterol-saturated foam cells in arterial walls, also referred to as plaque. Recent studies suggest that C1q, an innate immune protein, plays a protective role in early stages of atherosclerosis. C1q directly opsonizes targets like modified low-density lipoproteins, or “bad” cholesterol, which leads to an increase in macrophage foam cell phagocytosis, survival, and efflux. Cholesterol efflux and survival are often associated with oxysterol-mediated activation of the liver X receptor pathway in macrophages. mRNA levels of cholesterol modifying enzyme cholesterol 25-hydroxylase (CH25H) were investigated by qPCR in murine bone marrow derived macrophages (BMDM) from C1q-sufficient (wildtype) and C1q-decifient (C1q knockout) mice. BMDMs were treated with oxidized LDL as well as acetylated LDL to promote foam cell formation *in vitro* in the presence or absence of C1q. Levels of CH25H were increased in C1q-sufficient BMDM compared to C1q-deficient. Levels of CH25H also increased when C1q was bound to acLDL. Data presented show an increase in CH25H mRNA with the presence of C1q which is consistent with previous data showing that C1q upregulates

oxysterol 25-hydroxycholesterol, a known activator of LXR. Together, these data support a protective role for C1q in early stages of atherosclerosis through LXR mediated survival and cholesterol efflux.

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81. Inhibition of Protein Kinase B differentially affects the Unfolded Protein Response

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The endoplasmic reticulum (ER) is an organelle in eukaryotic cells that plays a vital role in many important cellular functions including proper folding of secretory and membrane proteins. Any disruption of ER function triggers ER stress leading to activation of an evolutionarily conserved signaling program called the Unfolded Protein Response (UPR). UPR initially aids in re-establishing normal ER functions and promotes cell viability. However, if the homeostasis is not restored in a timely manner, UPR eventually commits the cells to death. Cancer cells are known to be able to evade ER stress-induced cell death, which helps them acquire resistance to therapy. Our laboratory has recently shown that the pro-survival Protein kinase B *aka* Akt is activated and plays a role in enhancing survival of ER stressed cancer cells. Based on these findings, we hypothesized that Akt may upregulate cell survival by modulating UPR signaling. To test our hypothesis, we treated cells with a known small molecule inhibitor of Akt to reduce its activation and analyzed changes in the known UPR signaling proteins by immunoblotting. We tested the effect of Akt inhibition on two cell lines, HeLa – a cervical cancer cell line, and HEK293 – human embryonic kidney cells. ER stress was triggered using chemical inducers tunicamycin or thapsigargin. Our results indicate that Akt inactivation leads to differential effects on UPR signaling dampening one pathway whereas constitutively upregulating another. Our current experiments are focused on further delineating the mechanism by which Akt differentially regulates the UPR. We are also studying the effect of Akt inhibition on cell viability in multiple cancer cell lines. Many Akt inhibitors are currently being studied in clinical trials for different types of cancer. Our results will provide further insight into the molecular details of how Akt aids in cancer cell survival by tweaking the UPR.

82. Cuboid Arrays as Surface-Enhanced Raman Spectroscopy Substrates

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Surface-enhanced Raman spectroscopy (SERS) allows for the enhancement of intrinsically weak Raman signal and thus enables the detection of analytes at single-molecule level and chemical specificity. These capabilities make SERS a powerful multidisciplinary technique. Despite remarkable advancements in specificity and sensitivity however, SERS is not a routine chemical analytic technique. SERS suffers from a loss of signal reproducibility that depends critically on techniques for nanofabrication. In this project, we use cuboid arrays as an ideal platform for a SERS substrate with high sensitivity, high reproducibility, and low cost that is easy to manufacture. This study investigates plasmonic materials and structural parameters of the array to achieve resonant enhancement of the local electric field. Plasmonics offer unique capabilities to confine light to sub-wavelength dimensions and orders of magnitude field enhancement. Our previous studies revealed several configurations that exhibit relatively promising Raman enhancement factors, approaching 107 using self-assembled arrays of gold nanocubes. These enhancement factors can be further improved with outside parameters such as hybridization of material and using a waveguide arrangement structure. Guided by this preliminary data, and with the overall goal to fabricate the best performing SERS substrate, our objectives are to determine: (1) the dimensions and material configuration of the cuboid arrays that generate the highest enhancement factor in the visible and near-infrared range by using Lumerical's Finite Difference Time Domain software; (2) the best fabrication method to create the SERS substrate modeled in objective 1 that is the most reliable and reproducible; (3) the enhancement factor and range of target systems of the fabricated SERS substrate. The expected outcome of this work is the development of a low-cost user-friendly SERS substrate with high sensitivity, stability, and reproducibility. Collectively, our proposed research will broadly impact the field by assisting in the optimization of robust, lightweight, and efficient optical driven chemical sensing devices.

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83. Topological Analysis of ZIF-8 Using Atomic Force Microscopy

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Metal-organic frameworks (MOFs) are organic-inorganic crystalline molecular materials that resemble a cage like structure where metal nodes are connected to each other by organic ligands. The porous cage structure of MOFs allow them to have very large internal surface area per gram making them useful for applications in gas storage, liquid purification, and electrochemical energy storage. Zeolitic Imidazolate framework-8 or ZIF-8 is a MOF that is composed of tetrahedrally coordinated zinc connected by 2 methyimidazole, known for its overall stability and ease to synthesize. Because ZIF-8 is relatively easy to make it is prime candidate to study the growth patterns and how they affect the properties of ZIF-8 and other MOFs. Using an Atomic Force Microscope, will lead to the understanding of the growth of nanoscale ZIF-8 and their properties.

84. Bioengineered 3D Fibrosis Model

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Cardiac Fibrosis is one of the leading causes of heart failure post myocardial infarction. Fibroblast respond by rushing to the injured site and differentiate into excess proliferation of myofibroblast cells; resulting in cardiac fibrosis. The purpose of this research is to investigate methods to modulate fibroblast proliferation and myofibroblast activation in an in-vitro 3D model. Hydrogels from extracted porcine collagen type I was prepared within 3D PDMS molds with different micro-topographical environments at 1 and 5 days. Cells were stained using immunostaining of alpha-actin and F-actin. MTT Assay was used to correlate cell density. Quantitative Polymerase chain reaction was used to detect GAPDHA, alpha-smooth muscle actin, collagen 1 and cyclin D1. Preliminary qPCR results suggest that micro-channeled environments decrease proliferation of fibroblast. Microscope imaging showed that cells within the micro-channels proliferate with a defined structure than the cells in the flat environment. This suggests that fibroblast activation and proliferation are influenced by the micro-topographical environment; which can potentially be applied to minimizing cardiac fibrosis.

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85. Optimizing the Magneto Optical Kerr Effect (MOKE) Microscope

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The Magneto Optical Kerr Effect (MOKE) microscopy is a unique characterization method that locally probes the images of magnetic domains in thin films during magnetic switching. Previous work in our research group included the building and successful completion of a working MOKE system for hysteresis measurement and the initial set up of microscopy by introducing a new ccd-camera for imaging. Building from this previous work, current work focuses on improving the MOKE system by optimizing the gain setting of a new powered photo-detector, angle of the analyzer, and position of the ccd-camera for optimal focus. These optimizations have been conducted to establish and verify key parameters that directly affect the sensitivity and quality of the hysteresis loop measurement and image acquisition. A clear hysteresis loop with almost negligible noise was consistently obtained when the analyzer angle was set to 2 ° off the orthogonal position of the polarizer. The gain dependence of the photo-detector gave consistent energy levels and hysteresis data at 40dB. Labview imaging code was also implemented to streamline image acquisition. The upgrades of equipment and optimizations have resulted in the improved systematic research practices needed in the next phase of the MOKE. We are currently trying to detect the magnetic domain images of a patterned thin film and nanosphere structures but lack the magnification resolution to see individual domain changes. Future work with the MOKE system will attempt to rectify this issue by increasing the magnifying resolution of the ccd-camera. Additionally, the use of a new vector magnet will allow the MOKE system to be tested under different field configurations and MOKE geometry.

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86. Effect of electron withdrawing groups on benzoyl amino acids for butyrylcholinesterase inhibition in the potential treatment of Alzheimer's disease

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Alzheimer's disease (AD) is a neurodegenerative disease typically affecting 10% of people who are 65 and older in the United States. While there currently is no cure for AD, numerous approaches have been investigated to slow the progression of the disease and mitigate its effects. Previous studies have found that the activity of two major classes of cholinesterases changes in individuals with AD, acetylcholinesterase (AChE) activity shows a small decrease and butyrylcholinesterase (BChE) shows increased activity. The increased activity is suggested to deplete the neurotransmitter acetylcholine and may lead to dementia. This finding has led to the development of inhibitors that preferably inhibit BChE compared to AChE. Recently, our lab

identified amino acids with a 9-fluorenylmethoxycarbonyl (Fmoc) group were selective inhibitors of BChE. The Fmoc group contains multiple aromatic groups similar to other cholinesterase inhibitors, and these groups could facilitate binding via pi-pi interactions with active site aromatic residues. Previous studies evaluating the importance of electron withdrawing and donating groups on the energetics of pi-pi interactions in proteins showed that increasing incorporation of electron withdrawing groups such as fluorine lead to stronger interactions. If aromatic interactions are important for amino acid-based compounds interacting with the BChE active site, then incorporation of electron withdrawing substituents in the aromatic groups is predicted to lead to a better inhibitor. Fluoro-substitution on the aromatic Fmoc group is synthetically challenging, so we turned to amino acids bearing a benzoyl group, as reagents to generate fluoro-substituted amino acids are readily available. We first synthesized a series of benzoylated amino acids using the amino acid, benzoyl chloride, and aqueous sodium hydroxide. The compounds were purified using silica gel chromatography and characterized by NMR. Initial kinetics studies monitored by UV-Vis spectroscopy showed the compounds are weak BChE inhibitors with inhibition constants (K_I value) >200 μM. To overcome this limitation, a quaternary ammonium group is being introduced to the benzoylated amino acids, as previous studies showed the incorporation of the cationic group generates better inhibitors. Together, the results provide within this context a series of fluorobenzoyl-containing amino acids. We will then evaluate the effect of electron withdrawing groups on inhibition of BChE by determining and comparing the K_I values for the series of compounds. The important structural features identified in this study may then be used to guide the incorporation of electron withdrawing or donating groups in a variety of different classes of cholinesterase inhibitors.

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87. Band Structure and Polarizability of Twisted Bilayer Graphene

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Twisted Bilayer Graphene (TBLG) is a structure composed of two graphene sheets stacked with a relative twist angle between them. Cao et al. [Nature 556, 43 (2018)] recently reported the discovery of a superconducting state in TBLG at a “magic angle” of about 1.05°. The mechanism that causes this state is not yet known. We hypothesize that collective modes of the electrons known as plasmons could contribute to this state.The major difficulty of TBLG is that the periodic arrangement of atoms strongly depends on the twist angle. This in turn dramatically affects the motion of electrons in the system. This motion is determined by the relation between energy and momentum of electrons, called the band structure. At certain commensurate twist angles, TBLG exhibits a long-range periodic Moiré pattern which allows direct computation of the band structure. A method for performing this calculation with an exponentially decaying hopping parameter is presented with results for several twist angles. As

a prerequisite to the next step of computing the plasmon spectrum, we present a method for calculating the polarizability of monolayer graphene. Since applying this calculation to TBLG's complex band structure is a serious computational burden, we explore methods for optimizing numerical performance in the Python programming language.

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88. Ring Closing of Aromatic Alkynes and Gold Cavitand Substrate Selectivity

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Like enzymes, gold functionalized resorcin[4]arene cavitands have features that facilitate catalysis: an inwardly directed reactive center, adjacent to a well-defined binding pocket. Using the unique reaction conditions of this pocket, we hypothesize that an aromatic substrate could both enter and undergo a ring closing reaction with a terminal alkynyl functional group. We further hypothesize that reactivity will differ in cavitands that exhibit this pocket when compared to other gold complexes that do not. This will allow us to investigate the applications of these cavitands in molecular transformations. To accomplish this, a series of 3',5'-dimethyl-biphenyl-2-acetylene analogs have been prepared and tested with the cavitands. Nuclear Magnetic Resonance was used to screen for cyclization and the regiochemistry of cyclization. Our results have shown that cavitand-mediated cyclization occurs faster and with fewer byproducts than with simpler sans-cavitand Au compounds and that 6-membered ring formation is favored in a majority of the substrates. Limits exist however, and here we find exciting differences: when the guest's features do not pair well with the size of the cavitand interior, the reactivity of the cavitand changes. These substrates generally do not cyclize at all, mimicking the specificity of an enzyme with its substrate. The results of these experiments suggest that size specific cyclization of these compounds is indeed possible using the gold cavitands, provided that they are able to enter. This supplies additional information about the advantages and selectivity rules that cavitands provide when applied to catalytic problems.

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89. Quantum-Limited Interferometry: Angular Momentum Sorting at Very Low Light Levels

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We present a method of angular momentum selection at very low light levels using spatial interference between a strong local oscillator field and a weak beam. By using Fourier phase recovery techniques familiar in classical interferometry and by correcting the inhomogeneities

in the reference field, we can represent the quadrature components of a given spatial mode in the complex plane. Further, by post selection filtering (convolution and sampling), the method can distinguish states of different orbital angular momentum with a one-count standard deviation consistent with the quantum noise floor.

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90. Innate immune protein C1q decreases wound healing in human aortic endothelial cells

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Endothelial cells are cells that line the walls of the circulatory system. In atherosclerosis, the endothelium is damaged, which can be made worse by circulating oxidized low-density lipoproteins (oxLDL). Accumulation of oxLDL in the subendothelium can promote progression of advanced lessons in turn contributing to cardiovascular disease. Previous studies have shown that immune recognition protein C1q has the ability to bind oxLDL and improve removal of cholesterol while modulating macrophage functions. Interactions of C1q with endothelial cells are less well defined, although some studies have shown that C1q may promote chronic wound healing under ischemic conditions. To further investigate the role of C1q in endothelial migration/chronic wound healing, *in vitro*, the growth of primary human aortic endothelial cells (HAEC) were examined by a scratch assay. Treatments included untreated, serum, oxLDL, and oxLDL with C1q. After scratching an intact monolayer, HAEC growth was measured and analyzed by Image J during a 24 hour incubation. Data shows that oxLDL increased migration of HAEC, particularly at early time points, however the presence of C1q decreased the migration/wound healing process. Data were repeated with HAEC from 2 individual donors. These data are different to studies in HUVEC showing C1q increases migration, which may suggest that C1q provokes different responses in different cell types and in response to different targets.

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91. Characterization of *S. cerevisiae* Temperature-Sensitive Clathrin Heavy Chain Mutant *chc1-ts* for Protein Trafficking Studies

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The yeast vacuole of *Saccharomyces cerevisiae* is responsible for degradation of macromolecules, recycling of cellular waste, and responding to cellular stress to regulate cellular homeostasis. As such, it is functionally analogous to the human lysosome and is used as a model system to study lysosomal function, membrane fusion/fission dynamics and protein trafficking. Defects in lysosome function and trafficking can lead to various diseases including neurodegeneration, such as Alzheimer's Disease, and lysosomal storage diseases (LSDs), such as

Tay-Sachs. Studying lysosomal protein trafficking events at the molecular level can help better understand why and how defects occur. Specific interest lies in understanding how Env7, a protein kinase in the vacuolar membrane that is important for membrane fusion/fission during cell stress and budding, is trafficked from the Golgi to the vacuole. Past studies in the lab show that Env7 is potentially trafficked to the vacuole via a biosynthetic pathway called the carboxypeptidase Y (CPY) pathway. This pathway specifically requires clathrin heavy and light chains to function optimally. Therefore, biochemical and molecular studies on a temperature-sensitive clathrin heavy chain mutant (*chc1-ts*) will help shed light on Env7 protein mislocalization within the cell. We hypothesize that the *chc1-ts* cell line will have a WT-like localization of Env7 at permissive temperature and mislocalization of Env7 at restrictive temperature. Here, we describe initial characterization of the mutant cell line including studies directed at growth rates and phenotypes at permissive and restrictive temperatures to determine optimal temperature shift lengths and conditions. Biochemical assessment of Env7 localization under optimal temperature shift conditions is under way.

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92. Upregulation of the ryanodine receptor in response to non-dioxin like PCB exposure in embryonic zebrafish (*Danio rerio*)

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Exposure to polychlorinated biphenyls (PCBs) have been associated with certain cancers, neurotoxicity and adverse effects on the reproductive and endocrine system. Specifically, non-dioxin like PCBs, which contain *ortho* chlorine substitutions, interact with the ryanodine receptor, an intracellular calcium (Ca^{2+}) channel embedded in the membrane of the sarco/endoplasmic reticulum. The ryanodine receptor is critical to the excitation-contraction (EC) coupling in cardiac and skeletal muscle as well as neurological signaling. If disruption of the ryanodine receptor occurs it may contribute to disorders e.g. cardiac arrhythmias, Alzheimer's disease, and malignant hyperthermia (MH). Of the 209 PCB congeners, PCB 202, which is tetra-*ortho* chlorinated, is recognized to be the most potent ryanodine receptor activator. Current studies have not yet identified the consequence this congener may have on the ryanodine receptor in non-mammalian organismal exposure. The effects of PCB 202 on embryonic gene expression in zebrafish will be evaluated. It is hypothesized that the exposure to PCB 202 will result in the upregulation of the genes related to the ryanodine receptor and the genes activated in response to calcium-mediated signaling pathways. This research study will advance the understanding of the effects of PCB 202, and PCB mixtures, on human health and the potential environmental risk factors relevant to the air, water, and soil quality.

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93. Capping Metal-Organic Framework for X-Ray Photoelectron Spectroscopy Analyses

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Metal-organic frameworks (MOFs) have peaked the interest of the scientific community for their variety of structure, size, and high porosity. This enables applications such as targeted drug delivery, gas capture, and catalysis. MOFs consist of metal ion clusters coordinated by carboxylic acid containing organic ligands. Previous studies demonstrated trapping of loaded molecular guest species can possibly be achieved by steric hindrances utilizing carboxylic acids as capped substituents. Specifically, MOF-5 was capped with triphenylacetic acid and diffusion of crystal violet was monitored, but the wide variety of MOF shape, structure, and chemistry motivates explorations of other MOFs as well. The MOFs studied herein are copper based HKUST-1 and zinc based MOF-5 to compare and contrast results amongst different MOF structures. We hypothesize that capping substituents are primarily covalently bound to the surface of both MOF-5 and HKUST-1 samples. Capped MOFs were prepared by introducing *p*-trifluoromethyl benzoic acid under hydrothermal conditions for 48 hours. *p*-Trifluoromethyl benzoic acid was chosen as fluorine gives a unique photoelectron fingerprint for clear detection of capped species. Capped MOFs were then vacuum heated at 140 °C overnight to degas trapped solvent without degrading MOFs bulk structure or surface species. Powder X-ray diffraction and thermogravimetric analysis confirmed MOF stability against 140 °C *in vacuo* breakdown. Surface species and bulk material were analyzed by X-ray photoelectron spectroscopy (XPS) and argon ion sputtering. With both HKUST-1 and MOF-5, we observed detectable amounts of fluorine via XPS, and following argon ion sputtering of each MOF surface, spectra contained no fluorine signals within detection limits. The experimental results are consistent with a model wherein the fluorinated benzoic acid was successfully capped on the surface of HKUST-1 and MOF-5 material. In the future further control tests will be done for qualitative analysis to determine whether fluorinated capping groups are covalently bound or superficially adsorbed. Our preliminary findings show promising implications for understanding the mechanisms of carboxylic acids as capping reagent. This provides a simple method in encapsulating guest molecules within the pores of MOF structures for later controlled release.

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94. Innate Immune Protein C1q Modulates Macrophage Chemokines in Atherosclerosis

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Atherosclerosis is the predominant contributor to cardiovascular disease and is the leading cause of death in the USA. Macrophages are cells of the innate immune system and play a major role in atherosclerosis. These cells are derived from blood monocytes and differentiate into tissue macrophages. Resting macrophages can become M1 under inflammatory conditions

or M2, under resolving conditions. Macrophages remove cholesterol in the form of low-density lipoprotein (LDL), but during hyperlipidemia they store cholesterol in lipid droplets in the cell, forming foam cells, which form plaque, which can cause a heart attack or stroke. Macrophages also release chemokines, small protein molecules that attract more monocytes into the inflamed area. Innate immune protein C1q binds to modified atherogenic forms of LDL such as oxidized or acetylated LDL and modulates many macrophage functions during uptake like clearance of cholesterol, macrophage inflammation and survival. Preliminary RNA seq data from human macrophages ingesting oxLDL with C1q shows that C1q modulates certain chemokines. Here we want to validate this data using qPCR and will test the hypothesis that C1q will also modulate chemokines released by human monocyte derived macrophages ingesting acLDL. Our data showed that C1q modulates certain chemokines in human derived macrophages (HMDM) during clearance of modified lipoproteins. Importantly, our QPCR data validates our RNA-seq results. As a future step, we are also planning to run Luminex analysis to measure selected chemokine protein levels in supernatants. Since previous studies in the lab using a mouse model of disease indicate that C1q is playing a beneficial role in early atherosclerosis, modulation of chemokines by C1q may be one important way that C1q alters the atherosclerotic environment.

95. Identification of Androgen Receptor Isoforms Expressed in the Mouse Testis

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Androgens are essential for the development and maintenance of male sexual characteristics by acting on target organs and tissues via the activation of androgen receptor (AR). Previous studies have shown that androgen insensitivity in the testicularly feminized (Tfm) male mouse is caused by a frame-shift mutation in the *Ar* gene, which results in prematurely, C-terminally truncated AR isoform of 411 amino acids in length lacking the DNA-binding and ligand-binding domains. Despite this, a N-terminally truncated AR isoform containing the DNA- and steroid-binding domain of the AR might be produced from the internal translation initiation of the mutated Ar mRNA by *in vitro* translation. However, there is no evidence showing the existence of this internally translated AR isoform *in vivo*. To address this, we first performed sequence analysis of wild-type and Tfm mouse *Ar* cDNA by ATGpr (https://atgpr.dbcls.jp/) to search for potential translation initiation sites. We found 17 translation initiation sites, including amino acid positions 1, 503 and 517 as previously reported. Interestingly, amino acid 503 became most favorable site in Tfm AR mRNA for ribosome decking. To determine the *in vivo* expression of these potential AR isoforms, we performed immunoblotting of wild-type and Tfm male mouse testicular extracts with the antibodies recognized the N- or C-terminal regions of AR. So far, we observed the full-length AR protein (~100 kDa) in wild-type, but not in Tfm males. We will continue examining if these AR isoforms are similarly expressed in other mouse tissues.

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96. The Correlated Evolution of Tusks and Antlers in Ungulates.

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Larger ungulates lack tusks but instead possess antlers or horns, used as visual displays of social status, whereas tusks are mostly seen on smaller ungulates and used primarily as sexual weapons in battles over territory or mates. Two genera of deer have both antlers and tusks: *Muntiacus* and *Elaphodus*. In muntjacs, most fights are preceded by a "dominance display" which usually results in the subordinate male submission, therefore a gradual increase in reliance on this display may have led to the reduction in size of tusks and eventual evolution of complex, large antlers due to the rarity of actual fighting. Here, we analyze the relationship between overall body size (shoulder height, body mass, and skull length) and sexual weaponry amongst only tusked, both tusked and antlered, and only antlered ungulates. Developmentally, we hypothesize that the growth of larger body sizes favors the growth of disproportionately longer antlers and longer tusks when they are the sole sexual weapon available (i.e., positively allometric). When both types of weapons are present, however, we hypothesize that larger body sizes will favor disproportionately larger antlers but not tusks. Evolutionarily, we hypothesize that evolving larger body sizes favors disproportionately larger ornaments and weapons, regardless of whether one or two types of weapons are present. We examined these relationships both within several species of tusked ungulate, and between species of tusked and antlered deer using linear regression and phylogenetic generalized least squares (PGLS) analyses respectively. Intra-specifically, we found that in muntjacs antler length scales positively allometrically with overall body size, whereas tusk size scaled isometrically; though *Elaphodus* produced a positive allometric relationship with antler length, there was no relationship between tusk length and body size. Interspecifically, there was an overall isometric relationship between tusk length and skull length amongst all tusked species. However, when Muntiacinae was removed, there was a positive allometric relationship amongst only tusked species, suggesting it is still the preferred sexual weapon. Yet overall, as body mass increases, ungulates favor large complex antlers used as ornaments over tusks, used as pure sexual weapons.

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97. Micromagnetic Simulation of Magnetic Switching in Permalloy Capping Layers on Monolayers of Closed Packed Nanospheres

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Studying nanoscale materials presents an opportunity for the discovery of novel physical behavior. In this study, Permalloy (NiFe: Py) capping layers created by depositing Py on top of monolayers of closed packed nanospheres was used as an experimentally manipulated curved magnetic layer. Magnetic switching behavior of these thin films can be experimentally measured by a traditional magnetometry, such as, alternating gradient magnetometer. To understand the experimental data, especially for nanoscale magnetic materials, micromagnetic simulation software is used. Present work involved the choosing of appropriate software packages and the production of software to allow modeling of the Py capping layer. Following a survey of the NMAG, MuMax, and OOMMF software packages, OOMMF was selected as the best choice for the current state of the project. OOMMF uses the LLG (Landau Lifshitz Gilbert) equation to model the interaction across a region of rectangular prisms. The closed packed nanosphere geometry forms a repeated 7-sphere hexagonally organized grid, which can be generated for an arbitrary sized array of nanospheres. This geometry was encoded into a simulation for OOMMF. Thickness and curvature of the Py capping layer are the variables depending on the fabrication condition. The simulation is written to produce snapshots of the local magnetization configuration between each of the steps of a magnetic hysteresis loop. The MuView2 simulation visualization software package is used to display the simulation results. Future work will include extending the model system that will be more equivalent to the actual thin films sample and comparing the simulation result with an experimental data.

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98. Bioengineered Topographical Construct for Muscle Regeneration

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Volumetric muscle loss (VML) from major acute injuries can lead to both loss of tissue function and fibrosis. Although skeletal muscle demonstrates a capacity to regenerate minor damages, major injuries tend to be impossible to repair. For this project, we created a basis for the integration of engineered biomaterials with specified physical capabilities to support myoblast growth *in vitro* and skeletal tissue formation *in vivo*. Collagen type 1 was extracted from porcine tissue, purified using an acid solubilization method, and then casted upon a poly-dimethyl siloxane (PDMS) mold with micro channels. The mold was designed using SolidWorks and created using a Projet *6000 3D Printer*. To determine cell proliferation, C2C12 myoblasts were cultured for 1-3 weeks. Myoblasts cultured on molded collagen scaffolds showed enhanced

proliferation, desired physical orientation properties, and formation of multi-nucleated fibers. Successful experimentation of collagen bioengineered constructs continue to show possibility for future applications in tissue engineering.

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99. Coulomb Interaction on a Lattice

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Carbon, the building block of all known life, has an electronic structure that allows forming unique materials. For example, Carbon atoms can form a two-dimensional hexagonal structure a single atom thick with remarkable electrical and optical properties. Known as graphene, layers of this 2-D material can be stacked one atop the other. As the layers are stacked the electronic properties gradually change from those of graphene to those of graphite. To study electronic properties, one usually considers long wavelength and small energies. However, some properties require to go beyond this approximation. To this aim we determine an expression for the Coulomb interaction on a periodic lattice. This requires solving the Poisson equation to determine the electrostatic potential on a discrete lattice. The Poisson equation is a second order differential equation. To solve it on the lattice we use mathematical tools from Graph Theory. Most often, Graph Theory is used to solve computational problems such as the "Traveling Salesman" problem. However, the tools of Graph Theory lend themselves well to determining differential operators on a lattice. By constructing a logical graph that encapsulates information about the crystalline lattice structure of graphene we derive an expression of the Laplacian differential operator. We show how this is done on a linear chain and a two-dimensional honeycomb lattice. We then derive the expression of the Coulomb interaction for these cases. The extension of the graph theory to obtain the Coulomb interaction for a layered system is discussed.

100. Bayesian Inference of Neutron Star Equation of State

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The recent detection of gravitational waves from merging neutron stars by the Laser Interferometric Gravitational Wave Observatory (LIGO) opens a new window to understanding the densest objects in our Universe - Neutron stars. These stars are incredibly dense and

traditionally, one relies on models from nuclear physics to build an equation of state that predicts their properties such as mass and radius. Here, we present an alternative approach based on using Bayesian statistical methods to infer the equation of state of neutron stars from observational data on mass and radius. We evaluate the constraints set by the data on a generic parameterization of the equation of state using a set of density dependent polytropes.

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101. Fabrication and Characterization of Permalloy and Samarium Cobalt nanostructures created with multi-step spin-coated nanospheres

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A large area, monolayer of close-packed nanospheres can be used as a template or a mask to produce patterned nanostructures with interesting magnetic and optical properties. Spin-coating was used to create a densely packed monolayer of nanospheres of 400 nm, 1 micron, and 10 micron in diameter. To maximize the area of uniformly spin-coated monolayer of nanospheres, various parameters, such as spin speed, spin duration, and substrate size, need to be adjusted. A multi-step spinning process was employed to increase the monolayer spread along with assisting in the evaporation process. After a systematic study of samples made at various conditions and with Polystyrene and Silica nanospheres, recipes for 400 nm, 1 micron diameter, and 10 micron diameter nanospheres have been completed. Spin speed and nanosphere concentration turned out to be two critical tuning parameters to maximize the uniform deposition area. The chosen parameters yield 1 cm by 1 cm samples that are 90% covered with nanospheres of which areas of about 0.15 mm by 0.10 mm for 1 micron diameter nanospheres and 0.3 mm by 0.2 mm for 10 micron diameter nanospheres are monolayer. Silica nanospheres produced more uniform monolayers with less deformations than Polystyrene nanospheres. Permalloy or Samarium Cobalt were sputtered on the nanospheres and the magnetic properties of the nanocap layers were examined using an alternating gradient magnetometer, a vibrating sample magnetometer, and through the magneto-optical Kerr effect. Preliminary magnetic data shows a correlation between the coercivity of the material and the nanosphere spread. A long range nanosphere coverage tends to have a higher coercivity versus small area coverage. In addition, magnetic antidot nanostructures were obtained by removing nanospheres using Scotch tape after magnetic materials are sputtered. Similar characterization to the nanocap layers will be performed on the antidot nanostructures.

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102. Lysine Based Fmoc-Amino Esters as Butyrylcholinesterase Inhibitors in the Treatment of Alzheimer's Disease

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Butyrylcholinesterase (BChE) has recently been the cholinesterase of focus in the search to improve treatment of Alzheimer's disease (AD) and other neurodegenerative diseases. The decrease of the neurotransmitter acetylcholine and the significant proliferation of BChE in patients diagnosed with Alzheimer's have been connected with the decline of cognitive abilities. BChE activity is increased in individuals with AD, and this increased enzyme activity is suggested to reduce the acetylcholine BChE available for neurological function. Based on these observations, BChE inhibitors are sought to decrease enzyme activity and potentially restore acetylcholine levels to that of individuals without AD. Our lab found that amino acids with the 9-fluorenylmethoxycarbonyl (Fmoc) group were potent BChE inhibitors with Fmoc-Lysine being one of the more effective compounds. Building on the initial results, the Fmoc-amino acids provide an attractive scaffold to incorporate additional features that may lead to better inhibitors. Specifically, previous studies with other classes of inhibitors have shown that the incorporation of alkyl chains leads to more effective inhibitors, as the alkyl chains are suggested to increase binding interactions with hydrophobic groups in the enzyme active site. To test this hypothesis, herein we investigated a series of Fmoc-amino esters bearing alkyl chains of different lengths. Fmoc-Lysine esters containing a methyl, propyl, and octyl chain were synthesized and biochemically evaluated. The alkyl chain is expected to increase van der Waals interactions therefore forming a more potent inhibitor. Further, isopropyl-containing ester was tested to determine if branching and lowering the available surface area affects inhibition. The Fmoc-Lysine esters were synthesized using a series of alcohols, purified by silica gel chromatography, and characterized by NMR. The inhibition properties of the compounds were determined using kinetics experiments monitored by UV-Vis spectroscopy. All Fmoc-amino acid esters tested inhibited BChE, and while the methyl and propyl esters showed a modest ~three-fold increase in inhibition, the octyl ester showed a >20-fold increase in inhibition efficiency. Comparison of the propyl and isopropyl esters showed the branched isopropyl group with a smaller surface area was a less effective inhibitor relative to the linear propyl ester. Together, the results show that introducing alkyl groups within the compound leads to a more effective inhibitor, and increased binding interactions with the hydrophobic side chain are suggested to provide a basis for the tighter inhibitor binding. We are currently building on these results to identify maximum chain length that facilitates inhibitor binding. The results found in the Fmoc-amino ester scaffold may aid in the incorporation of similar features in other classes of BChE inhibitors.

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103. Investigation of Helium and Hydrogen Isotope Separation through Palladium and Palladium Nitride Foil Membranes for Use in the PFRC

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The Princeton Field-Reversed Configuration research experiment is a type of magnetic confinement device that utilizes odd-parity rotating magnetic fields to induce closed field lines, drive current, and heat the plasma. The fuel, D3He, that would be used in this type of device is aneutronic. However, deuterium (D) atoms in the plasma can fuse with each other to produce tritium (T). The T must be extracted to stop D-T reactions from occurring, which produce high energy (14 MeV) neutrons. Removing T from the plasma will allow for a cleaner and lower radioactivity plasma. One way to separate Hydrogen (H) and Helium (He) isotopes is to utilize a high Z material – permeation barrier – high Z material (ZBZ) configuration. Palladium (Pd) has a high H/He sorption rate and high selective permeability through conversion to a metallic hydride when heated to high temperatures, which increases H/He diffusion. This experiment focuses on how H permeability through a Pd foil is affected by temperature and pressure. In the conducted experiments, H and D were found to permeate through the Pd, while other atoms did not permeate which confirmed Pd selective permeability. The permeation was found to be temperature dependent, which was expected prior to the experiments. An increase in temperature was found to increase the permeation rate through the foil. Atomic H created in an unaccelerated ECR plasma source was found to be important in the overall permeation. Experimental values of the frequency factor and activation energy were close to those found in literature. With confirmation of selective H/D permeation, further experiments will be conducted.

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104. Gold Cavitand Catalyzed Alkyne-Acid Ring Closing: A Study in Regioselectivity

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Gold resorcin[4]arene cavitand-catalyzed transformations of small alkyne acids have piqued the interest of supramolecular chemistry researchers. The cavitand under investigation has 3-walls and one gold nanoparticle which creates a binding pocket around a reactive center. Simpler gold catalysts such as Au(I)Cl catalyze the cyclization of internal alkyne acids. We hypothesized the size-specific environment of the gold cavitand will result in significant regioselectivity differences in cyclization. Utilizing organic synthesis techniques (reflux, column chromatography, etc.) and NMR spectroscopy, we were able to synthesize 6 analogs of internal alkyne acids containing substituent groups ranging in size from methyl to pentyl chains. Each of the substrates were subjected to a 2.5% molar solution of cavitand in deuterated chloroform

and monitored by NMR over the course of 24hrs. We observed that the cavitand's influence in regioselectivity is related to the size of the alkyne's alkyl group. 5-membered lactones become favored as the chain lengthened (e.g. propyl and pentyl) while 6-membered lactones dominate with shorter groups (methyl and ethyl). For example, when the ethyl alkyne substrate a 2:1 conversion to the 6-membered ring under examination by NMR while the pentyl alkyne substrate exhibited a 3:1 conversion favoring the 5-membered ring closure. The results conclude the influence the size of the reactive pocket has with relation to the size of the substrates that are introduced in it. This specificity in regioselectivity can be furthered in a multitude of studies involving changing the size of walls attached to the cavitand or even the library of substrates that can be catalyzed.

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105. Proton couplings of Coenzyme Q across membrane mimics

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We will present the results of the control and regulation of proton gradient and coupling across membrane mimics using interfacial molecular assemblies of various Coenzyme Qs (CoQ). We use electrochemical and spectroscopic measurements to quantify proton gradient and investigate proton coupling modes across membrane mimics. The chemical interface produced between immiscible phases of water and 1,2-Dichloroethane is used as a model chemical interface and a membrane mimic. Electrochemical impedance spectroscopy analysis shows that proton gradient across such interfaces is controlled by the pH of the aqueous phase. We particularly show that fat-soluble molecules known for their proton coupling action in biological systems such as coenzyme $Q_{0\text{-}10}$ and quinone could change the impedance response associated with proton gradient across interfaces. We use interfacial molecular assemblies of ferrocene type redox agents and CoQs to control interfacial proton gradient. Interestingly, interfacial proton coupling varies between different CoQ type molecules, and impedance spectroscopy show signatures which are assigned to proton coupled electron transfer of these assemblies. We will discuss our results showing proton coupling regulation across membrane mimics and mechanistic differences shown in proton coupling activity of different CoQ type molecules.

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106. Synthesis of Cholinyl-Containing Phosphates to Evaluate the Steric Effects of the Cationic Group on Butyrlcholinesterase Inhibition

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Alzheimer's disease (AD), characterized by deterioration in memory and cognition, is the 6th leading cause of death within the United States. Patients with AD show evidence of the depletion of the neurotransmitter acetylcholine by the nonspecific enzyme Butrylcholinesterase (BuChe). Thus, the primary goal of our work is the creation of an inhibitor that can effectively mimic the chemical and physical properties of acetylcholine, competitively inhibiting BuChe. The inhibition allows the hydrolysis of acetylcholine by Acetycholinesterase, an enzyme that specifically hydrolyzes the neurotransmitter. To create the inhibitor, the pi cationic interactions and London dispersion forces between the amino acid, tryptophan, and the acetylcholine were mimicked. Due to tryptophan's hydrophobicity, we hypothesize that increasing the nonpolar environment around the cationic nitrogen will allow for better pi cationic interactions and Van der Waals forces. Thus, we synthesized methylated and ethylated amino alkyl phosphates, studying a pyrrolidinyl and diethyl amino group. The length of the alkyl chain was also varied (butyl, hexyl, and octyl) to determine if a bulkier chain results in improved binding to the acyl pocket in the BuChe active site. The assessment of the effectiveness of the molecules as inhibitors is being done by enzymatic inhibition assays. Previous assays, suggests increasing the alkyl chain and bulk of the cationic nitrogen, increased the ability of the molecule to inhibit BuChe evidenced by the decrease in K_i and IC_{50}. Further chiral shift studies will also be performed on the molecules.

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107. Studies to assess whether Hydrophobic Domain of S. cerevisiae Env9 is a bonafide lipid droplet localization signal

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One of the distinguishing features of the eukaryotic cell is that it contains specialized organelles whose function depend on the aid of various resident proteins. Lipid droplets (LDs) are cellular organelles involved in lipid metabolism functions, and their accumulation has been implicated in several physiological disorders such as obesity and diabetes. At their core, LDs contain nonpolar fat molecules surrounded by a phospholipid monolayer. However, much is still unknown regarding the localization signal and targeting of proteins to LDs. Bakers' yeast, *Saccharomyces cerevisiae*, is often used as a model system to study cellular processes, and its LDs are analogous to those of higher eukaryotes. Our laboratory uncovered *ENV9* gene as a

homolog to human RDH12 and has mapped the localization of its product, Env9, to LD's where it is involved in the regulation of LD biogenesis. We hypothesize that the hydrophobic domain (HD) of Env9, having been established as necessary for localization to LD's, is also sufficient for directing proteins to LD's; as such, we hypothesize that Env9 HD is a bonafide LD localization signal. To test this hypothesis, we will microscopically assess the localization of GFP-tagged reporter protein Env10-GFP that normally localizes to the endoplasmic reticulum, after addition of Env9 HD using recombinant DNA technology. To construct the *ENV10-HD-GFP*, yeast cells containing Env10-GFP encoding plasmid were prepared for plasmid isolation using Zymoprep™ Yeast Plasmid Miniprep II. Isolated plasmid DNA from yeast is currently being transformed into E. coli for amplification towards construction of *ENV10-HD-GFP* and assessing subcellular localization of its product.

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108. Environmental Polychlorinated Biphenyls Mixtures Inhibit the Dopamine Transporter

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Dopamine is a monoamine transmitter that contributes to the motor and reward system in in the body. When neurons experience a dopamine alteration it can cause symptoms of addiction, attention deficit hyperactivity disorder (ADHD), and Parkinson's. Polychlorinated biphenyls (PCBs) congeners are man-made environmental pollutants that can affect cognitive proficiency and disrupt the dopamine transporter (DAT). DAT is an integral membrane protein on the presynaptic neuron that uptakes dopamine from the synaptic cleft back into the presynaptic neuron. Non-dioxin like (NDL) PCBs with a higher chlorinated ratio in the *ortho* position and one *para* chlorine are the most active on DAT, where these NDL PCBs represent to majority of congeners found in environmental mixtures. When this protein is blocked it can increase the extracellular concentration of dopamine that gets deposited into the body while lowering dopamine concertation in the brain. To date, 15 of the 209 PCB congeners are known to alter the dopamine transporter (DAT) but it is unclear how PCB mixtures, common in the environment, may contribute to altered activity. The focus of this study is to examine the competitive activity of PCBs in binary mixtures towards DAT. We hypothesize that a binary mixture of PCBs will display an additive effect upon DAT, which will be assessed using female rat synaptosomes, a DAT antagonist binding assay and five PCBs with varying DAT potency. This work will aid in developing a neurotoxic equivalency scheme to predict DAT activity for complex PCB mixtures in the environment. The analysis of PCB exposure inducing DAT inhibition and altering dopamine concentrations can address its harmful persistent neural effects during developmental stages.

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109. Identification of Sexually Dimorphic Biomarkers in the Developing Mouse Amygdala Using Proteomics Approach

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The amygdala is an important brain region responsible for coordinating autonomic, behavioral, and endocrine responses to environmental stimuli with emotional content, most of which are different between the sexes. Accompanying functional differences, several neural structures of the amygdala are found to be sexually dimorphic. These differences are highly dependent on androgens and androgen receptors (AR), but the underlying mechanisms are unknown. This study was to identify proteins differentially expressed in the developing amygdala of male and female mice using the proteomics approach. Male mice carrying the testicular feminization mutation (Tfm) were included to investigate if the differences in protein expression were regulated by AR during early development. Tfm mice have a female phenotype and male genotype. Protein samples extracted from the amygdala of Tfm mice and their wild-type littermates (21 days of age, N=3 per group) were separated by two-dimensional (2D) gel electrophoresis. 2D gel images analyzed by Progenesis software, the resulting protein spots were visualized, and their intensities measured. Total of 300 protein spots on the 2D gels showed significant differences, and 31 of them displayed a fold-change of 1.5 or greater. Among them, three spots were excised from the gels, followed by in-gel digestion and protein identification using matrix assisted laser desorption ionization-time of flight (MALDI-TOF) mass spectrometry. From mass spectrometry analysis, we identified nucleoside diphosphate kinase A (NDK A) from one of the three spots. We will use immunoblotting to verify and profile the sex difference of NDK A expression in the mouse amygdala and the physiological role of NDK A in brain sexual differentiation.

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110. Innate Immune Protein C1q Increases Oxysterol 25-hydroxycholesterol in Microglia

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Lipids play a major role in both Alzheimer's disease (AD) and heart disease. We have previously shown that innate immune protein C1q binds to damaged forms of cholesterol such as oxidized low density lipoprotein (oxLDL) and modulates macrophage responses during ingestion. This includes increases in macrophage survival, phagocytosis of oxLDL, and efflux of cholesterol to HDL through the activation of the Liver X Receptor signaling pathway. Preliminary data also show that C1q changes the oxysterols produced in macrophages during ingestion of oxLDL. C1q

increases ingestion of oxLDL and efflux of cholesterol to HDL through the activation of the Liver X Receptor signaling pathway. C1q also increased levels of LXR-activating oxysterol 25-hydroxycholesterol (25-OHC) in human macrophages during ingestion of oxLDL. 25-OHC has also been shown to modulate immune responses and cell survival. The role of oxysterols in AD is complicated. There is evidence that 24- and 27-hydroxycholesterol are involved in the pathogenesis of AD, although other studies suggest 24-OHC is a mechanism to eliminate excess cholesterol from the brain, and thus, while levels increase with disease pathology, it may actually have a beneficial role. The role of 25-OHC in AD is also not well defined, however LXR activation in AD is known to regulate Aβ peptide transport and clearance. Since microglia are the resident phagocytic cells in the brain, we hypothesize that C1q increases 25-OHC and the cholesterol-modifying enzyme cholesterol 25-hydroxylase (CH25H) in microglia similar to peripheral macrophages. Primary microglia were isolated from adult wild-type and C1q-deficient murine brains, using a CD11b magnetic bead isolation kit. Microglia were cultured for 2-3 weeks in the presence of murine MCSF prior to treatment with oxLDL in the presence or absence of C1q. Cells and supernatants were collected for lipidomic analysis by liquid chromatography – mass spectrometry at the UCSD LIPID MAPS Core facility. Cells were also collected for RNA isolation and cDNA generation to analyze gene expression of cholesterol modifying enzymes. Lipidomic data show that oxysterol 25-hydroxycholesterol is increased in microglia in the presence of C1q. Lipidomic data also show that untreated microglia from C1q sufficient mice have higher resting levels of 25-OHC than C1q deficient mice. Additionally, C1q sufficient mice have higher mRNA expression for the CH25H enzyme than C1q deficient mice, which may provide the enzymatic mechanism by which 25-OHC levels are increasing. Understanding how the immune system affects lipid metabolism may provide novel avenues for therapeutic intervention in AD and heart disease.

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111. Effects of Microplastics on Feeding Rates of California Grunion Larvae, *Leuresthes tenuis*

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As human use of plastics has increased, so has the amount of microplastic debris in aquatic environments. Microplastics are now an abundant source of pollution that may pose a threat to marine ecosystems. Microplastics are small fragments that are less than 5mm in diameter, and can look a lot like the planktonic organisms that marine life such as fish feed on. In this study, we tested whether microplastics in sea water affected the feeding rates of larvae of the California Grunion, *Leuresthes tenuis*, a fish commonly found along the coast of Southern California. We measured feeding rates of grunion larvae within different levels of exposure to

75-90 µm Polyethylene (PE) and 125-250 µm High Density PE microplastics: control - no particles; medium – 250 particles/L; high – 1,050 particles/L; very high – 1,675 particles/L. Both experiments showed that exposure to microplastics can actually increase feeding rates compared to the control. In the experiment with 75-90µm PE, fish exposed to medium and high levels of microplastics had increased feeding rates compared to the control. However, exposure to a very high level of microplastics slightly decrease feeding rates. Similarly, in the experiment with 125-250µm High Density PE, increasing the level of microplastic concentration increased feeding rates with both high and very high as the highest peaks. In addition, in a separate experiment, the presence of microplastic debris in the environment increased grunion activity, though the effects were marginal. Future studies will be needed to understand why increasing microplastic concentration stimulated feeding. Overall, these results suggest that microplastics in seawater do not have a strong, negative effect on feeding rates of California Grunion during the early larval phase.

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112. Preparation of New Multi-Walled Gold Cavitands

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Our lab has an intense interest in understanding the catalytic characteristics of gold cavitands in molecular transformations. Gold cavitands place a reactive metal center inwardly directed to a small binding pocket where a molecule can enter and react. With that in mind, the preparation and synthesis of new multi-walled gold cavitands is a high-priority. We know that certain characteristics of the cavitand result in an increase in the rate of two reactions. We report herein the first preparation and catalytic results of a Hexanitro Gold Cavitand, which adds of six nitro groups to the cavitand's walls. The strong electron withdrawing effect has a high potential to influence the reactivity of entering substrates. In addition, the Hexanitro Gold Cavitand has somewhat shorter walls, so it potentially affords the insertion of bulkier substrates into the active site. The second newly prepared Gold Cavitand removes one of the three walls and thus opens a channel that faces the gold center. This may afford new opportunities to differently shaped substrates - or perhaps allow existing substrates to further intimately interact with the gold center. Future experiments are needed to explore the catalytic properties of these new cavitands. Ultimately, methodical exploration of reactivity vs. cavitand’s features will allow for more specialized chemical transformations, and perhaps for additional selectivity when multiple reaction centers are present in one substrate.

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113. Solution Methods for Relativistic Spin-0 Equations for Polynomial Potentials

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We compare two solution methods for relativistic quantum mechanical problems with spin-0 particles in polynomial potentials. These problems arise in describing mesons and baryons in a quark model. We adopted the Feshbach-Villars formalism that rewrite the Klein-Gordon equation in a two-component form. In this formalism the wave function components are referred to as particle and shadow antiparticle constituents. In the first method of choice we solve the Feshbach-Villars equation by representing the two-component Hamiltonian in a discrete Hilbert space basis and determine the resolvent by inverting the infinity by infinity matrix with the help of matrix continued fraction. In the other approach we determine the wave function by a direct numerical solution of the Klein-Gordon differential equation and then we get the particleantiparticle components by invoking the Feshbach-Villars procedure. We discuss the respective advantages of these methods.

114. Self-Assembly of Liposome Bilayer-embedded Pd Nanoparticle Hybrids in Water: Formation, Stability, and Phase Behavior

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The scientific community has been encouraged to search for new therapeutics that can help prolong the life of our aging populace. Nanoparticle research is one of several fields that have overseen developments in biomedical applications including magnetic resonance imaging and targeted drug delivery. The properties of nanometer sized particles vary drastically from those of higher dimensions or bulk materials. Much hope is being placed in their usefulness for biomedical applications due to their unique optical, catalytic, and electric properties. In this research, palladium nanoparticles with hydrophobic coatings were synthesized using the thiosulfate protocol and subsequently hybridized with dialkylphosphatidylcholine to form vesicles. The self-assembly of hydrophobic nanoparticles inside the bilayer of liposome took place as a result. By characterizing the resulting colloidal mixtures both physically and chemically, we are trying to understand the formation, stability, structural changes, and phase behaviour associated with Pd nanoparticle incorporation. The results so far have shown that the inclusion of Pd nanoparticles in liposome bilayers may decrease colloidal stability of the vesicles and the catalytic activity of the hybrids may be dependent on the vesicle phase transition temperature. This indicates that the bilayer-embedding of Pd nanoparticles reduce the zeta potential and lower the phase transition temperature of the hybrid vesicles we have prepared. This research also targets developing a model that can accurately predict the properties of nanoparticle-containing liposomes based on the preparation methods, either the thin film hydration (TF) or the reverse-phase evaporation (RP), and composition. These studies

will serve as a foundation for developing nanoparticle-loaded liposomes for a variety of applications such as bioorthogonal catalysis or drug delivery.

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115. Investigation of Particle-Hole Symmetry In the Fractional Quantum Hall Effect at the lowest Landau Level using realistic Hamiltonians

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Electrons confined to two-dimensions experience the fractional quantum Hall effect (FQHE) at low electron densities, high magnetic fields, and low temperatures. FQHE states are topologically ordered phases characterized by the fractional filling factor ν which is the electron number divided by the Landau level (LL) degeneracy. Alternatively, under particle-hole conjugation one can consider system in terms of holes (the absence of an electron). The total number of holes in a fractionally filled LL is simply the LL degeneracy minus the number of electrons. Hence, the fractional filling factor of holes is $\nu_h = 1 - \nu$. Naively, if the system maintains particle-hole symmetry, then if the FQHE occurs at filling factor ν it will also occur at filling factor 1- ν with all the same properties. However, realistic effects such as finite magnetic fields, disorder, etc. can break particle-hole symmetry at the level of the Hamiltonian. We study the nature of particle-hole symmetry on the FQHE in the lowest Landau level under realistic conditions numerically using exact diagonalization.

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116. Wirtinger Width

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Knots are loops in 3-dimensional space. The mathematical study of knots has broad applications to the sciences including DNA synthesis and quantum mechanics. One of the main goals in knot theory is to find methods for determining when two apparently different knot diagrams actually represent the same knot. This is partially accomplished with knot invariants. One such invariant is the Gabai width. In this project, we define the Wirtinger width of a knot and show it is equivalent to Gabai width. The Wirtinger width is algorithmically computable and leads to a new and efficient combinatorial technique for calculating the Gabai width of a knot.

117. Colloidal Palladium Nanoparticle for Selective Hydrogenation of Styrene Derivatives with Reactive Functional Groups

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The application of nanoparticles is promising in the biofuel industry and medicine because of their high surface area to volume ratio properties that could be useful as catalysts. Alkylthiolate-capped palladium nanoparticles were used in this investigation to observe their hydrogenation selectivity with different styrene derivatives. The selectivity and percent conversion between two different ligand-capped palladium nanoparticles were compared. Ligand-capped palladium nanoparticles were synthesized by using sodium borohydride to nucleate the palladium core followed by sodium s-octylthiosulfate or sodium s-phenylethylthiosulfate to passivate the palladium cores; octanethiolate-capped palladium nanoparticle (C8 PdNP) and phenylethanethiolate-capped palladium nanoparticle (PhC2 PdNP) were prepared using this method. The two catalysts were tested in different styrene derivatives varying in different electron withdrawing and electron donating functional groups in deuterated chloroform solvent, 1 atm H_2 for 24 hours. Samples from each reaction after 24 hours were analyzed using ^1H NMR to measure its product conversion. All styrene derivatives with the C8 PdNP catalyst were observed to have undergone reduction of the vinyl group with >99% product conversion. Styrene derivatives with the PhC2 PdNP catalyst were also observed to have undergone reduction of the vinyl group but ranged from 25 to 60% product conversion depending on the functional group. Both catalysts demonstrated selectivity for the hydrogenation of the vinyl group without reducing other reactive functional groups in the styrene derivatives, but C8 PdNP had a higher catalytic activity than PhC2 PdNP. No trends were observed between the functional group of the styrene derivatives and product percent conversion in the reactions treated with the PhC2 PdNP. Results suggest that vinyl group on the substrate can interact with the catalytic surface easier on the C8 PdNP than the PhC2 PdNP to form the palladium-alkyl intermediate. A proposed mechanism for PhC2 PdNP's lower catalytic activity is that the aromatic group between the ligand and substrate creates a pi-pi interaction which lowers the interaction between the catalytic palladium surface and the substrate's vinyl group.

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118. Second Order Relativistic Quantum Mechanical Equations

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We develop a computational approach to solve the basic equations of relativistic quantum mechanics, like the Klein-Gordon and the Dirac equations. We use the second order form these

equations due to their similarity to the Schrödinger equation. In our method we map the Coulomb Klein-Gordon and Dirac solutions to the corresponding Schrödinger Green's operator. The equations are solved in the Coulomb-Sturmian basis representation and we approximate the short-range part of the potentials by finite rank operators. The method seems to be superior to existing methods as it is applicable for non-local potentials as well, and the method converges super-fast.

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119. Temperature dependence of the neutron star crust equation of state.

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The lowest energy nucleus at zero temperature is calculated for different neutron star mass densities, and from this information an equation of state is calculated. From that equation, many interesting properties of the neutron star are discovered. This is the standard approach to calculating equations of state, but this approach does not present the whole picture. To discover more properties of neutron stars, temperature is added into the equation. When temperature is treated as a non-zero variable, the nuclei at different densities might change in comparison to the single nuclei picture, but more importantly, multiple nuclei now have the capability of existing at the same density. Using this new method, the lowest energy nucleic species are calculated at varying temperatures and densities. An equation of state is calculated, and its clear the results can be drastically different than that of the single nuclei model.

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120. Effects of Solvent Polarity on the Catalytic Activity and Selectivity of Colloidal Palladium Nanoparticles

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Evaluations of metal nanoparticle catalysts functionalized with well-defined and well-ordered alkanethiolate ligands are considered important because such systems can provide valuable fundamental understandings on the structure-function relationships of nanoscale catalysts. Due to the presence of hydrophobic alkanethiolate ligands on the surface of colloidal Pd nanoparticles (PdNP), these nanoscale catalysts will interact with surrounding solvents distinctively depending on the polarity of solvents. This research investigates how solvents with varying polarities influence the catalytic activity of colloidal PdNP capped with thiolate ligands. Our previous work using allyl alcohol catalysis suggested that the conformation of

alkanethiolate ligands changes upon the type of solvents, resulting in varying degree of available space close to the nanoparticle surface. However, more detailed investigations using various solvents and catalysis reactions are necessary to fully grasp on this important concept. A synthetic method applying Bunte salts (sodium s-dodecylthiosulfate) is used for the generation of PdNP capped with alkanethiolate ligands (dodecanethiolate). Catalytic activity of PdNP is tested in different solvents (protic, aprotic, and nonpolar) using hydrogen gas and 1-octene as the substrate. The reaction mixture is allowed to stir for a set amount of time (1,4,8, and 24 hours) at room temperature for kinetic analysis. The preliminary catalysis results of alkene hydrogenation and isomerization are investigated using ^{1}H NMR and gas chromatography. The catalysis results in methanol and benzene indicated that the polar protic solvent (methanol) favor the hydrogenation of 1-octene to octane and the nonpolar solvent (benzene) promote the isomerization of 1-octene to 2-octene. More studies will confirm the high regioselective "switching" behavior of PdNP in different solvents with varying polarities.

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121. Liposome Bilayer-Embedded Hydrophobic Pd Nanoparticles with Varying Surface Ligand Density for Colloidal Catalysis in Water

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Ligand-capped metal nanoparticles exhibit promising properties as catalysts, because their large surface to volume ratio allows for high catalytic activity, while their ligands dictate the immediate environment around the catalytic surface allowing for directed catalytic selectivity. Our research group has recently reported the isolated effects of surface ligand density on the catalytic activity and selectivity of Pd nanoparticles (PdNPs) with same core size and shape but with varying surface ligand density. Overall, enhanced catalytic activity of hydrogenation/isomerization of alkenes and dienes was observed for PdNPs with a lower ligand density. Surface ligand density is also shown to influence the hydrogenation/isomerization product selectivity of the catalytic reactions by regulating the formation of certain Pd-substrate intermediates and the kinetic diffusion of surface hydrogen/substrates. Our research now aims to study the influence of liposome bilayer embedding on the catalytic activity and selectivity of PdNPs with varying surface ligand density. In particular, this poster research focuses on understanding the influence of surface ligand density on bilayer-embedding of PdNPs and the colloidal stability of these hybrid liposome-nanoparticle complexes (HLNC). First, colloidal Pd nanoparticles are synthesized using the reversed thiosulfate addition protocol, completing the nucleation growth of PdNP before adding alkylthiosulfate ligand; this step is completed using tetraoctylammonium bromide (TOAB), in a way to control the size of PdNP. The PdNPs are then self-assembled with 1,2-distearoyl-sn-glycero-3-phosphocholine (DSPC) lipids in water. This

process creates hybrid liposome-nanoparticle complexes with a hydrophobic region where the hydrophobic PdNP catalysts reside. The presence of hydrophobic bilayer allows the concentration of substrates and hydrogen gas molecules near the catalytic sites for hydrogenation/isomerization to occur in aqueous environments. The preliminary catalysis results of alkene hydrogenation and isomerization are investigated using ^{1}H NMR and gas chromatography.

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122. Photo–enhanced Catalysis of Palladium Nanoparticles Supported on Titanium Oxide.

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The field of nanomaterials has been getting more attention the last few decades because of their unique optical, electrical and physical properties compared to those of bulk materials of the same type. One of the most studied nanomaterials is colloidal metal nanoparticles (NP) because of the tunability to control their structural parameters such as core size, shape, and chemical functionality using organic capping ligands. The head group of these ligands interacts with the surface of the metal nanoparticle whereas the organic chain of the ligand prevents aggregation and the terminal group controls the chemical properties such as solubility and chemical interactions. The adsorption of metal nanoparticles on semiconductor supports has recently been studied increasingly for the application of hybrid nanoparticles in photocatalysis or photoenhanced catalysis. Photoenhanced catalysis is a type of catalysis that uses light to further enhance the rate of a reaction. Titanium oxide (TiO_2) is one of the most common semiconductors that has been used for photoenhanced catalysis. The mechanism has to do with the production of electrons and holes whenever TiO_2 absorbs ultraviolet (UV) light. More specifically, when UV light hits the surface of TiO_2, the electrons are excited from the valence band to the conduction band and therefore creating the negative electron (e-) and positive hole (h+) pair. Herein, we investigate the influence of TiO_2 particles on the activity and selectivity of colloidal palladium nanoparticle (PdNP) for the hydrogenation and/or isomerization of allyl benzene derivatives. It is hypothesized that the positive hole that is formed on the surface of TiO_2 particles breaks apart the water molecules that are present forming two protons and half mole of oxygen, whereas the negative electrons can be transferred to PdNP and change the electronic property of Pd. The synthesis of water-soluble alkanethiolate capped palladium nanoparticle (PdNP) is achieved using the thiosulfate protocol developed by our group. The produced PdNP is characterized by ^{1}H NMR and UV-Vis Spectroscopy. The catalytic activity of PdNP for the hydrogenation/isomerization of allyl benzene is tested in different conditions. The preliminary results suggest that despite the overall low conversion yield the catalytic activity of

the colloidal PdNP increases with the use of semiconductor TiO_2 in the presence of UV light supporting the initial hypothesis.

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123. Numerical Methods for Multiscale Modeling in Bacterial Colony Growth

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The spatial heterogeneity of nutrients and metabolites in a developing bacterial colony can affect cell local growth rate, and hence the morphology of the colony. We model the essential elements (Carbon source, oxygen, and metabolite) as coupled reaction diffusion Partial Differential Equations. These equations in practicality are difficult to solve, due to the multiple temporal and spatial scales from coupling and disparate kinetic rates that imposes a severe restriction on the numerical time stepping. In this study, we propose a modified Newton-Multigrid method and implement it to a 1D similar and simplified system. The result demonstrates clear advantage of our method in both accuracy and efficiency, in comparing with other numerical methods such as Forward Euler, Crank-Nicolson, and Newton's method. We will apply this proposed method to the modeling of 3D bacterial colony.

124. Pd Nanoparticle - Quantum Dot Nanodisc Hybrids for Photo-enhanced Colloidal Catalysis

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Our group has employed the thiosulfate protocol, using sodium S-alkylthiosulfates instead of alkanethiols, to generate catalytically active Pd nanoparticles (PdNP) capped with the lower density of alkanethiolate ligands. The controlled alkanethiolate capping has provided nanoparticles the partial poisoning that is necessary for selective hydrogenation and/or isomerization of olefins. To further increase the utility of Pd nanoparticle catalysts, the colloidal hybrids of PdNP with graphene quantum dots (GQD) and bismuth selenide (Bi_2Se_3) nanodiscs (BSD) were prepared. GQD was found to be an excellent UV-vis active semiconductor, with its optical and electronic properties induced by the quantum confinement effect. The strong near-infrared (NIR) absorption of Bi_2Se_3 nanodiscs also allowed it to utilize a large range of solar spectrum. Upon irradiation, electrons in the valence band of the semiconductor will transfer to its conduction band and holes are left in the valence band. The ligand-capped PdNP, PdNP/GQD, and PdNP/BSD were characterized using UV-vis spectroscopy, fluorescence spectroscopy, Raman spectroscopy, and transmission electron microscopy (TEM). The catalytic alkene hydrogenation was monitored using gas chromatography-mass spectrometry (GC-MS) and nuclear magnetic resonance (NMR). Our research hypothesized that the photo-generated

electrons or holes might have strong effects on the catalytic activity and selectivity of colloidal PdNPs. The catalytic activity of both PdNP/GQD and PdNP/BSD hybrids decreased dramatically toward hydrogenation of our first trial substrate, 1-octen-3-ol. This proved that it is the photo-generated electrons that transfer to the PdNPs from quantum dot discs and the hybrid catalysts become less adsorptive for alkenes. The next step for our research is to examine the catalytic activity and selectivity of the hybrid catalysts toward substrates with electrophilic and reducible functional groups such as nitrophenol.

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125. Impact of the Tsallis Distribution on the Thermodynamics of Fermions.

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Distribution functions describe the probability distribution of all possible energy states in a system of particles. There are many different distribution functions that can be applied to different types of systems, depending on the physical properties of the particles. However, in some extreme astrophysical environments, such as neutron star interiors and supernovae explosions, these physical properties depend on particle interactions which are not well known, and thus it is not obvious which distribution function is best to use. Experiments involving heavy ion collisions, which are in some ways similar to the environments we are interested in, can be accurately described using the Tsallis distribution. In order to determine whether the Tsallis distribution can be applied to these astrophysical environments, we compare calculations of physical quantities found using the Tsallis distribution to those found using the Fermi-Dirac distribution. Our results show significant differences between the two distributions at all temperatures in the low density regime and smaller differences for high temperatures at higher densities. This suggests that the Tsallis distribution may be useful for investigating the matter surrounding a neutron star just after its formation, which has densities similar to our low-density results.

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126. Incorporating Substrate Features in Fmoc Amino Acids to Develop More Potent and Specific Butyrylcholinesterase Inhibitors for the Potential Treatment of Alzheimer's Disease

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Alzheimer's Disease (AD) is a chronic neurodegenerative disease leading to irreversible memory loss and is the most common form of dementia. While a cure for AD is not available, numerous approaches including cholinesterase inhibitors are under investigation to mitigate the effects of this disease. For the two major classes of cholinesterases, acetylcholinesterase (AChE) and butyrylcholinesterase (BChE), previous studies showed that BChE activity increased in individuals with AD while AChE activity was similar. The increased BChE activity is suggested to deplete the pool of the neurotransmitter acetylcholine, and this depletion may contribute to dementia. We recently identified Fmoc-amino acids as BChE inhibitors, and Fmoc-Lys-O^- was one of the most potent inhibitors. The structural similarities of the Fmoc-Lys-O^- cationic ammonium group and trimethylammonium group of the enzyme's substrate, acetylcholine, may contribute to the potency of Fmoc-Lys-O^- as an effective inhibitor. Building on this result, we hypothesized that methylalting the Lysine side chain will lead to more potent inhibitors, as the methyl groups will mimic the acetylcholine substrate. We first synthesized a dimethylamino analog of Lysine, characterized the product by NMR, and used the compound in biochemical assays. To compare to previous Fmoc-Amino Acids the inhibition constants (K_I values) were determined using kinetics assays followed by UV-Vis spectroscopy. While the K_I value for Fmoc-Lys-O^- was 150 □□□, the K_I value for Fmoc-Lys$(CH_3)_2$-O^- was 40□□□□, indicating that the dimethylamino compound is a four fold better inhibitor. The results support the hypothesis that adding substrate features lead to a more potent BChE inhibitor. Additional studies indicated that the compound selectively targets BChE relative to AChE. Currently we are synthesizing the trimethyl ammonium compound to further test the model that the methyl groups contribute favorably to binding. As including substrate features is often a powerful component in inhibitor design, incorporation of methyl groups in Fmoc-amino acid based cholinesterase inhibitors may potentially help in the development of compounds to treat AD and help with slowing the harsh effects of dementia.

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127. Abstract not available.

128. Development of Robust Protocols in IC_{50} Determination of MCF-7 Cancer Cell Lines for Combination Chemotherapy Using Hybrid Collagen/Cell-Penetrating Peptides

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Combination chemotherapy studies in metastatic breast cancers have shown increased efficacy compared to single-agent chemotherapy. Unfortunately, most multi-agent treatments need to be administered sequentially rather than in one combination due to the difficulties of delivering agents with different chemical properties; therefore, limiting the possible synergistic effects of combination chemotherapy. We have designed a new hybrid collagen/cell-penetrating peptide drug carrier and hypothesize that this carrier will be able to deliver multiple agents simultaneously and in a controlled manner. The drugs to be tested will include Paclitaxel (PTX), Doxorubicin (DOX), 5-Fluorouracil (5FU), and a combination containing the three drugs. To test their effectiveness, the hybrid peptide drug carrier will be evaluated on MCF-7 cells, a model breast cancer cell line, with drug efficacies expressed as half-maximal inhibitory concentration (IC_{50}). The IC_{50} of PTX, DOX, and 5FU will be determined individually and in combination using luminescence cell viability assay (CellTiter-Glo 2.0). A challenge in determining IC_{50} of drugs on MCF-7 cells is their strong tendency to form clumps, preventing accurate measurements in cell counting. We try to overcome this challenge by separately treating the cells with a commercially available anti-clumping agent and a concentrated cell dissociation reagent. Preliminary data shows that there is no significant change in obtaining accurate cell counts for cells treated with the anti-clumping agent or cell dissociation reagent compared to cells not exposed to either reagent. We plan to further optimize and change parameters for our anti-clumping protocols to improve cell viability assays and advance drug delivery methods.

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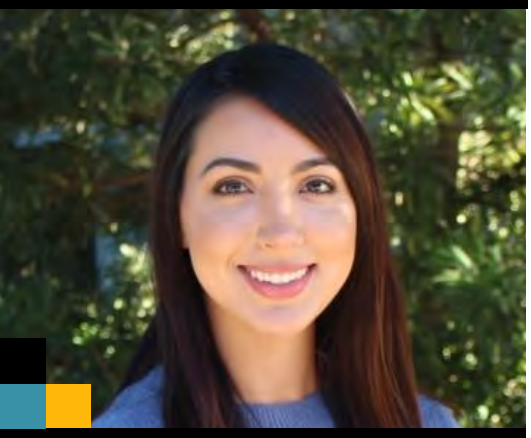
Lena Njoku, M.Ed.
Coordinator, Health Professions Advising



Cynthia Alarcon, M.A.
Coordinator, Research Programs

David Goulet
Technician, G2 Computer Lab

Resources @ JENSEN SAS CENTER

The Jensen SAS Center serves to support, prepare, and advance the education of students in all fields of science and mathematics through active participation in research, scholarship, and co-curricular activities.

TUTORING
Free drop-in tutoring led by upper-class students

G2 LAB
CNSM computer lab with printing, posters + more

PRE-HEALTH
Health professions advising for a variety of med careers

WORKSHOPS
Free topical workshops on academic + career success

MENTORING
For first-year students in the learning communities

RESEARCH
Advice on finding a lab and research training programs

EVENTS
Orientation and transition events for new students

Study Space:	8:00 am - 8:00 pm (Mon - Thurs) 8:00 am - 5:00 pm (Friday)
Research Programs:	8:00 am - 5:00 pm (Mon - Fri)
Health Professions:	8:00 am - 4:30 pm (Mon - Fri)
Tutoring:	8:00 am - 8:00 pm (Mon - Thurs) 8:00 am - 4:00 pm (Friday)

*hours are subject to change

@CSULBjensenSAS

HSCI-164

CNSM TUTORING

TUTORING SERVICES OVERVIEW

The university and college offer several tutoring options to assist students with their math and science courses. All tutoring services are free and operate on a "drop-in" basis which means you do not need to make an appointment.

CNSM TUTORING CENTERS

Jensen SAS Center: located in HSC1-164 + tutors BIOL, CHEM, MATH, PHYS, and STAT
Lindgren Math Tutoring Center: located in LA5-345 + tutors MATH and STAT
Math Education Tutoring Center: located in LA5-249 + tutors MTED
Physics Learning Assistants: located in HSC1-222 + tutors CHEM, MATH + PHYS

TUTORING TIPS + TRICKS

TUTORING BEGINS AS EARLY AS SEPT 3

Top reasons for receiving tutoring:

- To review material before a test.
- To review exam results and incorrect homework problems.
- To gain study skills and time management strategies.
- To overcome struggling with a particular concept or problem.
- To build your confidence in a subject matter.
- To stay on top of your homework and study routine.

Tutoring can take different forms:

- Come to the tutoring center with a set of questions with which you need assistance.
- Study in the tutoring center and engage a tutor when questions arise.
- "Teach" the tutor what you have learned so they can review your knowledge.
- Have a tutor quiz you before a test.
- Visit with a group of friends and invite the tutor to help with problem areas.

You can benefit from tutoring by:

- Increasing your confidence in a particular subject or overall academic skills.
- Building connections with upper-class students and classmates.
- Increasing your opportunity for success in forthcoming courses.
- Learning new study and problem-solving strategies.

FOR DROP-IN HOURS AND COURSES TUTORED, CHECK THIS OUT!

Undergraduate Research

Research at CSULB provides undergraduates the opportunity to benefit from faculty mentorship, engage in active learning, and create new knowledge through original work.

Set yourself up for success after graduation by participating in undergraduate research!

Benefits of Research

- Gain valuable skills that transfer to any career path
- Become a competitive applicant for graduate school, medical school, and the job market
- Collaborate and network with experts
- Apply classroom knowledge to real-world situations

Get Started

- Identify your personal research interests
- Ask faculty members you would like to work with about research opportunities in their lab
- Learn about funded research opportunities
- Contact the Research Programs Coordinator:

Cynthia Alarcón
Cynthia.Alarcon@csulb.edu
Office: HSCI-164A

CNSM Student Research Symposium 2019