CALIFORNIA STATE UNIVERSITY LONG BEACH

College of Natural Sciences and Mathematics

STUDENT RESEARCH SYMPOSIUM

CNSM
COLLEGE OF NATURAL SCIENCES AND MATHEMATICS
CALIFORNIA STATE UNIVERSITY LONG BEACH

BOOK OF ABSTRACTS

Friday, September 14, 2018

Supported by: Jensen Student Access to Science and Math Center &
College of Natural Sciences and Mathematics

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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 14, 2018. 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
Origins of a Research Career: it's never a strait path
Dr. Michael Harris, Assistant Professor of Integrative Physiology and Neuroscience

10:30-10:50am: How to Get Involved in Research
Chantra Nhien, Program Coordinator

10:50-11:00am: Poster Session 1 Set Up

11:00-11:55am: Poster Session 1 (Odd Abstracts)

11:55-12:05pm: Poster Session 2 Set Up

12:05-1:00pm: Poster Session 2 (Even Abstracts)

Coffee and orange juice will be served in the Alamitos Bay Room at 11:00am.

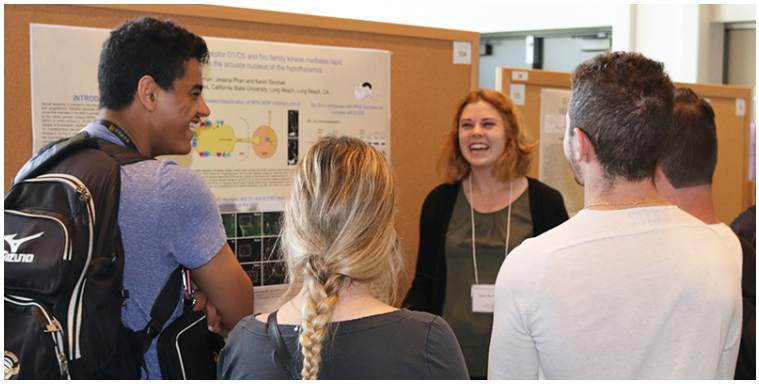
Pizza will be served in the Alamitos Bay Room at 11:30am.

Undergraduate Research

As a student in STEM (Science, Technology, Engineering, Mathematics), it is highly recommended that you explore, discover, and collaborate through undergraduate research. Regardless of whether research will be a part of your future career, participation in research will help you develop critical thinking, creative problem solving, and communication; these skills are highly valued in any career. Within the College of Natural Sciences and Mathematics (CNSM) at California State University Long Beach, you have the opportunity to conduct *original* research with amazing faculty.

How to Get Involved

- **Search Faculty Bios:** Search your department's web site to find faculty research interests.
- **Start a Conversation:** Talk to faculty and upperclassmen about their research.
    - **CNSM Student Research Symposium:** Held annually at the start of the Fall semester, the symposium is a great opportunity for you to learn about the research that is being done by your fellow students in our college across all STEM fields. This year's symposium will be held **Friday September 14, 2018 from 10am-2pm**.



- **Join a Research Lab:** Once you have identified a faculty member you would like to work with, ask them directly if you may join their lab. You may join as a volunteer or get course credit.

Federally-funded research training programs are available for students. These programs provide partial tuition assistance, stipends/hourly wages, graduate school preparation, summer research experiences, professional development, conference travel, and much more!

Get Started at www.csulb.edu/sas

Project Abstracts

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1. **Role of oxygen deficiency in Perovskite-Based Electrocatalysts in Oxygen Evolution Reaction**
Jiam H.Vuong, Charles J. Bloed, Alexis Enriquez, Sharan Raghavan, Hadi Tavassol, Ph.D., Shahab Derakhshan, Ph.D.
Department of Chemistry & Biochemistry, California State University, Long Beach, CA 90840

Hydrogen produced through water electrolysis is a key component of a sustainable energy cycle. Water splitting involves two half reactions, hydrogen evolution reaction(HER) at the anode and oxygen evolution reaction (OER) at the cathode of an electrolyser. Both of these reactions are slow and electrocatalysts are required to increase the rate of the reaction. OER is a more challenging reaction and requires high overpotentials to be viable IrO2, RuO2 or CoOx are materials often used for this reaction, which suffer from high cost of the metal, lack of stability, high overpotential, and toxicity. Here we investigate iron based perovskite structures as a candidate for OER electrocatalysis We focus on the physical and electrochemical characterization of perovskite and brownmillerite structure of Sr2-xCaxFe2O6-δ system, where δ=0-1 and x = 0, 0.25, 0.50, 0.75, 1, 1.25, 1.50, 1.75, 2. Solid state synthesis and gas phase synthesis was employed to rationally design compounds with varying oxygen deficiency and vacancies order. Interestingly some of these compounds exhibit higher activity than LaCoO3 in alkaline solution.

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

2. **Abstract not available**

3. **Synthesis and Characterization of Dinitrosyl Iron Complexes Using Pyrazole-Derived Ligands**
Mike T. Le, Vinh Q. Tran, Erik Galicia, and Lijuan Li, Ph.D.
Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840

Nitric oxide (NO) plays major roles in facilitating muscle relaxation, lowering blood pressure, and preventing memory loss. The half-life of NO is only a few seconds, so a carrier mechanism is required for pharmaceutical application. Non-heme dinitrosyl iron complexes (DNICs) have shown potential in the controlled release of nitric oxide. These DNICs are paired with ligands that can interact with proteins or DNA in the body. A potentially beneficial ligand exists in the five-membered heterocycle pyrazole. Pyrazole moieties are found in several pharmaceutical drugs that work against inflammation, viruses, bacteria, or fungi. Novel DNICs were synthesized and characterized by reacting $Fe(NO)_2(CO)_2$ with pyrazole-derived ligands. Crystal structure data revealed two pyrazole ligands coordinating to two iron centers. Chemical and electronic properties were studied using spectroscopic techniques such as IR, NMR, UV-vis and X-ray crystallography. Investigation of these properties as well as nitric oxide release may prove valuable for pharmaceutical research.

This project has been supported by the National Institute of Health (NIH-SCORE). We also thank Xiang Zhao and Xianhui Bui for research collaborations

4. **Abstract not available**

5. **Abstract not available**

6. Identifying mRNA Modification in Glioblastomas

Marvin Huynhle[1,2], Qi Cui[2], and Yanhong Shi[2]
[1]Department of Biotechnology, California State University, Long Beach; Long Beach, CA 90840
[2]Department of Developmental and Stem Cell Biology, City of Hope; Duarte, CA 91010

Glioblastoma is the most common and deadly of the malignant brain cancers. Treatment combinations that include surgical techniques, radiation, and chemotherapy have only produced median survival rates of less than 15 months after diagnosis. One of the greatest struggles to treating glioblastoma has been suggested to be from the treatment resistance of glioblastoma stem cells (GSCs), which carry a great capacity to promote tumor growth and invasion. Therefore, treatment approaches to glioblastoma will absolutely need to target these cancer stem cells to address overall resistance and recurrence.

While the importance of RNA modifications in biological processes has been reported, the complete list of effects from many classes of these modifications still have yet to be fully identified. One such case is the impacts of N6-methyladenosine (m6A) mRNA modification in cancer biology and cancer stem cells. We recently demonstrated that mRNA m6A levels are crucial for maintaining GSCs and revealed that m6A methylation may be a high-value target for anti-glioblastoma therapy. To further explore the role of RNA modifications in GSCs, here we knocked out known RNA modification modulators using CRISPR/Cas9. These gene knockout cells will be used to define the role of RNA modifications in GSC growth, self-renewal and tumorigenesis.

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

7. Developing Approaches to Incorporate Fluorotyrosines in Peptides via Solid Phase Peptide Synthesis

Noel M. Chau, Alexander Colla, and Jason P. Schwans, Ph.D.
Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840

The incorporation of unnatural amino acids in peptides and proteins has furthered the investigation of numerous protein structures and enzyme functions. Enzyme residues suggested to be important for catalysis are readily mutated using site-directed mutagenesis and measured for energetic effects. However, the limited repertoire of naturally occurring amino acids constrains the available substitutions. To obtain a deeper understanding of how enzymes work, unnatural amino acids are needed to systematically and incisively perturb enzymatic residues. In a recent study to evaluate the catalytic contribution of oxyanion hole hydrogen bonds, a feature often suggested as important for enzymatic catalysis, a series of fluorotyrosine analogs were used to perturb the pK_a value of a tyrosine hydrogen bond donor in the oxyanion hole of ketosteroid isomerase. However, challenges in the synthesis of fluorotyrosine analogs within the protein limited the pK_a range that could be investigated. To overcome these challenges and extend the series of fluorotyrosines used in enzymatic studies, we are developing an approach to selectively incorporate fluorotyrosines in peptides using silyl-based and fluorenylmethyloxycarbonyl (Fmoc) based chemistry. Air and moisture-sensitive reactions were conducted under argon, products were purified by flash chromatography, and isolated products were characterized by ^{1}H NMR. Initial synthesis incorporated the direct addition of the Fmoc protectant group on the N-terminal, followed by the esterification of the carboxylate to minimize unfavorable interactions with the phenolic hydroxyl group. Dual protected tyrosine was afforded at 60% yields post silylation and reduction of the allylic ester; however, lower yields were reported with Fmoc-2F-Tyrosine. Currently, a series of silylation conditions and additional protecting groups on the amino

acid are being evaluated. After optimization, the dually protected fluorotyrosines will be used to generate synthetic peptides via solid phase peptide synthesis.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; 5UL1GM118979-03; 5TL4GM118980-03; 5RL5GM118978-03. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

8. **Transplantation of Directly Reprogrammed Neural Precursor Cells into Mouse Cervical Spinal Cord Injury Model to Promote Improved Locomotor Recovery**

Javier Lepe, Chris Nelson, Katja Piltti PhD, Rebecca Nishi, Aileen Anderson PhD, Brian Cummings Ph.D.

Spinal cord injuries can lead to a debilitating condition resulting in chronic deficits in sensory and/or motor function. Currently, The World Health Organization (WHO) estimates that every year the number of new spinal cord injuries range from 40-80 new cases per million people, world-wide. In the US alone, Christopher and Dana Reeve Foundation survey puts the incidence of SCI at over 17,000 new cases each year, with a prevalence of ~282,000 individuals living with chronic SCI. The extent of the damage caused by spinal cord injuries vary by the severity of the insult. Novel therapeutic approaches to help treat/cure this debilitating condition are essential to help those in need. Several trials of stem cells therapies have been completed or are underway for SCI; however, none make use of an autologous cell source. Direct reprogramming of fibroblasts into neural precursor cells (drNPCs) offer personalized treatment for patients and circumvents immune system rejection and ethical acceptance. Reprograming fibroblasts into neural progenitor cells also offers a faster derivation method for neural stem cells (NSCs) for experimental analyses and potentially, human transplantation. Direct reprogramming of fibroblasts bypasses a cellular pluripotent state which reduces the amount of time compared to the classical derivation of induced pluripotent stem cells (iPSCs) needed for producing neural precursor cells and may increase safety, as the cells are never pluripotent. We hypothesize that transplantation of directly reprogrammed precursor cells into the spinal cord, can produce functional recovery months after transplantation. In a mouse cervical contusion injury model, we investigated the functional recovery of animals after transplantation of three directly reprogrammed cell lines oligo-progenitor cells (drOPCs), neural progenitor cells (drNPCs) and a line which produces both OPCs and NPCs. Animals were transplanted 2 weeks post injury with a dose of 75,000 into four rostral/caudal injection sites. Transplanted animals will be compared to sham control animals and injured animals injected with vehicle. Recovery of function will be assessed by performing locomotor tasks one, two and three months after transplantation by individuals blind to treatment group. Allodynia and hyperalgesia (increased sensitivity to pain) will also be assessed to confirm safety.

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

9. **Reversed Alkyl Thiosulfate Addition Synthesis of Mono- and Binary Ligand-capped Palladium Nanoparticles: Isolating the Catalytic Influence of Surface Ligand Density and Surface Morphology.**

Kevin M. Vargas and Young-Seok Shon, Ph.D.
Keck Energy Materials Program and Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840.

Ligand-capped metal nanoparticles exhibit promising properties as catalysts. Its large surface to volume ratio allows for high catalytic activity, while its ligands dictate the immediate environment around the catalytic surface, allowing for directed catalytic selectivity. Alkanethiolate-capped palladium nanoparticles (PdNPs) have previously been synthesized using a modified Brust-Schiffrin synthesis (using alkyl thiosulfate instead of alkanethiol), in which the nanoparticle core size is established during alkyl thiosulfate ligand passivation of the nanoparticle nucleation-growth initiated by borohydride reduction. Due to the dependence of core size on amount of ligand present, surface ligand density decreases with increasing core size. Herein we present a method in which core size is established independent to ligand addition, allowing the formation of PdNPs with similar core sizes, yet different surface ligand density. In this method, core size is established during the temporary passivation of growing nanoparticles by borohydride and tetraoctylammonium bromide (TOAB), allowing nucleation to reach completion. Various molar equivalents of alkyl thiosulfate are then added, prompting the replacement of borohydride and TOAB and the formation of alkanethiolate-capped PdNP. The resulting PdNPs were characterized via ^{1}H NMR, UV-Vis spectroscopy, thermogravimetric analysis (TGA), transmission electron microscopy (TEM), FT-IR, and inductively coupled plasma atomic emission spectroscopy (ICP-AES). Enhanced catalytic activity was observed for hydrogenation/isomerization of dienes and alkenes using PdNPs with lower surface ligand density proving the isolated effect of surface ligand density from other parameters such as core size and shape. PdNPs with lower surface ligand density demonstrated decreased selectivity for isomerization of alkenes possibly due to less steric hindrance and ligand-induced poisoning of the di-σ-bonded intermediate formation needed for hydrogenation. Future experiments aim to characterize the surface morphology (random organization, Janus, phase-separated) of binary ligand-capped PdNPs prepared with varying ratios of two dissimilar ligands. The influence of surface morphology on catalytic activity and selectivity can then also be determined. The summed results of each project help us build towards our goal of constructing well-defined and easily modulated enzyme site mimics.

This project is supported by the National Institute of General Medical Science (#SC3GM089562).

10. **Using CRISPR/Cas9 to Model *SCN1A* Epilepsies in Human iPSCs**

Carmen M. Ramos[1], Yunyao Xie[2], Nathan N. Ng[2], Olga S. Safrina[2], Martin A. Smith[2], Diane K. O'Dowd[2]
[1]Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840
[2]Department of Developmental and Cell Biology University of California, Irvine, Irvine, CA 92697

Epilepsies are chronic neurological disorders characterized by recurrent seizures affecting approximately 1.2% of the U.S. population. Over 1200 mutations associated with epilepsies occur in the SCN1A gene, which encodes the alpha subunit of voltage-gated sodium channel $Na_V1.1$. Mutations in this gene cause a spectrum of epilepsy disorders ranging from genetic epilepsy with febrile seizures plus (GEFS+) to the more catastrophic disorder, Dravet syndrome (DS). These two disorders are characterized by febrile seizures that persist past childhood, however DS causes more severe seizures with additional comorbidities including developmental delays and learning deficits. The

large number of single amino acid mutations that cause GEFS+ and DS has made understanding the underlying cellular mechanisms difficult. Using CRISPR/Cas9 gene editing technology, we successfully introduced and corrected these epilepsy-causing mutations in human induced pluripotent stem cell (iPSC) lines, creating both mutant and isogenic lines. The mutations that cause GEFS+ and DS, R1648H and R1648C, respectively, were introduced into an unaffected patient-derived cell line. Another mutation which causes GEFS+, K1270T, was corrected in an affected patient-derived cell line. Future directions include using these CRISPR/Cas9 generated lines for differentiation into iPSC-derived neurons and conducting electrophysiology. These studies can create a platform to support the development of future therapies and cures.

Thanks to the O'Dowd lab and the CSULB CIRM directors for their support. The project was supported by funding from CIRM Grant EDUC2-08383.

11. Assessing Protein-Ligand Binding Modes Via Ensemble Molecular Dynamics

Parker Bremer[1] , Walter Alvarado[1] , Eric Joseph Sorin[2]
[1]Chemistry, California State University at Long Beach, Long Beach, California 90840
[2]Chemistry Biochemistry, California State University at Long Beach, Long Beach, California 90840

The inhibition of butyrylcholinesterase (BChE) can lead to cognitive improvement for those suffering from mild to moderate Alzheimer's disease. A family of inhibitors, dialkyl phenyl phosphates (DAPPs), have demonstrated inhibitory potency equal to, or greater than, some pharmaceuticals currently prescribed in the United States. Using the GROMACS simulation suite within the Folding@Home network, we have collected one-thousand explicit-solvent simulations of approximately 100 ns each for a dozen inhibitors as well as the protein *sans* inhibitors, yielding a total simulation time of approximately 1.4 milliseconds. In order to maximize the potency of DAPPs and further understand protein-ligand binding conformations as a whole, we propose a method to elucidate binding modes through correlation and clustering. Analysis of these data based strictly on chemical interactions, which will be unaffected by the flexibility inherent to the BChE-inhibitor complex, will allow for the proposal of new, potent inhibitors for our collaborators to synthesize and analyze.

This project is supported in part by the Office of Summer Research Assistantship Program at CSULB.

12. Translational Potential of Optimized Choroid Plexus Epithelium Based in vitro Blood-CSF Barrier System

Robert J. Sims[1], Edwin S. Monuki MD, PhD[2].
[1]Department of Biological Sciences, California State University Long Beach, Long Beach CA, 90840 and [2] Department of Pathology University of California Irvine, Irvine CA, 92697

Transmembrane culture systems are often used to model the blood-brain barrier with micro vascular endothelial cells or the blood-cerebrospinal fluid barrier (BCSFB) with choroid plexus epithelial cells (CPECs).

However, several technical limitations impede establishment of effective and reproducible transmembrane culture modeling of the BCSFB formed by choroid plexus epithelial cells:

-Multiple refractive indices of Transwell® culture plates are prohibitive to real time, phase contrast inspection of confluence by live cell imaging

-The post mitotic nature of CPECs presents challenge to sustainable confluence required for BCSFB modeling

-Lack of robust in vitro barrier and transport data from primary CPECs impedes translatable characterization of these features required for competent assessment of their stem cell derived counterparts and development of preliminary drug screens

Utilizing transgenic mice bred to express fluorescent reporter CPECs, we develop a stepwise series of analyses for optimization of the choroid plexus epithelial cell-based in vitro BCSFB model.

Such optimization will prove an invaluable tool in BCSFB studies; for modeling disease processes that affect the choroid plexus such as Alzheimer's disease, screening drugs that rely on CPEC permeability to enter the brain, and as a quality control tool for evaluating functionality of human stem cell derived CPECs.

We apply our optimizations in the survey of the beta amyloid clearing capacity of primary mouse and human stem cell derived CPECs respectively, using fluorescent-labeled beta amyloid (Aβ 1-42).

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

13. Synthesis, Crystal Structure, and Magnetic Properties of $Li_3Mg_2RuO_6$ a Geometrically Frustrated Ruthenium(V) Oxide with an Ordered Rock Salt Structure

Marie Donato[1], Thomas Gredig Ph. D [2] and Shahab Derakhshan Ph. D[1]
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Compounds with triangular cationic sublattices with nearest neighbor antiferromagnetic (AFM) exchange cannot satisfy spin constraints simultaneously and exhibit a phenomenon, which is 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.[2] Non-frustrated lattices have values between 2 and 4 while highly frustrated lattices are 10 or higher.[2] Previous work has been done by our group on $Li_3Mg_2RuO_6$ from the family of ordered NaCl structure type with an orthorhombic crystal structure with a frustration index of , $f \approx 109/17 = 6.4$ implying that the system is mildly frustrated.[1] Through solid-state methods $Li_3Mg_2RuO_6$ was re-synthesized under high temperature and made in the monoclinic crystal phase. The monoclinic phase had a magnetic frustration index, $f \approx 94/10 = 9.4$. With the monoclinic phase having a higher value than the orthorhombic suggests that the monoclinic crystal structure of Li_3Mg_2RuO is more frustrated. Our preliminary results show that compounds with the same chemical composition can be made into different crystal structures, which may exhibit different magnetic properties. To further investigate this concept a series of compounds namely $Li_{3+x}Mg_{2-x}RuO_6$ (x=0, 0.25, 0.50, 0.75, and 1.0) are being investigated. By varying synthesis conditions of annealing temperature and amount of Li^+ and Mg^{2+} added into the system we can study the effect on crystal structure. Characterization of crystal structure was confirmed using powder x-ray diffraction. Temperature dependent magnetic susceptibility data collected by physical property measurement system (PPMS) were collected to evaluate the effect of the crystal structure on their magnetic properties.

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14. Inositol Alters Gene Expression of myo-Inositol and Drosophila Insulin-Like Peptides in Drosophila melanogaster Larvae

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Myo-inositol is a six-carbon sugar alcohol that is a precursor for 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 also been implicated in diseases and complications such as polycystic ovary syndrome, cancer, and type 2 diabetes. Myo-inositol supplementation of pregnant women's diets has been shown to reduce the incidence of gestational diabetes and type 2 diabetes, by decreasing insulin resistance. It is hypothesized that dietary inositol supplementation will be useful for alleviating hyperglycemia and obesity diet-induced type 2 diabetic flies. With this main goal in mind, there are multiple aims: 1) examining the regulation of myo-inositol synthase transcripts and 2) examining the regulation of Drosophlia insulin-like peptide (DILP) 2 and 5 transcripts in response to dietary inositol. In this study, to determine the effects of dietary inositol, wild-type larvae were grown on high- and low-sucrose diets, with and without inositol supplementation. The levels of mRNA transcript encoding DILPs and MIPS were determined using qPCR. The results indicate that addition of dietary inositol resulted in lower expression of both MIPS and DILPs transcripts. Furthermore, third instar larvae fed high sucrose have slightly decreased MIPS expression and increased DILPS expression compared to the larvae fed low sucrose. These studies were further expanded to include a preliminary examination of the expression levels of the MIPS protein via western blots. Taken together, this begins to provide an understanding on how inositol affects diabetes.

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15. Semiconducting Langmuir-Blodgett Films of Copper Paddlewheel Frameworks

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Porphyrin-containing metal-organic frameworks (MOFs) have attracted a significant amount of attention due to their photocatalytic potential that can be applied in light-harvesting devices. These porphyrin-containing MOFs are composed of carboxylate porphyrin and various transition metal ions, such as Zn^{2+},Cu^{2+},Fe^{2+}, and Pd^{2+}. In this work, we synthesized two Cu-porphyrin MOFs consisting of paddlewheel porphyrin frameworks (PPFs), PPF-1 and PPM-2, both of which have a layered structure consisting H_2TCPP (5,10,15,20-tetrakis(4-carboxyphenyl)porphyrin) and copper ions. To compare their electronic and optical properties, we prepared ultra-thin film of each MOF by a Langmuir-Blodgett method. Our studies found PPM-1 exhibiting a higher conductivity compared to PPM-2 due to the porphyrin centers occupied by copper ions. The structural difference was confirmed by UV/Vis/NIR spectra. The photocatalytic efficiency of both materials was also tested through a series of light harvesting experiments in light and dark conditions.

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16. Constitutive Inositol Synthesis Reduces Obesity, Increases Hyperglycemia, and Causes a Developmental Defect in *Drosophila melanogaster*.

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Myo-inositol is a six-carbon sugar alcohol that is known to be a precursor for 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. This study focuses on these diseases by utilizing the model organism *Drosophila melanogaster*. In this study, a high sucrose diet was used to induce obesity and hyperglycemia. Larvae grown on this semi-defined food had an obese-like phenotype, as was demonstrated in a float-buoyancy assay. Previous experiments in the laboratory suggest that increasing the inositol concentration of this semi-defined food reduces the number of obese-like larvae. These previous studies have also shown that deletion of the inositol synthase gene, *Inos*, increases the amount of obese-like larvae. This study also addresses hyperglycemia by measuring the glucose concentration in the hemolymph of the larvae. Further investigation of the role of the *Inos* in obesity and hyperglycemia was done using a strain ("D") with a UAS_{GAL4} inserted upstream of the 5' *Inos* UTR. The prediction is that increased constant (deregulated) synthesis of inositol should reduce the proportion of obese-like larvae. This was achieved by constitutive provision of GAL4 using an actin promoter. Float-buoyancy experiments revealed that this was accurate; there were fewer obese-like larvae. Another interesting result is that the levels of glucose in the hemolymph of "D"/Act-Gal larvae were greater than in wild-type larvae. Surprisingly, no viable "D"/Act-Gal adult flies have been observed. The deregulation of *Inos* in this strain results in nearly no progeny developing beyond pupal stage. These studies should contribute to a better understanding of inositol's role in diseases such as obesity, hyperglycemia, diabetes and other developmental defects.

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17. In vitro characterization of the interaction between tau and lipid membranes

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Alzheimer's disease, the most prevalent form of dementia, is a neurodegenerative disorder which has been associated with the presence of intraneuronal neurofibrillary tangles that are composed of Tau aggregates. Tau is a microtubule-associated protein that regulates microtubule assembly/stabilization and axonal transport. Under pathological conditions, Tau detaches from microtubules and misfolds into protein aggregates. Previous studies have demonstrated that aggregated Tau can be transported to the extracellular matrix, where it can be taken up by recipient cells and seed further aggregation. The interaction of Tau with membrane has been purported to be important for both its physiological function as well as its trafficking between cells that leads to the propagation of aggregates and neurodegenerative disease. However, there are still questions about the exact nature of Tau's interaction with membrane and its effect on physiological function and disease. We hypothesized that the interaction between Tau and lipid membranes contributes to Tau aggregation. To approach this

hypothesis, we generated amino-terminal (Tau-NT) and carboxyl-terminal (Tau-CT) deletion constructs of Tau via cloning and expressed and purified these constructs from bacterial lysates using affinity chromatography. We utilized in vitro flotation assays with synthetic endoplasmic reticulum-mimetic membrane to show that both termini of Tau bind to lipid membranes. After, we utilized variable-sized liposomes and giant unilamellar vesicles to demonstrate that the interaction between Tau and membrane is not affected by membrane curvature, an important factor for membrane localization specificity. Using microtubule recruitment assays, we show that microtubule binding does not perturb the Tau-membrane interaction. Finally, we utilized site-directed mutagenesis and aggregation assays to determine that the 'VQIVYK' membrane-binding region within Tau-CT exacerbates and is sufficient for aggregation of Tau. Taken together, this work increases our understanding of the interaction between Tau and lipid membranes and will be valuable for further research in delineating the molecular mechanisms involved in the pathogenesis of various neurodegenerative disorders.

18. Simulation and Analysis of Self-Assembled Silver Nanowires Networks

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With Moore's law coming to an end, new ways of building on-chip computing and communication fabrics has become necessary to keep pace of progressing electronics. It follows the trend for Moore's law that scaling the data processors, namely the transistors, makes them exponentially faster. The opposite is true for wires. One way to go around current limitations of the wires is to use self-assembly as a way to build electronic chips. The major challenges of traditional chips are related to delays of non-scalable global interconnects and reliability in general, which leads to the observation that simple scaling will no longer satisfy performance requirements as feature sizes continue to shrink. Self-assembled nanowire networks have previously been explored as a way to generate on-chip communication networks. Such networks can also be used for sensing and information processing. Self-assembly as a fabrication technique has the potential to lead to large-scale systems that can be built cheaper and easier than traditional top-down engineered electronic chips. In this project, self-assembled nanowire network models were developed, simulated, and evaluated. Our primary goals were: (1) to investigate and understand the characteristics of such self-assembled networks; (2) to simulate these networks in software; and (3) to analyze their communication properties. We built a MATLAB toolbox that allowed us to simulate a wide variety of nanowires by changing the model parameters, such as curvature, relative wire length, and number of wires. Bezier curves, essentially a parametric polynomial generated by a set of defined control points, were used to describe the nanowires mathematically. We used the average shortest path in the network to quantify its communication property. The total number of wires in the network was used as a cost measure and also indicates the efficiency of other factors that are proportional, such as wire length and power consumption. Different network models with different wire-length distributions were also generated: uniform, power law, exponential, and Gaussian. Our results show that some of these distributions allow to build more communication-efficient networks, or networks with a low average shortest path with the least amount of wires, than other distributions. Our work is relevant for future computing and communication fabrics, smart biomedical sensors with on-sensor data processing and analysis capabilities, and for self-assembled systems.

19. **Title: Synthesis of Mixed Efficacy Peptidomimetics as Potential Opioid Analgesics with Reduced Tolerance and Dependence**

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Opioid analgesics are valuable assets in the treatment of severe and chronic pain as they are capable of producing potent analgesia. Although commonly prescribed, opioids can generate tolerance, dependence, and respiratory depression. Mixed efficacy mu-opioid receptor (MOR) agonist/delta-opioid receptor (DOR) antagonist peptidomimetics have shown great promise as of late in being able to produce antinociception with reduced tolerance and dependence. Previously, it was found that peptidomimetics containing the pharmacophore regions of a dimethyl tyrosine and benzyl group linked by a benzylic core with an O-n-propyl substituent demonstrated the desired MOR-agonism/DOR-antagonism profile. Although moderately stable and highly efficacious in MOR binding in vitro, the compound was found to be inactive in vivo. In an attempt to enable in vivo activity, we replaced the benzyl pendant with various cyclic basic amine pendants which have been suggested to increase metabolic stability and promote MOR/DOR efficacy. From initial competitive displacement and agonist-induced stimulation assays, the O-n-propyl monocyclic basic amine pendant analogs synthesized were found to have substantial MOR-agonism/DOR-antagonism. This study also included a probing molecule featuring a stereocenter that was previously found to enhance metabolic stability, but greatly reduce MOR-agonism. This was to test if the addition of a basic amine pendant could overcome this poor agonism. Initial in vitro tests of the probing molecule have found that the addition of the basic amine pendant lead to similar binding, decreased potency, and similar MOR-efficacy compared to the benzyl pendant analog. In this study, we report the synthesis and activity of basic amine pendant monocyclic core peptidomimetic analogs as novel opioid analgesics.

20. **Study of the Electronic Properties of Ruthenium Chloride ($RuCl_3$)**

Naomy Marrufo, Amirari Diego, Francisco Ramirez, James Analytis, Claudia Ojeda-Aristizabal

Ruthenium Chloride ($RuCl_3$) is an insulating material with exciting properties. It is arranged in layers, where central ruthenium ions form an almost ideal honeycomb lattice. This configuration results in bond-directional interactions, that give rise to interesting phenomena predicted in the frame of the Heisenberg-Kitaev model. When cooled down, spins in the ruthenium ions align in a very particular way, forming a zig-zag antiferromagnetic pattern. They can also go through a spin liquid state, where the spins are constantly fluctuating. The layered nature of this material allows the extraction to very thin layers, close to the thickness of a single atom, allowing us to explore its properties in the 2-dimensional limit by using nanofabrication techniques to produce an electronic device that we can measure. We have used techniques of nanofabrication such as mechanical exfoliation, electron beam lithography, and electron beam evaporation to print circuits at the microscale on thin crystals of $RuCl_3$ and test how electrons travel in this material at low temperatures. We have additionally implemented the technique of ionic liquid gating to tune the conductivity of our thin crystals.

21. Surface Modification of Iron-Based Metal-Organic Framework for Drug Delivery

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According to the Center for Disease Control and Prevention, 25% of all deaths are related to coronary artery disease causing symptoms such as thrombosis and restenosis. To treat these symptoms, polymer-based drug eluting stent coatings have been developed and have exhibited great advantages over bare metal stents alone. However, clinical studies have shown that the polymer coating has been linked to numerous cases of hypersensitivity reactions and inflammatory responses. Our goal is to replace the polymer coating with an iron-based metal organic framework (Fe-MOF) due to its non-toxicity, high porosity, and biodegradable characteristics. Specifically, we used Material from Institute Lavoisier-88B (MIL-88B), which is composed of an iron ion connected by aromatic dicarboxylate groups forming a 3D cage-like structure. One of the greatest advantages of using an Fe-MOF is the ability to chemically bond to metal unlike the physical adsorption of polymer-based coatings. Our approach involves a three-step method starting with the synthesis of MIL-88B followed by using stainless-steel (SS) as metal substrate to obtain a uniform surface-supportive thin film of Fe-MOF using a direct crystallization method; subsequently, we used ibuprofen as a model drug to test for its capabilities of drug encapsulation and release kinetics. We applied two independent surface analytical techniques, X-ray photoelectron spectroscopy and Fourier Transform Infrared (FT-IR) spectroscopy to quantitatively analyze the elemental composition as well as for chemical characterization of the thin film. The FT-IR data indicate that the Fe-MOF is chemically bound to the SS substrate based on the observation of the carboxylate groups at 1600 cm^{-1}. We also observed that the Fe-MOF thin film on SS was composed of trivalent elements (Fe, Co, V, Ru, Mn); these results agree with those of previous literature on MIL-88B. Subsequently, we loaded a solution of ibuprofen in hexane onto the Fe-MOF thin film through a simple submersion technique and allowed to incubate for 24 hours. FT-IR spectroscopy confirmed the presence of ibuprofen through a series of C-H peaks ~3100 nm. To ensure that the peaks are from encapsulated ibuprofen rather than ibuprofen in solution, the SS sample was triple rinsed with hexane and dried with N_2. We are currently analyzing the drug loading capacity of the Fe-MOF film by measuring the ibuprofen/hexane solution before and after incubation by UV-Vis spectroscopy and drug release kinetics by HPLC. In summary, we have successfully grown Fe-MOF thin film onto SS substrate, and demonstrated encapsulation of ibuprofen into the MOF structure. Our preliminary findings show promise in increasing the understanding of MOF thin film formation on a metal substrate and it's role as a drug delivery system.

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22. Exploring the Relationship Between TBI and Violence with Personality Disorders

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Traumatic brain injury (*TBI*) is a lesion resulting from a blow to the head that can be detrimental to cognitive performance depending on the location and severity of the wound. Hypoactivity in the *prefrontal cortex*, an area of the brain responsible for executive functioning such as decision making and inhibition, is related to *TBI* and violence. However, the relationship between *TBI* and violent crimes may be dependent on other factors such as personality disorders. Certain personality disorders, like

borderline personality disorder or *avoidant personality disorder*, are associated with brain functionality or structural anomalies. Exploring what other circumstances make *TBI* patients more likely to commit crime is important for health officials to better intervene patients from engaging in risky behavior after injury. The aim of this study is to identify personality disorders that mediate the relationship between *TBI* and violent crimes. The Structured Clinical Interview for DSM-5 Personality Disorders (SCID-PD) assesses for 13 different personality disorders. Violent crime history was collected using the violent crime subscale of the Self-Report Crime Questionnaire. *TBI* incidence was collected using Ohio State University TBI Identification Method interview. Homeless men recruited from a local rescue mission ($n = 92$) were used in the sample of this study because crime and *TBI* are prevalent in this population. A path analysis was constructed using PROCESS macro, a path analysis modeling tool for SPSS, to understand the role of mediation for personality disorders on the relationship between *TBI* and violent crimes. In our findings, the introduction of *antisocial personality disorder* (*ASPD*) reduced the significance of the direct relationship between *TBI* and violent crime, ($t = 1.54$, $p = .13$). However, the indirect effect was significant, (95% CI [.07, 1.04]). A sobel test revealed that the mediation was not significant, ($z = 1.56$, $SE = .26$, $p = .12$), which could be because of the insignificant direct effect affecting the measures of the test and high correlations among predictors in addition to a small sample size. Individuals with *ASPD* have increased rates of *TBI*, hypofunctioning in prefrontal brain regions, and increased rates of crime and violence. The comorbidity of *ASPD* and *TBI* explains the relationship between *TBI* and violence better than the comparison alone. The findings should encourage health professionals to assess for *ASPD* when screening for *TBI* and suggest rehabilitation to intervene further likeliness of risky behavior which may lead to crime. In addition, when offenders are tried in court, consideration of comorbidity should be standardized.

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23. Synthesis of Tyrosine-based Polysulfates

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Click Chemistry refers to reactions that are high yielding, easy to perform, produce little to no byproduct, and selective, thus allowing one to make connections between diverse building blocks. Click Chemistry has been widely used to synthesize potential pharmaceuticals, molecular probes, and complex macromolecular structures. We have previously reported the synthesis of high molecular weight bisphenol A(BPA)-polysulfates using Sulfur(VI) Fluoride Exchange (SuFEx) chemistry; however, using BPA as a starting material limits the utility of these polymers in biological systems and humans because of the adverse effects of BPA. It is therefore important to develop tunable macromolecules using biocompatible scaffolds that will have minimal impact in living systems. Here we report the successful synthesis of novel biocompatible and biodegradable polysulfates with good yield (70-80%), accomplished by a series of straightforward reactions (DCC coupling, addition) and confirmed by NMR. These polysulfates were synthesized from bioavailable starting materials such as L-tyrosine and coumaric acid. Additional "clickable handles," such as a propargyl group, were installed on the synthesized monomers to perform future post-polymerization modifications that are useful in

altering/enhancing the properties of macromolecules. We will analyze and characterize our polymers with NMR, GPC, and Mass Spectrometry.

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24. Nickel-catalyzed Heterocycle Assembly via Intramolecular C-N Coupling

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Modern pharmaceuticals are largely comprised of small molecules containing heterocyclic moieties. Facile methods for the development of such structures are of high importance since bioactivity cannot be readily predicted based on structure alone. Synthetic methodologies are necessary to assist in the construction of heterocycles by elucidating efficient and cost-effective syntheses. As an alternative to other costly, less abundant, and more commonly used group ten metals, nickel was employed to perform intramolecular C-N coupling of vinyl halide and aryl halide sulfonamides to afford their cyclic amino derivatives. Optimization of these reactions was carried out to determine the ligand, base, and solvent parameters that afforded the highest isolated yields under relatively benign conditions. The study proved successful in determining conditions that afforded the respective pyrrolidine enamide and indoline products in high yields and without the use of metal reductants. The investigation and optimization of these reactions will be discussed. To our knowledge, this study represents the first documented example involving successful nickel-catalyzed intramolecular *N*-vinylation of a sulfonamide.

25. An Accessible Method to Enantiomeric Purity Determination of P-Stereogenic Compounds With Eu(hfc)$_3$: the Terminal Methyl Signal is Highly Resolved, Rather Than the Alpha-Carbon Protons

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Compounds with chiral phosphorus atom centers play increasingly important roles in the development of pharmaceutical drug candidates, agrochemicals, and chiral ligands in catalysis. A variety of methods are currently available to determine the enantiomeric excess (ee) of chiral organophosphorus compounds, including chiral high-performance liquid chromatography and gas chromatography-mass spectrometry methods; however, they are not widely accessible to all institutions. Therefore, we examined the use of proton nuclear magnetic resonance in conjunction with the lanthanide shift reagent, Eu(hfc)$_3$ (Europium tris[3-(heptafluoropropylhydroxymethylene)-*d*-camphorate]) to assay the ee for phosphate triesters. Previous studies employing this reagent focused on the alpha-carbon protons of the ester for ee determination studies. In our search for specific cholinesterase inhibitors for the treatment of Alzheimer's Disease, we have found a drug-precursor scaffold: alkyl phenyl 2-(dimethylamino)ethyl phosphate. The terminal methyl group of the alkyl substituent was observed to have the most highly resolved signal in chemical shift and proved to be most useful in the determination of ee. We hypothesize that this sharp contrast to earlier reports is due to the Lewis basic nitrogen atom coordinating to the Lewis acidic europium atom center. To further investigate the mechanism of this effect, we have synthesized a series of racemic phosphate triesters with various alkyl chain lengths and analogs with heteroatom-containing substituents. Overall, protons of the alpha-carbon showed broadening and little separation even without the nitrogen atom, but highly resolved separation of signals was observed for protons more distal to the oxygen atom. Additionally,

the *N*-methylated series required much less shift reagent to determine ee, indicating that charge may play a large role in affecting how each enantiomer feels the magnetic field present in the ligand-Lewis acid complex. This work will contribute to the development of a widely accessible technique to rapidly determine ee of *P*-stereogenic compounds using $Eu(hfc)_3$.

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26. Synthesis of Membrane Transporters: Calix[4]arene Tetra Phosphonic Acid

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The delivery of small molecules across biological membranes has been a long-standing challenge to medicinal chemistry. Often, *in vitro* active drugs are challenged by an impenetrable cell membrane. Our lab has demonstrated that host-guest chemistry, using synthetic receptors, can effectively transport drugs and drug-like molecules across 3-phase liquid membranes, as well as vesicle bilayers. Calixarenes are an example of a synthetic receptor species containing ionizable groups capable of transporting several payloads. We hypothesize that calix[4]arene tetra phosphonic acid will be able to effectively transport complex drugs across cellular plasma membranes. Calix[4]arene tetra phosphonic acid is lipid soluble, and can recognize and bind to drug-like molecules. Furthermore, it affected transport of these molecules. We synthesized calix[4]arene tetra phosphonic acid in a five-step process starting from 4-tert-butylcalix[4]arene following known methods. The synthesis provided the desired compound in a 6.7% overall yield. The final product was analytically pure by nuclear magnetic resonance spectroscopy. If drug delivery is successful in subsequent cell based studies, this technology will be a significant compliment to existing transport systems.

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27. Proteomic Characterization of the CFD1-NBP35 Scaffold Protein Complex Interactome

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Eukaryotic cells require close regulation of iron-sulfur (Fe-S) clusters because they play essential roles in nucleotide metabolism, transcription, DNA replication, and DNA repair. The mitochondrial and cytosolic Fe-S protein assembly machineries (ISC and CIA) facilitate the maturation of Fe-S proteins, however, the molecular basis of the connections within and between the machineries is unclear. An essential protein in the CIA is the CFD1-NBP35 scaffold protein complex which is essential for cytosolic Fe-S cluster biogenesis. We were interested in studying the interactome of the CFD1-NBP35 scaffold complex in HEK293 cells. Immunoprecipitation, immunoblotting, and bottom-up proteomics were utilized to study the interactome. The known interactor IOP1 was confirmed and new interactors like FAM96B and CIA substrates were found. By elucidating the interactome of the CFD1-NBP35 scaffold complex we will better understand the extramitochondrial Fe-S protein biogenesis process.

This project is supported in part by the National Institutes of Health Grant 5R01GM112763-04.

28. Structural and Functional Consequences of Apolipoprotein E3 and E4 Modification by 4-Hydroxynonenal, A Lipid Peroxidation Product.

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Apolipoprotein E3 (ApoE3) and apolipoprotein E4 (ApoE4) are exchangeable apolipoproteins that play a critical role in cholesterol transport and homeostasis. Structurally, they differ by a single amino acid with the most common isoform, apoE3, having a cysteine and an arginine at positions 112 and 158, respectively, and apoE4 containing arginine at both positions. ApoE4 is considered a risk factor for age-related neurodegenerative disorders and cardiovascular disease. Neurodegenerative diseases, such as Alzheimer's, Parkinson's and Huntington's disease are correlated to age-related oxidative stress, including lipid peroxidation. Lipid peroxidation damages lipids in membrane lipid bilayers and in lipoproteins by reacting with polyunsaturated fatty acids, and forming, among other products, 4-hydroxynonenal (4-HNE). 4-HNE is a cytotoxic, secondary lipid peroxidation product, elevated levels of which were reported in brain tissues and plasma of age-related neurodegenerative disease patients, along with various HNE-protein adducts including 4-HNE modified-apoE3 and -apoE4. In the present study, we will test the hypothesis that 4-HNE modification of apoE3 and apoE4 leads to impairment of structure and function of these proteins. The specific objectives are to: (i) prepare purified recombinant apoE3 and apoE4, (ii) modify purified apoE3 and apoE4 by 4-HNE, (iii) confirm modification by Western blot and mass spectrometry, (iv) determine effect of modification on secondary and tertiary structure of protein, and, (v) examine effect of modification on apoE function in terms of ability to bind lipoprotein receptors. Recombinant apoE3 and apoE4 bearing a His-tag at the N-terminal end were overexpressed, isolated and purified by affinity chromatography from *E. coli*. Purified apoE3 and apoE4 were modified by 4-HNE by incubation of 25x molar excess of 4-HNE over apoE3 at 37°C for 3 hours. The modification was confirmed by Western blot analysis using a 4-HNE specific antibody, which showed major bands at 36 kDa and 72 kDa. Subsequent steps will involve mass spectrometric analysis to identify specific amino acids and nature of modification, circular dichroism and fluorescence spectroscopy to determine changes to the secondary structure and tertiary fold, respectively, and assays to identify potential functional alterations to the isoforms in terms of lipid binding activity, cholesterol efflux ability, and LDL receptor binding activity. The findings from this study will aid in understanding isoform-specific differences in modification of apoE3 and apoE4, and help us understand the molecular basis for the role of apoE4 as a risk factor for age-related Alzheimer's disease.

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29. Liposome-Encapsulated Hydrophobic Palladium Nanoparticles for Biphasic Catalysis of Olefins in Water

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Despite the availability of many water-soluble organometallic and nanoparticulate catalysts, the direct application of water-soluble catalysts for the reaction of immiscible and hydrophobic substrates has been hindered by the low solubility of nonpolar reactants in water. Our research group has shown that alkanethiolate-capped palladium nanoparticles (PdNP) exhibit excellent catalytic activity and selectivity for hydrogenation of unsaturated compounds in organic solvents. This PdNP was synthesized using

the thiosulfate protocol using sodium S-dodecylthiosulfate as ligand precursor. The purpose of this study is to examine the catalytic activity of PdNP encapsulated in phosphatidylcholine (PC) lipids in water. After the liposome assembly of PdNP with PC in dichloromethane, the solvent was removed under vacuum and the hybrid was hydrated with phosphate buffered saline (PBS) solution. The resulting liposome-PdNP hybrids dissolved in water were characterized by UV-vis spectroscopy, inductively coupled plasma atomic emission spectroscopy (ICP-AES), dynamic light scattering (DLS), and transmission electron microscopy (TEM). During the catalysis reaction, the micellar characteristics of liposome-PdNP hybrid would allow the hydrophobic substrate such as 1-octene to momentarily enter the hydrophobic region of the catalysts with adequate stirring force. After the reaction, the resulting products from bi-phasic system were subsequently extracted with organic solvents and analyzed using ^{1}H NMR spectroscopy. The results suggested that the transformation of 1-octene to octane could be completed within 1 h of catalysis reaction under atmospheric pressure and at room temperature. Liposome catalysis results are then compared to control experiments without PC. The recycling tests of catalysts indicated that the aqueous phase containing the liposome-PdNP hybrids could be reused multiple times with only small decreases in the overall reaction rate.

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30. Cholinyl Esters of Fmoc-Amino Acids as Cholinesterase Inhibitors

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Alzheimer's is one of the most common central nervous system diseases, affecting more than 5.7 million Americans today and is the 6th leading cause of death in the United States. Cholinesterases are one of many enzymes needed for the proper neuronal cholinergic transduction of the nervous system, and perturbation of transduction results in a reduced concentration of acetylcholine in the synapse contributing to cognitive dysfunction. Of the two major forms of cholinesterases in the brain, acetylcholinesterase (AChE) and butyrylcholinesterase (BChE), catalyze hydrolysis of choline-based esters, and previous studies reported BChE activity to be elevated in patients with Alzheimer's, while AChE activity slightly decreased or remained the same. On this basis, BChE is a potential therapeutic target for the development of potent and specific inhibitors to alleviate neurodegenerative symptoms. We previously reported that amino acids bearing the Fmoc protecting group inhibit BChE preferentially with measured K_I values in the μM range. The Fmoc-amino acids provide a scaffold to readily evaluate a variety of modifications on inhibition properties. Specifically, the carboxy terminus provides a handle to introduce a cholinyl group. As enzymes have specificity towards their substrates, incorporation of substrate features such as a cholinyl group in enzyme inhibitors offers a powerful approach to generate potent and specific compounds. To evaluate if cholinyl-containing Fmoc-amino acids are BChE inhibitors, we synthesized the desired compound in two steps from the starting Fmoc-amino acid. The products were purified and characterized by chromatography and NMR, respectively. Whereas inhibition was not observed for Fmoc-Alanine at 200 μM, initial tests with a cholinyl-containing Fmoc-Alanine did show inhibition. The results suggest substrate analogs can potentially be used to increase the specificity and potency of inhibitors. We are currently synthesizing a series of cholinyl-containing Fmoc-amino acids and are evaluating their ability to inhibit BChE.

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31. Expression and Purification of Recombinant CDK5-p25 Complex from *E. coli* SoluBL21-DE3 Cells

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Cyclin-dependent kinase 5 (CDK5) is a serine/threonine protein kinase involved in regulation of several cellular processes including cell migration, proliferation and differentiation. It needs a cognate activator, p35 or its truncated form p25, to adopt a catalytically active conformation. The goal of this project was to express and purify recombinant CDK5-p25 complex from bacterial cells. We cloned the cDNAs of CDK5 and p25 into the pET-DUET-1 vector. We tested different growth media (Luria Bertani and Terrific broth), bacterial strains (*E. coli* BL21-DE3 as well as SoluBL21-DE3 cells) and temperature/time of induction (18°C, 25°C and 37°C for 1h, 2h and 18h) to optimize the expression and solubility of the complex. Our results showed that while majority of CDK5 was found in the inclusion bodies in *E. coli* BL21 cells under the conditions tested, expressing the complex in SoluBL21-DE3 cells greatly improved its solubility. The complex was then purified using immobilized metal affinity chromatography using the Ni-NTA and Co-NTA beads. The elutions were analyzed using SDS-PAGE followed by instant blue staining and western blotting. Our current and future goals include purifying the complex further and testing its catalytic activity using *in vitro* kinase assays.

32. Folding and Uptake Kinetics of Collagen Peptides in Temperature Controlled Drug Delivery to MCF7 Breast Cancer Cells

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Collagen peptides, when folded into triple helix conformation, forms nanoparticles that can be used as drug carriers for cancer drugs. The peptide can be designed such that only in a folded, helix conformation is cellular uptake permitted. The coil-to-helix transition is temperature dependent and can be controlled by the length and sequence of the collagen peptide. While we have previously tested a static model, where lowering the temperature by 12C allows for cellular uptake of the peptide, the dynamic model of prodrug uptake under physiological conditions has not been tested. Here we present a model to mimic an in-vivo-like environment where breast cancer cells (MCF7), are incubated with the peptide in the flow chamber, much like in the bloodstream. A syringe pump is used, producing a continuous flow of growth media containing the collagen peptide carrier modified with fluorescence marker over the cell culture. The flow chamber is placed in a temperature gradient with the flow rate of 0.3 mm/sec, imitating the flow rate of blood through capillaries. Confocal images are used to determine the efficiency of peptide uptake for varying temperatures and flow rates. These data will allow us to predict feasibility of the developed static methodology to dynamic in vivo models, and future clinical applications.

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33. Formation of Chlorinated Disinfection By-Products from Hypochlorite Solution

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Wastewater treatment consists of three main processes: standard initial treatment, primary and secondary treatments that clear overall waste chemicals. Additional treatments use microfiltration, reverse osmosis, and advanced oxidation processes (AOP) to create potable water. Our interest is in

studying the UV-hydrogen peroxide (H_2O_2) AOP where hydroxyl radicals (●OH) are generated from the photolysis process. These radicals have high reactivity, and have the ability to non-selectively oxidize any remaining chemicals in the wastewater. The presence of chloramines (NH_2Cl, $NHCl_2$, NCl_3) in the AOP in addition to excess added hypochlorite to prevent the creation of algae and other microorganisms in the RO membranes will therefore interfere with the AOP chemistry. An unwanted side effect is that the highly energized species made from chloramines and hypochlorite can produce organochlorinated byproducts that cannot be removed by AOPs. As such, we are studying the thermal reactivity of only hypochlorite with amino acids (simulated organic contaminants). Kinetic measurements are performed using stopped-flow kinetics. Second-order rate constants were determined from several amino acids (such as Alanine, Glycine, and Cysteine). 2.5 mM hypochlorite solution is used to react with amino acids ranging from 5 mM to 20 mM with 5 mM increments. Rate constants of these reactions are compared to literature data that was found in relation with this project. Although, these tests have conclude that some form of disinfection by product (DBPs) are created when reacting hypochlorite with amino acids. In the future, we're interested in looking into what these DBPs are and whether or not this can lead to viable cleanup using AOPs.

34. Distribution and Behavior Patterns of Mammalian Carnivores Across an Urban-to-Rural Landscape Gradient

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As land development continues to infringe on natural landscapes, habitat loss and fragmentation have prompted efforts to understand how land development and anthropogenic land use affect wildlife communities. We addressed this issue at a community and behavioral level by asking how the distribution and diurnal-nocturnal activity patterns of mammalian carnivores varies across an urban-to-rural landscape gradient. Using an extensive camera trapping transect to survey mammalian communities across landscapes of varying degrees of disturbance, we can gather presence/absence data to estimate occupancy and co-occurrence of carnivores at and across sampling stations. Furthermore, using the time at which species are detected we can elucidate any behavioral shifts in diurnal-nocturnal activity across the landscape gradient. The study hypothesizes a gradual reduction in complexity for mammalian communities and a shift to nocturnal activity patterns as natural habitats transition into urban areas and human presence becomes prevalent. Preliminary data show that coyotes (*Canis latrans*), striped skunks (*Mephitis mephitis*) and other mesocarnivores occur throughout the landscape gradient; but cryptic carnivores like mountain lions (*Felis concolor)* and bobcats (*Felis rufus*) prevail exclusively in rural landscapes, with the presence of former becoming less apparent as the degree of disturbance increases. A study of this magnitude can convey knowledge necessary to better understand how populations, communities and animal behavior change in response to landscape alterations. It expands on established statistical models of occupancy and co-occurrence patterns that incorporate detection probability and contributes to nationwide efforts by the Urban Wildlife Information Network to study and understand urban wildlife.

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35. Genetic Analysis of HAC1 and MED25 in *Arabidopsis thaliana* Leaf Senescence

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During leaf senescence plants recycle nutrients from older leaves into newer tissues. Recycling of essential nutrients such as nitrogen allows for nutrient conservation and is important for sustainable agriculture. Leaf senescence in *Arabidopsis thaliana* is regulated by changes in gene expression. HAC1 is an enzyme that attaches acetyl groups to histone proteins, allowing for relaxation of chromatin and transcription. Previous research suggests that HAC1 physically interacts with MED25, a subunit of the mediator complex. This interaction brings HAC1 to target genes, resulting in histone acetylation and gene transcription. We are using a genetic approach to determine if HAC1 and MED25 work together to promote leaf senescence. We hypothesize that histone acetylation by HAC1, in concert with the MED25 mediator subunit, contributes to changes in gene expression associated with senescence. Both *hac1* and *med25* mutants show a "staygreen" delayed-senescence phenotype, suggesting that both genes are positive regulators for leaf senescence. DNA isolation from leaves, PCR, and gel electrophoresis were conducted on 19 F_2 plants from a cross between *med25* and *hac1* to identify *med25/hac1* double mutants. A line that was a *med25* homozygous mutant and heterozygous for *hac1* was recovered. F_3 seeds from this plant should contain one quarter *med25/hac1* double mutants. Our purpose is to better understand the relationship between both genes by isolating a *hac1/med25* double mutant and analyzing leaf senescence in WT, single and double mutants. If HAC1 and MED25 work together in the same pathway, the double mutant should have a similar delay in senescence as that of each single mutant. A more severe phenotype in the double mutant would suggest independent roles for HAC1 and MED25. By better understanding leaf senescence, we can reduce the need for nitrogen fertilizer.

36. La-filled & Heavy Element Transition Metal Doped Thermoelectric Skutterudites; $La_{0.2+x/3}Co_{4-x}Ru_xSb_{12}$

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Filled skutterudites have attracted a great deal of interests due to their ability to host various physical properties. They have shown to be promising thermoelectrics (TE), heavy- fermion compounds, and superconductors and also exhibit various phenomena such as metal– insulator transition. Their general formula is A_yBX_3 where B is typically a group eight or group nine transition metal ion and X is a pnictogen, which forms X_4^{4-} polyatomic ions. Accordingly, these materials are placed in the class of zintl phases and are generally expected to obey the electron precise formula [1]. Electronic properties of these materials show strong dependency to their constituent elements along with the electron count scheme. The maximum value of y in the filled variants is equal to 1. Selection of y value is critically important as it simultaneously affects the charge carrier density and the lattice thermal conductivity. Through implementation of high pressure synthesis methods, La-filled $CoSb_3$ base compounds with $y_{max} \sim 0.3$ resulted in an enhanced zT of ~1.06 at 863K largely due to reduced lattice thermal conductivity caused by point-defect phonon scattering [2]. Ideally, a greater La filling fraction should translate to further lowering of the lattice thermal conductivity and thus improving zT. However, due to lack of charge balance compensation, the incorporation of La^{3+} in $CoSb_3$ is restricted, thus emphasizing the importance of electron counting. Here we report on our recent work on heavy

element transition metal doped analogs of the materials. More diffused *d* orbitals of *4d* elements compared to those of *3d* elements along with their stronger spin-orbit coupling is expected to improve the effective mass of charge carriers in favor of enhanced Seebeck coefficient. By selecting $La_{0.2}Co_4Sb_{12}$ as our baseline composition, a new series of compounds namely $La_{0.2+x/3}Co_{4-x}Ru_xSb_{12}$ (x = 0.2, 0.4, 0.6, 0.8, and 1.0) were synthesized via solid-state methods under high-temperature and high-pressure conditions. These compounds were extensively characterized by a combination of powder x-Ray diffraction(PXRD), scanning electron microscopy (SEM), and electron probe microanalysis (EPMA) to confirm phase homogeneity. TE properties of these novel variants were also studied. Interestingly, a very low thermal conductivity was observed for the compound with nominal composition $La_{0.467}Co_{3.2}Ru_{0.8}Sb_{12}$, resulting in a promising zT of ~1.1 at 825K.

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37. Transport of Chemotherapeutic Agent Paclitaxel by ApoE3 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, apo-AII and apoE3, several molecules of lipids, and cholesterol. Amongst these apolipoproteins, apoE3 has the ability to bind lipoprotein receptors that facilitate cellular uptake of lipoproteins via receptor-mediated endocytosis. We propose to use this feature of apoE3 to incorporate hydrophobic chemotherapeutic agents such as paclitaxel (pac) into HDL for eventual uptake into cells. We will test the hypothesis that pac delivered via apoE3-containing HDL nanodiscs is more efficient and specific in cellular uptake in glioblastoma cells than that delivered as such via cremophor, a polyoxyethylated oil. The objectives of the current study are to: (i) overexpress, isolate and purify recombinant human apoE3 bearing the lipoprotein receptor binding N-terminal (NT) domain (residues 1-191) with a His-tag; (ii) prepare reconstituted HDL (rHDL) using synthetic phospholipids and apoE3 NT domain; and, (iii) incorporate pac into rHDL and characterize pac loaded-rHDL. Overexpression of apoE3 NT domain was accomplished using *E. coli* BL21- Gold (DE3) pLysS cells and the protein purified by affinity chromatography using a Nickel Hi-Trap chelating column. SDS-PAGE analysis revealed that the protein was ~ 95% pure. The protein was reconstituted with 1,2-dimyristoyl-*sn*-glycero-3-phosphocholine by sonication at 24 ºC and intermittent vigorous vortexing to form reconstituted HDL (rHDL). The rHDL was separated from lipid-free protein and protein-free lipid vesicles by density gradient ultracentrifugation. Lastly, we employed a fluorescent pac analog, Paclitaxel Oregon Green™ 488 Conjugate (f-pac), which is known to have a fluorescence emission peak at 545nm when dissolved in DMSO. A mixture of pac and f-pac was incubated with rHDL for ~48 h at 4 ºC while rotating. Unbound pac and f-pac were separated from rHDL preparations using Ni-conjugated Dynabeads to capture rHDL bearing His-tag-apoE3 NT domain, and eluting bound protein with 0.5 M imidazole. Fluorescence emission spectra of the eluted samples revealed a peak at 525 nm following excitation at 390 nm. This significantly blue-shifted emission peak compared to emission of f-pac in DMSO suggests that f-pac is located in a highly hydrophobic environment such as that expected in the core of HDL. In control reactions, the pac mixture was treated with buffer, and yielded no major fluorescence emission peak. These preliminary studies suggest that pac was incorporated into rHDL to yield pac/rHDL. Further studies will be pursued to determine the effect of pac delivered via rHDL to glioblastoma cells. Successful

intracellular delivery of pac via rHDL nanodiscs offers a specific mode of entry of chemotherapeutic agents into cancer cells, which have high expression levels of lipoprotein receptors.

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38. Bis-Gold Cavitands: Stabilizing Reactive Intermediates in Alkyne-Coupling Reactions.

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The effect of metallocatalytic cavities, flanked by various aromatic rings on the dimerization of terminal alkynes is studied through comparisons with formerly studied catalysts. Previously, diquinoxaline-spanned resorcin[4]arene provided an adequate cavity for the catalytic event to take place.

The research naturally follows to modify the walls of the cavity; that is, modifying the electronic characteristics inside the cavitand to examine the effects on the coupling reaction of terminal alkynes. It has been observed that using "shorter" walls such as pyrazine, as well as no walls, greatly reduced catalytic activity. Herein, we investigate the addition of 2,3-dichloro-6,7-dimethylquinoxaline walls to the resorcin[4]arene base in order to determine if the hypothesis that increasing the electronic shielding of reactive intermediates can further enhance the efficiency of alkyne-coupling reactions.

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39. Investigating Transcytosis of apolipoprotein AI in bovine aortic endothelial cells

Kyle Meyer, Tina Nguyen, Vasanthy Narayanaswami

Despite the vast amount of literature indicating low plasma levels of high density lipoproteins-cholesterol (HDL-C) as a risk factor for cardiovascular disease (CVD), the last decade has seen a paradigm shift in the concept that the functionality of HDL-C may be much more important than its overall level within the body as a determining factor in CVD. The inverse correlation between plasma HDL-C levels and CVD risk has been questioned by numerous studies showing evidence that neither pharmacological nor genetic intervention to increase HDL-C levels lowered the risk for CVD. Thus, there is a need to understand the role of HDL in CVD from a mechanistic perspective and understand structure-function relationships in HDL. HDL are large lipid-protein complexes with apolipoprotein (apo) AI being an important component and player in cholesterol transport. The overarching goal of this project is to understand HDL transcytosis as it traverses across the endothelial layer lining the arterial intima and to investigate possible structural and functional alterations to the HDL as a consequence of this transcytosis. We tested the hypothesis that apoAI undergoes transcytosis in either the lipid-free or lipid-associated state. To address this issue, bovine aortic endothelial cells (BAOEC) were grown to confluence on Transwell inserts, establishing tight junctions. Recombinant apoAI bearing a hexa-His tag was over-expressed in E. *coli*, and purified by affinity chromatography and size exclusion chromatography. The protein was complexed with 1-palmitoyl-2-oleoyl-*sn*-glycerol-3-phosphocholine by the cholate dialysis method yielding discoidal reconstituted HDL (rHDL) particles.

BAOEC were treated with lipid-free or rHDL-associated apoAI on the apical side (representing the vasculature side) for 18 h. The conditioned medium from the basolateral side (representing the sub-endothelial intima side) was incubated with cobalt-coated Dynabeads to capture apoAI. Lipid-free apoAI appeared on the basolateral side of BAOEC as revealed by Western blot analysis using anti-His tag antibody. Further studies will focus on identifying the precise sites and nature of modification, other protein or lipid components acquired by rHDL during transcytosis through mass spectrometry, as well as alterations in the functional status of the HDL. The long-term goal is to identify direct relationship between structure/composition and changes to the atheroprotective property of HDL as a consequence of transendothelial transport.

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40. Studying the Effects of Ser326 Mutations on p50

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The NF-kB family of transcription factors serves as a master regulator of inflammation and the immune response. Aberrant activity of transcription factor NF-kB is characteristic of many inflammatory diseases, including arthritis, multiple sclerosis, asthma, and other immune diseases. The NF-kB family is of high interest, as a deeper understanding its components will enhance therapeutic efforts. Despite structural insight into DNA binding by NF-kB through X-ray crystallography, it is still not clear how NF-kB binds DNA. Additionally, recent studies suggest that under DNA damaging conditions, the p50 subunit of human NF-kB undergoes phosphorylation at residue Serine-329, altering its DNA binding activity in a sequence dependent manner. To further look at the mechanisms of NF-kB binding to DNA, we used purified NF-kB subunits and *in vitro* biochemical experiments to study the role of p50 phosphorylation in DNA binding. We employed site-directed mutagenesis to introduce a mutation of mouse p50 at Serine-326 to a neutral alanine and phosphomimetic aspartic acid. Expression conditions were empirically optimized, and proteins were purified through nickel affinity chromatography. These mutants will be used in DNA binding assays, which include EMSA and fluorescence anisotropy, to mechanistically determine how p50 phosphorylation alters DNA binding and how the DNA sequence plays a role in this regulation.

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41. Spatiotemporal Establishment of Growing Bacterial Colonies

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Bacterial growth is a complicated process. To understand the key components that control the morphology and dynamics of bacterial growth, we conduct an experiment on the growth of *Escherichia coli* cells on an agar dish. We also construct a minimal, multiscale, three-dimensional computer model to explore various factors in determining the growth laws and patterns. Initially, our minimal model cannot capture the transitioning of colony height from a linear growth regime to another with a much

flatter slope as observed from experiments. Our initial hypothesis was that the observed transition could be replicated by implementing a more complex nutrient profile by including oxygen and modeling aerobic cell growth; also included was a "toxic effect", where acetate, a byproduct of growing cells, accumulates in the colony and inhibits its growth. However, results from the simulation with these models included did not produce the transit of linear regimes as initially hypothesized; a simplified 1D model was developed and gradually increased in complexity to gain insight in the nutrient profile used in the simulation. This 1D model finally helped us to fill in a missing piece of the puzzle, the maintenance uptake of cells that breaks down nutrient source without contributing to growth. Moreover, the accumulation of acetate due to cell maintenance eventually leads to significant slowing down of colony vertical growth, corresponding to the experimental observations.

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42. CHARACTERIZATION OF THE PROTEIN-RNA INTERACTIONS THAT NUCLEATE THE HIV-1 VIRUS ASSEMBLY

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The HIV virus infects roughly 40 million people worldwide; the retrovirus compromises the immune system, paving way for other diseases. While there are treatments for this disease, only about half of the people infected receive it, and a fraction of them also have side effects or reject the treatment, making it ineffective. A better understanding of the molecular mechanisms of different processes during the HIV replication cycle will benefit the development of new anti-viral therapeutics. We are focused on studying how Gag can selectively package the viral dimeric genome. Although there is a large excess of non-viral RNA in the cytosol, more than 90% of the progeny virions contain viral genomic RNA. Gag is a multi-domain polyprotein which includes the Matrix (MA), Capsid (CA), and Nucleocapsid (NC) domains. The NC domain of Gag binds to unpaired or weakly base-paired Guanines on the 5' UTR region of the dimeric RNA genome. We propose that the clustering of Gag proteins on the 5' UTR promotes the formation of Gag hexamers, which will function as the nucleation site to initiate the assembly of the Gag protein shell.

We seek to characterize the different binding sites on the 5' UTR that Gag interacts with, as well as providing evidence that the RNA promotes the formation of Gag hexamers. By using gel shift and ITC we located sixteen binding sits in the core encapsidation signal. Chemical crosslinking and electron microscopy reveals that the gag hexamer was formed when bound to RNA. Our ultimate goal is to solve the structure of the Gag/RNA nucleation complex by cryo-electron microscopy, which will reveal the detailed molecular mechanism for HIV selective genome packaging.

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43. Screening 43 million non-redundant microbial genes for carbohydrate-active enzymes

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Glycoside hydrolases (GHs) produced by microbes are involved in the breakdown of polysaccharides (e.g., cellulose, chitin, starch, xylan) in the environment and are important enzymes for environmental processes and biotechnology (e.g., biofuel, mammal nutrition). These enzymes are often found as single domain GHs (SDGH), secreted by microbes to deconstruct complex substrates outside the cell. GHs are sometimes associated with accessory non-catalytic domains such as carbohydrate binding modules (CBMs) aimed at anchoring catalytic domains (i.e., GHs) to their substrate. These multi-domain GHs (MDGHs) display reduced diffusion and improved catalytic efficiency.

Here, using a custom bioinformatic approach, referred to as the GeneHunt approach, we first reannotated the 7,920 biochemically characterized GHs listed on the carbohydrate active enzyme database to validate our algorithm. Next, we analyzed the 43 million sequences in the M5nr and identified the detailed domain architecture of 322,068 total sequences for GHs. Although variable across GH families, the vast majority of identified sequences (>98% sequences scanned) corresponded to single domain enzymes. Next, we searched for GHs in assembled metagenomes derived from various ecosystems and identified ecosystem-specific GH distributions and multidomain architecture. Finally, we investigated the possibility to screen M5nr-annotated short read metagenomes for GHs.

Globally, we demonstrated that GeneHunt can be used to identify GHs in large sequence datasets. Collectively, this information will help better understand the function of microbial communities across environments and will help identify new interesting proteins for biotechnological applications.

44. Phosphoregulation of Cyclin Dependent Kinase 5 (CDK5)

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Cyclin–dependent kinase 5 (CDK5) is a proline-directed serine/threonine kinase involved in the regulation of cell migration and proliferation. Because of its role in these important cellular processes, dysregulation of CDK5 has been implicated in various diseases such as Type 2 Diabetes, cancer metastasis and neurodegeneration. Previous research in our laboratory has demonstrated that CDK5 can be negatively regulated by phosphorylation at Serine 47 (S47). S47 is a conserved residue present in the cyclin binding region of CDK5 whose phosphorylation inhibits CDK5 binding to its activator p35. This study focused on determining the effect of phosphorylation on another conserved serine residue (S46) that also interfaces with the p35 binding surface. We hypothesized that phosphorylation at S46 will also inactivate CDK5 by inhibiting CDK5-p35 interaction. To test this hypothesis, cell lysates of Cos7 cells co-transfected with p35 and wild type, phosphomimetic (S46D) or non-phosphorylatable (S46A) mutants of CDK5 were immunoprecipitated using an anti-p35 antibody. Western blot analysis of the immunoprecipitates showed that the S46D mutant disrupted binding between CDK5 and p35. Together, these data suggest that phosphorylation of either S46 or S47 is sufficient to inactivate CDK5. Our future studies are focused on determining the effect of S46 phosphorylation on cell migration and proliferation.

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45. Do Changes in Cytosine Methylation Affect *UGT78D1* Expression During Leaf Senescence?

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In plants, senescence is the final stage of leaf development in which nutrients are mobilized from older leaves to new growth and storage organs. 5-methyl cytosine methylation, a form of epigenetic modification, can activate or repress transcription depending on its location. In the promoter region, a decrease in cytosine methylation can parallel activation of transcription. Cytosine methylation is associated with dimethylation of histone 3 at lysine 9 (H3K9me2) in a positive feedback loop. A negative correlation between promoter cytosine methylation and *UGT78D1* gene expression was observed as leaves age in *Arabidopsis thaliana* suggesting *UGT78D1* may be a cytosine methylation regulated-senescence up-regulated gene (CMR-SURG). *ros1-1* (cytosine demethylase) mutants are hypothesized to have increased cytosine methylation and decreased *UGT78D1* expression in comparison to WT. *suvh4* (H3K9me2 methyltransferase) mutants are hypothesized to have decreased cytosine methylation and increased *UGT78D1* expression. Mature *A. thaliana* leaf tissue will be collected at 28d, 35d, 42d, and 49d. Additionally, WT tissue will be collected at T0 (time of bolting) and T12 (12 days after bolting). Genomic DNA will be subject to sodium bisulfite treatment to measure cytosine methylation at the *UGT78D1* promoter. RNA will be isolated to measure *UGT78D1* and *NIT2* (leaf senescence marker) expression by real-time qPCR using *ACT*2 as a reference. Data show an increase in *NIT2* expression ($p=0.019$) and a trend of increased *UGT78D1* expression in WT tissue at T0 and T12. Data at 49d show *ros1-1* has reduced *UGT78D1* expression ($p=0.003$), as predicted. Further data consistent with my hypothesis would support a cause and effect relationship between the loss of promoter cytosine methylation and mRNA induction during leaf senescence.

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46. Probing the Function of Apolipoprotein A-I using Chimera Proteins

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Human apolipoprotein A-I (apoA-I) is a 243 residue, 28 kDa protein that consists of an N-terminal (NT) helix bundle domain and a less structured C-terminal (CT) domain. ApoA-I is the major protein component in high-density lipoprotein (HDL) and is known to play an important role in reverse cholesterol transport promoting the removal of excess cholesterol from peripheral tissues to the liver. The CT domain of apoA-I has a high affinity for phospholipids and initiates lipid binding, whereas the NT domain harbors the site of lecithin-cholesterol acyltransferase activity. A recent study showed that removal of residues 231-243 led to a decrease in lipid binding affinity. Other studies have suggested that segments in the NT domain, residues 1-43 and 44-65, initiate lipid binding. Thus, conflicting data exists regarding the location of high-affinity lipid binding in apoA-I. A chimera protein was recently designed in which the CT domain of apoA-I was attached to insect apolipophorin (apoLp-III). The insect apolipoprotein acquired apoA-I like properties, including high affinity lipid binding. Thus, this

system allows for the identification of apoA-I segments that have a high affinity for lipid surfaces. To identify potential lipid binding regions within apoA-I, three chimeric constructs were designed using *L. migratoria* apoLp-III. Residues 1-43 or 44-65 of apoA-I were attached to the NT of apoLp-III. In addition, residues 231-243 of apoA-I were attached to the CT of apoLp-III. The apoA-I/apoLp-III chimeras were successfully expressed in *E. coli* and purified using an NT poly-histidine tag. SDS-PAGE analysis confirmed that the chimeras were of expected size. Secondary structure of each chimeric protein was analyzed through circular dichroism. The chimeras had α-helical content similar to parent proteins. The exposed hydrophobic surface area of each chimera was analyzed through aninilinonapthalene-8-sulfonic acid fluorescence (ANS). The chimeric protein, apoA-I (44-65)/apoLp-III, showed increased binding sites for ANS, in comparison to apoLp-III. The chimeras apoA-I (1-43)/apoLp-III and apoA-I (44-65)/apoLp-III were able to solubilize phospholipid vesicles at a faster rate in comparison to apoLp-III. The chimeric protein, apoLp-III/apoA-I (231-243) solubilized phospholipid vesicles at a rate comparable to apoLp-III. Overall, the structural properties of the proteins were not affected through the addition of apoA-I segments to apoLp-III. The addition of apoA-I segments 1-43 and 44-65 to apoLp-III led to an increase in solubilization rates enhancing lipid binding. However, no change in the solubilization rate for apoLp-III/apoA-I (231-243) was observed, indicating that the addition of apoA-I segment did not have an effect on lipid binding. This is possibly due to the apoA-I residues 231-243 containing an insufficient number of residues to form an amphipathic α-helix.

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47. Determining the Binding Sites for the WRKY75 Transcription Factor During Leaf Senescence in *Arabidopsis thaliana*

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Leaf senescence is the final stage of leaf development when leaf tissues degrade as a strategy to reallocate nutrients from older leaves to developing structures (i.e. roots, leaves, and inflorescences). This controlled, degradative process is largely influenced by differential gene expression. Genes that exhibit increased expression during leaf senescence are senescence-associated genes (SAGs). Expression of the *WRKY75* gene, encoding a WRKY-family transcription factor, is strongly up-regulated during age-associated leaf senescence and predicted to be a positive regulator. Our previous research show genes related to salicylic acid response are down-regulated during age-associated leaf senescence in *wrky75* mutant plants. Other studies describe WRKY75's involvement in flowering initiation and root development highlighting the range of developmental roles for WRKY75. This study aims to 1. locate WRKY75 binding sites within the Arabidopsis genome to identify a conserved binding region for WRKY75 and 2. find direct targets (WRKY75 bound genes) to provide a set of genes that are likely directly regulated by WRKY75 during senescence. We predict WRKY75 binds to the promoter region of genes that it regulates. To elucidate the direct targets and the functional role of WRKY75, chromatin immunoprecipitation followed by Illumina sequencing (ChIP-seq) will be performed to identify the DNA bound by WRKY75. We have obtained a transgenic line that expresses HA-tagged WRKY75 driven from the WRKY75 promoter. An anti-HA antibody will be used to pull-down genomic DNA regions bound by WRKY75, and these regions will be subject to Illumina sequencing. Identification of WRKY75 gene targets might allow fine tuning of senescence to increase nitrogen recycling and reduce the amount of nitrogen fertilizer in agriculture.

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48. Collagen Peptide Supported Organometallic Catalysts for Dual Transformations

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Collagen-mimetic peptides (CMP) in their folded conformation form nanoparticle-like support for immobilization of metallic and organometallic catalysts. This catalyst immobilization method carries an advantage over other catalyst-supports due to control over the number and localization of the catalytic sites. In particular, different catalysts can be placed in the well-defined spatial arrangement allowing for more than one transformation simultaneously. This arrangement can lead to enhanced catalytic efficiency of multistep catalysis, and prevention of possible interference between reactions that often results in low product yields and purity. We tested this hypothesis by immobilizing two organometallic catalyst: 4-carboxy-1,10-phenanthroline copper (II) complex and arginine palladium complex on a 30AA collagen peptide. The former was immobilized via cysteine residue and the latter via arginine. Additionally, the spacing can be controlled by choosing the position of the residue in the peptide sequence. The catalytic reactions tested, copper-catalyzed oxidative hydroxylation and palladium-catalyzed Suzuki-Miyaura carbon coupling, are carried in green chemistry conditions to emphasize a sustainable industrial process. Circular Dichroism Spectroscopy and Gas Chromatography/Mass Spectrometry are used to optimize peptide modification and efficiency of the catalytic reactions.

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49. Haloalkaliphilic viruses in Searles lake: Do they exist?

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We believe that lytic, extreme haloalkaliphilic viruses are present in Searles Lake. We will test our hypothesis by isolating cells from the lake to obtain pure cultures and then using them as hosts to isolate potential viruses via the top agar plaque assay. Currently, 18 pure cell cultures have been isolated, and our data suggest that the cells exposed to higher levels of peptone and yeast during culturing in the SL2 nutrient medium yield higher cell densities in comparison to their counterparts exposed to lower levels of peptone and yeast in the SL1 culture medium. Future steps include identification of the isolated cells via DNA extraction, PCR, and gene sequencing, and then conducting a top agar plaque assay using filtered water samples from Searles Lake, which will detect the presence of lytic viruses. If lytic viruses are found, we will study their morphology, life cycle, genome, and additionally, we will test their physico-chemical tolerances to pH, salinity, temperature, and desiccation.

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50. Alternative Splicing of Tau Exon 10 in the Developing Mouse Cortex and Hippocampus

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Formation of neurofibrillary tangles (NFTs) is one of the defining neuropathological hallmarks of Alzheimer's disease (AD). NFTs result from aberrant tau proteins, which are encoded by the gene of microtubule associated protein, tau (*Mapt*). Alternative splicing of *Mapt* exon 10 is highly regulated by a variety of splicing factors, producing two MAPT isoforms with three (3R, minus exon 10) or four (4R, plus exon 10) microtubule-binding repeats. For example, splicing factor, suppressor of white-apricot (SFSWAP) and RNA-binding motif protein, X chromosome (RBMX) inhibit the inclusion of *Mapt* exon 10. On the other hand, CUGBP Elav-like family members 3 (CELF3) and 4 (CELF4) promote the exon 10 inclusion. We have previously found that in the developing mouse cortex/hippocampus, mRNA levels of *Sfswap* decrease with age. Thus, we hypothesized that there would be an age-dependent increase in the inclusion of *Mapt* exon 10 in the developing mouse cortex/hippocampus due to down-regulation of *Sfswap*. Aside from looking at *Mapt*, we also expected that *Rbmx* expression would decrease with age while *Clef3* and *Celf4* would display an age-dependent increase in their expression during early development.

To test our hypothesis, we used reverse transcription with polymerase chain reaction (RT-PCR) and quantitative polymerase chain reaction (RT-qPCR) to characterize and measure the expression of total, 3R, and 4R *Mapt* mRNA in the cortex/hippocampus of male and female C57BL/6J mice collected on postnatal day (PN) 0, 7, 14, and 21 (N=8 per sex per age). We first observed that regardless of sex, mice expressed only 3R variant at PN0 and equal amounts of 3R and 4R isoforms at PN7, while only 4R was produced at PN14 and PN21. Next, we used RT-qPCR to quantify relative levels of total and 4R *Mapt* as well as *Rbmx*, *Celf3*, and *Celf4*. While total *Mapt* mRNA levels in the developing mouse cortex/hippocampus showed an age-dependent decrease ($p<0.001$) and were female-biased ($p=0.008$), the ratio of 4R to total *Mapt* increased with age ($p<0.05$). Along with the changes in *Sfswap* expression and *Mapt* exon 10 inclusion, we observed an age-dependent decrease in *Rbmx* and *Celf3* mRNA levels ($p<0.05$), but two elevations in *Celf4* expression at PN7 and PN21 ($p<0.05$). Overall, our data indicate that during early development, the inclusion of *Mapt* exon 10 in the mouse cortex/hippocampus increases with age possibly due to the regulation of differential expression of its upstream splicing regulators, including SFSWAP, RBMX, CELF3, and CELF4.

Keywords: Alternative splicing; Alzheimer's disease; Neural development; Tau

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51. Decoding Molecular Evolutionary Signals in *Barleria*

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Barleria is a genus of approximately 300 species in the family Acanthaceae. Species of *Barleria* are widely distributed across the paleotropics, with variable habit, and vegetative and reproductive morphologies. *Barleria* are typically herbs and shrubs, and can be recognized by three synapomorphies:

four sepals in the calyx, a small inner pair and larger outer pair; double cystoliths in epidermal cells; and globose, honeycombed pollen. Historically, natural groupings within the genus have proven elusive because so many morphological characters that are consistent in other Acanthaceae genera are highly variable in *Barleria*. Previous morphological studies have subdivided the genus into two subgenera and seven sections, but these groupings have come under scrutiny in light of molecular analyses based upon chloroplast loci and the nuclear locus nrITS. The aim of this study is to estimate relationships in the genus through a phylogenetic analysis that samples 180 *Barleria* taxa, representing all sections and the geographic range of the genus, as well as five outgroups from closely related genera *Andrographis*, *Crabbea*, *Lepidagathis*, and *Whitfieldia*. Single nucleotide polymorphism data were generated using restriction-site associated DNA sequencing, a next generation sequencing technique. Loci were assembled *de novo* and used in a maximum likelihood analysis to estimate phylogenetic trees. Our results support the monophyly of *Barleria* and more broadly inform our understanding of diversity and evolution in one of the largest genera in Acanthaceae.

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52. Abstract not available

53. Comparative leaf anatomy in selected species from major lineages of Acanthaeae

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Acanthaceae is a tropical and subtropical plant family with approximately 4000 species, but relatively few anatomical studies have been attempted on these plants. The family includes lineages such as Acantheae, Barlerieae, Justicieae, and Ruellieae. The objective of this study is to investigate whether leaf anatomy characteristics are a potential synapomorphy for the genus *Barleria*, a genus of interest in our lab. We collected fresh leaf tissue from the Huntington Library Botanic Gardens and plants grown in the CSU Long Beach greenhouses. We preserved the leaves in a solution of formalin, propionic acid, and alcohol. Then we embedded the tissue in paraplast and sectioned the leaf transversely on a microtome. Sections were mounted on slides and stained with tannic acid, iron alum, safranin and orange G, that selectively stain for cellular components. We compared a total of 52 sectioned leaves from eight *Barleria* species and 44 species representing the other major lineages in the family. Acanthaceae leaves consist of a midvein, two distinct layers of mesophyll, known as the spongy mesophyll and palisade parenchyma. We found that in 34 Acanthaceae species the palisade parenchyma continues across the midvein region, whereas in 6/8 *Barleria* species sampled and 6/8 Acantheae species sampled, the palisade parenchyma is interrupted by the midvein. We also found that 7/23 Justiceae species sampled had interrupted palisade parenchyma. Crystals of calcium carbonate called cystoliths were found across the leaf tissue, in various orientations, and were especially prevalent in Justiceae. Cystoliths were absent or reduced in 6/8 Acantheae species sampled. We found that interrupted palisade parenchyma cells and cystoliths lacking were common traits in Acantheae and *Barleria*, yet these lineages are not thought to be closely related. Future studies that incorporate additional sampling from these lineages will allow us to understand how often this anatomy evolved and if it has a functional role. This work was supported by an award to Ms. Do from the Bennett and Peggy Kayser Field Research Award.

54. Comparison of Feeding Morphology between Urban and Rural Coyote Populations

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Humans are capable of drastically changing their environment within a relatively short time frame, turning vast landscapes into bustling cities. Few organisms can adapt quickly enough to survive this drastic change, forcing many species to evacuate human territory or risk extinction. Those who remain in urban environments will subsidize their natural food source with anthropogenic food since an animal's typical food source may not be readily available. A species with populations living in both urban and rural settings may exhibit different facial adaptations due to selective pressures from food diversity, availability, and the acquisition difficulty. This study focuses on comparing the skull morphology and bite force of the coyote urban population located in the Greater Los Angeles with the rural population found in Fresno County. Specimens had their upper jaw length and width, lower jaw lever lengths, and mastication muscle masses recorded to calculate an upper jaw length/width ratio and bite force at the large molar and canine for each specimen. Based on current findings there appears to be not significant difference between the skull morphology of urban and rural coyote populations.

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55. Tree Water Relations Across an Urban Temperature Gradient

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Temperatures in Portland, Oregon are significantly higher than in surrounding areas, and are likely to continue to increase in the near future. There is a lack of information on the health of the urban canopy but evidence of increased tree mortality rates is mounting. Water status of three of Oregon's native species was studied across an urban temperature/exposure gradient. Ground based measurements were performed, including leaf water potential and percent loss in hydraulic conductivity. Clear and consistent patterns of increasing water stress were found, correlating with an increase in temperature and exposure across all species and sites.

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56. Effects of Mammalian Aposematic Pattern and Contrast Variation on Predator Avoidance Learning

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Aposematic coloration makes prey defenses easier for predators to learn and remember, reducing mistaken attacks. Coyotes (*Canis latrans*) are potential predators of the striped skunk (*Mephitis mephitis*) but are highly vulnerable to the latter's noxious defenses. To determine how contrast intensity and pattern structure influence avoidance learning in canid predators, we initially conditioned captive coyotes to attack brown benign baited prey models and subsequently presented them with noxious spraying prey models that vary in pattern structure and contrast intensity. Differences in the latency to attack the novel spraying models are compared with respect to the contrast intensity and pattern

structure of the model. Past research shows that coyotes can easily learn to avoid attacking black and white prey models and can generalize this avoidance to models with more white (high contrast) but not to models with more black (low or no contrast). Preliminary findings suggest that coyote subjects demonstrate greater latency to attack all black and white (maximum contrast) models, regardless of pattern structure, compared to the black and gray (minimal contrast) model. Our next steps will entail installing camera traps at sites along a transect and observing avoidance learning in wild coyotes in response to prey models that vary in color contrast intensity and pattern structure.

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57. Pollination of the rare plant, *Clinopodium chandleri*

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There are many rare plants around the world that are in need of conservation. In order to conserve them however, they have to be researched first in order 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 mountain chaparrals in Orange, Riverside, and San Diego counties. Little to no research has been done into the pollination of *C. chandleri*, therefore putting this plant at risk if its populations further decline. Pollinator studies of other plants that have been done, however. Some studies have shown that the most abundant pollinators are not always the most efficient. Less abundant native pollinators have been shown to lead to a higher seed set than their more abundant relatives. Pollinators may also be excluded due to morphological constraints of the plant. Plants in the legume family, for example, have a lever mechanism that must be tripped in order to reach the nectar rewards. The lever excludes pollinators that are unable to produce sufficient force to trip the lever. Flower size may also play a role in pollinator exclusion if the flowers are too small for larger pollinators. For this research, we hypothesize that native pollinators will be more efficient than the abundant and ever present honey bee. We plan to study seed set and make observations at Cleveland National Forest during the spring season of 2019 to gain an understanding of its specific pollinators. We will also begin testing forces required to open the flower of *C. chandleri* and forces that can be generated by pollinators in late 2018. These studies will undoubtedly give valuable insight into the reproduction of *C. chandleri* that can be in turn used for its conservation.

This project is supported in part by RISE

58. Abstract not available

59. Investigating the relationship between locomotion and cross-sectional bone geometry between aquatic and terrestrial salamanders

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Bones have different roles throughout the skeleton that allow animals to move through their environment. Scientist have had historical interest on how tetrapods evolved to move onto land almost 375 million years ago, but behavior is difficult to preserve in the fossil record. Alternatively, living salamanders are a common model for early tetrapod's due to their morphological similarities.

Examining the relationship between bones and locomotion in living animals can help us build a model to infer the locomotor capabilities of extinct species from fossilized bones. Quantifying the locomotion of living salamanders with different ecologies can help us model different stages along the evolutionary transition from water to land, providing new insights into the different physical demands that may have affected how walking evolved. To determine how bone morphology relates to locomotor capabilities and ecology, we integrated tools from engineering and biomedical imaging to compare the internal anatomy of the limb bones between salamanders ranging from fully aquatic (e.g., *Necturus lewisi*) to primarily terrestrial (e.g., *Ambystoma tigrinum*). First, cross-sectional area was calculated as a proxy for bone density. Second, we quantified the second moment of area and polar moment of area to estimate the ability of limb bones to resist different physical demands (e.g., bending and twisting) that could lead to bone fractures while walking on land. Differences observed between aquatic salamanders (e.g., *Necturus lewisi*) and terrestrial salamanders (e.g., *Ambystoma tigrinum*) could help resolve how ecology relates to bone mechanics. The second moment of area (resistance to bending) is predicted to be greater in *Ambystoma tigrinum* compared to *Necturus lewisi* in order to better resist gravitational forces on land and accommodate the different roles that the humerus plays on land (digging, amplexus, walking). Bone strength will be greater in *Necturus lewisi* than *Ambystoma tigrinum* when comparing cross-sectional area of the humerus due to aquatic animals having denser bones. Findings from this work will serve as a valuable blueprint to breathe new life into fossils and reconstruct how vertebrates, like us, became terrestrial.

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60. 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 (wt) male and female mouse pups as well as testicular feminization mutation (Tfm) males, lacking functional AR, at postnatal days 21-24 (n=8 for wtm, n=7 for wtf and n=6 for Tfm). The brains were post-fixed in 4% paraformaldehyde, sectioned, and stained with cresyl violet. After cover-slipping, measurement of thickness and area size of pyramidal cell layers in the CA1 and CA3, and granular cell layer in the DG of the hippocampus were taken under a light microscope using ImageJ. We found that the area size, not thickness, of the CA1 in wt males was smaller than wt females, and Tfm males had a similar CA1 pyramidal cell area of wt females. Additionally, in the CA3, wt males showed larger thickness and area size of the pyramidal cell layer than wt females and Tfm males while no difference was observed between Tfm and wt female animals. In contrast, none of those stereological measurements in the DG was different among the

three groups of mice. Overall, our preliminary data support our hypothesis, suggesting the essential role of the AR in mediating the effect of perinatal androgens on CA1 and CA3 pyramidal cell morphology of mice during development.

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61. Analyzing Interactions between the 18-Wheeler Gene and X-chromosome Linked Genes in Salivary Gland Development

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The *18-wheeler* gene found in *Drosophila melanogaster* directs epithelial cell migration during embryonic development. Previous work has demonstrated that homozygous *18-wheeler* mutant embryo express abnormal salivary glands. Drosophila salivary glands are an excellent model for mammalian organ development because their development is similar to our own. 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 with18-wheeler will produce 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 both 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 mated with females heterozygous for an X-linked deficiency. Their other X-chromosome is a GFP-expressing "balancer". Control embryos are obtained by using males that are wild type at the 18-wheeler locus, but still carry the GFP salivary gland reporter (stock 15-1). Embryos are collected, fixed, and subjected to immunocytochemistry to detect GFP, which is expressed in the salivary glands of the 18-wheeler; Df(1) embryos. If the mutations interact, salivary gland morphogenesis will be abnormal. Defects include, but are not limited to, glands lengthening, shortening, or migrating asymmetrically. Df(1)BSC719 (stock 26571) shows a gene interaction, but not in the manner predicted. When crossed to the 18-wheeler mutant, wild type glands are observed, but when crossed to wild type 18-wheeler, the glands possess morphological difference in migration pattern and development. This suggests that the deficiency causes a defect in gland morphogenesis that is rescued by reducing the dosage of the 18-Wheeler protein. Further work will examine the genes within Df(1)BSC719. Df(1)ED7374 (stock 8954) shows a genetic interaction. Heterozygous embryos for the deficiency and mutant *18-wheeler* expresses abnormalities in migration and morphology. The homozygous 18-wheeler wildtype and heterozygous for deficiency express wildtype glands. From these results we can conclude in this deficiency there may be candidate gene(s) interacting with *18-wheeler*. Current work focuses on using smaller deficiencies that map within Df(1)BSC719 and Df(1)ED7374 to further define the location of the gene(s) that interact with 18-wheeler during salivary gland morphogenesis.

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62. Gold Cavitands: Regioselective Ring Closing of Alkyne Acids

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Gold cavitand usage and diversity in the transformations of small molecules have piqued the interest of our lab. Our gold cavitands in particular have varying wall sizes creating a sort of pocket in which we introduced monosubstituted alkyne acids of varying sizes to see whether or not a 5 or 6 membered cyclization occurred. Various analogs of alkyne acids were synthesized each with different R-group attachments to the end of the alkyne chain (ex. methyl, ethyl, and propyl groups). Upon introduction and reaction to the cavitand at room temperature and with heat, we anticipated some variation in the reactivity and cyclization patterns and we very much saw that. Each of the substrates cyclized, but they favored different products. For example, the substrate with a methyl R-group favored a 1:1 conversion of 5-membered and 6-membered rings. Conversely, the substrate with the propyl attachment favored 5-membered cyclization 9:1. These results were unexpected and were indicative of not only the size of the interior pocket but also which cyclization pattern is favored in general. To understand the nature of our gold cavitand, we will expand the collection of R-group substrates by varying the size and length of the analogs.

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63. Abstract not available

64. Regioselective Ring Closing of Aromatic Alkynes and the Influence of Gold Cavitands

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Gold cavitands have some features resembling enzymes and can therefore facilitate catalysis. They have been of great interest in our lab as we investigate their applications in molecular transformations. The experiments we have designed test the cavitand's functionality, focusing on ring closing reactions with aromatic terminal alkynes. We can test special features of our gold cavitands by comparing them directly to the simple salt AuCl. We hypothesize that the substrate can both enter and cyclize intramolecularly using the terminal alkyne functional group. Furthermore, upon influence of the cavitand, the substrate can either close into a 5-membered or 6-membered ring. We also anticipate the cavitand can cyclize substrates that otherwise would not transform using AuCl alone. To date, 5 analogs of the substrate have been synthesized and tested using the gold cavitands. We have found the cavitand favors 6-membered rings for a majority of the substrates and cyclization occurs faster and more cleanly than with the simple AuCl salt. The results of these experiments can provide a gold mine of information, with further understanding of the capabilities and limitations of the cavitands as they are applied to catalysis.

This project is supported by RISE (LR) (NIH 2R25GM071638-09A1), NSF (MPS) (RUI CHE-1708937) 6/1/2017 - 5/31/2020, NMR instruments on NSF (MPS) (MRI CHE-1337559)

65. Identification of Multi-Activity Proteins from the Environment for Improved Biomass Degradation

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The growing worldwide demand for energy and to the predicted limitations of fossil fuel motivate the development of alternative energy sources. In this context, biofuels derived from plant biomass could be produced using agricultural residues and cultivation of energy crops. However, the conversion of biomass into useable fuel requires the development of improved enzymatic systems such as Carbohydrate Active enZymes (CAZymes) to break down polysaccharides into fermentable sugars. The incomplete biomass deconstruction by individual enzymes reflects the complexity of this process and highlights the need for multiple catalysts acting synergistically to completely degrade linear (e.g., cellulose), branched (e.g., starch), and substituted (e.g., xylan) polysaccharides, and prevent the inhibition by the product, among others. In this context, multi-activity proteins (MAPs), combining several catalytic domains, display increased synergistic interaction amongst associated domains and thus represent an interesting alternative to complex mixtures of enzymes. Here, we used the GeneHunt algorithm developed in the Bioinformatics Lab, to identify MAPs for polysaccharide deconstruction in publicly accessible sequence datasets. Five proteins, namely RJ1.2, RJ3, RJ5, RJ7, and RJ8, were then selected for biochemical analysis based on predicted activities. The corresponding DNA sequences engineered, optimized for production in *E. coli*, synthesized, and cloned into the pET151 plasmid for heterologous expression. Finally, we tested, the recombinant proteins on the chromogenic substrate (e.g., AZCL-Xylan). Among others, three and four proteins (out of five) displayed the expected xylanase and cellulase activities, respectively.

Globally, as shown here, combining the GeneHunt approach with the synthetic biology and recombinant protein expression system provides a new way to identify new enzymes for biotechnological applications.

66. Quantifying extracellular tachyzoite survival and invasion-capability under a wide range of environmental conditions in the human parasite, *Toxoplasma gondii*.

Emmanuel Cuevas, Haley Gause, Viviana Valencia, Alyssa Gimenez, Dr. Douglas Pace

Toxoplasma gondii is an obligate intracellular parasite whose acute stages of infection occur during the tachyzoite stage. Despite this important life stage, quantitative measures of tachyzoite survivability have not been undertaken with respect to different extracellular ionic conditions, temperature, and time in the extracellular stage. The present study examined the survivability of two different strains of *T. gondii* with differences in virulence: PRU (less virulent) and RH (more virulent). Survivability in conditions that mimicked serum, gastric juices, and seawater were assessed using three different techniques: 1) Giemsa staining to determine invasion efficiency, 2) plaque assays, and 3) the use of a Live/Dead fluorescent staining technique. For all conditions, the more virulent RH strain had more robust survival and invasion capability relative to the less virulent PRU strain. Focusing on RH strain results, Live/Dead fluorescent staining revealed that extracellular tachyzoites had 17% survivorship for up to 48 hours in serum-like conditions. However, the fraction that were invasion-capable, as determined using invasion and plaque assays, was much less at ~6%. Quantification of survival and invasion ability in gastric conditions demonstrated that while most parasites could not survive the acidity of such extracellular conditions, a small, but significant, fraction (~ 1%) did survive for up to 30 minutes and was subsequently able to invade host cells when returned to serum-like conditions.

Interestingly, tachyzoites also demonstrated survivability even under seawater conditions. While under seawater conditions, parasites lost motility, but still could elevate their conoid invasion machinery. Tachyzoites incubated for 6 hours in full strength seawater (34 ppt) at 16˚C could survive (Live/Dead staining = 56%) and subsequently invaded human host cells (invasion and plaque assays = 6%). This suggests that significant parasite dissemination to other major organs via the host cardiovascular system may be accomplished during the extracellular tachyzoite stage. Overall, Live/Dead fluorescent staining over-estimated the number of cells that could engage in *in vitro* host cell invasion and replication. This study demonstrates a coordinated method for determining tachyzoite survival and can be used for testing phenotypic outcomes of genetically modified parasites. Biologically, this study further demonstrates the robustness of the extracellular parasite to stressful conditions and time outside of a host cell.

67. Abstract not available

68. Structural and Functional Analysis of Apolipoprotein E3/apoE4 Heteromer

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Apolipoprotein E (apoE) is a 299 residue, exchangeable apolipoprotein that has essential roles in cholesterol homeostasis and reverse cholesterol transport. In humans, the *APOE* gene is polymorphic with 3 common alleles, ε2 ε3 and ε4, occurring in frequencies of 8, 77 and 15%, respectively in the population. Heterozygotes expressing both apoE3 (C112) and apoE4 (R112) isoforms represent the highest population of ε4 carriers, an allele highly associated with Alzheimer's disease. ApoE is a two-domain protein with the C-terminal (CT) domain mediating protein self-association to form dimers and tetramers via helix-helix interactions. The objective of this study is to determine if apoE3 and apoE4 can hybridize to form a heteromer in lipid-free state. Refolding an equimolar mixture of His-tagged apoE3 and FLAG-tagged apoE4 (or vice versa) followed by co-immunoprecipitation and immunoblotting indicated formation of apoE3/apoE4 heteromers. Forster resonance energy transfer (FRET) between donor fluorophore on one isoform and acceptor on the other, both located in the respective CT domains, revealed a distance of separation of ~ 40 Å between the donor/acceptor pair. Similarly, a quencher placed on one was able to mediate significant quenching of fluorescence emission on the other, indicative of spatial proximity within collisional distance between the two. The α-helical content apoE3/apoE4 heteromer was comparable to that of the parent proteins. ApoE3/apoE4 heteromer association was also noted in lipid-associated state in reconstituted lipoprotein particles. The possibility of heteromerization of apoE3/apoE4 bears implications in the physiological behavior of these isoforms.

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69. The Effect of GIV Depletion on ATF6 Processing During Endoplasmic Reticulum Stress

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The endoplasmic reticulum (ER) is an organelle that plays a role in many important cellular functions including post-translational modification and folding of secretory and membrane proteins. Various pathophysiological conditions that result in disruption of ER function such as cancer,

neurodegeneration and type II diabetes can trigger ER stress. Upon facing ER stress, the cell activates an evolutionarily conserved signaling program called the Unfolded Protein Response (UPR) that aids in re-establishing normal ER functions. Our laboratory has recently identified that Gα-Interacting vesicle associated protein (GIV) plays a role in promoting cell survival during ER stress by activating the AKT pathway. This project focused on the role of GIV in the UPR, specifically focusing on one of the UPR sensors called the Activating Transcription Factor 6 (ATF6). We treated control and GIV-depleted HeLa cell lines expressing FLAG-tagged ATF6 construct with ER stressor dithiothreitol to test the effect of GIV depletion on ATF6 processing. Our western blotting analysis showed that GIV depleted cells express ~2X higher level of ATF6 as compared to control cells. These cells also showed a higher level of ATF6 processing resulting in the release of the active N-terminal fragment of ATF6 from the rest of the protein. Our current and future goals include determining the molecular mechanism by which GIV negatively regulates ATF6 levels and processing during ER stress.

70. Deciphering the Molecular Connection between Flowering Time and Age-Dependent Leaf Senescence in *Arabidopsis thaliana*

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In plants, the vegetative to reproductive growth phase transition precedes age-dependent leaf senescence. Understanding the timing of this phase transition and its molecular connection to leaf senescence is agriculturally important. During leaf senescence, nitrogen and other macromolecules are recycled from leaf sinks and relocated to reproductive organs. In many species, these reproductive organs, such as the fruits and seeds, are harvested for human consumption. Homozygous *Arabidopsis trithorax* (*ATX)* triple T-DNA insertion mutants (*atx1/atx3/atx4*) display significantly early flowering coupled to significantly accelerated leaf senescence. A BrAD-seq (RNA-seq) time-course experiment highlighted 228 genes with differential expression (DEGs) in flowering *atx* triple mutants relative to vegetative wildtype plants of the same age. We hypothesize that some of these DEGs, which change expression soon after the transition to reproductive growth, are signaling the onset of leaf senescence. Twenty-one genes from this list contain predicted regulatory domains. T-DNA insertion mutants for each gene were isolated to screen for mutations that uncouple flowering and leaf senescence. Flowering time and above-ground fresh weight along with *NIT2* expression and chlorophyll concentration are being analyzed in a time course experiment to characterize leaf senescence phenotypes in single mutants. We aim to identify mutants that display leaf senescence that is uncoupled from flowering. Preliminary data from the candidate screen shows four transcription factor single mutants that display uncoupled flowering and senescence phenotypes. Currently, data support the hypothesis that there are flowering-time specific gene expression changes of senescence-related genes, and further study of regulatory gene candidates may elucidate the molecular connection between flowering and age-dependent leaf senescence.

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71. Effects of Indole Glucosinolate Metabolic Pathway during Developmental Leaf Senescence in *Arabidopsis thaliana*

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Leaf senescence is the ultimate stage of leaf development in which nutrients are recycled and reallocated to newly developing organs. In a previous study, gene ontology analysis revealed an enrichment for the indole glucosinolate (IG) biosynthesis biological process among Senescence-Upregulated Genes (SURGs), which suggests IGs influence senescence. Indole glucosinolates (IG) are secondary metabolites present in the Brassicaceae plant family, and which possess protective properties against herbivory and fungal infections. We have shown that inhibition of IG synthesis at the beginning of the pathway results in premature senescence, however blocking this portion of the pathway can lead to loss of other metabolites as well. Recent data demonstrated that an IG transport double mutant *pen1/pen3* exhibited premature leaf senescence implicating the IG metabolites as playing a protective role.

This study hypothesizes that IGs play a protective role preventing premature leaf senescence. Furthermore, we intend to identify the IG metabolites that play this protective role. The IG biosynthetic pathway will be investigated through mutant lines for biosynthesis gene families *CYP81F* and *IGMT*, transport genes *PEN1* and *PEN3*, myrosinase gene *PEN2*, glutathione transferase gene *GSTU13*, regulatory genes *MYB51* and *MYC2*, and signaling gene *MPK3*. The progression of senescence will be analyzed in homozygous mutant plants, and compared to *Arabidopsis thaliana* wild-type (WT) plants. Relative SURG expression and leaf chlorophyll content show *pen1/pen3* as the only mutant exhibiting premature leaf senescence. It is likely that redundancy in these gene families may compensate for single gene mutations, thus preventing premature senescence.

The quantification of the IG leaf content in double mutant *pen1/pen3* and single mutants, *pen1* and *pen3,* and WT was performed by our collaborators at University of Florida. The single mutants do not display early senescence, and thus IG metabolites missing or reduced in the double mutants, but not in the single mutants, will be of interest. The results demonstrated a significant increase in two downstream metabolites in *pen3* and *pen1/pen3* while only the *pen1/pen3* double mutant shows a decrease in one upstream metabolite. The accumulation of upstream combined with the reduction of downstream IG metabolites may result in accelerated senescence. Currently, the *pen1/pen3/sid2* triple mutant is being analyzed to determine whether premature senescence is dependent on the plant hormone, salicylic acid.

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72. Abstract not available

73. Functional Analysis of Three TIR-NBS-LRR Genes in the Regulation in Leaf Senescence in *Arabidopsis thaliana*

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The molecular events of leaf senescence can be studied through genetic analysis. Different observed phenotypes can reflect specific biological processes, which can be attributed to certain mutant genes. The TIR-NBS-LRR (TNL) gene family encodes disease resistance proteins with an estimation of 149 TNL genes in the *Arabidopsis thaliana* genome. It was previously noted that expression of three TNL genes from the H family, AT1G63860, AT4G14370, and AT4G11170, are up-regulated during leaf senescence, suggesting they play an important role in leaf senescence regulation. T-DNA insertion mutants that disrupted each of the three genes were isolated. The single mutants display no obvious changes in senescence. We hypothesize that the TNL-H genes compensate for one another, and that a triple mutant may show altered leaf senescence. An experiment will be carried out by producing triple mutants, then the quantification of senescence-associated gene expression by real-time qPCR and chlorophyll loss will be performed to determine if there is a significance difference in leaf senescence among single, double, and triple mutants. Double mutants have been isolated and crossed together to produce the triple mutant. Determining whether TNL proteins contribute to the regulation of leaf senescence can help decipher the complex pathways that signal leaf senescence in *Arabidopsis thaliana*.

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74. Synthesis and Characterization of Esters of Fmoc-Amino Acids as Potential Butyrylcholinesterase Inhibitors

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Neurodegenerative diseases such as Alzheimer's disease (AD) is the sixth leading cause of death in the United States and affects 5.7 million Americans. While cures for this disease have not yet been discovered, several pharmaceuticals are available to alleviate symptoms. These compounds typically target the enzymes acetylcholinesterase (AChE) and butyrylcholinesterase (BChE). Specifically, for individuals with AD it has been found that while AChE activity is slightly decreased or unaffected, BChE activity is increased. The increased BChE activity leads to a depletion of the neurotransmitter acetylcholine, and this depletion is implicated in the progression of dementia. Thus, inhibitors of BChE are sought in the treatment of AD. We previously found Fmoc-amino acids selectively inhibit BChE, leading to a potential new class of cholinesterase inhibitors. While the role of the amino acid side chain was explored, the effects of modifying the carboxylate group were not investigated. Specifically, the enzyme binds the cationic substrate acetylcholine, but the Fmoc-amino acids are anionic. We postulated Fmoc-amino acid esters may be more potent inhibitors, as the ester ablates the negative charge. In addition, the ester allows incorporation of substituents that increase van der Waals interactions that may interact favorably with the enzyme. To test this model, a series of Fmoc-amino acids were esterified using an alcohol and EEDQ (*N*-Ethoxycarbonyl-2-ethoxy-1,2-dihydroquinoline), purified by chromatography, and characterized by NMR and HPLC. The solubility and inhibition properties for the Fmoc-containing esters were evaluated using UV-Vis spectroscopy. Kinetic studies

suggest the Fmoc-Leu-esters are more potent inhibitors compared to the Fmoc-Leu-O^- but are limited by solubility. We are now investigating additional Fmoc-amino acid esters bearing cationic groups to enhance solubility such as lysine, and our initial results suggest the lysine-based compounds are potent BChE inhibitors. Overall, the results may guide the design of new Fmoc-containing compounds that specifically and effectively inhibit BChE.

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75. Phenotypic Analysis of Three Negative Regulators of Leaf Senescence: WRKY54, WRKY70 & WRKY58 in *Arabidopsis thaliana*.

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Leaf senescence is a degradation process in which the nutrients from older leaves are recycled and remobilized to the reproductive organs of the plant. The visible manifestation of leaf senescence is when the green leaves turn yellow/brown due to chlorophyll degradation. In the model plant organism, *Arabidopsis thaliana*, a network of transcription factors (TF), many of them members of the *WRKY* family, play key roles in regulating leaf senescence. It has been previously shown that WRKY70 and its close homolog, WRKY54, function as negative regulators of leaf senescence. The double mutant *wrky54/wrky70* shows a faster rate of senescence compared to WT and single mutants. Our lab showed that single *wrky58* mutants senesced at a faster rate than WT, suggesting that WRKY58 is a negative regulator of leaf senescence. Based on our lab's previous work, we hypothesize that although the mechanisms used by these TF's to slow down senescence are not identical, they may have overlapping properties. As such, triple mutants would be expected to show a greater acceleration in leaf senescence as compared to single and double mutants. The additive effect of these three *WRKY* transcription genes will be tested by analyzing the senescence phenotypes of wild type, double and triple mutants. The mutants were identified through PCR analysis of genomic DNA. I am currently measuring the expression of senescence up-regulated genes and chlorophyll levels. If the WRKY TFs are additive, the triple mutants will show a faster rate of senescence than double and wild type plants. Preliminary data suggest a more complicated relationship among the three TFs.

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76. Progesterone receptor-Src family kinase signaling mediates neuroprogesterone induction of the luteinizing hormone surge

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In the female rat, estradiol positive feedback is mediated by astrocyte-neuronal interactions. Estrogen positive feedback is regulated by astrocyte-neuronal interactions in the rostral periventricular region of the third ventricle (RP3V). Estradiol upregulates progesterone receptors (PGR) in RP3V kisspeptin (kiss1) neurons and induces neuroprogesterone (neuroP) synthesis in hypothalamic astrocytes. This

neuroP acts to augment RP3V kiss1 expression and stimulate kisspeptin release to trigger the luteinizing hormone (LH) surge. In vitro, PGR signals via Src in mHypo51A.cultured neurons that are a model for RP3V kiss1 neurons. Therefore, we tested the hypothesis that neuroP induction of the LH surge is mediated by PGR-Src signaling. In Experiment I, ovariectomized (OVX)/adrenalectomized (ADX) rats primed with 2μg of estradiol benzoate (EB) received two sequential infusions into the RP3V. The first infusion was either DMSO or the Src antagonist (PP2, 50 nmol; Tocris) 51.5 hours after EB, followed by a Src agonist (Src Family Activator, 50 nmol; Santa Cruz Biotechnology) or DMSO 4.5 hours later. Two hours later, the rats were anesthetized, then trunk blood and brains were collected. Animals infused with Src Family Activator demonstrated significantly increased serum LH compared to DMSO controls, and PP2 inhibited the increase of serum LH by Src Family Activator. In Experiment II, OVX/ADX animals were primed with 50μg EB, inducing neuroP, which triggers the LH surge. For three consecutive days, PP2 (50 nmol) was injected into the DBB to inhibit Src activity, which blocked the LH surge. In Experiment III, we established that PGR and Src are co-localized in the RP3V using immunohistochemistry in oil or estradiol-treated (EB, 2μg) OVX. Estradiol upregulated the number of cells expressing either PGR or Src in the RP3V compared to oil controls. PGR and Src co-expression was also increased by estradiol. In Experiment IV, we demonstrated that PGR and Src are in close proximity in the plasma membrane using Duolink Proximity Ligation Assay. Taken together, these results indicate that PGR and Src are colocalized in the RP3V, and neuroP may be activating a membrane associated PGR-Src complex to trigger the LH surge as predicted from in vitro experiments.

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77. Nitrogen Mobilization by DUR3, AAT1, and PTR3 Transporters During Leaf Senescence in *Arabidopsis thaliana.*

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During the final stages of leaf development, plants undergo the process of leaf senescence a nutrient recycling event in which nitrogen and other nutrients are reallocated to other plant tissues to promote growth. Previous data have shown that transporters such PTR3, AAT1, and DUR3, which function in transporting dipeptides, amino acids, and urea respectively, underwent an increase in mRNA abundance in Arabidopsis thaliana plants during leaf senescence. Creating triple T-DNA insertion mutants of the three transporters will cause the genes coding the PTR3, AAT1, and DUR3 transporters to become non-functional and stop the synthesis of these transporters. With non-functional nitrogen transporters, mutant plant lines will be tested to determine if there is a decrease in nitrogen mobilization and an increase in Rubisco retention during senescence. Rubisco is a highly-abundant leaf protein that is the major source of mobilized nitrogen. Immunoblotting techniques will be used to quantify Rubisco levels during senescence in each genotype: single, double, and triple mutants. Triple T-DNA insertion mutants will be produced by crossing single mutants of each gene to create heterozygous F_1 plants. F_1 plants will self-fertilize to create the F_2 generation of which 1/16 will be a double mutant. Double mutants from the F_2 generation will be crossed together to obtain the triple T-DNA insertion mutant. Currently, I am collecting F_2 seeds for double mutant isolation.

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78. Dopamine receptor D1 in close proximity with progesterone receptor and Src kinase mediates progesterone signaling in the arcuate nucleus of the hypothalamus

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Progesterone facilitation of sexual receptivity (lordosis) in ovariectomized (OVX) rats requires classical progesterone receptors (PGR). PGR are found in the arcuate nucleus of the hypothalamus (ARH) and are upregulated by estradiol benzoate (EB) priming. Progesterone infused into the ARH region of EB-primed OVX rats facilitates lordosis within 30 minutes. The rapid action of progesterone is mediated by extranuclear PGR (PGR-B) that appear to directly inhibit ARH β-endorphin (β-END) neuronal transmission to induce lordosis. PGR-B complexes with and signals through Src family kinase (Src) to rapidly facilitate lordosis. This PGR-Src signaling is interdependent with the dopamine receptor (D1/D5) signaling; blocking either PGR, Src, or D1 activity blocks the ability of the other two to facilitate lordosis. Using immunohistochemistry, we demonstrated that PGR, Src, and D1 are all expresses in ARH β-END neurons. Co-immunoprecipitation experiments revealed that PGR-B and Src form complexes in membrane fractions of ARH tissue. However, D1/D5 was not shown to form complexes with either Src or PGR. Thus, we tested the hypothesis that D1 is in close proximity to the PGR and Src in ARH using Duolink In Situ Fluorescence (Sigma Aldrich) technique. This technique labels two proteins in close proximity by linking together two host specific antibodies, and nuclei were counterstained with DAPI. OVX Long Evans rats were treated with EB (2μg) or oil, and 30 hours later were fixed and perfused with chilled saline followed by 4% paraformaldehyde. Initially, free floating sections taken through ARH probed for PGR and Src (cell signaling) as positive control for Duolink staining. Next, we tested whether D1 and Src were in close proximity. Duolink analysis showed that D1 and Src are in close proximity as indicated by speckled immunopositive staining located on the membrane of a subpopulation of ARH neurons. Our results suggest that D1 may not be complexed to PGR or Src, but is in close proximity to Src, which allows for the interdependence of PGR, Src, and D1 signaling in the ARH that facilitates lordosis.

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79. C1q increases 25-hydroxycholesterol in macrophages during atherosclerosis

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Heart disease is the leading cause of death in the USA today. A major contributor is atherosclerosis, which is characterized by chronic inflammation and the build up of fatty deposits and cholesterol-saturated foam cells in arterial walls. Recent studies suggest that innate immune protein C1q plays a

protective role in early stages of atherosclerosis. C1q directly binds and opsonizes targets including modified low-density lipoproteins (so-called "bad cholesterol") leading to improved macrophage foam cell phagocytosis, survival, and efflux. We have preliminary data that one of the mechanisms by which C1q promotes macrophage survival is via activation of Liver X Receptor signaling. Several oxysterols are known to activate LXR. C1q is investigated here for its possible role in modulating oxysterol levels in murine bone marrow derived macrophages (BMDM) under conditions of high cholesterol. Levels of oxysterols were measured in BMDM from C1q-sufficient and C1q-deficient atherosclerosis-prone (LDLR knockout) mice that were fed a high fat diet *in vivo* using mass spectrometry. Data showed that the BMDM from C1q sufficient LDLR-/- had significantly higher levels of 25-hydroxycholesterol compared to C1q deficient LDLR-/- BMDM. To investigate the mechanism, mRNA levels of cholesterol modifying enzyme cholesterol 25-hydroxylase were investigated by QPCR in these same BMDM as well as in BMDM from wild-type (C1q-sufficient) and C1q-deficient mice that were administered oxidized LDL *in vitro* in the presence or absence of C1q. Levels of CH25H were increased in C1q sufficient BMDM compared to those from C1q-deficient mice under high fat conditions. The addition of exogenous C1q also increased CH25H levels in wild-type macrophages. The presented data support the protective role of C1q in decelerating atherosclerosis by upregulating the macrophage production of oxysterol 25-hydroxycholesterol, a known activator of LXR.

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80. Proton Coupled Electron Transport Reaction Through Soft Interface

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In this project, a soft interface is formed by two immiscible electrolyte solutions, comparable to cell membranes. This can be used as a proton pump to speed up the rate of proton coupled electron transfer reactions. We are interested particularly in studying the rate of PCET reactions that occur between the two solutions with the presence of simple cofactors and coenzymes that are known for transporting protons and electrons in a biological setting. We estimate the rate of PCET reactions by impedance spectroscopy by measuring the resistance of the electrochemical cell. Through this research we hope to gain a better understanding of performing PCET reactions in an artificial cell in laboratory conditions. Such information could prove invaluable in designing new biochemical energy storage options in the future. What has been discovered thus far is the effects of different pH levels on the rate of PCET reactions is significant due to the higher concentration of protons at lower pH values. We have also been exploring the effects of different coenzymes like CoenzymeQ10, 2,4-Dinitrophenol, and Quinone on the rate of PCET reactions. The results are still inconclusive, and further experiments are planned to ascertain the relationships these coenzymes might have on the rate of our PCET reactions in our electrochemical cell. In the future we would like to work with enzymes and other proton shuttling compounds that could prove even more efficient than what we have currently been testing.

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81. Abstract not available

82. Recombinant C1q variants do not activate the Classical Pathway, but modulate phagocytosis and cytokine production in phagocytes

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C1q plays a dual role in a number of inflammatory diseases such as atherosclerosis. While in later stages Classical Complement Pathway (CCP) activation by C1q exacerbates disease progression, C1q was demonstrated to also play a beneficial role in early disease. Independent of its role in complement activation, we and others have identified a number of potentially beneficial interactions of C1q with phagocytes *in vitro*, including triggering phagocytosis of cellular and molecular debris and polarizing macrophages toward an anti-inflammatory phenotype. These interactions may also be important in preventing autoimmunity. Here, we characterize variants of recombinant human C1q (rC1q) which no longer initiate complement activation, through mutation of the C1r/C1s binding site. For insight into the structural location of the site of C1q that is important for interaction with phagocytes, we investigated the effect of these mutations on phagocytosis and macrophage polarization, as compared to wild-type C1q. Phagocytosis of antibody coated sheep erythrocytes and oxidized LDL was measured in human monocytes that had interacted with rC1q wild-type or variants. Secreted levels of cytokines were also measured in C1q stimulated human monocyte-derived macrophages (HMDM). All variants of C1q increased phagocytosis in human monocytes compared to controls, similar to native or wild-type rC1q. In addition, levels of certain pro-inflammatory cytokines and chemokines secreted by HMDM were reduced in cells that interacted with C1q variants, similar to wild-type rC1q and native C1q. This includes downregulation of IL-1b, TNFa, MIP-1a, and IL-12p40 by native and rC1q in both resting and M1-polarized HMDM. This suggests that the site responsible for C1q interaction with phagocytes is independent of the C1r/C1s binding site. Further studies with these CCP-null variants of C1q should provide greater understanding of the complement-independent role of C1q, and allow for potential therapeutic exploitation.

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83. Oxidative Modification of Apolipoprotein E3 by Myeloperoxidase

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High density lipoproteins (HDL) are large spherical anti-atherogenic complexes composed of ~ 70 different proteins and ~ 200 different types of lipids. A major class of proteins on HDL are apolipoproteins (apo) such as apoAI, apoAII, apoE, which are exchangeable proteins with an ability to exist in lipid-free and lipid-associated state. In lipid associated state, these proteins, along with amphipathic lipids such as phospholipids encompass a core of non-polar lipids. HDL plays a critical role in reverse cholesterol transport from macrophages to liver for eventual disposal, a process that earned its popular designation as the "good cholesterol." In addition, it also bears anti-inflammatory, antithrombotic, and antioxidant properties. However, there are naturally occurring oxidative processes that could impair HDL function; one such process is oxidation mediated by myeloperoxidase (MPO),

an enzyme expressed by granulocytes to mediate antimicrobial activity. In the current study we hypothesized that MPO mediated oxidative modification impairs the structure and function of apoE3. The specific objectives are to: (i) prepare purified recombinant apoE3, (ii) modify purified apoE3 by MPO, and (iii) confirm modification by Western blot and mass spectrometry. Recombinant apoE3 bearing a His-tag at the N-terminal end was overexpressed, isolated and purified by affinity chromatography from *E. coli*. Purified apoE3 was modified by MPO buffered in sodium acetate solution (pH=6.0) with the addition of pentetic acid (DTPA) and hydrogen peroxide. SDS-PAGE analysis under reducing conditions revealed the presence of bands at ~ 36 and 72 kDa, corresponding to monomeric and dimeric species, respectively, suggesting possible formation of a covalently cross-linked species. In-gel digestion of the monomeric and dimeric band was performed using trypsin followed by tandem Matrix-Assisted Laser Desorption/Ionization- Time of Flight (MALDI-TOF) mass spectrometry (MS). MS data revealed modification of Tyr 74 in the monomeric band and Tyr 162 in the dimeric band to 3-chlorotyrosine. Further studies are required to determine the effect of MPO modification on the secondary structure and tertiary fold of apoE3 by circular dichroism and fluorescence spectroscopy respectively, and to identify potential functional alterations to apoE in terms of lipid binding activity, cholesterol efflux ability, and LDL receptor binding activity. The findings from this study will aid in understanding the role of MPO in rendering the HDL dysfunctional and identifying factors that reduce the anti-atherogenic properties of HDL.

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84. The OFQ/N-ORL-1 System Mediates Rapid Facilitation of Lordosis by Estradiol Activating Plasma Membrane G Protein-Coupled Estrogen Receptor-1 (GPER) in ARH

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In the arcuate nucleus of the hypothalamus (ARH), the sequential activation estrogen receptor-α (ERα) followed approximately 48 hours later by G protein-coupled estrogen receptor-1 (GPER; aka GPR30) activation facilitates sexual receptivity (lordosis) in ovariectomized (OVX) rats. The initial actions of estradiol include priming lordosis circuits and inhibiting lordosis by activating ARH β-endorphin (β-END) neurons that project to the medial preoptic nucleus (MPN). β-END neurotransmission, in turn, activate MPN μ-opioid receptors (MOP) producing inhibition of lordosis. ARH infusion of non-esterified 17β-estradiol (E2) 47.5 hours after 17β-estradiol benzoate (2 μg EB) priming facilitates lordosis rapidly within 30 minutes through the deactivation of MPN MOP. Previous results from our laboratory demonstrated that like E2, the selective estrogen receptor modulators (SERMs), ICI 182,780 (ICI) and tamoxifen (TAM), facilitate lordosis via activation of GPER in EB primed rats that deactivates MPN MOP. Using cell fractionation techniques and western blot, we demonstrated that GPER are expressed both in plasma membrane and cytosolic ARH fractions (Feri et al 2016). However, it appears that plasma membrane associated GPER mediates E2 effects. Previously, we showed that membrane impermeable estradiol (17β-estradiol conjugated to biotin; E-biotin) infused into the ARH of EB primed rats facilitated lordosis within 30 minutes. However, we did not confirm that the E-biotin was reducing β-END neurotransmission. Therefore, we tested the hypothesis that E-biotin rapidly facilitate lordosis via membrane GPER through the OFQ/N-ORL-1 system and reduces β-END neurotransmission as measured by a reduction in MPN MOP activity. ARH infusion of E-biotin ARH 47.5 hours after EB priming, facilitated lordosis within 30 minutes and significantly reduced MPN MOP activation as measured by MOP immunoreactive intensity staining. Pretreatment of UFP-101, an ORL-1 selective antagonist, or G-15, GPER selective

antagonist, blocked the facilitation of lordosis and deactivation of MPN MOP by ARH infusion of E-Biotin. These data indicate that membrane GPER mediates the E2 facilitation of lordosis by activating OFQ/N neurotransmission, which inhibits β-END neurotransmission to reduce MPN MOP activation. Multiple ER pathways are activated sequentially over time to facilitate sexual receptivity. Understanding the location, and timing and type of ER signaling pathway(s) that are activated to regulate reproduction is important for enhancing SERM therapies for women's health.

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85. Proteomics Analysis of Sexual Dimorphism in the Developing Mouse Amygdala and Hypothalamus

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One of the most important factors responsible for brain sexual differentiation is testosterone secreted by the developing testes. During late gestation and on the day of birth, testosterone and its metabolites cause male brains to develop differently, which is mediated by androgen receptors (AR), and after aromatization to 17β-estradiol, by estrogen receptors. However, the molecular mechanisms downstream to sex steroid hormones and their receptors to control the sexual dimorphic development remain unclear. The hypothalamus is the brain region implicated in regulation of various sexually dimorphic reproductive, parental, and aggressive behaviors, and it contains abundant AR. The aim of the present study was to identify the androgen-regulated sexually dimorphic proteins in the developing mouse hypothalamus using proteomic approach. First, we observed male mice androgen receptor protein expression slightly higher than female in hypothalamus but contrary in amygdala. We further explored the whole Proteome profiling with a total four 2D gels of the amygdala and the hypothalamus proteins from wild-type male, wild-type female, and Tfm mice. The overall protein spot patterns on these gels were similar, but more than five spots showed differential expression among the groups. Some of spots showed male-biased and female-biased changes. One protein spot was selected for in-gel digestion, mass spec, and bioinformatics analysis. From mass spec results, shown myelin basic protein (MBP) was identified with three unique peptides and 100% protein sequence confidence. We further confirm this results by immunoblotting assay in hypothalamus and showing the same expression trend with mass spec results.

MBP is a cationic protein of 169 amino acids that plays a critical role in the process of myelination in the nervous system. The myelin sheath functions as an insulator to greatly increase the velocity of axonal impulse conduction. MBP maintains the correct structure of myelin sheath by interacting with the lipids in the myelin membrane.

Our data suggested the AR-dependent regulation of MBP expression might be critical for sexual differentiation of the hypothalamus through myelination.

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86. How Various Sources of High Fat Diets Affect *Drosophila melanogaster's* Developmental Timing and Lifespan

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Approximately two-thirds of the adult population in the United States is considered to be either overweight or obese, meaning that around two-thirds of adults are likely to suffer from obesity-related illnesses such as diabetes, atherosclerosis, heart disease, high blood pressure and sleep disorders. Many of these diseases are common and preventable causes of death in the United States. Obesity and its related illnesses continue to increase in the United States.

Drosophila melanogaster was used in this study as a model organism to examine the effects a high fat diet has at physiological and molecular levels over multiple generations. *Drosophila melanogaster* is an ideal model organism to study the effects of obesity due to its ease of breeding and maintenance, easily trackable developmental stages, and short lifespan. The *Drosophila melanogaster's* short lifespan makes it an ideal organism for multigenerational studies, allowing us to monitor the developmental effects of a high-fat diet on the resulting offspring.

We hypothesize that *Drosophila melanogaster* raised on various types of high fat diets will become obese which will cause upregulation of genes involved in lipid metabolism and will also overall have a shorter lifespan than flies raised on control food. We also hypothesized that differences in developmental timing will be observed. Two different sources of fat were used, coconut oil and vegetable shortening. Physiologically, the lifespan and lipid storage of *D. melanogaster* third instar larvae were observed. Molecularly, expression of the intestinal lipase gene, *magro (mag)*, was studied. Our initial results indicate that there is a difference in the amount of lipid stored over multiple generations based on the Triglyceride Assay. As for *magro,* despite the increasing trend showing a difference in gene expression, the differences between larvae raised on control and vegetable shortening were not statistically significant. We are currently investigating how the different sources of fat affect the timing of larval development to pupation and eclosion, which is known to be sensitive to nutrient levels. Our results indicate that a high fat diet does affect the lifespan of *Drosophila melanogaster.*

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87. The Urbanization of Diatoms Along the Santa Ana River

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Water is fundamental for Earth's biological processes and the existence of human life. The impact of humans' land usage due to urbanization, however, can have a significant effect on surrounding water quality. Scientists have conducted many studies on how urbanization affects water quality and in several countries, research has been conducted relating water quality to the bioindicative usage of diatoms. Studies, such as the ones done in Beijing, China, Melbourne, Australia and Portland, Oregon, correlate assemblages of diatom species to elements found in water samples- specific conductivity, pH, salinity, and temperature, in particular. Diatoms are photosynthetic algae and serve as excellent

bioindicators of their surroundings due to their ability to absorb and recycle nutrients in the ecosystem. In relation to the aforementioned studies, we hypothesized that there would be a significant change in diatom species moving along the Santa Ana River in California from an urban-to-rural gradient. Prior research has shown that certain diatom species are tolerant to specific levels of pollution. Data, obtained from the CEDEN database, was collected for 20 sites along the river and analyzed through multivariate statistical tests. We concluded that there was a staggering difference in water chemistry between sites characterized as urban and rural. This difference also resulted in diatom species assemblages unique to each respective site. For example, *Nitzschia palea* is known to be very tolerant of high levels of pollution; unsurprisingly, it was found more abundantly in our urban sites as compared to the rural locations along the Santa Ana River. Using our knowledge of diatoms and their assemblage diversity in urbanized areas, we will be able to assess the health of water in other regions as well. Possible studies to conduct could include relating our findings to other bodies of freshwater found in Southern California, such as sites found along the Los Angeles and San Gabriel Rivers.

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88. Effects of Micro-plastics 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 micro-plastic debris in aquatic environments. Micro-plastics are an abundant source of pollution that may pose a threat to marine ecosystem. Micro-plastics 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 experiment, we tested whether micro-plastics 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 micro-plastics: control - no particles; low - 25 particles/300mL; high - 66 particles/300mL; very high – 315 particles/300mL. The higher levels of micro-plastics (high and very high) reduced feeding rates of larvae over a 14-day period. However, exposure to a low level of micro-plastics significantly increased feeding rates compared to the control. Future studies will be needed to understand why a small increase in micro-plastic stimulated feeding. Overall, these results suggest that presence of micro-plastics in coastal water may have harmful effects on larvae by reducing their feeding efficiency and subsequent growth.

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89. Quantifying the Effect of Larval Culturing Density on Morphology and Physiology of the Echinoid Echinoderm, *Dendraster excentricus*

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Echinoderms are unique model organisms with many biomedical research applications such as cell-fate mapping, studying molecular regulation of development, and eco-toxicology studies related to water quality. However, interpretations of experimental variables can be confounded by the culture

conditions used to rear embryos and larvae. The objective of this study was to quantify the potential effect of larval culture density on a number of morphological and physiological variables. To accomplish this, we cultured larvae of the common sand dollar, *Dendraster excentricus* at the following larval densities: 0.1, 0.25, 0.5, and 1.0 larvae/mL (i.e., ranges that are achievable in typical culturing conditions). Larvae were reared in triplicate vessels for each density at 16℃ and fed *Rhodomonas* algae at 10,000 cells/mL. Morphological measurements were made using ImageJ at 7 and 11 days post-fertilization (DPF) and included post-oral arm length, midline body length, stomach length, and stomach width. Physiological rates of algal feeding and protein biomass growth were also determined. No effect of larval density was observed for all morphological variables (ANOVA, $P > 0.05$). All larvae were observed to have significant rudiment development as well, suggesting no noticeable overall effect on developmental rates. Preliminary analysis suggests that rates of feeding and protein biomass growth were likewise similar between all treatments. Larvae at 11 DPF had a protein biomass of 2,360 (+/- 181) ng/larva (average; +/- SD). These results will aid future biomedical studies utilizing echinoderm larvae by minimizing extraneous sources of variance emerging from inappropriate husbandry and culturing conditions.

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90. Correlated Evolution of Antlers and Tusks in Ungulates

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Tusks are mostly seen on smaller ungulates and used primarily as sexual weapons in battles over territory, whereas larger ungulates lack tusks but instead possess antlers or horns, used as a visual display of social status. Two genera of deer have both antlers and tusks: *Muntiacus* and *Elaphodus*. In muntjacs, all fights are preceded by a "dominance display", typically performed by the dominant male, resulting with the subordinate male's withdrawal. 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 examine the correlation between antlers and tusks in relation to overall body size and other ecological factors. We hypothesized: (1) that as body size increases, then relative size of tusks will decrease, and the relative length of antlers will increase, and (2) transitioning into more open habitats and evolving larger body sizes made dominance signaling more efficient than tusk-based combat. Antler and tusk measurements from 39 cervid species was collected from four museums and from the literature and subjected to allometric and comparative phylogenetic analyses. With body size, we found positive allometric relationships with antler size and isometric relationships with tusk size. Results also suggest as the species move from closed to open habitats, from solitary to group living lifestyles, and from small to large body sizes there is a significant trend of tusk size decrease and antler size increase. This study demonstrates the selective forces that led to the transition between primitive small solitary tusked deer and the large social/polygynous antlered deer that dominate today.

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91. The Mouse Gut System is Home to Many Structurally and Functionally Distinct Microbial Communities

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The community of microbes (i.e., microbiome) in the gut of mammals, including humans, affects the physiology of its host. Frequently, feces are used as a proxy to describe the microbes in the gut however, the "gut" is composed of multiple distinct ecosystems (e.g., stomach, small intestine) with various environmental parameters (e.g., pH, salt composition and concentration). This compartmentalization of the gastrointestinal tract might influence the structure (what lineages are present) and functions (e.g., what Carbohydrate-Active enZYmes – aka CAZYmes - are detected) of the microbiomes. In this context, we hypothesized that using only fecal microbiota may limit the understanding of gut functioning. To address this limitation, we collected the digesta in the stomach, small intestine, cecum, and the large intestine, of 5 mice. Next, the microbial DNA was extracted, sequenced, and analyzed using custom bioinformatic approaches. Finally, we investigated the variation in the structure and the function (CAZYmes) of the sequenced microbiomes.

Both the structure and the function of the sampled microbial communities varied extensively. First, regarding the structure, microbial communities in the stomach were highly variable and diverse whereas within the small/large intestine, and in the cecum, microbiomes were different and displayed reduced variability. This likely reflects the variation in DNA from the microbial community and the food in the stomach and some well-established, more conserved, microbiomes in the other parts of the gut. Second, regarding CAZYmes, samples from the stomach and the large intestine were variable and diverse. Next, in the small intestine and in the cecum, we identified conserved high frequency of many CAZymes including glycoside hydrolase (GHs) 106 in small intestine and GH42 in the cecum, respectively. Finally, we tested the correlation between structural and functional changes across microbial communities and identified a high correlation between structural and functional variations in the stomach, large intestine, and cecum. This suggests that in these communities structure and function are strongly connected because similar communities tend to have the same functions whereas distinct communities have distinct functions. However, the exact CAZyme composition is unlikely to be essential for the selection of the lineages within these environments as functionally distinct communities were observed herein. In the small intestine, the CAZyme-rich microbial communities, although being highly conserved, displayed a relatively high functional variability suggesting that closely related lineages with abundant and variable sets of CAZyme-genes are being selected. Together these findings highlight how microbial communities are assemble in the gut and support the polysaccharide deconstruction, an essential function of the digestive system.

92. Open-source Devices for Biological, Chemical, and Engineering Applications

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Commercial and custom-built instruments play an essential role in most laboratories and experimental investigations, such as for data acquisition and process control. However, these instruments are typically built for specific tasks, unable to modify for one's specific or unique purposes. This is especially the case for commercial instruments, whose patents do not allow users to customize the

programming or configuration for their specific intents and tasks. For custom-built instruments, and even standard high-quality equipment, the major issue is the high cost that by default excludes less affluent institutions and their experimental abilities. With recent advances in open-source electronics and 3D printing technology, the technical barrier and cost for custom-built instruments have been significantly reduced. This has presented new opportunities for the new generation of scientists and engineers in both academia and industry. Open-source hardware allows for the creation of products driven by capitalism and not monopolies, and the opportunity for companies and individual to learn and improve from one another. Using a combination of programming languages, open-source technologies, and 3D printed parts, we will design and construct six different instruments used commonly in biology, chemistry, and engineering, including pH meter, viscometer, spectrophotometer, water level controller, water flow controller, and gel electrophoresis chamber. We will test our open-source hardware and compare their performance with that of their commercial counterparts. With our model of building the instruments, we hope to give students the tools to learn how to do more with the instruments they work with than just pressing a button on a specialized machine, and to provide them with training with practical knowledge and skills in this area of growing importance.

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93. Abstract not available

94. Reactivity of Monochloramine with Amino Acids Under Wastewater Conditions

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The Orange County Water District (OCWD) 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). During the final AOP polishing step, the water undergoes exposure to an irradiation (UV light) in the presence of strong oxidizing agents (e.g. H2O2) which destroys the remaining organic compounds that were not removed in the previous steps. However, the efficiency of the AOP depends on the chemicals present in the wastewater at that stage. One particular problem are the disinfectant chloramines that are generated by adding bleach to the wastewater train to prevent membrane biofouling. This is usually performed before the microfiltration step, by adding bleach, which reacts with the natural ammonia present to produce a mixture of monochloramine (NH2Cl), dichloramine (NHCl2) and trichloramine (NCl3). Although chloramines are beneficial, they can also react with organic matter present in the wastewater to give chlorinated disinfection byproducts (DBP's). These toxic and hazardous chemicals are highly regulated, and as such, understanding their formation chemistry is essential. The focus of this project is to determine the temperature-dependent rate constants of NH2Cl's reactivity with a set of amino acids at pH 12 in different concentrations. Amino acids were selected as prototypical organic matter, and this basic pH was used to ensure that fully deprotonated nitrogen atom centers occurred. These reactions were monitored through the decay of the NH2Cl absorbance peak at 242 nm in a UV-Vis spectrophotometer. From the changes in the decay rate of monochloramine with different amino acid

concentrations, second-order rate constants for these reaction kinetics were obtained at different temperatures. By attempting to construct reactivity-structure relationships for these reactions, we can better understand this chemistry.

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95. Assessing the Stability of *tert*-Butyl Carbonate (Boc) and *tert*-Butyl (*t*-Butyl) as Protecting Groups for Flourinated Phenols Under Solid Phase Peptide Synthesis Conditions: Model Studies for the Incorporation of Fluoro-substituted Tyrosines in Peptides and Proteins

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While the importance of enzymes in biological function is well known, our understanding of the energetics of enzymatic catalysis and comparison to the corresponding non-enzymatic reactions remains limited. Generally, enzyme residues suggested as important for catalysis are mutated via site-directed mutagenesis and the effect the mutation on activity is measured. However, the chemical diversity of the naturally occurring amino acids limits our ability to introduce the systematic changes necessary for quantitively evaluating enzyme energetics. Incorporation of unnatural amino acids (UNAAs) in enzymes allows us to overcome this limitation and introduce multiple systematic perturbations. Recently, in a study to evaluate the energetics of hydrogen bonds in an enzyme active site, a series of fluorotyrosines were used to perturb pK_a value for a tyrosine hydrogen bond donor in the oxyanion hole of ketosteroid isomerase. Yet methods used to incorporate the unnatural amino acid limited the set of fluorotyrosines used. To combat this issue, we are currently exploring methodologies to introduce fluorotyrosines in enzymes using *tert*-butyl carbonate (Boc) and *tert*-butyl (*t*-butyl) protecting groups. These protecting groups are often used in peptide synthesis, but their use to incorporate a series of fluoro-substituted tyrosines in peptides has not been reported. We are first using a series of fluorophenols as model compounds to evaluate the effect fluoro substituents on protecting group stability. A series of protected phenols were synthesized, and our results show that *t*-butyl protected 2-fluorophenol was stable under 4-methylpiperidine (4mp) in dicholoromethane (DCM), while Boc protected 2-fluorophenol was not. Regarding the tetrafluorophenols, the Boc protected and *t*-butyl protected 2,3,5,6-tetrafluorophenols were both deprotected under this condition. On the other hand, both protecting groups, regardless of which compound they protected, were removed when subjected to trifluoroacetic acid in DCM. Our results suggest *t*-butyl and Boc may be useful in generating fluorotyrosine containing peptides for use in biochemical studies.

96. Electrical Stimulation of Myoblasts for Muscle Repair Applications

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Certain victims of trauma-induced skeletal muscle injuries experience volumetric muscle loss (VML), in which large amounts of tissue are damaged and consequent permanent reduction in functionality of damaged tissue results; innate repair mechanisms are successfully limited to smaller wounds and not those resulting from VML injuries. The purpose of this study is to investigate the effect of electrical pulse stimulation on the proliferation and differentiation of a mouse muscle cell line. Over a set amount of time and using both a control group and an experimental group, this study analyzed the relative proliferation and differentiation of C2C12 myoblasts seeded on treated, 8-well plates

containing growth medium. Our preliminary fluorescent staining results suggest the application of electrical pulses via a C-Pace EP multi-channel stimulator increased both the proliferation and differentiation of C2C12s. Future experiments will include qPCR analysis and additional immunostaining characterization. Results from this work will help design new therapeutic systems for muscle repair.

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97. CRITICAL TEMPERATURE OF SUPERCONDUCTING-MAGNETIC HYBRID SYSTEMS

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We study proximity systems made of coupled thin films with superconducting and magnetic ground states. We study the change of the superconducting critical temperature T_c when varying the parameters of the magnetic component. Singlet Cooper pairs formed in the superconducting layer permeate through the magnetic layer resulting in the generation of triplet pair correlations that modify the T_c of the system. The critical temperature is calculated by solving Usadel's equations using an involved transformation to an eigenvalue problem. In previous work of the group, we investigated the behavior of T_c for a homogeneous ferromagnet. We generalize the method to include various inhomogeneities of the magnetic component. In particular, we present the critical temperature behavior as a function of the ferromagnet's thickness and the magnetization twisting angle of a trilayer of the type SF_1F_2 where F_1 and F_2 have different magnetic properties.

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98. Localization of Laplacian Eigenfunctions

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Localization of eigenfunctions for a Dirichlet Laplacian had not been noted in previous studies, this is believed to be caused by the boundary conditions imposed on the fractal structure of the Koch Snowflake. A Laplacian is applied to graph approximations of the Koch Snowflake. Graph approximations and visualizations of the Koch Snowflake and its corresponding eigenfunctions are generated using Python programming and symbolic algebraic algebraic software. Numerical approximations indicate a form of localization of the Laplacian eigenfunctions at high energies consistent with *whispering gallery modes*.

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99. Measuring the Degree of Optical Limiting of Metallophthalocyanine Thin Films

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Phthalocyanines and their metal complexes have been shown to demonstrate optical limiting, a process by which increases in light intensity incident on the material, past a certain point, do not result in a proportional increase in transmitted light intensity. Phthalocyanines are known to exhibit a third order optical nonlinearity, making them excellent candidates for use in practical optical limiters, shielding sensitive equipment and human eyes from dangerous light levels. While much work has been done on this subject, relatively little has been done on phthalocyanine thin films, and none has been done to quantify the effects of structural characteristics such as film thickness or grain size on the optical limiting phenomenon. This project seeks to determine what effect changes in the physical structure of these thin films have on the degree of optical limiting. To this end, a laser of beam of varied intensity is fired through a phthalocyanine thin film, and the incident and transmitted light levels are measured to observe changes in the absorptivity of the film as incident light increases. Preliminary results have shown the experimental setup to be viable, producing consistent measurements across many trials. Additionally, an unexpected decrease, rather than increase, in the absorptivity of the film at high incident intensities was observed, indicating an as yet unknown effect that is overwhelming the optical liming properties of the sample. This phenomenon, in addition to the effects of changes in film structure, will be studied further.

100. Fabrication of Nanosphere Monolayers with Langmuir Blodgett Method

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Nanospheres have various applications in multiple disciplines, ranging from the medical sciences to environmental engineering. The Langmuir Blodgett method was used to create nanosphere monolayers. Samples were created on a silicon substrate using a Langmuir Blodgett trough and polystyrene nanospheres. Altering processing conditions produced samples of greater quality. A decreased surface pressure, as well as slower compression and dipper arm speed, resulted in more comprehensive nanosphere layers. Through experimentation and variable manipulation, the quality of the nanosphere samples improved as evident by the optical microscope images. Thus, understanding of the Langmuir Blodgett technique and fabrication of nanosphere monolayers was achieved.

This project was also completed through McNair Scholars Program at California State University, Long Beach (P217A170271), which is funded by the U.S. Department of Education.

101. Structurally Induced Magnetic Transition

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Manganese phthalocyanine (MnPc) thin films were fabricated on both insulating and metallic substrates at different deposition temperatures ranging from 32°C to 260°C using thermal evaporation. Two crystals are found, one set shows the MnPc (200) peak ranging from 6.732° to 7.004° position corresponding to a lattice constant of a ranging from 2.302 nm to 2.395 nm. The second set of thin film samples deposited at 230°C and 260°C, has a MnPc (001) peak 2θ peak at 7.12° consistent with MnPc in the β – phase and a lattice constant corresponding to c = 1.133 nm. The structural change is

accompanied by changes in the magnetism. The magnetic properties of all MnPc thin films are characterized with the vibrating sample magnetometer. The temperature-dependent static susceptibility shows a large increase at low temperatures for samples deposited at high temperatures, similarly the low-temperature magnetic hysteresis loops have a large saturation magnetization for the same set of samples. The net magnetization almost disappears for the low-temperature sample set. This is characteristic for a magnetic transition with the parameter being the crystalline order of the material.

This project is supported by the CSULB Graduate Research Fellowship, the ORSP Summer Student Research Assistantship.

102. Design and Build an Apparatus for Nanoparticle Self-Assembly at Air/Water Interface

Miguel Bugayong[1], Norberto Gallegos[1], Alex Beach[1], Fangyuan Tian[2], Ph.D., Jiyeong Gu[1], Ph.D., Chuhee Kwon[1], Ph.D.
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[2] Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA

We design and build an apparatus to form nanostructures by simply using the properties of the nanoparticles self-assembling and the interface in which the assembly occurs. We investigated the process of self-assembly and Brownian motion using an optical microscope, but this setup has space limitations and restrictions. We are designing an apparatus to monitor *in situ* the self-assembly and nanosphere film deposition processes in a realistic setting. The new apparatus using a monocular, CCD camera, lenses, metal posts, and clamps can reach about ½ of the magnification of the x500 optical microscope. We will present our current observations and progress. Further improvements are being developed, including the inclusion of O-rings to confine the nanospheres, temperature controlled bath, and other additions to help stabilize the observing apparatus. Our results so far show that the current apparatus has the ability to observe nanoparticles despite the on-going Brownian motion. When the apparatus is optimized, the self-assembly process at air/water interface will be studied with a goal to produce high quality nanostructured films.

This project is supported by the CSULB Small Faculty Grant.

103. Fabrication of Close-Packed Polystyrene Nanospheres by Spin Coating

Victor De La Cruz, Dr. Jiyeong Gu, Ph.D.
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A large area, monolayer of close-packed nanospheres can be used as a template to produce nanocomposites with interesting magnetic properties. Spin coating was used to create the densely packed monolayers of nanospheres of 400 nm in diameter. To maximize the area of uniformly deposited monolayer of nanospheres fabricated by spin coating, various parameters, such as spin speed, spin duration, and substrate size, need to be adjusted. After a systematic study of samples made at various conditions, a recipe has been narrowed down to two critical parameters, spin speed and nanosphere concentration. The chosen parameters yield 1 cm by 1 cm samples that are 90% covered with nanospheres of which some parts are monolayer. Future samples will be made by changing the concentration of the nanospheres in the solution to continue optimizing the monolayer spread. Some of the samples were sputter coated with Permalloy to examine and characterize the magnetic properties using an alternating gradient magnetometer, a vibrating sample magnetometer, and through the magneto-optical Kerr effect. Preliminary magnetic data with these thin films will be discussed.

This project is supported in part by Small Faculty Grant 2018-2019 from College of Natural Sciences and Mathematics.

104. Neutron Star: Equations of State and Phase Transitions

Marc Salinas, Thomas Klaehn, Ph.D., Prashanth Jaikumar, Ph.D., and Wei Wei, Ph.D.
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Neutron stars are among the densest objects in the universe. The uncertainty of the internal structure of these stars have led to different ideas for modeling the core of these stars. In order to solve for the structure of the star, the Tolman-Oppenheimer-Volkoff (TOV) equations are derived and solved to yield Mass-Radius curves of different neutron star structures. Such different structures investigated include a purely nuclear core and a core composed of two layers, an inner quark plasma and a nuclear outer core. These classes of stars are probably the only place in the universe where such a quark plasma can exist. Because of the possibility of quark deconfinement, Quantum Chromodynamics (QCD) plays an important role in modeling the core of these stars. Although QCD is unsolved, we can still use some of the main principles to obtain some possible Equations of State (EoS) to be used in conjunction with the TOV equations. With an equation of state for both the nuclear and quark layers of the core, we can assume the star is in an equilibrated state and perform a maxwell construction for the phase transition from nuclear to quark matter and can come up with a combined EoS for the core. Although the core is the main focus of the research, the crust is also explored, as well as it's resulting effect on the Mass and Radius. The results are different Mass Radius curves that we can compare to observation. Since these stars that are modeled are likely the only objects in the universe where the extreme density allows for quark deconfinement, they provide us with one way to test out the QCD framework. Lastly, a core structure with three layers: a pure quark layer, a mixed nuclear and quark layer, and a pure nuclear layer, will be investigated in the future using a so called Gibb's construction.

105. The Effects of Varying Stacking Order on Superconducting and Magnetic Properties of Niobium/Cobalt Hybrid Thin Films

Gabriel Rocha, Jiyeong Gu, Ph.D
Department of Physics and Astronomy, California State University, Long Beach, Long Beach, CA 90840

It is known that superconducting and magnetic properties of superconductor (SC)/ferromagnet (FM) hybrid thin film structures depend on the parameters of the bilayer thin films, such as the thicknesses of FM and SC layers and interface roughness, etc. In this research, the effect of stacking order of the SC and FM layers was investigated. Niobium (Nb) and Cobalt (Co) were used as superconducting and ferromagnetic layers, respectively. Co(10nm)/Nb(100nm)/Si and Nb(100nm)/Co(10nm)/Si thin films were created where the only difference between two samples is the stacking order of Nb and Co layers. Nb(100nm)/Si sample was also fabricated for the comparison. Resistivity and magnetic hysteresis measurements showed distinguishable differences in critical temperature (T_c) and magnetic hysteresis loops among three samples. T_cs for both bilayer thin films were lower than the T_c of Nb single layer (~4.2 K), however, there was a difference in by how much the T_c was lowered due to the Co layer (~3.25 K for Nb/Co/Si and ~2.6 K for Co/Nb/Si). Magnetic hysteresis loops show more drastic difference possibly due to the CoO layer formed when Co was deposited as a very top layer. For future work, more bilayer samples need to be fabricated and measured with various thicknesses. Also, Co/Nb/Co/Si trilayer structure will be fabricated as well.

This project is supported in part by the Robert E. McNair Scholars Program

106. Analyzing Tidal Deformations of Neutron Star with Phase Transitions from Nuclear to Quark Matter

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An exploration of how the tidal properties measured in gravitational wave (GW) sources from coalescing neutron star mergers can be utilized to constrain the elusive neutron star (NS) Equation of State (EoS) was conducted. For the purpose of this study, realistic EoS models that featured phase transitions from nuclear matter to quark matter were employed to simulate behavior that is more consistent with quantum chromodynamics (QCD) calculations. From these models, the relation between the mass-weighted tidal deformability, $\tilde{\Lambda}$ and the binary mass ratio, $q = M_2/M_1$, was analyzed to determine if a given EoS, meets the criterion determined by the GW170817 signal of $400 \leq \tilde{\Lambda} \leq 800$ for $0.7 \leq q \leq 1.0$. By comparing the tidal deformability of a single star, $\tilde{\Lambda}$, constraints on the mass and radii of neutron stars can be placed.

107. Calculation of Primary Variables Affecting the g-mode Oscillations in Neutron Stars.

Megan Barry, Marc Salinas, Thomas Klaehn, Ph.D., and Prashanth Jaikumar, Ph.D.
Department of Physics and Astronomy, California State University, Long Beach, Long Beach, CA 90840

Other than black holes, neutron stars are the only known source of gravitational waves. Unlike black holes, however, neutron stars contain matter at extremely high density. Thus, studying gravitational waves from neutron stars helps us discover new forms of matter. We study particular oscillations of neutron star matter driven by chemical gradients, called g-modes, that couple to gravitational waves. Using a theoretical model for the neutron star, we derive the trends in proton fraction with mass density and the Brunt-Väisälä frequency at which the g-mode oscillates. The trends confirm published results from literature for baryon densities greater than .07 fm^{-3}, but differ below this range. We plan to extend this benchmark to new regimes of dense matter that include a mixed phase of quark and nuclear matter.

This research was funded by a grant from the National Science Foundation PHY 1609859.

108. A Morphology and Magnetism Study of Permalloy Nano-cap Thin Magnetic Film through AFM/MFM/SEM.

Adriana Rincon, Terence Baker, Alexander Beach, Jiyeong Gu, Ph.D., Chuhee Kwon, Ph.D.
Department of Physics and Astronomy, California State University, Long Beach, Long Beach, CA 90840.

A single-layer permalloy (Ni80Fe20) films deposited on polystyrene nanospheres were used to explore the limits in the formation of magnetic nanostructures. The magnetic structures and surface topology were investigated with the atomic force microscopy (AFM), magnetic force microscopy (MFM), and scanning electron microscopy (SEM). These techniques were utilized to capture necessary images that would help us understand the correlation between the unusual curved magnetic structure and topographical data of the nanospheres. During the study, we were able to see a special advantage with Conical vs. Rotated AFM tips. Conical tips maintain the contact with the sample better—which provides better details on captured images. Next, we were able to corroborate a remarkable doughnut-shaped magnetic state with multiple rings to be present on the MFM images; these were previously

viewed by Terence Baker during his initial MFM scans. In addition, we detected multiple outer rings between nanospheres with encapsulated gaps. This may occur when there is a substantial amount of space between the spheres. However, from the structural morphology of nanospheres, the SEM gave us a possible insight into how these spheres self-assemble through the Langmuir-Blodgett trough. The images uncovered an unexpected shape of the end-product—the spheres seemed compressed together. There might a possibility that they lost their spherical shape during self-assembly. Likewise, the AFM images coincided with what was found on the SEM images. This newly gathered information will be applied to further characterize and understand the nanosphere self-assembly process.

This project is supported by the CSULB 2018 ORSP Summer Student Research Assistantship Award and FY 2018/19 Small Faculty Grant.

109. Solving Neutron Star Structure using Enthalpy Method:

Benjamin Diaz, Prashanth Jaikumar, Ph.D.
Department of Physics and Astronomy, California State University, Long Beach, Long Beach, CA 90804

Neutron stars and Black Holes are prominent sources of gravitational waves. We compute the general relativistic structure of the Neutron Star using a variation of the standard Tolman-Oppenheimer-Volkoff (TOV) equations. Our method is based on computing the dimensionless enthalpy from a given equation of state. We test our method using a polytropic equation of state to model nuclear matter and thermodynamic Bag model to describe quark matter. Our method is more efficient and accurate at finding the surface of the star, which is important for calculating the frequency of gravitational waves emitted by the star.

This project is supported by Natural Science Foundation Grant PHY-1608959

110. Monitoring Foaming Bacteria's (*Gordonia amarae*) Growth in a Partially Nitrifying Water Reclamation Plant

John Nguyen, Dr. Pitiporn Asvapathanagul

Usable water in Southern California's dry climate is very scarce, so it must be recycled. Water Reclamation Plants (WRPs) convert wastewater into usable forms for irrigation, toilets, and etc. Nevertheless, solids separation problems (foaming incidents) frequently occur in activated sludge, which lowers the quality of reclaimed water and increases energy, labor, and chemical costs to eliminate foams. Overgrowth of filamentous bacteria causes foaming incidents. Our study goals are to identify the foaming bacteria and to discover the causes of the overgrowth of filamentous bacteria in the water samples. The wastewater samples were obtained from a partially nitrifying wastewater plant located in Southern California. Molecular techniques, including gene amplification (PCR) and gene sequencing, were combined with statistical analysis to determine correlations between environmental and operational parameters with the overgrowth of foaming bacteria. The results found *Gordonia amarae* was sequenced and was identified as the major foaming bacterial group. Our results showed a strong correlation between low temperature with high *G. amarae* cell population (r = -0.56 and P = 0.0011). Additionally, *G. amarae* cells increased when nitrification was not completed, and there was NO^-_2-N accumulation in the system and in second effluent (r = 0.68, P = 0.00; r = 0.46, P = 0.01), and elevated pH levels. Both findings implied low temperature associated with incomplete nitrification and nitrite accumulation were favorable factors to *G. amarae*'s growth compared to other bacteria.

This study was funded by Louis Stokes Alliances for Minority Participation (CSULB-LSAMP NSF HRD 1302873) and Chancellor's Office of the California State University). The authors thank Ronnie Johnson of the Santa Margarita Water District at the Oso Water Reclamation Plant for supplying the sample collection, and the laboratory specialists at SMWD for wastewater analysis data.

111. Calculating Gravitational Wave Frequencies of Neutron Stars

Michael Lanoye, Prashanth Jaikumar, Ph.D
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Neutron Stars are a prominent source of gravitational waves. To compute the frequency of the gravitational waves we first calculate the general structure of a neutron star by using a polytropic equation of state, using a dimensionless variation to the Tolman-Oppenheimer-Volkoff (TOV) equations. We then calculate the spacetime oscillations of the star at its surface and determine the frequency of the gravitational waves that it will emit. We solve a system of 4 coupled linear differential equations in the star and determine the values of the metric variables at the stellar surface. These values are in good agreement with published results. We then solve the Zerilli equations and determine the frequency of the fundamental non-radial spacetime oscillations that generate gravitational waves. Our results differ at the few percent level from published results, motivating us to explore more robust numerical techniques in future calculations.

This project is supported in part by National Science Foundation Grant PHY-1608959.

112. The Development and Characterization of Different Nano-Graphite Sizes filled Bisphenol A-Based Benzoxazine/ Cycloaliphatic Epoxy

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A novel class of thermoset matrix of composite with higher thermal stability and enhanced glass transition temperature (T_g) was engineered from Bisphenol A-based Benzoxazine (BZ), Cycloaliphatic Epoxy (CER), and Graphite Nanoparticles (GNPs). The mechanical and thermal properties of BZ/CER systems filled with different loadings (0.1, 0.3, 0.6, and 0.9wt%) of GNPs were investigated by using DSC and DMA. Desirable wettability and processability were achieved with the 37.5wt% epoxy by decreasing the viscosity of the BZ. Several mathematical models were used to predict the modulus of the BZ/CER/GNP system and were compared with the experimental data. The BZ/CER/GNP composite provided higher mechanical and electrical properties while having the similar processability compared to the BZ/CER composites.

113. The Effect of Bagnold Dune Slopes on the Short Time-scale Temperature Fluctuations at Gale Crater on Mars

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In-situ measurements of how Mars air temperature near the surface responds to changing topography are rare. The Bagnold dunes were investigated by MSL's Curiosity rover during its second winter in Gale crater on Mars. The effect of Bagnold dune slopes on the local microclimate and how it changes

the variability of short-lived air temperature fluctuations is described. The temperature signal is characterized using Fourier analysis to isolate oscillations of periods under 24 minutes. Comparing the analyzed sols during the Bagnold dunes exploration to a typical southern winter sol, we determine the trends in short-duration temperature oscillations near the east-facing High Dune, the west-facing Namib Dune, as well as in the area between the dunes. We find each of the regions having distinct signatures, with the west and east orientation of the dunes reflected in the data.

This work was carried out under the NASA MSL and a M2020 grant.

114. Advancing Hydrogen as a Renewable Chemical Fuel

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Energy storage is vital to the development of renewable energy systems. Our lab is working toward identifying abundant electrocatalysts for storing renewable energies in hydrogen bonds, through the hydrogen evolution reaction (HER, $2\,H^+ + 2e^- \rightarrow H_2$), due to their light weight and high energy storage capacity. Electrocatalysts allow for reactions to be accelerated without altering the chemical composition. The precious metal platinum is an efficient HER catalyst however, due to its high cost, we investigate alternatives. We hypothesize that two transition metal dichalcogenides (TMD), molybdenum disulfide (MoS_2) and molybdenum diselenide ($MoSe_2$), can become economical yet efficient alternatives for HER. MoS_2 has been shown to be active for HER. MoS_2 has an asymmetric layered structure, while the location and mechanism of HER catalysis remain unknown. It is believed that the active sites are on the edges rather than the basal planes of MoS_2. To understand the catalytic mechanism, we utilize Chemical Vapor Deposition in order to synthesize these materials with an emphasis on the absence of precursors making our process different than previously studied. This will help reduce the financial burden of fabricating MoS_2 and $MoSe_2$ further as well as prevent the contamination of volatile materials such as Sulfur. Characterization is carried out through Raman Spectroscopy to understand the vibrational modes present as well as the layers which are imperative to the catalytic behavior for HER. Through optical images of triangular features and the Raman signature of our desired materials present, we demonstrate successful synthesis of both MoS_2 and $MoSe_2$ thus promoting the advancement of hydrogen as a renewable chemical fuel.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; 8UL1GM118979-02; 8TL4GM118980-02; 8RL5GM118978. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health

115. Chemomechanical Effects of Surfaces with Respect to Hydrogen Evolution

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Hydrogen gas is a clean-burning alternative energy source compared to fossil fuels and has about three times the energy per kilogram compared to gasoline. H_2 can be produced through water splitting which requires a catalyst since it is a slow reaction. The catalysts for this reaction are usually rare metals making this an expensive process. We need alternative Earth abundant metals to make this a

commercially viable option. Our group is investigating the chemomechanics of different thin film electrodes with the goal of improving catalysis of the hydrogen evolution reaction (HER). We are currently investigating the effect of doping rare metal electrodes with Earth abundant transition metals. In particular, Ni is highly abundant and is significantly less expensive when compared to the best-known catalyst for HER: Pt. If a viable catalytic Ni-based alternative is found, it could significantly lower the cost of hydrogen gas production, offering a more accessible alternative to fossil fuels.

Research expenses for this project are supported in full using capital from Dr. Tavassol's laboratory start-up funds

116. Chemomechanical Evaluation of HER-Active Earth-Abundant Thin Film Electrocatalysts

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Recent authors have discussed the emerging viability of a new "hydrogen economy", a means of storing and distributing energy – particularly those generated from renewable sources – within the chemical bonds of molecular hydrogen. Such a fuel can be used as an energy source, releasing only water vapor as exhaust. The hydrogen evolution reaction (HER) is the process by which gaseous molecular hydrogen is produced and which is a crucial part of a sustainable "hydrogen economy". Precious metal platinum is a very efficient catalyst for this reaction, and remains the industry standard HER catalyst for commercially-available low temperature water electrolysers. Significant loadings of platinum are required for the volume of evolved hydrogen to become commercially viable. The loading of platinum for catalysis alone has been estimated by some authors to constitute as much as 50% of the stack cost of polymer electrolyte fuel cells (PEFCs). Therefore, cost will remain an intractable barrier to scalability unless the amount of Pt applied for HER catalysis can be reduced without compromising the performance requirements of the electrolyser.

One approach to this topic involves the integration of the Pt surface with earth-abundant 3d transition metals. Emergent electrochemical behaviors are characterized for these systems, with the goal of tuning properties deemed beneficial for this goal. The in-situ chemomechanical response of a surface during electrochemical experiments manifests also as a stress diagnostic of the underlying surface process. Measuring the surface stress of a thin film during cyclic voltammetry may precisely identify the relationship between that surface's catalytic performance and its associated surface processes. This can then be used to inform the iterative optimization of that surface to maximize the current density while also minimizing the use of costly precious materials.

Recent work has focused on systems of polycrystalline Pt thin films in acidic media with and without dissolved transition metal salts. In the absence of other metals, the dependence of polycrystalline Pt on scan rate, pH, and on atmospheric conditions is explored. The adsorption of hydrogen onto the Pt surface from a hydrogen-saturated acidic solution was surprisingly found to induce extreme stresses on that surface. For investigations in the presence of transition metal salts, the bulk deposition of copper metal in the presence of sulfuric acid has been observed to eliminate the chemomechanical changes associated with hydrogen adsorption. Future investigations will establish a volcano curve identifying the performance of Cu against Pt thin films with varying thicknesses of overlying Pt.

117. Characterization of Zigzag Inverse Semigroups

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Motivated by examples of C*-algebras generated by semigroups, we investigate constructions of inverse semigroups from left cancellative categories such as the inverse semigroup of the path category of a directed graph. We give axioms that characterize inverse semigroups that are isomorphic to the set of zigzag maps on a left cancellative category.

This work was completed as part of the REU program at University of Texas at Tyler, funded by the NSF Grant 1659221.

118. Size Control on Zeolitic Imidazolate Framework-8 Particles for Gas Sensing

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2. Department of Chemistry and Biochemistry, California State University Long Beach

Zeolitic imidazolate framework 8 (ZIF-8), a type of metal-organic framework (MOF), is composed of tetrahedral zinc ions connected with 2-methylimidazole ligands forming a sodalite structure. ZIF-8 has demonstrated great potential in gas sensing due to its intrinsic characteristics of large surface area and porosity. In an endeavor to improve upon this quality, we successfully synthesized ZIF-8 particles with a controlled size ranging from 100 nm to 10 um in diameter. Two distinct methods of synthesis were utilized. First, by modulating the ratio between zinc nitrate hexahydrate and 2-methylimidazaole, we were able to vary the ZIF-8 particle size in nanoscale. Second, switching synthesis solvent from methanol to dimethylformamide promoted particle growth in the microscale range. The chemical composition, crystal structures, and porous properties of the produced ZIF-8 particles were analyzed using infrared spectroscopy, X-ray diffraction, and nitrogen gas sorption analysis, respectively. Additionally, scanning electron microscope (SEM) studies confirmed that uniform particles were produced with diameters of 100nm, 300nm, 400nm, and 10μm, respectively. Interestingly, atomic force microscope (AFM) imaging studies revealed that the three larger particles were in fact aggregations of 100nm particles. To address this, future work will be geared towards the mechanism studies of ZIF-8 particle formation and its impact on gas adsorption.

119. Dynamic Wirtinger Number

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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 bridge number. In this project we define a new way to calculate bridge number given a diagram of a knot.

120. Abstract not available

Student Resources

GROWTH MINDSET 101

The College of Natural Sciences and Mathematics firmly believes in mindset theory and the power of developing a growth mindset. Through tutoring, your faculty, advising, NSCI courses, and the SAS Center, you will hear about the importance of growth mindset many times this year. Browse the following pages for more information.

Mindsets are beliefs about yourself and your most basic qualities such as intelligence, talent, and skills.

In a **fixed mindset**, *people believe their basic qualities, like intelligence or talent, are fixed; they can't be changed.*

In a **growth mindset**, *people believe their basic qualities can be developed through dedication and hard work.*

MINDSET CHARACTERISTICS

FIXED MINDSET		GROWTH MINDSET
SKILLS ARE BORN YOU CAN'T LEARN & GROW	**BELIEFS**	SKILLS ARE BUILT YOU CAN LEARN & GROW
PERFORMANCE & OUTCOMES NOT LOOKING BAD	**FOCUS**	THE PROCESS GETTING BETTER

KEYS TO GROWTH

NOT NECESSARY NOT USEFUL	EFFORT	USEFUL WILL LEAD TO GROWTH
BACK DOWN & AVOID FRAME AS A THREAT	CHALLENGES	EMBRACE & PERSEVERE FRAME AS AN OPPORTUNITY
HATE THEM & GET DISCOURAGED TRY TO AVOID MAKING THEM	MISTAKES	USE THEM TO LEARN TREAT THEM AS OPPORTUNITIES
NOT HELPFUL GET DEFENSIVE & TAKE PERSONALLY	FEEDBACK	USEFUL INFORMATION APPRECIATE IT & USE IT TO GROW

10 WAYS TO DEVELOP GROWTH MINDSET

Embrace the word **"yet".** Whenever you feel like you are struggling with a task, tell yourself you just haven't mastered it yet.

Try different **learning** *tactics. There's no one-size-fits-all model for learning. What works for one may not work for you.*

View challenges as **opportunities**. *Having a growth mindset means relishing opportunities for self-improvement.*

Redefine "genius". The myth's been busted: genius requires **hard work**, *not talent alone.*

Celebrate growth in others. If you appreciate growth, you'll want to **share** *your progress with others.*

Accept the concept of "brain training". The brain is like a muscle that needs to be **worked out.**

Place **effort** *before talent. Hard work should always be rewarded before inherent skill.*

Think logically about time and effort. It **takes time** *to learn. Don't expect to master a topic in one sitting.*

Acknowledge and embrace imperfections. Hiding from your weaknesses means you'll never **overcome** *them.*

Replace the word "failing" with the word "learning". When you make a mistake or fall short of a goal, you **haven't failed**; you've learned.

ADAPTED FROM "25 WAYS TO DEVELOP GROWTH MINDSET" BY SAGA BRIGGS; OPENCOLLEGES.EDU.AU/INFORMED/FEATURES/DEVELOP-A-GROWTH-MINDSET

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JENSEN SAS CENTER

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CNSM computer lab with printing, posters + more

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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
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EVENTS
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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

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 HSCI-164 + tutors ASTR, BIOL, CHEM, MATH and PHYS
Lindgren Math Tutoring Center: located at LAS-345 + tutors MATH and STAT
Math Education Tutoring Center: located at LAS-245 + tutors MTED
Physics Learning Assistants: located at HSCI-222 + tutors ASTR, MATH + PHYS

TUTORING TIPS + TRICKS

TUTORING BEGINS AS EARLY AS SEPT 4

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!

CNSM STUDENT CLUBS + ORGANIZATIONS

pre-health orgs

American Medical Student Association
amsacsulb.info@gmail.com

Black Medical Student Association
csulbbmsa@gmail.com

Neuroscience at the Beach
neuroscienceatthebeach@gmail.com

Minority Focused Alliance of Pre-Health Scholars (MAPS)
csulbmaps10@gmail.com

Association of Pre-Pharmacy
app.csulb@gmail.com

Long Beach State Pre-Dental
csulb.lbpd@gmail.com

college orgs

CNSM Student Council
csulbcnsmsc@gmail.com

Environmental Science + Policy Club
csulbesp@gmail.com

Student Chapter of the American Society for Microbiology
asmcsulb@gmail.com

Marine Biology Student Association
csulbmbsaboard@gmail.com

Society of Physics Students
president@csulbsps.org

Society of Wetland Scientists
wetlandia@gmail.com

Mathematics + Statistics Student Association
mssa.csulb@gmail.com

Society for the Advancement of Chicano/Latino and Native American Scientists
csulb.sacnas.org@gmail.com

American Association of Petroleum Geologists
csulbaapgchapter@yahoo.com

FIND MORE INFO ON BEACHSYNC

STEMx
SISTERS IN MOTION

MEET STEM STUDENTS, FACULTY, ALUMNI & STAFF

- GAIN SUPPORT TO PERSIST IN YOUR MAJOR
- BUILD COMMUNITY AND SISTERHOOD
- CAREER AND PROFESSIONAL DEVELOPMENT
- MEETINGS ONCE A MONTH!

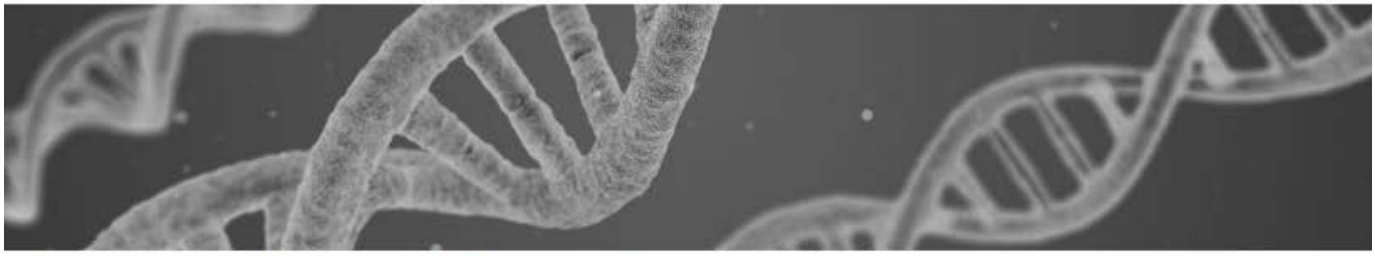
IF INTERESTED CONTACT SONIA SANTOS
COLLEGE OF NATURAL SCIENCES AND MATHEMATICS
SONIA.SANTOS@CSULB.EDU

FIND US ON BeachSync!

IMPORTANT CAMPUS RESOURCES

Career Development Center (CDC)	Brotman Hall Room 250	562-985-4151	careers.csulb.edu
Disabled Student Services (DSS)	Brotman Hall Room 270	562-985-5401	csulb.edu/dss
Enrollment Services	Brotman Hall Room 101	562-985-5471	csulb.edu/enrollment
Financial Aid	Brotman Hall Room 101	562-985-8403	csulb.edu/financialaid
Learning Assistance Center (LAC)	Horn Center Room 104	562-985-5350	csulb.edu/lac
Lindgren Math Tutoring Center	Liberal Arts 5 Room 345		csulb.edu/math
Student Access to Science and Math Center (SAS)	Hall of Science Room 164	562-985-4682	csulb.edu/sas
Writer's Resource Lab (WRL)	Language Arts (LAB) Room 206	562-985-4329	csulb.edu/wrl

BIOLOGICAL SCIENCES



DEPARTMENT INFO

The biological sciences include all of the areas of scientific endeavor centered around the general question of the nature of life. The Department of Biological Sciences is dedicated to the teaching of biology and discovering new biological truths for society. Students have access to valuable research opportunities that contribute to current innovations. The department also participates in the Desert Studies Consortium and the Ocean Studies Institute.

DEGREE OPTIONS

B.S. IN BIOLOGY: This degree is designed for students pursuing careers that involve the study of life. The four options are:

- General: most flexible option with a wide variety of classes
- Education: for those wishing to be middle school or high school science teachers
- Molecular Cell and Physiology: popular among those wishing to enter the medical field
- Organismal: focuses on biology in relation to the environment

B.S. IN MARINE BIOLOGY: This degree focuses on the study of biology and ecology of organisms found in diverse marine habitats.

B.S. IN MICROBIOLOGY: This is the study of microorganisms and their interactions with humans, other organisms, and the environment.

CAREERS IN BIOLOGY

- Dentist
- Technical writer
- High school teacher
- Lab technician
- Medical illustrator
- Pharmaceutical sales
- Fish + Game warden
- Tree surgeon
- Veterinarian
- Biomedical engineer
- Criminologist
- Zymurgy
- Aquarium curator
- Coastal restoration
- Naturopathic physician
- Nutritionist
- Food + drug inspector
- Environmental lawyer
- Animal behavorist
- Congressional aide
- Museum curator

DEPARTMENT OF BIOLOGICAL SCIENCES
Hall of Science Room 104 (HSCI-104) | 562-985-4806 | csulb.edu/biology

CHEMISTRY + BIOCHEMISTRY

DEPARTMENT INFO

The Department of Chemistry and Biochemistry is committed to rigorous and innovative curriculum that focuses on developing problem-solving, critical thinking, and communication skills, and provides high-quality education in chemistry and biochemistry. The award-winning faculty are vigorously involved in research projects with undergraduate and graduate students alike and receive significant external grants and contracts annually. The department offers extensive opportunities for students to participate in novel research projects across a broad spectrum of areas in the chemical sciences.

DEGREE OPTIONS

B.S. IN BIOCHEMISTRY: This is the study of chemical processes within and relating to living organisms. This field utilizes chemical knowledge to solve biological problems.

B.A. IN CHEMISTRY: This degree will provide a background in chemistry and can be used for preparation in secondary science education.

B.S. IN CHEMISTRY: This degree is designed to provide students a thorough background in chemistry for those planning to pursue careers as professional chemists or to do graduate study in chemistry or biochemistry. There is an opportunity to focus your degree as such:

- Materials Science option: the study of materials in relation to their applications

CAREERS IN CHEMISTRY

- Patent attorney
- Flavor chemist
- High school teacher
- Perfumer
- Crystallographer
- Carbon trader
- Sustainability consultant
- Social activist
- Pharmacologist
- Dentist
- Food + drug inspector
- Geochemist
- Hazardous waste management
- Materials scientist
- Medical librarian
- Toxicologist
- Industrial hygienist
- Pharmaceutical sales
- Forensic document examiner

DEPARTMENT OF CHEMISTRY + BIOCHEMISTRY
Hall of Science Room 370 (HSCI-370) | 562-985-4941 | chemistry.csulb.edu

ENVIRONMENTAL SCIENCE + POLICY

PROGRAM INFO

This program, a collaboration between the College of Natural Sciences and Mathematics and the College of Liberal Arts, is designed for students who are interested in conservation of our natural world through interdisciplinary collaboration. Students in this program will have a broad understanding of Earth systems, an ability to apply economic principles to analyze environmental programs, an ability to integrate legal principles with environmental science and policy, work as a member of an interdisciplinary team, and apply natural and social sciences to solve environmental problems.

DEGREE OPTIONS

B.A. IN ENVIRONMENTAL SCIENCE AND POLICY: Graduates of this degree are especially well-prepared for positions in state and local government, private consulting firms, energy companies, news organizations, and environmental advocacy groups.

B.S. IN ENVIRONMENTAL SCIENCE AND POLICY: The Bachelor of Science degree cultivates an advanced level of understanding of Earth systems, living systems, and the role and effect of chemicals in natural systems. Graduates are trained for entry positions in industry and government.

CAREERS IN ES+P

- Environmental analyst
- Teacher
- Ecologist
- Geochemist
- Urban planner
- Recycling manager
- Environmental advocate
- Social activist
- Wildlife manager
- Ecotourism
- Political aide
- Park ranger
- Waste water treatment specialist
- Materials scientist
- Hazardous waste specialist
- US Coast Guard
- Environmental lawyer
- Pollution prevention technician

ENVIRONMENTAL SCIENCE + POLICY PROGRAM
Hall of Science Room 136 (HSCI-136) | 562-985-8432 | prog-esp@csulb.edu

GEOLOGICAL SCIENCES

DEPARTMENT INFO

The geological sciences includes the study of the solid earth, the hydrosphere, and the atmosphere. The department's programs are based solidly in fundamental geological skills with an emphasis in field experiences. Geology integrates the principles of chemistry, physics, biology and math in the study of Earth processes and its history. The mission of the Department of Geological Sciences is to educate students who will fill critical roles in industry and teaching, protect the environment, and develop natural resources. The department is committed to preparing students for professional careers or further post-graduate education. The department participates in the Southern California Marine Institute for our marine geology, oceanography, and seismic studies.

DEGREE OPTIONS

B.S. IN EARTH SCIENCE (APPLIED GEOSCIENCE): This degree prepares students to understand the natural environment, Earth resources, land and ocean use, pollution, geology of the sea floor, and other areas of critical importance to present and future world problems.

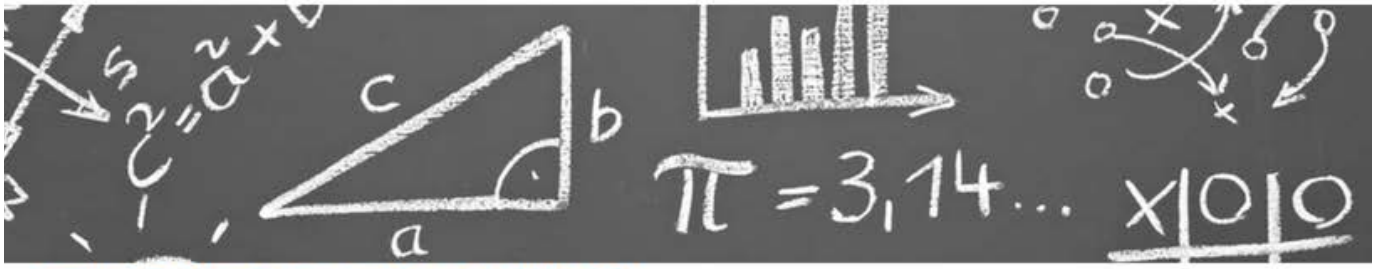
B.S. IN GEOLOGY: With this degree, students learn about fundamental geological processes and materials, cultivate skills in integrative three-dimensional thinking, actively engage in lab and field activities, and pursue interests in elective courses or research in the many disciplines of the geological sciences.

CAREERS IN GEOLOGY

- Geophysicist
- Mineralogist
- Science writer
- Teacher
- Hydrologist
- Paleontologist
- Oceanographer
- Seismologist
- Soils engineer
- Park ranger
- Petroleum engineer
- Geochemist
- Hazards analyst
- Volcanologist
- Glacial geologist
- Meteorologist
- Mining engineer
- Crystallographer
- Stratigrapher
- Environmental consultant

DEPARTMENT OF GEOLOGICAL SCIENCES
Hall of Science Room 322 (HSCI-322) | 562-985-4809 | csulb.edu/geology

MATHEMATICS + STATISTICS



DEPARTMENT INFO

Mathematics is fundamental to all scientific knowledge, including not only the traditional natural sciences but increasingly the social and economic sciences. Mathematics is also a vital aid to critical and philosophical thinking. The department offers instruction for students at all levels beyond high school mathematics. Its courses provide the computational and analytic skills needed for a variety of majors, as well as the advanced theoretical topics for specialists in mathematics. The faculty actively engage in outstanding research and teaching and in interdisciplinary and outreach activities within the surrounding communities and throughout southern California.

DEGREE OPTIONS

B.S. IN MATHEMATICS: This degree requires that a selection of fundamental courses in algebra statistics, and analysis be taken. There are four options for the B.S. in Mathematics degree.

- General (Pure): most flexible option with a widest choices of electives and career options
- Applied Mathematics: emphasizes math frequently used in real-world applications
  - Suboption: Science and Engineering
  - Suboption: Economics and Management
- Mathematics Education: focuses on preparing teachers for the secondary school level
- Statistics: develops a foundation in statistical methods

CAREERS IN MATHEMATICS

- Mathematician
- Statistician
- Computer programmer
- Teacher
- Systems analyst
- Corporate accountant
- Surveyor
- Efficiency engineer
- Securities analyst
- Econometrist
- Information scientist
- Actuary
- Operations research analyst
- Technical writer
- Demographer
- Meteorologist
- Financial analyst
- Salary analyst
- Biostatistician
- Forensic accountant

DEPARTMENT OF MATHEMATICS + STATISTICS
Faculty Offices 3 Room 120 (FO3-120) | 562-985-4721 | csulb.edu/math

PHYSICS + ASTRONOMY

DEPARTMENT INFO

This discipline helps us understand phenomena we observe in our world. Physics students acquire skills and knowledge that are unlike most other degree programs. The combination of solving intricate theoretical constructs, mastering hands-on experimental techniques, wrangling data acquisition and analysis, error analysis, technical writing, and more develops critical thinking and problem-solving skills that can be applied to nearly any kind of challenging situation. The mission of the Department of Physics and Astronomy is to train students through coursework and hands-on research to become physicists who will excel in applying their knowledge, talents and practical skills to solve problems in STEM.

DEGREE OPTIONS

B.A. IN PHYSICS: This Bachelor of Arts degree is appropriate for those preparing for teaching careers in the physical sciences at the secondary level as well as those whose goal is a liberal arts education with an emphasis in physics or for engineers interested in a double major.

B.S. IN PHYSICS: This degree requires significant courses in mathematics and introductory courses in biology and chemistry. The Bachelor of Science degree is designed for students interested in immediate employment in industry or wishing to continue on to a Master's or Ph.D. degree in physics or a related field.

CAREERS IN PHYSICS

- Astrophysicist
- Computer scientist
- Electro-optical engineer
- Meteorologist
- Acoustical engineer
- Medical physicist
- Cosmologist
- Teacher
- Physicist
- Industrial health engineer
- Aerospace engineer
- Metallurgist
- Systems analyst
- Mathematician
- Technical writer
- Astronomer
- Materials researcher
- Planetarium exhibit curator
- Nuclear engineer
- Geophysicist

DEPARTMENT OF PHYSICS + ASTRONOMY
Hall of Science Room 220 (HSCI-220) | 562-985-7925 | csulb.edu/physics

SCIENCE EDUCATION

DEPARTMENT INFO

The Science Education department offers a Master's degree in Science Education Information and is strongly committed to the improvement of teaching and learning of science at all levels (pre-Kindergarten through University) and in all settings (classrooms and non-classroom locales). The department also offers advising and courses to aid undergraduate and post-baccalaureate students in earning a California Science Teaching Credential to teach middle and/or high school science.

This is also the home of the Science Learning Center, the Young Scientists' Camp, and the Long Beach Science Educators Network.

DEGREE OPTIONS

M.S. IN SCIENCE EDUCATION INFORMATION: This degree is designed primarily for credentialed K-12 teachers and experienced informal educators.. There are three options for the M.S. in Science Education Information degree.

- Elementary and Middle School Science Education: for those who are K-8 generalists
- Informal Science Education: aimed at those currently working in non-classroom settings
- Secondary Science Education: for those with a Single Subject credential in Science.

SINGLE AND MULTIPLE SUBJECT CREDENTIALS: While housed in the College of Education, the Science Education department offers assistance to students seeking a credential.

AFSE STUDENT CHAPTER

The Association of Future Science Educators (AFSE) is sponsored by the Science Education Department to support future K-12 science teachers with programs that include "how to" workshops regarding job interviews, field trips, and content-based inquiry learning techniques. AFSE is a student chapter of the National Science Teachers Association and the California Science Teachers Association.

DEPARTMENT OF SCIENCE EDUCATION
Hall of Science Room 205 (HSCI-205) | 562-985-4801 | csulb.edu/scied

CNSM Student Research Symposium 2018