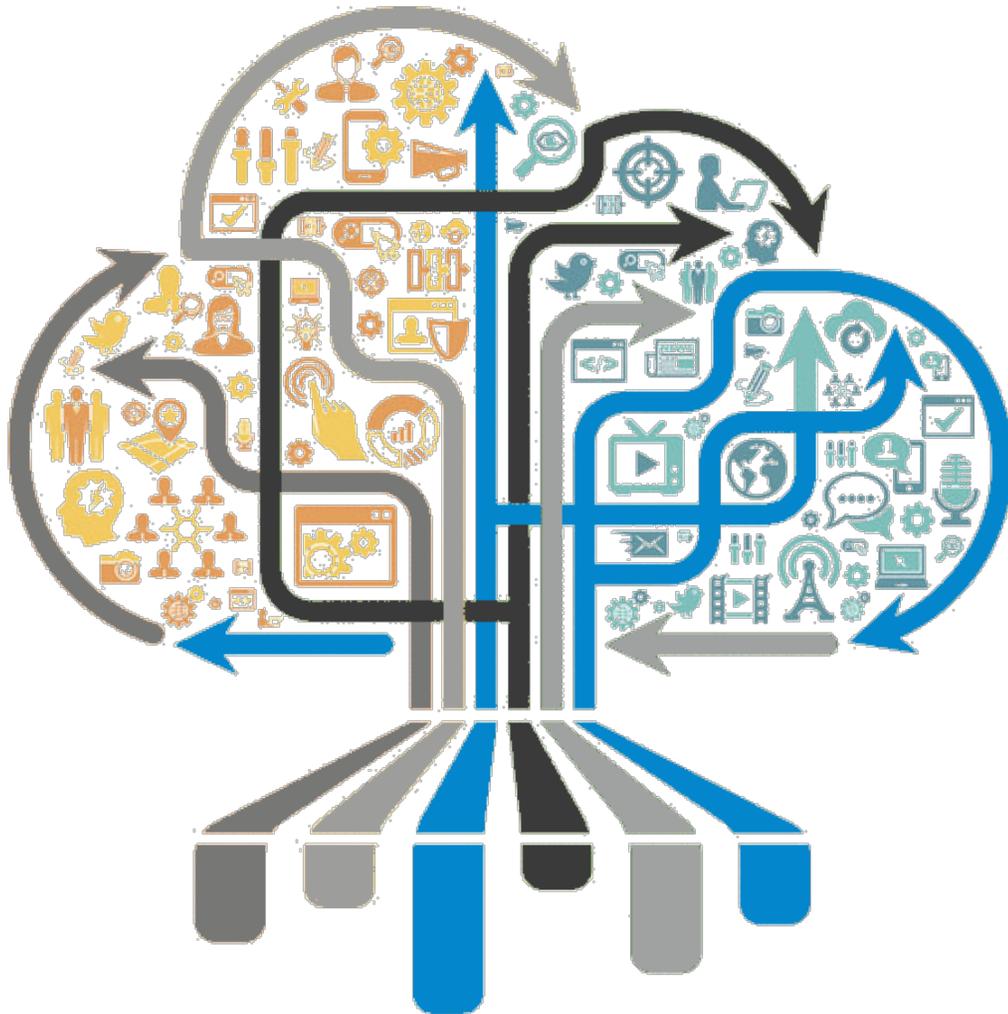


6th Annual

Physical and Biological Sciences Summer Research Symposium



Summer 2015

University of California, Santa Cruz

Participant	Poster	Title of Poster
Alhakim, Kaisar	1	Estimation of Iron Concentration in a Sample Solution by Spectrophotometry
Alvarenga, Aubrey	2	Metal-Organic Frameworks: Anion Exchangers for Environmental Applications
Andrade , Rodrigo	3	Mutation of Agouti Signaling Protein for Improving the Treatment of Melanoma
Antoni, Andrea C.	4	How Does a Moving Mass Accrete Matter from its Environment?
Apolinario, Francis Albert	5	The Effect of Wind and Current Direction on The Swimming Patterns of the Western Grebe (<i>Aechmophorus occidentalis</i>)
Aranda, Andres	6	Designing Smart Demand for Frequency Regulation in a Micro-Grid Test Bed
Ashley, Guinevere	7	The Role of Synaptonemal Complex Components in the Meiotic Synapsis checkpoint
Blanc, Nicolas	8	A High-Pressure Infrared Spectroscopic Study of Chromium Pyrophosphate to 18 GPa
Bolaños, Daniela	9	Structural Analysis of pUC19 in NEB 5-alpha Competent <i>E. coli</i> Cells Treated with <i>Bam</i> HI and Topoisomerase I Enzymes
Brandt, Daniel	10	Galaxy Superwinds and the Circumgalactic Medium
Brown, Elise	11	Discovering Novel Compounds to Stabilize the E2F-retinoblastoma Protein Complex in the Cell Cycle
Campos, Jocelyn	12	Structure-Driven Analyses of the Human Astrovirus Receptor-Binding Site
Carter, Evan	13	Simulated Infrared Observations of High-Mass Star-Forming Regions
Cervantes, Miguel Angel	14	Single Molecule Assay to Identify and Characterize Telomere-binding Drugs as Potential Anti-Cancer Therapeutics
Chen, Sami	15	Constraining Seasonal and Vertical Distributions of Planktonic Foraminifera for Paleoclimate Reconstruction Since Marine Isotope Stage 3 at the Axial Seamount, Juan de Fuca Ridge
Coppage, David	16	Investigation of Naturally Derived Compounds From Indonesian Sea Sponges
Correa, Erika	1	Estimation of Iron Concentration in a Sample Solution by Spectrophotometry
Cruz, Daniel	17	The Effect of Stress on Hematopoietic Stem Cell Differentiation Pathways
Del Cid, Anthony	18	Is the Increased Virulence of LasA Protease Mutants Due to Increased Expression of LasB Protease?
Escobar-Zamora , Marlyn	19	The Effects of Developmental Manganese Exposure on Norepinephrine Transporters in the Prefrontal Cortex
Estevam, Gabriella	20	The Design and Functional Characterization of Minimal Telomerase Essential N-terminal Constructs
Ferrer, Erica	21	Effects of Ocean Acidification on Estuarine Fish Predation
Flores, Shaneece	22	Phylogenetic Signal in Plant Pathogen Sporulation: Host Species that are Closely Related to Main Host Allow the Production of the Most Spores
Flores Silverio, Miguel	23	Smart Grid: Designing an Algorithm for Autonomous Load Balancing to Maintain Grid Health
Garcia, Jose	24	Investigating the Bioavailability and Stability of N-Alkylated Cyclic Peptides
Gebremedhin, Selam	1	Estimation of Iron Concentration in a Sample Solution by Spectrophotometry
Gotfrid, Taylor	25	Designing Mini-Games for Speech with Sam
Hadley, Stephanie	26	Cosmology: Stellar Mass vs. Stellar Velocity Predictions from the Bolshoi-Planck Simulation using Age Matching
Hernandez, Jazel	27	Over Expression of the Aldehyde Dehydrogenase Gene from <i>Halopiger xanaduensis</i> in <i>Haloferax volcanii</i> to produce Butanol
Herrera, Jessica	28	Modeling of the Ideal Microgrid and Analysis of Solar Photovoltaic Systems with Electric Vehicle Charging
Kayede, Emmanuel	29	Printed Circuit Board Stators for Brushless DC motors
Kyane, Sandrine	30	Introduction of Cancer Mutations into Human Embryonic Stem Cells
Lai, Cynthia	31	Increasing the Binding Affinity of ASIP to MC1R by Modification of the Ligand's C-terminal Loop
Landeros, Adriana	32	Isolation of Salt Tolerant Cellulase Producing Halophiles for Biobutanol Production in <i>Haloferax volcanii</i>
Lara-chavez, Jbenjamin	33	Design, Construction, and Implementation of a Renewable Energy Integrated Test Bed to Regulate Frequency Deviation
Leija, Alex	34	A Search for Marine Sponge-derived Natural Products As Novel Inhibitors of Human 12-Lipoxygenase
Lemseffer, Nassim	35	Searching for Variants of Wolbachia Through Apoptosis Rates
Little, Benjamin	36	One-Pot Synthesis of Triphenylphosphine-Capped Palladium Nanoclusters
Lopez, Jose	37	Simulations of Red Giant Star Cluster Wind Collisions
Lopez, Aaron	38	Understanding the Stream-Disk Interaction in Mass-Transferring Binary Star Systems
Mama-Farah, Abyan	39	Testing Kinesins 4-14 for Roles in Axonal Transport of <i>Drosophila melanogaster</i>
Maravilla-Mendoza, Jazmin	40	Stellar Explosions: A Shocking Look into Supernova Propagation

Participant	Poster	Title of Poster
Mehic, Sanjin	41	Comparing Bacterial Attachment on the Marine Diatom <i>Pseudo-Nitzschia</i>
Mendoza, Sarah	42	Alternative Hematopoietic Differentiation Pathways Under the Effect of Hematopoietic Stress
Meyer, Rachel	28	Modeling of the Ideal Microgrid and Analysis of Solar Photovoltaic Systems with Electric Vehicle Charging
Morales, Juan	43	Neptune's Dual Capture of Triton and Nereid in Gravitational Encounter With Binary Pluto-like Kuiper-Belt System
Moran, Daniel	44	Synthesis of a Rhodamine Based Profluorescent Nitroxide for Catechol Detection
Munoz, Alexis	45	Chemical Profiling of a Marine-derived Gram-negative Bacteria, <i>Achromobacter spanius</i>
Navarro, Hector	46	How do Broken Chromosomes Segregate?
Nguyen, Khanh	47	In vivo Heterodimeric Transcription Elongation of Spt4 & Spt5
Nwakudu, Kindness	48	Synthesis of Bis-Nitroxide Alkynes from TEMPOL
Ostrander, Kalia	49	The Role of Conserved Lysines in DNA Polymerase
Padilla, Hugo	50	RNAi Screen of Potential Factors Required for Germline Mediated Lifespan Extension
Palmer, Theron	51	Comparative Genomic Analysis of Human Naïve and Memory B-Cell Immunoglobulin Switch Regions
Perez, Ivette	52	Finding Potent Wolbachia Strains to Deter Viral Infection in Mosquitoes
Perez, Edmundo	53	Functional Studies on a Human Astrovirus-Neutralizing Antibody
Perez, Joanna	54	Quartz Nanopipette for Intracellular Superoxide Sensing
Pineda, Linda	55	Evidence for Decadal and Century Scale Climate and Oceanic Variability in the Guaymas Basin, Gulf of California, over the Last Millennium
Pinson, Justin	6	Designing Smart Demand for Frequency Regulation in a Micro-Grid Test Bed
Rios, Mayra	56	Factors in Nuclear Extract that Contribute to their Activity and Splicing Efficiency
Rodriguez, Anthony	47	In vivo Heterodimeric Transcription Elongation of Spt4 & Spt5
Rodriguez, Ramiro	57	MEMS-based Adaptive Optics Multi-photon Microscopy for Deep Tissue Imaging
Samimi, Thooba	58	Climate Change Associated Sea Level-rise in Marshall Islands
Sanchez, Marisol	59	Assessing Cyclophilin Activity On the Regulation of a Circadian Clock Protein
Sanchez, Santiago	60	Finding Site of Pre-mRNA and snRNA Binding to Splicing Proteins CUS2, HSH49, HSH155, PRP5, and PRP9 During Spliceosome Assembly and Splicing
Sanchez, Michael	61	Soybean Lipoxygenase as a model for the Human Lipoxygenase Enzyme
Sanchez, Nancy	9	Structural Analysis of pUC19 in NEB 5-alpha Competent <i>E. coli</i> Cells Treated with <i>Bam</i> HI and Topoisomerase I Enzymes
Santo Tomas, Chad	62	Resistance to the Antibiotics Ampicillin and Kanamycin in <i>Escherichia coli</i>
Schenone, Dominic	27	The Design and Overexpression of Aldehyde/Alcohol Dehydrogenase Genes in <i>Haloferax Volcanii</i> : For the Conversion of Butyryl-CoA to Butanol.
Serrano, Maria	63	Analysis of the Effects of Amyloid- β on Axonal Transport of Mitochondria in <i>Drosophila</i> Motor Neurons
Sharifi, Masuda	64	Autophagosome Transport in <i>Drosophila</i> Motor Neurons
Sheppard, Georgia	65	Laminar Fate Determination of Neocortical Progenitor Cells
Simlick, Jocelyn	32	Isolation of Salt Tolerant Cellulase Producing Halophiles for Biobutanol Production in <i>Haloferax volcanii</i>
Stewart, Chelsea	47	In vivo Heterodimeric Transcription Elongation of Spt4 & Spt5
Tan, Raymond	66	The Regulations of How Cln3 is Made Proportional to Growth.
Tena, Jennyfer	67	Synthesis of Rhenium Carbonyl Complexes as photoCORMs: Contrast in Denticity Depending on the Flexibility of the Ligand
Torres, Ivette	62	Resistance to the Antibiotics Ampicillin and Kanamycin in <i>Escherichia coli</i>
Valdez, Jesus	61	Soybean Lipoxygenase as a model for the Human Lipoxygenase Enzyme
Weaver, Ian	68	Simulating Accretion Disk and Stream Interaction in Exoplanetary System WASP-12/b
Wedel, Zachary	33	Design, Construction, and Implementation of a Renewable Energy Integrated Test Bed to Regulate Frequency Deviation
Yxcot, Michael	52	Finding Potent Wolbachia Strains to Deter Viral Infection in Mosquitoes
Zamora, Alvaro	69	Saturn as an Exoplanet
Zavala-Chavez, Alfonso	70	Enhancing the Stability of an Appetite Stimulating Peptide

POSTER 1

Estimation of Iron Concentration in a Sample Solution by Spectrophotometry

Kaisar Alhakim, Erika Correa, Selam Gebremedhin, Pradip Mascharak

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRI - IMSD

Iron is an essential element found in nature ranging from a variety of minerals to living organisms including animals and plants. In addition, iron is also found in the human body in the ferric form coordinated to hemoglobin, an oxygen transport protein found in red blood cells. Even though it is an essential element, iron can be detrimental to a person's health if found at relatively high concentrations. Iron overload can lead to diseases like hemochromatosis which results in the damaging of vital organs like the liver. In order to determine the concentration of iron in an unknown solution, five standard solutions of different dilutions were made. The reductant hydroxylamine hydrochloride was used to guarantee the ferric form of iron over the ferrous form. 1,10 phenanthroline was the ligand used to bind the iron in solution and sodium acetate was used as a buffer. By the usage of a spectrophotometer, we measured the absorbance at 490 nm and 510 nm to estimate the iron concentration in a sample of water which resulted to be 0.0001344M. The overall goal of the experiment was to use basic lab techniques to get accurate results and to determine the iron concentration in a sample solution using a standard curve.

POSTER 2

Metal-Organic Frameworks: Anion Exchangers for Environmental Applications

Aubrey Alvarenga, Susan Citrak, Scott Oliver

Department: Chemistry and Biochemistry

Home Institution: Cabrillo College

Summer Program: ACCESS

Perchlorate, a byproduct of rocket fuel, has a history with contaminating drinking water and causing hypothyroidism by inhibiting the uptake of iodine in the thyroid gland. In children, hypothyroidism leads to intellectual and developmental delays. Silver bipyridine acetate (SBA), a potentially new analog of the previously studied silver bipyridine nitrate (SBN), was considered for an environment-friendly ion exchange material to exchange the pollutant perchlorate, an oxoanion. It was believed that acetate, bonded electrostatically between the layers of the metal-organic framework (MOF), would exchange for perchlorate. For initial studies, the oxoanion permanganate (in the same family as perchlorate) was used first because its violet color was easiest to analyze. The oxoanion exchange reaction ran simultaneously for both SBN and SBA under identical conditions and was analyzed quantitatively using Ultraviolet-Visible Spectroscopy and qualitatively using Powder X-Ray Diffraction. SBA exchanged permanganate at an appreciable rate, relative to SBN. For the environment, acetate proves to be a better alternative anion than nitrate in the exchange of perchlorate.

POSTER 3

Mutation of Agouti Signaling Protein for Improving the Treatment of Melanoma

Rodrigo Andrade, Jillian Miller, Glenn Millhauser

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - CUSP-HLLC

Melanoma causes a large majority of skin cancer deaths. According to the American Cancer Society, approximately 10,000 people are expected to die of melanoma this year in the United States. Melanoma is difficult to treat because melanosomes, organelles containing the pigment eumelanin, prevent chemotherapy from working. Agouti signaling protein (ASIP) binds to melanocortin receptor 1 and suppresses the production of eumelanin; thus, fewer melanosomes are formed and their ability to absorb and inactivate chemotherapeutics is minimized. When cells are treated with ASIP, chemotherapy has been shown to be three times more successful in treating melanoma. In order to continue using ASIP to treat melanoma, ASIP is synthesized using solid phase peptide synthesis, oxidative folding, and purification using HPLC. It will then be further tested for its effectiveness in melanoma treatment in model organisms.

POSTER 4

How Does a Moving Mass Accrete Matter from its Environment?

Andrea C. Antoni, Jill P. Naiman, Enrico Ramirez-Ruiz

Department: Astronomy and Astrophysics

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - LAMAT

We investigate the accretion of matter onto a point mass moving at constant velocity through a uniform medium in two ways. First, we use a numerical solver to demonstrate the Hoyle-Lyttleton concept of an accretion radius, R_a , of a point mass due to gravitational focusing. We show that the mass accretion rate, M , is given by the mass flux through a circle with radius R_a far upstream from the point mass. The Hoyle-Lyttleton Accretion (HLA) model is a particle model that neglects fluid pressure. As such, we perform a hydrodynamic simulation to compare the mass accretion rate of a point mass in a gas to the theoretical HLA rate. We find that the accretion of mass in the gas is, in fact, proportional to the HLA rate. However, the rate is reduced because the gravitational pressure exerted on the gas by the accretor is overwhelmed by the fluid pressure of the gas at short distances from the accretor.

POSTER 5

The Effect of Wind and Current Direction on The Swimming Patterns of the Western Grebe (*Aechmophorus occidentalis*)

Francis Apolinario and Nan Ho

Department: Biology

Home Institution: UC Santa Cruz

Summer Program: No Program Affiliation

The effect of wind and water current directions on the swimming patterns of Western Grebes (*Aechmophorus occidentalis*) were measured in 60 minute intervals. The Western Grebes were thought to swim mostly in a pattern that had the wind or the water current hitting the posterior sides. My hypothesis was that the western grebes prefer to swim with either the water flowing or the wind blowing at their posterior side. The observations showed that the western grebes swam in a pattern that had the wind or water current flow hitting their backs. The wind and the water hitting their lateral sides were the second most preferred. The wind and water hitting the anterior side of the western grebe were least preferred. The preference of having the wind or water current hit the posterior of the western grebe is mostly likely related to the conservation of energy that occurs while swimming.

POSTER 6

Designing Smart Demand for Frequency Regulation in a Micro-Grid Test Bed

Andres Aranda, Justin Pinson, Zachary W. Graham, Tela Favaloro, Michael Isaacson

Department: Electrical Engineering

Home Institution: Hartnell College

Summer Program: CUSP-HLLC STEM Internship

One challenge of integrating renewable energy generation into the electric grid is that it may induce deviations in the frequency of power resulting in instability in the electrical service quality. This has the potential to damage equipment and lead to power outages. We propose a method that uses frequency as a signifier of the current state of the grid and regulates this quantity by way of deferrable 'smart' loads employed at the residential level. These loads can be directly controlled to mediate the frequency excursion by deferring consumption whilst preserving their respective duty cycles. Here, we discuss the characterization of potential 'smart' loads as well as the design and implementation of embedded systems that perform the logic to control load behavior and sense frequency in a home-built test microgrid. Thermal loads, refrigerators and water heaters, were selected for their energy storage and their regulation will not cause a noticeable disruption in service. We measure frequency of the mains power using a microcontroller that transmits data wirelessly to a single-board computer for processing. Once data are analyzed, an ancillary algorithm rooted at the specified deferrable load responds to queries and commands from the computer to advance or postpone power usage. This manner of demand regulation allows the test bed to successfully stabilize frequency and improve the state of the power delivered with no disturbance to the consumer. Furthermore, this test bed can be modified for other investigations when direct implementation into the grid is neither practical nor an available resource.

POSTER 7

The Role of Synaptonemal Complex Components in the Meiotic Synapsis Checkpoint

Guinevere Ashley, Kyra Firestone, Evan Eggelston, Tisha Bohr, Needhi Bhalla

Department: Biology

Home Institution: UC Santa Cruz

Summer Program: DeAntonio-Estabrook Undergraduate Research Award

For meiosis to be successful, chromosomes must synapse to promote crossover recombination, allowing them to properly orient on the meiotic spindle. In *C. elegans*, synapsis is complete when the four central elements of the synaptonemal complex (SYP-1, SYP-2, SYP-3 and SYP-4) are loaded between homologs. In *syp-1* mutants, chromosomes cannot synapse and therefore cannot repair double strand breaks through recombination resulting in highly elevated levels of apoptosis due to activation of the synapsis checkpoint and the DNA damage checkpoint. It is assumed that any *syp* mutant backgrounds will resemble *syp-1* mutants because they are interdependent when loading between homologs. However, preliminary data in the Bhalla lab indicates that *syp-3* mutants fail to activate the synapsis checkpoint while robustly activating the DNA damage checkpoint suggesting that SYP-3 is required for the synapsis checkpoint. This led us to ask if the other SYP proteins are also required for the synapsis checkpoint like *syp-3* mutants or, if their absence would lead to synapsis checkpoint activation, like *syp-1* mutants. To address this question, we monitored apoptosis levels in live animals using a CED-1::GFP signal that surrounds apoptotic nuclei in the gonad. Our results show that, like *syp-1* mutants, *syp-2* and *syp-4* mutants exhibit very elevated levels of apoptosis supporting the idea that both the DNA damage checkpoint and the synapsis checkpoint are being activated in each mutant. We also utilized genetic backgrounds that allow us to monitor activation of one checkpoint at a time to confirm both the checkpoints are being activated in *syp-2/4* mutants.

POSTER 8

A High-Pressure Infrared Spectroscopic Study of Chromium Pyrophosphate to 18 GPa

Nicolas Blanc and Quentin Williams

Department: Earth and Planetary Science

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - UC LEADS

The infrared spectra of chromium pyrophosphate, $Cr_2P_2O_7$, have been studied under pressures up to ~18 GPa. $Cr_2P_2O_7$ is a prospective battery component, and understanding its behavior under volumetric compression can lead to insights into possible behavior-modulating chemical substitutions. Our study explored the compound's response to pressure by investigating the shifts of vibrational modes under compression and pressure-induced phase transitions occurring within the crystal lattice. Our preliminary results constrain the pressure response of the symmetric and asymmetric bending and stretching modes of the tetrahedrally-coordinated PO_4 -phosphate groups between 600 to 800 cm^{-1} , and 950 to 1200 cm^{-1} , respectively. Modes show a normal constant shift to higher frequencies with pressure up to ~4 GPa where a transition occurs. At ambient pressures, seven bands are resolvable at 1190, 1150, 1100, 1060, 1030, 1015, and 950 cm^{-1} , but only the four lowest frequency modes persist to the highest pressure of

our experiment (18 GPa): at this pressure, these modes are at 1100, 1070, 1030, and 990 cm^{-1} , respectively. The three lower frequency bands between 600 and 800 cm^{-1} are resolvable at pressures up to ~ 6 GPa; at higher pressures, these modes appear to merge into one broad band near 740 cm^{-1} . Decompression data suggests that all bands, except one at ~ 730 cm^{-1} , reappear. Our results indicate that a phase transformation occurs within the lattice of $\text{Cr}_2\text{P}_2\text{O}_7$ at ~ 4 GPa, and is likely associated with a subtle shift in crystallographic symmetry.

POSTER 9

Structural Analysis of pUC19 in NEB 5-alpha Competent *E. coli* Cells Treated with BamHI and Topoisomerase I Enzymes

Daniela Bolaños, Nancy Sanchez, Michael D. Stone

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRI - CUSP-HLLC

DNA is widely known for its double helix structure, but rarely recognized for the properties it harbors. The goal of this experiment was to understand DNA in its structure through the use of competent *E. coli* cells and pUC19 plasmid. DNA transformation was used to introduce pUC19 into AMPR *E. coli* cell cultures. Purified pUC19 DNA was treated with a restriction endonuclease digest, BamHI, and Topoisomerase I. The enzyme BamHI allowed us to cut the DNA resulting in linear structures. Topoisomerase I gave us control of relaxing the DNA into a circle. With the use of gel electrophoresis, and 1kb ladder, we were able to analyze the different structures in DNA: supercoiled, relaxed, nicked, and linear. An overview of magnetic tweezers was seen to demonstrate how DNA supercoiling relates to its DNA function. For example, DNA supercoiling allows for RNA/DNA synthesis and compacting DNA. Understanding the structural properties of DNA can lead to a better understand of DNA regulation.

POSTER 10

Galaxy Superwinds and the Circumgalactic Medium

Daniel A. Brandt, Jessica K. Werk, J. Xavier Prochaska

Department: Astronomy and Astrophysics

Home Institution: Case Western Reserve University

Summer Program: STEM Diversity - LAMAT

We present equivalent width and column density measurements for Mg-II ions and Na-I atoms in the circumgalactic medium (CGM) surrounding 11 low-z galaxies and their background quasi-stellar objects (QSOs) sourced from the COS-Halos survey. Spectra for measuring Mg-II and Na-I absorption from the galaxies was obtained from Keck/LRIS, spectra for measuring Mg-II absorption in the quasars was obtained from Keck/HIRES, and 3 spectra used for measuring Na-I absorption in the quasars was obtained from ESI. The sample was selected such that all background quasars have impact parameter $R < 75$ kpc to their target galaxies. All galaxies were chosen to be star-forming with a specific star formation rate (sSFR) greater than or equal to 10^{-11} yr^{-1} . Our equivalent width measurements result in an average value for Na-I of $W_{\text{NaI}} = 0.28 \pm 0.07 \text{ \AA}$ and an average value for Mg-II of $W_{\text{MgII}} = 0.5 \pm 0.1 \text{ \AA}$, which is far lower than equivalent width measurements of corresponding to outflows emanating from the galactic

center. We interpret this result as indicating that the ionization parameter of Na-I falls off rapidly as a function of height from the galactic disk, while the varying strength of Mg-II in each spectrum suggests a dependency on environment and galaxy morphology. Future work will corroborate current data to provide insight on the rate of baryon transfer between the CGM and galactic plane, with estimates of mass, temperature, and velocity allowing for rudimentary empirical relationships to be established between star formation rate, average galactic metallicity, and CGM baryon content.

POSTER 11

Discovering Novel Compounds to Stabilize the E2F-retinoblastoma Protein Complex in the Cell Cycle

Elise Brown, Cameron Pye, Tyler Liban, Jason Burke, Scott Lokey, Seth Rubin

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: ACCESS

The retinoblastoma protein (RB) is a key cell cycle regulator. Mutations in the RB pathway cause rapid cell division, which is a hallmark of cancer. RB binds and inhibits the E2F transcription factor until cells are ready to divide. RB is then phosphorylated by cyclin-dependent kinases, which leads to E2F dissociation and its activation of cell cycle genes. The structure of phosphorylated RB was previously determined, and it was found that when phosphorylated, it changes conformation altering the active site and releases E2F. Many cancers have increased kinase levels, which leads to phosphorylated RB, unbound E2F, and rapid cell division. It is hypothesized that if a novel compound can be found to cause phosphorylated RB to have an increased affinity to E2F, a drug can be developed that stops rapid cell proliferation. Such a compound may block the site of pocket-N-terminal association or work by some other mechanism. We previously used a high-throughput fluorescence polarization (FP) anisotropy assay to identify lead compounds that increase E2F binding to phosphorylated RB. In current work, I have repeated the FP assay on screen hits prepared from fresh powders and followed up those results with Isothermal Titration Calorimetry (ITC) experiments. The goal of ITC is to determine the affinity of the RB-E2F complex in the presence of the compound. To date, I have found three compounds that may show promise of enhancing binding of E2F to phosphorylated RB.

POSTER 12

Structure-Driven Analyses of the Human Astrovirus Receptor-Binding Site

Jocelyn Campos, Lucy Yin, Rebecca DuBois

Department: Biomolecular Engineering

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - Packard

Human astrovirus (HAstV) is the second leading cause of viral diarrhea in young children. Astroviruses are about 28nm in diameter and are composed of an icosahedral capsid protein shell surrounding a single-stranded positive-sense viral RNA genome. The molecular mechanisms by which HAstV attaches to human cells are poorly understood. The goal of this

study is to identify the location of the receptor-binding site(s) on the HAstV capsid protein. To do so, we are investigating several recombinant astrovirus capsid protein structural domains and assessing their ability to attach to human cells. First, DNA expression plasmids were constructed in order to inducibly express recombinant capsid domains in *E. coli*. Capsid domains were expressed as fusion proteins after enhanced green fluorescent protein (eGFP) to allow for its subsequent visualization in cell attachment studies. Protein purification was accomplished on an AKTA fast protein liquid chromatography (FPLC) system with affinity and size-exclusion chromatography steps. These studies resulted in the production of several recombinant eGFP-capsid domain samples with high yields (several mgs) and high purity >98%. In collaboration with another researcher in the lab, the purified eGFP-capsid domain samples were incubated with human colon cancer (Caco-2) cells (a model cell line for human astrovirus studies), and cell binding was observed by confocal fluorescence microscopy. Together, these studies will provide exciting new insights into the mechanisms by which HAstV enters human cells.

POSTER 13

Simulated Infrared Observations of High-Mass Star-Forming Regions

Evan S. Carter, Anna L. Rosen, Christine M. Koepferl, Mark R. Krumholz

Department: Astronomy and Astrophysics

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - LAMAT

Understanding the relationship between the prestellar cores from which stars form and the initial distribution of stellar masses remains a significant issue in astrophysics. Infrared observations of the dusty star-forming regions where cores are found, such as those carried out by Herschel, have greatly increased our understanding of these regions. In order to determine how accurately physical structures including prestellar cores are identified by actual observations, we perform synthetic observations on a numerical simulation of a turbulent high-mass star-forming region. We generate dust emission maps from the temperature and density distribution of the dust at wavelengths observed by Herschel. These maps are post-processed with the FluxCompensator code to create synthetic Herschel observations. We then compute dendrograms from the synthetic observations in order to identify dense structures, including prestellar and star-forming cores. By comparison of the synthetic data to the original simulation, we discuss to what degree these structures may fail to be detected by real observations.

POSTER 14

Single Molecule Assay to Identify and Characterize Telomere-binding Drugs as Potential Anti-Cancer Therapeutics

Miguel A. Cervantes, Shankar Shastry, Michael D. Stone

Department: Chemistry and Biochemistry

Home Institution: Hartnell College

Summer Program: ACCESS

The stability and fidelity of eukaryotic chromosomes is shielded by end capping structures called telomeres, which include double stranded DNA repeats of TTAGGG nucleotides. Because the

cell cannot completely copy the lagging strand DNA template, after each round of cell division, the telomeres undergo attrition, leading to cell aging and ultimately cell death. Cancer cells have shorter telomeres than healthy cells, but maintain their telomere length after cell division, implying that they can divide limitlessly. Drugs that bind to telomeres and perturb their structure, thus leading to cell death, can be developed as potential anti-cancer therapeutics. Magnetic tweezers are specialized instruments that can exert force and torque on biological molecules, similar to the forces cells experience during cell division, to study their structural properties. The Stone lab has developed a magnetic tweezers-based assay to probe the effects of torque-induced forces on telomere DNA molecules. This technique will be utilized to investigate the mechanism of action of telomere binding drugs that disrupt telomere structure. Preliminary results have demonstrated that, N-methyl-mesoporphyrin-IX (NMM), binds to negatively supercoiled telomere DNA and stabilizes the formation of structures called G-quadruplexes in the telomere DNA, thus perturbing its global structure. We propose to characterize the mechanism of action of this drug and others, and obtain quantitative information about the telomere-drug interactions including the ligand binding affinity and critical torque for drug binding. This research will serve to develop a single molecule assay as a tool for investigating and characterizing telomere binding molecules as potential anti-cancer drugs.

POSTER 15

Constraining Seasonal and Vertical Distributions of Planktonic Foraminifera for Paleoclimate Reconstruction Since Marine Isotope Stage 3 at the Axial Seamount, Juan de Fuca Ridge

Sami Chen, David Clague, Ana Christina Ravelo

Department: Ocean Sciences

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - IMSD

The ocean plays a critical role in the Earth's climate by absorbing and redistributing heat and storing CO₂. These processes can be effectively investigated using paleoceanography, or the study of past ocean conditions. One region of climatic interest is the California Current, where upwelling brings cold nutrient rich waters to the surface, creating high productivity and a dynamic interaction between circulation and ecology. A 77 cm piston push core was taken from the Juan de Fuca Ridge Axial Seamount using a Remotely Operated Vehicle (2213m, 45.55° N, 130.08° W), an active submarine volcano ~480 km off Oregon's coast. Five radiocarbon dates taken of the core, ranging from 42.6 ka at 77 cm to 17.6 ka at 15 cm, define an average sediment accumulation rate of 2.47 cm/ka and 0.85 cm/ka during the postglacial period (<17.6 ka). Foraminifera, single celled protists, build calcium carbonate shells that record current environmental conditions. Measurements of oxygen isotopes and Mg/Ca ratios of subtropical, subarctic, and arctic planktonic foraminifera species from the core have been used to constrain changes in vertical and seasonal temperature since Marine Isotope Stage 3 (MIS3). Bulk nitrogen isotopes and nitrogen flux provide additional constraints on upwelling strength and insight into local biological productivity and nutrient dynamics. These records provide insight into the regional effects of climate change in the California Current and near seamount volcanism. By reconstructing past environmental conditions, we can better understand present and future climate change patterns.

POSTER 16

Investigation of Naturally Derived Compounds from Indonesian Sea Sponges

David Coppage, Nicholas Lorig-Roach, Phillip Crews

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - MARC

All organisms produce a variety of different compounds which are used for intercellular communication, cellular regulation and defence against foreign organisms. It has been shown that several naturally derived compounds or their derivatives are biologically active as effective treatments for a variety of diseases and for pain management. Because of their versatility, natural products and their derivatives have made up the vast majority of new and effective drugs for the past 20 years, making them a powerful resource in combating illness and disease. The main objective of our work was extracting and analyzing naturally derived compounds from multiple Indonesian sea sponges looking for compounds that express cytotoxicity towards HeLa cancer cells and compounds that could have new novel structures. Compounds were extracted from the sponges and the bacterial colonies that lived in them through exhaustive methanol extractions and separated through solvent partitioning and prep high-performance liquid chromatography (HPLC) into 7 pre-fractions containing different groups of compounds. Tandem liquid chromatography-mass spectroscopy (LCMS) was then used to analyze the different compounds in each fraction based on their mass and isotope patterns to identify possible new compounds. These target compounds were further purified through analytical HPLC and their structures determined through nuclear magnetic resonance spectroscopy (NMR). The 7 pre-fractions from each sponge were plated in a 96 well plate and sent to the Ford Medical Center where they were the cytotoxic activity towards HeLa cancer cells was determined.

POSTER 1

Estimation of Iron Concentration in a Sample Solution by Spectrophotometry

Erika Correa, Kaisar Alhakim, Selam Gebremedhin, Pradip Mascharak

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRI - IMSD

Iron is an essential element found in nature ranging from a variety of minerals to living organisms including animals and plants. In addition, iron is also found in the human body in the ferric form coordinated to hemoglobin, an oxygen transport protein found in red blood cells. Even though it is an essential element, iron can be detrimental to a person's health if found at relatively high concentrations. Iron overload can lead to diseases like hemochromatosis which results in the damaging of vital organs like the liver. In order to determine the concentration of iron in an unknown solution, five standard solutions of different dilutions were made. The reductant hydroxylamine hydrochloride was used to guarantee the ferric form of iron over the ferrous form. 1,10 phenanthroline was the ligand used to bind the iron in solution and sodium acetate was used as a buffer. By the usage of a spectrophotometer, we measured the absorbance at 490 nm and 510 nm to estimate the iron concentration in a sample of water which resulted to be 0.0001344M. The overall goal of the experiment was to use basic lab

techniques to get accurate results and to determine the iron concentration in a sample solution using a standard curve.

POSTER 17

The Effect of Stress on Hematopoietic Stem Cell Differentiation Pathways

Daniel Cruz, Sarah V. Mendoza, Gloria E. Hernandez, Anna E. Beaudin, Camilla Forsberg

Department: Chemistry and Biochemistry

Home Institution: Hartnell College

Summer Program: ACCESS

Recent use of lineage tracing models has provided further insight into the normal differentiation pathways that hematopoietic stem cells (HSCs) take. The Forsberg lab has utilized a fate-mapping model, herein referred to as the “FlkSwitch” model, in which expression of the tyrosine kinase receptor Flk2 drives switching of a ubiquitously expressed dual-color transgenic reporter from tomato to green fluorescent protein (GFP), which signifies differentiation through a Flk2+ stage. As reporter-switching results from an irreversible genetic change, this model can be used to track HSC-derived blood cells with history of Flk2 expression. Previous characterization of the FlkSwitch model revealed that all adult HSCs express tomato and that all mature lineages express GFP, reflecting their differentiation through a Flk2+ intermediate. Recently our lab has demonstrated that a GFP+ HSC that is restricted to fetal development plays a role in innate immunity. Here, we use the FlkSwitch model to determine whether the introduction of the immunostimulant polyinosinic-polycytidylic acid (poly I:C), a synthetic analog of a double stranded RNA, causes a deviation in normal adult HSC differentiation pathways. We also want to resolve whether there is a persistence of fetal-restricted GFP+ HSCs into adulthood, and if they can be induced out of quiescence by the introduction of poly I:C. Using flow cytometry to analyze peripheral blood following poly I:C injections in FlkSwitch mice, we have observed subtle changes in reporter expression within myeloid cells which could be indicative of a change in normal HSC differentiation pathways.

POSTER 18

Is the Increased Virulence of LasA Protease Mutants Due to Increased Expression of LasB Protease?

Anthony Del Cid, Aaron Sullivan, Suzanne Fleiszig

Department: Vision Science

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - MARC

Microbial Keratitis (MK) is an infection of the cornea resulting in ocular pain, reduced visual prowess, heightened photo-sensitivity, and ocular discharge. Untreated MK can lead to permanent blindness. The bacterium *Pseudomonas aeruginosa* is the #1 cause of contact lens related MK. Previously the Fleiszig lab elucidated a relationship between the bacterial Type 2 secretion system (T2SS) and its affect on corneal traversal, the first stage in MK. The focus of this project is to investigate the proteases secreted by the T2SS; proteases are enzymes that break down proteins. *P. aeruginosa* mutants that lack the protease LasB are unable to traverse through the corneal epithelium, diminishing virulence. Intriguingly, mutant strains that lack a different T2SS protease, LasA, phenotypically appear more virulent than WT strains. One

possibility is that mutant LasA strains up-regulate expression of LasB, in order to compensate for loss of LasA. To investigate if this is true relative transcription expression in unaltered bacteria (WT), bacteria lacking LasA (-LasA), and lacking both LasA and B (-LasAB) were compared by Real Time PCR by extracting RNA from overnight cultures. Results from Real-Time PCR is currently inconclusive; fifty percent of the -LasA samples showed more than 50% reduction in LasB transcription, while the rest showed no change. We believe this to be attributed to inefficient growth conditions used for inducing the T2SS required for maximum LasB production. In addition, the optical densities' used for experimentation were not as tightly standardized as could be. Further work is necessary in order to elucidate the relationship between LasA deficient strains and LasB production during corneal traversal.

POSTER 19

The Effects of Developmental Manganese Exposure on Norepinephrine Transporters in the Prefrontal Cortex

Marlyn Escobar-Zamora, Travis Conley, Donald Smith

Department: Microbiology and Environmental Toxicology

Home Institution: Cabrillo College

Summer Program: ACCESS

Exposure to elevated manganese (Mn) levels from environmental sources has been linked to attention, cognitive, and fine motor deficits in children. The catecholaminergic system, of which the neurotransmitter norepinephrine and its transporter (NET) are members, plays an important role in prefrontal cortex (PFC) function, and the PFC brain region is essential for regulating many of the neurobehavioral functions (attention, impulse control, etc.) that appear to be affected in Mn-exposed children. In fact, changes in the norepinephrine system may help explain the deficits we see in young individuals exposed to Mn. I hypothesize that Mn exposure alters expression of NET in the prefrontal cortex (PFC). To determine the effect of Mn on NET protein levels, immunohistochemistry was used to detect the protein in rat brain tissues. In order to visualize the rat PFC and target the NET protein, the application of a primary and secondary antibody (containing a fluorescent tag) was used to target the NET antigen. Following staining, rat tissue was imaged using fluorescence microscopy and fluorescence was measured using Imaris quantification software. In conclusion, we expect Mn-exposed individuals to express more of the NET protein.

POSTER 20

The Design and Functional Characterization of Minimal Telomerase Essential N-terminal Constructs

Gabriella O. Estevam, Christina D. Palka, Michael D. Stone

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - Packard

Telomerase is an enzyme that extends the telomeric ends of eukaryotic chromosomes. Improper activation of telomerase has been associated with various diseases including 90% of cancers. Jointly, telomerase reverse transcriptase (TERT) and telomerase RNA (TER) form a distinct ribonucleoprotein complex necessary for catalytic activity. Specifically, the telomerase essential N-terminal (TEN) domain of TERT has been shown to play a crucial role in telomerase catalysis and a high-resolution crystal structure has been solved of this domain from the model organism *Tetrahymena thermophila*. Although the TEN domain is implicated in binding to both telomere DNA and TER, the molecular details of these interactions and the manner in which TEN contributes to telomerase activity remains unclear. Here, we employed protein engineering using site-directed mutagenesis to create several truncated constructs of the *Tetrahymena* TEN domain. Primers were designed to generate protein end deletions, in addition to the removal of unstructured regions of the protein as shown in the crystal structure, through the polymerase chain reaction (PCR). The goal of this project is to generate improved TEN domain constructs that are amenable to biochemical and high-resolution structural analysis by NMR and X-ray crystallography. Ultimately, we aim to obtain an atomic resolution model that explains how the evolutionarily conserved TEN domain orchestrates multiple sites of nucleic acid binding to facilitate telomerase function.

POSTER 21

Effects of Ocean Acidification on Estuarine Fish Predation

Erica Ferrer and Kristy Kroeker

Department: Ecology and Evolutionary Biology

Home Institution: UC Santa Cruz

Summer Program: No Program Affiliation

The presence of carbon dioxide (CO₂) in the atmosphere has risen at an unprecedented rate over the last two centuries. As of today, there is roughly 400 ppm of CO₂ in the atmosphere, versus an estimated 280 ppm at the start of the Industrial Revolution. This concentration continues to grow exponentially and threatens the ecological functioning of several terrestrial and marine ecosystems. Such a shift in marine chemistry must have significant consequences, but as of yet, very few studies document what those consequences are or will be. My project addresses the effects of ocean acidification on the predatory behavior of fish in estuarine ecosystems, like the seagrass beds of Elkhorn Slough. I am examining predation rates among Shiner Surf Perch (collected from Elkhorn Slough) under ambient and low pH conditions. If decreased pH leads to an increase in the rate by which perch feed on invertebrate grazers, the onset of ocean acidification could negatively affect estuaries via detrimental trophic change.

POSTER 22

Phylogenetic Signal in Plant Pathogen Sporulation: Host Species that are Closely Related to Main Host Allow the Production of the Most Spores

Shaneece Flore and Gregory S. Gilbert

Department: Environmental Studies

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - MARC

Fungal plant pathogens are known to be more likely to infect a plant and cause more severe symptoms if the host is closely related to the pathogen's main host. However, pathogens may be unable to reproduce in certain host plants even if the plant shows symptoms of disease. The amount of inoculum produced by the pathogen in different potential host plants may also vary through phylogenetic signal. In this experiment, we collected necrotrophic fungi from plants found in the UCSC natural reserve. We then inoculated those fungi onto leaf pieces of plants of varying phylogenetic distances to the main host. After a few weeks, we counted the spores generated on the leaf pieces for each species. We expect the fungi to sporulate more on species closely related to the main host than those that are more distantly related. In natural and agricultural ecosystems, symptomatic hosts that are close relatives to the main host may contribute more inoculum than more distantly related symptomatic hosts. A phylogenetic signal in fungal pathogen sporulation may further explain the mechanisms by which pathogens help shape the diversity of natural ecosystems.

POSTER 23

Smart Grid: Designing an Algorithm for Autonomous Load Balancing to Maintain Grid Health

Miguel Flores Silverio, Kapil Sinha, Zachary Graham, Tela Favaloro, Michael Isaacson

Department: Electrical Engineering

Home Institution: Hartnell College

Summer Program: CUSP-HLLC STEM Internship

As result of increased use of renewable energy sources for power generation, the overall quality of electrical services has degraded due to instability caused by reliance on natural factors. A proposed approach to mediate this effect is to stabilize mains frequency. In order to demonstrate the feasibility and efficacy of this method as potential solution, we designed and implemented an algorithm for a home-built micro-grid testbed that regulates frequency by controlling deferrable residential loads. The main algorithm runs on an industrial single board computer in conjunction with driver programs whose main purpose is to monitor and control their respective loads. The primary purpose of the main algorithm is to monitor frequency and orchestrate each of the driver programs accordingly to bring the frequency within an acceptable range. Each of the driver programs takes into account certain characteristics unique to each load, such as duty cycle and temperature, all with minimal impact on the consumer. The modular design allows the main algorithm to be load-independent and together with the testbed will allow for further development of 'smart' loads. Having loads autonomously adjusting their power consumption based on the state of the grid will help maintain the health of the power grid, and thus potentially prevent crises such as blackouts in a variety of situations – both emergency situations and everyday deviations –with imperceptible effect on the consumer.

POSTER 24

Investigating the Bioavailability and Stability of N-Alkylated Cyclic Peptides

Jose Garcia, Christain Ettiene, Rushia Turner, Scott Lokey

Department: Chemistry and Biochemistry

Home Institution: Hartnell College

Summer Program: ACCESS

Peptides have many key roles in biology, from transmitting signals in the brain to binding to receptors on cells. N-methylated cyclic peptides have gained attention in drug discovery because they are more stable to proteolysis and they are more likely to exhibit passive membrane permeability. The Lokey Research Group has exhaustively examined the pharmacokinetics of the multiple N-methylated cyclic peptide cyclo[L-Leu-L-Leu-NMe-D-Leu-NMe-L-Leu-L-Tyr-NMe-D-Pro], also known as 1NMe3. This compound was shown to have oral bioavailability of 28% in rats, but it was extensively metabolized in the liver via N-demethylation. Three analogs of 1NMe3 are being synthesized in which the N-methylated leucine residues are replaced with N-isobutyl alanine residues, both individually and in tandem. These analogs represent the starting point for a larger investigation into the effect of bulky N-alkyl substituents on the membrane permeability and hepatic stability of cyclic peptides. The passive membrane permeability of the three N-isobutyl alanine-containing compounds will be tested using both cell-free and cell-based assays. Hepatic stability will be evaluated using an *in vitro* human liver microsome assay. The membrane permeability and hepatic stability data will then be used to develop and synthesize more extensive N-alkylated cyclic peptide libraries.

POSTER 1

Estimation of Iron Concentration in a Sample Solution by Spectrophotometry

Selam Gebremedhin, Kaiser Alhakim, Erika Correa, Pradip Mascharak

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRI - IMSD

Iron is an essential element found in nature ranging from a variety of minerals to living organisms including animals and plants. In addition, iron is also found in the human body in the ferric form coordinated to hemoglobin, an oxygen transport protein found in red blood cells. Even though it is an essential element, iron can be detrimental to a person's health if found at relatively high concentrations. Iron overload can lead to diseases like hemochromatosis which results in the damaging of vital organs like the liver. In order to determine the concentration of iron in an unknown solution, five standard solutions of different dilutions were made. The reductant hydroxylamine hydrochloride was used to guarantee the ferric form of iron over the ferrous form. 1,10 phenanthroline was the ligand used to bind the iron in solution and sodium acetate was used as a buffer. By the usage of a spectrophotometer, we measured the absorbance at 490 nm and 510 nm to estimate the iron concentration in a sample of water which resulted to be 0.0001344M. The overall goal of the experiment was to use basic lab techniques to get accurate results and to determine the iron concentration in a sample solution using a standard curve.

POSTER 25

Designing Mini-Games for Speech With Sam

Taylor Gotfrid, Zachary Rubin, Sri Kurniawan

Department: Computational Media and Computer Engineering

Home Institution: UC Santa Cruz

Summer Program: SURF-IT

Speech With Sam is a game that acts as a virtual form of speech therapy for children recovering from corrective surgery for cleft palate. After corrective surgery, children often still need speech therapy outside the supervision of their therapist. This position is often delegated to the parents who are unfamiliar with what to look out for, so mistakes often go unnoticed which lowers the effectiveness of speech therapy. Traditional speech therapy is also boring for children, which is poor motivation to continue sessions. Speech With Sam is a mobile system that integrates voice recognition to accurately assess a child's progress throughout a series of mini-games. These games must be motivating to ensure that kids want to play. They also need to keep their attention so that the game can be played multiple times a week for maximum impact. Using the Cocos2d framework, three mini-games were created: Bounce, Space Invaders, and Road Trip. In each of these mini-games the player is presented with a game in which he or she must use voice input to solve. Each game evaluates a different group of phonemes that children going through speech therapy have trouble pronouncing distinctly. Each mini-game is tailored to a certain vocal structure and is designed to get the child to repeat the target phrase as much as possible.

POSTER 26

Cosmology: Stellar Mass vs. Stellar Velocity Predictions from the Bolshoi-Planck Simulation Using Age Matching

Stephanie J. Hadley, Aaron J. Romanowsky, Aldo Rodriguez-Puebla, Joel Primack

Department: Physics

Home Institution: San Jose State University

Summer Program: STEM Diversity - LAMAT

A 2011 study compared the rotation velocity of spiral galaxies and the velocity dispersions of elliptical galaxies with predictions from the high-resolution Λ CDM n-body Bolshoi cosmological simulation in which stellar masses were assigned to galaxies using abundance matching, and the predictions rather well reproduced the observed Tully-Fischer and Faber-Jackson relations. In 2013 it was shown that putting old red galaxies with little star formation in early-forming dark matter halos and young blue galaxies with ongoing star formation in late-forming halos, a method called Age Matching, correctly predicts the spatial correlations of red and blue galaxies. In order to obtain a better understanding of galaxies and their associated dark matter halo properties, we use a simulation with updated cosmological parameters, the Bolshoi-Planck simulation, and we study the effects of applying different Age Matching assumptions. We also improve the previous treatment of the gravitational response within the dark matter halos due to the stellar mass. The previous work calculated the circular velocities of galaxies at a radius of 10 kpc assuming that all the stellar mass was within that radius. We will improve the analysis by considering the statistics of more massive galaxies for which the stellar mass is more broadly distributed. We predict that our results will show a bimodal distribution of the red and blue galaxies without adherence to conformity as previous studies suggest. This will lead to further studies to better understand the galaxy to dark matter halo connection.

POSTER 27

The Design and Overexpression of Aldehyde/Alcohol Dehydrogenase Genes in *Haloferax volcanii* for the Conversion of Butyryl-CoA to Butanol

Jazel Hernandez, Dominic Schenone, Alonzo Lee, Sanusha Bijj, Derek Brekke, Jackson DeKloe, Vijay Jayant, Megana Kunda, Isabel Madau, Kendal Prokopakis, David Bernick

Department: Biomolecular Engineering

Home Institution: UC Santa Cruz

Summer Program: iGEM - CUSP-HLLC

Using fossil fuels as the world's dominant source of energy is no longer sustainable and has led to lasting negative effects on the environment and irreversible changes to our climate. As a result, the development of energy-dense carbon neutral biofuels has gained increased research interest. Butanol, a four carbon alcohol that can be metabolized from glucose and from cellulose, a glucose polymer is one possible solution. Continuing previous work done to engineer a glucose to butyryl-CoA pathway in the halophilic archaeon *Haloferax volcanii*, research is now being done to quantify the presence of butyryl-CoA and butanol in the engineered mutant and at the same time aldehyde-alcohol fusion and single genes are being designed to convert butyryl-CoA to butanol. Several approaches are being developed for the design and quantification of the of the genes. These include the identification, optimization and overexpression of fusion and single genes found in other halophilic organisms and the creation of fusion genes using native aldehyde and alcohol dehydrogenase genes(aldy3, aldy5 and adh2) from *H. volcanii*. At the same time, there is evidence that *H. volcanii* under acidogenic conditions activates these same native genes and work is being done to detect the existence of butanol under those conditions. The plasmid constructs are currently being designed using a overexpression plasmid via gibson assembly and will soon be transformed into *H. volcanii*. Once successful transformants are found, an *in vitro* protein assay will be performed on the expressed proteins to quantify their activity with butyryl-CoA as the substrate.

POSTER 28

Modeling of the Ideal Microgrid and Analysis of Solar Photovoltaic Systems with Electric Vehicle Charging

Jessica Herrera, Rachel Meyer, Robert D. Cormia, Joel Kubby

Department: Electrical Engineering

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - CAMP/Advanced Studies Laboratories

Low-carbon and zero-emission electric vehicle (EV) charging solutions are a key engineering and development focus in sustainable energy design for transportation. Combinations of solar photovoltaic (PV) arrays and battery storage offer standalone and off-grid capability with zero greenhouse gas (GHG) emissions. By analyzing data collected from Ames' Photovoltaic Testbed (PVOT) and the managed grid at Foothill College, we in Energy and Sustainability Solutions at the Advanced Studies Laboratories are gaining insights into power flows, PV arrays and energy storage for use in EV charging, and the optimal microgrid configuration. Key figures researched include total zero emission electric vehicle miles traveled (EVMT), amount of carbon displaced, and costs and benefits of various solutions and microgrid configurations. This project will benefit NASA-ASL and Foothill College's District in developing examples of integrated energy/Zero Net Emission (ZNE) buildings, and can be extended as a research template for scalable and sustainable energy solutions for developing countries without reliable electrical

grids. Project deliverables include analysis of existing and ongoing PV-EV charging data for Ames' PVOT and solution modeling for Foothill's proposed 14 EV chargers.

POSTER 29

Printed Circuit Board Stators for Brushless DC Motors

Emmanuel Kayede, Dmitriy Rivkin, Gabriel Elkaim

Department: Computer Engineering

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - UC LEADS

Brushless DC (BLDC) motors can be coupled with momentum wheels to achieve attitude control for small satellites (CubeSats). These tiny satellites present extreme size and weight constraints, which often cannot be satisfied by off-the-shelf solutions. In general, a motor/momentum wheel combination should be as flat and wide as possible, thus minimizing its weight while maximizing its moment of inertia. If one is willing to design a custom motor, performance can be maximized by integrating the motor and inertial wheel into the same component, making this motor wide and with a heavy rotor. The stator is most easily fabricated by making use of existing PCB manufacturing technology. Leveraging this technology allows for high precision coil placement and significantly reduced build time as compared to wound stator coils, as well as producing an exceptionally thin product. Computer-aided drafting (CAD) was used to design a six-layer stator PCB. Back electromotive force (back EMF) and torque constant was predicted. The design was shipped off to a fab house for fabrication.

POSTER 30

Introduction of Cancer Mutations into Human Embryonic Stem Cells

Sandrine Kyane, Olena Morozova, Ian Fiddes, Sofie Salama, David Haussler

Department: Biomolecular Engineering

Home Institution: UC Santa Cruz

Summer Program: Research Mentoring Institute

Gliomas are the most common malignant brain cancers diagnosed in the United States. They arise from three types of glial cells of the brain known as astrocytes, oligodendrocytes, and ependymal cells. Among other factors, gliomas are classified by their World Health Organization (WHO) grade, grade I-IV. While many grade II and grade III gliomas are known to be associated with mutations in genes IDH1 and ATRX, the exact tumorigenic mechanisms of these mutations remain unknown. Using the recently described CRISPR-Cas9 system, IDH1 and ATRX mutations can be introduced into human embryonic stem cells. In this work, an existing line of human embryonic stem cells (H9) was adapted to stem beads FGF2 for the preservation of cell pluripotency. We will use CRISPR to introduce IDH1 and ATRX mutations into these stem cells. Successful generation of embryonic stem cell lines carrying glioma mutations would provide an invaluable model system to study glioma development in the laboratory.

POSTER 31

Increasing the Binding Affinity of ASIP to MC1R by Modification of the Ligand's C-terminal Loop

Cynthia Lai, Jillian Miller, Glenn Millhauser

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - IMSD

The melanocortin system regulates pigmentation, UV protection, inflammation and energy balance. The melanocortin 1 receptor (MC1R) specifically has a role in pigmentation and UV protection. The disulfide-rich antagonist agouti signaling protein (ASIP) binds to MC1R resulting in the production of pheomelanin. On the other hand, the agonist α -melanocyte-stimulating hormone (α -MSH) results in the production of eumelanin. Melanocytes naturally produce eumelanosomes which are small granules containing eumelanin that protects DNA from UV radiation. In melanoma, chemotherapy is ineffective because eumelanosomes export anticancer drugs out of the cell. By modifying ASIP we can enhance its binding affinity to MC1R and decrease the production of eumelanosomes. We focused on varying the sequence of the C-terminal loop of ASIP because the C-terminal loop is necessary for inverse agonist activity specifically at MC1R. We replaced serine, the 129th amino acid of wild type ASIP, with leucine, to improve hydrophobic interactions with the receptor. Using a CEM liberty microwave peptide synthesizer, mutant ASIP S129L was prepared on a H-rink amide resin and then cleaved under acidic conditions. The peptide was purified with reverse-phase high performance liquid chromatography (HPLC) and electrospray mass spectrometry. We have purified pure unfolded ASIP S129L and are currently optimizing the oxidative fold conditions. We plan to vary the solvent, adjust the levels of oxidizing agents, and change the amount of disulfide shuffling enhancers. Overall, folded ASIP S129L is predicted to have stronger hydrophobic interactions with MC1R and become a helpful therapeutic for skin cancer chemotherapy.

POSTER 32

Isolation of Salt Tolerant Cellulase Producing Halophiles for Biobutanol Production in *Haloferax volcanii*

Adriana Landeros, Jocelyn Simlick, Sofia Menendez, Tina DeLeon, Andre Baxter, Raymond Bryan, Henry Vilas, David L. Bernick

Department: Bio Molecular Engineering

Home Institution: UC Santa Cruz

Summer Program: iGEM - CUSP-HLLC

Production of butanol via microbiological metabolic processes is being investigated as an alternative for fossil fuels. *Haloferax volcanii* is an ideal microbe that can be utilized in breakdown and fermentation of saline treated plant matter [cellulose rich biomass] for butanol biofuel production. Our study will focus on finding halophiles with cellulases that can fold and work in high saline environments. We (iGEM field team) have collected samples from the Salt Ponds near Fremont, California and performed single species isolations from colonies that have shown robust growth. The inoculation and enrichment process was performed to select for cells that will produce a cellulase using microcrystalline cellulose as the sole carbon source in their growth media. Next, we will test for glucose abundance, in order to select for high activity cellulases. From there, we will identify the species by using its small subunit rRNA and performing PCR [polymerase chain reaction] to amplify regions that are specific for archaea.

The amplified DNA will be sequenced to identify species. If species have previously been identified we will use BLAST [a database that compares and correlates similar sequences] to identify target cellulase enzymes and attempt to transform *H. volcanii*. If we find a novel organism, we can then use whole genome sequencing to produce a draft sequence of its genome, and learn about its cellulose and carbohydrate metabolizing capabilities.

POSTER 33

Design, Construction, and Implementation of a Renewable Energy Integrated Test Bed to Regulate Frequency Deviation

J. Benjamin Lara-Chavez, Zachary Wedel, Zachary Graham, Tela Favaloro, Michael Isaacson

Department: Electrical Engineering

Home Institution: Hartnell College

Summer Program: CUSP-HLLC STEM Internship

With the increase in renewable energy generation contributing to the production of power in the grid, over or underproduction of power due to fluctuations of environmental conditions induce instability in the frequency of the AC power within the grid. A potential solution that would ensure electrical service quality is by direct control of load behavior in response to the frequency deviation. Thus, power consumption can be deferred to stabilize the frequency using devices that have the ability to convert electrical energy into thermal energy for storage. To implement these “smart” loads, we have designed and constructed a Test Bed that models a residential electrical system. The Test Bed integrates solar energy generation with a grid tie-in and/or generator, while a mounted single board computer senses frequency through a smart meter and modifies the load power usage. The Test Bed was built to National Electric Code to accommodate safety standards; which includes accounting for maximum current-draw by selecting appropriately sized circuit breakers and wire gauges. By creating a model grid that incorporates renewable sources, we can identify and test different types of deferrable loads on a small scale and then use these results for replication on a larger scale.

POSTER 34

A Search for Marine Sponge-derived Natural Products As Novel Inhibitors of Human 12-Lipoxygenase

Alex Leija, Steven R. Perry, Theodore R. Holman

Department: Chemistry and Biochemistry

Home Institution: Gavilan College

Summer Program: ACCESS

Lipoxygenases (LOXs) are a group of iron-containing enzymes that accelerate the oxidation of polyunsaturated fatty acids. They are associated with cell proliferation, differentiation and the pathogenesis of multiple diseases such as cancer, inflammation, and diabetes. The catalyzed oxidation of the polyunsaturated fatty acid Arachidonic Acid, leads to bioactive hydroxyeicosatetraenoic acid metabolites (HETES) that are paramount in signaling certain physiological responses. Human platelet-type 12-LOX catalyzes the oxidation of Arachidonic Acid at the twelfth carbon, and is significant for its exhibited function in diabetes, a disease that

affects more than 380 million people worldwide. In this study, a group of Indonesian marine sponge extracts and fractions were tested for LOX inhibitory activity. A UV-Vis spectrophotometric assay was employed to measure IC50 inhibition values. Of the twenty samples tested, two extracts exhibited significant inhibitory activity. Sample 95648F inhibited both 12-LOX and 15-LOX. Sample 96613F inhibited only 15-LOX. Testing of less complex fractions of the crude extracts is in progress.

POSTER 35

Searching for Variants of *Wolbachia* Through Apoptosis Rates

Nassim Lemseffer, Heather DeBruhl, William Sullivan

Department: Molecular, Cell and Developmental Biology

Home Institution: UC Santa Cruz

Summer Program: DeAntonio-Estabrook Undergraduate Research Award

Currently no techniques are available to generate *Wolbachia* variants in the lab. Consequently, we have taken an alternative approach in which we isolate *Wolbachia* from insects captured in the wild and screen for natural *Wolbachia* variants. To this end, fifty lines of *Drosophila* from nature were generated and analyzed by PCR for the presence of *Wolbachia*. Each of the lines was assayed for its affect on apoptosis, programmed cell death, in the *Drosophila* oocyte. The basis of the hypothesis stems from *Wolbachia* robustly suppressing apoptosis in other insects and nematodes. Therefore, if stable variants in the rate in which *Wolbachia* influences apoptosis can be identified, the responsible *Wolbachia* genes could be mapped and identified. The two species of *Drosophila* from nature assayed for apoptosis rates were *D. melanogaster* and *D. simulans*. By staining oocytes of *Wolbachia*-cured and infected *Drosophila* lines with acridine orange, a marker for cells undergoing apoptosis, the effect to *Wolbachia* on cell death rates could be determined. To date, fifteen *D. melanogaster* lines have been stained. Currently we find that paired uninfected and infected lines exhibit similar rates of cell death.

POSTER 36

One-Pot Synthesis of Triphenylphosphine-Capped Palladium Nanoclusters

Benjamin Little, Mauricio Rojas-Andrade, Shaowei Chen

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: No Program Affiliation

Triphenylphosphine-protected palladium nanoclusters were synthesized by a facile, one-pot reduction of palladium triphenylphosphine complex with sodium borohydride. The resulting nanoclusters were characterized via AFM and were found to have an average diameter of 1.7 +/- 0.82 nm corresponding cluster sizes of < 10 atoms. High-resolution UV-vis spectra show stereotypical staircase-like peaks throughout the 200 nm region corresponding to the molecular-like electronic transitions characteristic of small metal nanoclusters and relatively strong fluorescence was observed at 305 nm upon excitation at 265 nm. The electrocatalytic activity for the oxygen reduction was determined with these nanoclusters exhibiting an onset potential at 0.95 +/- 0.1 V vs RHE, an improvement over commercial palladium catalysts of approximately

200 mV. The facile synthesis and relatively high electrocatalytic activity of these nanoclusters make them promising candidates for fuel cell applications.

POSTER 37

Simulations of Red Giant Star Cluster Wind Collisions

Jose Lopez, Melinda Soares-Furtado, Enrico Ramirez-Ruiz

Department: Astronomy and Astrophysics

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - CUSP-HLLC

Modern advances in technical science require sophisticated computer simulations to make further explorations possible. The simulations should be able to depict the various physical phenomena that are difficult to observe directly, either due to extremely large or small length scales, or across time scales ranging from microseconds and millions of years. The collisions between the stellar winds of red giant stars in clusters present such a scenario, as they are difficult to observe directly and must be studied using simulations. The FLASH hydrodynamical physics simulator was used to evolve the structure of stellar winds from a cluster of red giants over time. FLASH produces a series of HDF5 files containing vast arrays of physical parameters, representing individual snapshots of these events over the desired time interval. For the sake of physical fidelity and to maintain comprehensiveness, the files were rendered and analyzed at different camera angles using Yt, a Python package tailored specifically for visualization of astrophysics simulations. I employed Yt to demonstrate manipulations of the HDF5 files and stitched them together to create equally useful and aesthetic animations. The animation created for the star cluster simulation aptly shows how the winds expand over time. The ultimate goal of this project is to create a program which would allow the user to stop the animation at any point in time and manipulate the viewing angle in 3-space in any way desired by means of input more intuitive than keystrokes; doing this on a 3-D screen would be ideal.

POSTER 38

Understanding the Stream-Disk Interaction in Mass-Transferring Binary Star Systems

Aaron Lopez, Ian Weaver, Phil Macias, Enrico Ramirez-Ruiz

Department: Astronomy and Astrophysics

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - LAMAT

Observations of a wide range of interacting binary stars show that accretion disks in these systems display pronounced deviations from axisymmetry, for which the most obvious agent is the impact of the gas stream from the mass-donating companion star onto the accreting star's disk due to Roche lobe overflow. The complexity of this stream-disk interaction mandates the use of sophisticated hydrodynamic simulations to fully explore its consequences, though it is reasonable to expect each class to share some common disk interaction features. Here I use multi-dimensional, high-resolution simulations via the FLASH hydrodynamical physics code in conjunction with Yt, an open source astrophysics Python package, for visualization and analysis these phenomena. I focus primarily on the various system parameters and their effects on the

ensuing angle of impact, structure of the hotspot region, and other relationships overlooked in previous analyses.

POSTER 39

Testing Kinesins 4-14 for Roles in Axonal Transport of *Drosophila melanogaster*

Abyan Mama-Farah, Inna Djagaeva, William Saxton

Department: Molecular, Cell and Developmental Biology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - IMSD

Understanding how cells move, organize and distribute the organelles containing the building blocks for life is one of the fundamental goals of cellular biology. My project studies the mechanisms driving intracellular and cytoplasmic organization *in vivo*, using *Drosophila melanogaster* as a model organism. The focus is on motor proteins in the kinesin superfamily and their roles in long distance axonal transport. While kinesins 1&3 have been shown to be involved, it is unclear whether any of the other kinesins (4-14) are. We attempt to answer this question using real-time imaging of live larva through the body wall. We employ the UAS/GAL4 system that allows precise control over spatial and temporal expression of specific transgenes. Flies containing a motor neuron specific driver (OK6-GAL4) and a responder (UAS-ANF-GFP) are crossed with UAS-RNAi transgenic flies. These crosses produce progeny containing fluorescent-protein tagged dense core vesicles in a subset of tissues while also expressing short hairpin RNA (shRNA). The shRNA knock down the function of the specific kinesin in motor neurons only and thus allows us to test for genes essential in early fly development. By imaging larvae with confocal microscopy, the movement of organelles can be recorded and analyzed for differences in flux and velocity. The same animals are also examined for the presence of focal accumulations and distal paralysis. With further imaging and investigation we hope to answer the broader question of what role do the less studied kinesins play in long distance axonal transport of various organelles.

POSTER 40

Stellar Explosions: A Shocking Look into Supernova Propagation

Jazmin Maravilla, Gabriela Montes, Enrico Ramirez-Ruiz

Department: Astronomy and Astrophysics

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity – LAMAT – California Space Grant

The sudden release of a large amount of energy into a background of fluid density creates a strong explosion. This type of explosion has a shock wave or blast wave, from the point where the energy was released. Also known as the Sedov-Taylor explosion, this problem provides a useful test to validate a hydrodynamical numerical scheme. By running simulations using a hydrodynamical Fortran code called Mezcal, we were able to manipulate the factors that characterize the explosions. Such factors include internal and external density, pressure, and radius. From these factors we can derive key components of the explosion, including volume, kinetic and thermal energy, and post-shock pressure.

POSTER 41

Comparing Bacterial Attachment on the Marine Alga *Pseudo-nitzschia*.

Sanjin Mehic and Marilou Sison-Mangus

Department: Ocean Sciences

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - Packard

Harmful algal blooms are an increasing threat to the Pacific Coast. 2015 had one of the spatially largest, and temporally longest, *Pseudo-nitzschia* blooms in nearly twenty years. *Pseudo-nitzschia* blooms are known to often be highly toxic and detrimental to wildlife. The neurotoxin produced by the algae can ripple through the entire food chain creating a direct risk for seafood consumption. Research has implicated numerous environmental factors to the rise and demise of *Pseudo-nitzschia* blooms, but it is still unclear whether or not bacterial interactions are mainly responsible for this ecological phenomenon. In addition, previous experiments find differences in *Pseudo-nitzschia* physiology when co-cultured with specific bacteria; however, it remains unknown whether or not the attachment of bacteria to the host is a contributing factor to the differences in physiology. In this study, we seek to identify direct and indirect interactions between bacteria and *Pseudo-nitzschia* cells. We employed epifluorescent and scanning electron microscopy to visualize attachment of bacteria to *Pseudo-nitzschia*. DAPI and ATTO dyes were used for staining cultures for epifluorescent imaging. Imaging of laboratory grown cultures will also be compared to fresh environmental samples and subsequently discussed.

POSTER 42

Alternative Hematopoietic Differentiation Pathways Under the Effect of Hematopoietic Stress

Sarah Mendoza, Daniel Cruz, Gloria Hernandez, Anna Beaudin, Camilla Forsberg

Department: Chemistry and Biochemistry

Home Institution: Monterey Peninsula College

Summer Program: ACCESS

Flk2 is a receptor tyrosine kinase whose expression is associated with differentiation and loss of self-renewal capability. Hematopoietic stem cells (HSCs) give rise to all mature blood cell lineages through a Flk2+ progenitor stage. The Forsberg lab has established a "FlkSwitch" lineage tracing model that uses Flk2 expression to drive the irreversible switching of a fluorescent reporter system from red (Tomato) to green fluorescent protein (GFP). Characterization of this model revealed that self-renewing HSCs are Tomato+ and must differentiate through a Flk2+ stage to give rise to all GFP-expressing mature cell lineages. Recently, a fetal-restricted GFP+ HSC was shown to exist and contribute to innate immunity. We hypothesize that acute hematopoietic stress, such as viral infection, may induce alternative differentiation pathways by causing Tomato+ HSCs to bypass the Flk2+ progenitor stage and therefore give rise to Tomato+ mature progeny. Alternatively, acute stress may induce the emergence of the developmentally-restricted GFP+ HSCs from quiescence in adulthood. We tested whether treatment with polyinosinic-polycytidylic acid (plpC), an immunostimulant that mimics viral infection, could induce alternative differentiation pathways from HSCs. Peripheral blood samples were analyzed using flow cytometry following plpC injection in adult FlkSwitch mice. A slight decrease in the proportion of GFP+ platelets was observed in the peripheral blood of plpC-treated males, as well as a slight decrease in the proportion of GFP+ GMs in the

peripheral blood of plpC-treated females. These changes suggest that viral stress stimulates the rapid production of mature lineages downstream of HSCs by bypassing the Flk2+ progenitor stage.

POSTER 28

Modeling of the Ideal Microgrid and Analysis of Solar Photovoltaic Systems with Electric Vehicle Charging

Rachel Meyer, Jessica Herrera, Robert Cormia, Joel Kubby

Department: Electrical Engineering

Home Institution: Foothill College

Summer Program: Advanced Studies Laboratories

Low-carbon and zero-emission electric vehicle (EV) charging solutions are a key engineering and development focus in sustainable energy design for transportation. Combinations of solar photovoltaic (PV) arrays and battery storage offer standalone and off-grid capability with zero greenhouse gas (GHG) emissions. By analyzing data collected from Ames' Photovoltaic Testbed (PVOT) and the managed grid at Foothill College, we in Energy and Sustainability Solutions at the Advanced Studies Laboratories are gaining insights into power flows, PV arrays and energy storage for use in EV charging, and the optimal microgrid configuration. Key figures researched include total zero emission electric vehicle miles traveled (EVMT), amount of carbon displaced, and costs and benefits of various solutions and microgrid configurations. This project will benefit NASA-ASL and Foothill College's District in developing examples of integrated energy/Zero Net Emission (ZNE) buildings, and can be extended as a research template for scalable and sustainable energy solutions for developing countries without reliable electrical grids. Project deliverables include analysis of existing and ongoing PV-EV charging data for Ames' PVOT and solution modeling for Foothill's proposed 14 EV chargers.

POSTER 43

Neptune's Dual Capture of Triton and Nereid in Gravitational Encounter With Binary Pluto-like Kuiper-Belt System

Juan E. Morales and Gregory Laughlin

Department: Astronomy and Astrophysics

Home Institution: UC Berkeley

Summer Program: STEM Diversity - LAMAT

Our research objective was to explain the origin of Neptune's irregular satellites, Triton and Nereid, by using methods of computational analysis. Numerical Integrations were used to simulate a large number of N-body encounters between the Pluto system and an "original" Neptune-like system, which we modeled by substituting Uranus's current satellites as proxies for Neptune's original satellites. After the suited of chaotic encounters have been simulated, we check to see if any satellites left orbiting Neptune have irregular orbits with properties such as Triton's retrograde orbit or Nereid's high eccentricity. If such examples are frequently found, we can conclude that both Triton and Nereid were once part of a Pluto-Charon-like Kuiper-belt system and were captured by a gravitational N-body interaction involving Neptune.

POSTER 44

Synthesis of a Rhodamine Based Profluorescent Nitroxide for Catechol Detection

Daniel Moran, Wiley Schultz-Simonton, Rebecca Braslau

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - IMSD

Urushiol is a catechol derivative found in poison ivy, poison oak, poison sumac, and Asian lacquer trees. Detection of urushiol is important since physically avoiding the oil is the best way to avoid contact dermatitis. Unfortunately, this does not save one from contacting urushiol through secondary contact from tools or clothing that has been contaminated. Profluorescent nitroxides, in conjunction with boronic acids, are capable of detecting urushiol via fluorescence restoration. Attaching organic fluorophores to nitroxide radicals decreases the fluorescence to give profluorescent nitroxides. Once the profluorescent nitroxide comes in contact with urushiol and a boronic acid, the fluorescence returns to indicate that urushiol is indeed present. Improved profluorescent nitroxides are needed to make this urushiol detection a commercially viable product. The specific profluorescent nitroxide synthesized in this project was derived from a rhodamine B fluorophore and 4-amino-TEMPO. The final step is a copper mediated click reaction. Thin layer chromatography and proton nuclear magnetic resonance are used to identify all intermediate products.

POSTER 45

Chemical Profiling of a Marine-derived Gram-negative Bacteria, *Achromobacter spanius*

Alexis Danielle Munoz, Christine Theodore, Patrick Still, Phillip Crews

Department: Chemistry and Biochemistry

Home Institution: Hartnell College

Summer Program: ACCESS

Secondary metabolites, unlike primary metabolites, are not involved in growth, development, or reproduction of an organism and often play a role in chemical defense and communication. Within the marine environment, secondary metabolites from non-photosynthetic Gram-negative bacteria are considered to be a promising source of new natural products. A bacterial strain that was isolated from a backshore (dry sand) sample collected at Zmudowski State Beach in California was identified as *Achromobacter spanius* (100% identical to *A. spanius* by partial 16S rRNA gene sequence). The ethyl acetate crude extract of a liquid culture of this strain was subjected to pre-fractionation by high performance liquid chromatography (HPLC). The pre-fractions were analyzed using ultra high performance liquid chromatography (UPLC) and high-resolution accurate mass spectroscopy. The accurate masses (to four decimal places) obtained for each peak (A-R) were used to generate molecular formulas. These molecular formulas were then used to search compound databases such as DNP Dictionary of Natural Products (DNP) and ChemSpider, with the goal of prioritizing the isolation of potentially new natural products. Upon examination of the mass spectra data obtained by the Orbitrap for peaks A-R, peak J proved to have an interesting mass due to its few matches in databases DNP and ChemSpider. Further examination of peak J revealed two potential molecular formulas through the dereplication process of F-4 fraction, indicating a potential structure ($C_{14}H_{33}N_4O_4S$) sulfaquinoxaline.

POSTER 46

How Do Broken Chromosomes Segregate?

Hector Navarro, Brandt Warecki, William Sullivan

Department: Molecular, Cell and Developmental Biology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - IMSD

How do broken chromosomes segregate? In mitosis, chromosomes are segregated via kinetochore attachments to microtubules at special sites called centromeres. Environmental insults can result in chromosome fragments lacking centromeres (acentrics) that would not be expected to properly segregate, potentially causing aneuploidy, a hallmark of cancer. Surprisingly in *Drosophila melanogaster*, artificially generated acentric fragments exhibit delayed but ultimately successful segregation (Royou et al., 2010). Acentrics rejoin segregated daughter nuclei through channels in the reforming nuclear envelope specifically at re-entry sites (Karg et al., 2015). Given these channels represent a mechanism of last resort for maintaining genomic integrity and are potentially novel cellular structures, it is of interest to identify genes that are important for the coordination of acentric segregation with channel formation. One possible candidate is Megator, a component of the nuclear pore complex that is necessary for proper chromosome dynamics during mitosis. Using live imaging and fluorescence microscopy, we monitored mitotic cells in which acentric fragments were induced and found an increase in improper acentric segregation in cells depleted of Megator compared to controls. This suggests a potential role for the nuclear envelope in mediating proper acentric segregation.

POSTER 47

In vivo Heterodimeric Transcription Elongation of Spt4 & Spt5

Khahn Nguyen, Anthony Rodriguez, Chelsea Stewart, Grant Hartzog

Department: Molecular, Cell and Developmental Biology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRI - CUSP-HLLC

Spt4/5 is a multi-domain protein complex that regulates transcription elongation and processing of pre-mRNAs and is essential for life in eukaryotes. Spt4 is universally conserved throughout all organisms - archaea, bacteria, and eukaryotes - suggesting that it is an ancient regulator of gene expression. We previously showed that Spt4/5 binds RNA Polymerase II and many proteins involved in transcription elongation and RNA processing. Our objective here is to construct tools that will allow us to determine what proteins specifically interact with Spt5's KOW4 and KOW5 domains. This will help us understand the individual functions of these two domains of Spt5. We hypothesize that the KOW4 and KOW5 domains are protein-protein interaction domains that interact with and recruit other factors to the RNAPII elongation complex. Our ultimate goal is to perform protein-affinity chromatography with forms of Spt5 that lack the KOW4 or KOW5 domains. We predict that a subset of proteins that interact with full-length Spt5 will not co-purify with forms of Spt5 that lack KOW4 or KOW5 domains. In this experiment, we cloned particular regions of the KOW plasmid and inserted it into pGH231. We know that these sites are compatible because they both have the Bgl II and Eag I restriction digest sites. The clones then must be cultivated in *E. coli* to grow the plasmid and eventually be expressed in the recombinant plasmid yeast. We ultimately hope to find a temperature regulant mutation to observe cell activity fully before and after the introduction of the Spt 4/5 protein.

POSTER 48

Synthesis of Bis-Nitroxide Alkynes from TEMPOL

Kindness Nwakudu, Chad Higa, Rebecca Braslau

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - CAMP

Nitroxides are very effective in controlling living polymerizations, which lead to polymer chains with controlled lengths. Attaching nitroxides to pre-formed polymers allows for making materials with pendant nitroxides. TEMPOL, a nitroxide bearing an alcohol, was synthesized from 2,2,6,6-tetramethylpiperidin-4-one. An attempt to make the acetylene bis-nitroxide using TEMPOL through Fischer esterification did not work; therefore, another approach was taken. The bis-nitroxide electron-poor alkyne was synthesized via the Steglich reaction using carbodiimide coupling. When N,N-dicyclohexylcarbodiimide (DCC) was used, it formed the urea as a byproduct, which was difficult to remove from the desired product. Alternatively, 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide (EDCI) is now being used in place of DCC to prevent any byproducts. Huisgen dipolar cycloaddition reaction among an azide and this electron-poor alkyne will be used to append polymers with nitroxides.

POSTER 49

The Role of Conserved Lysines in DNA Polymerase

Kalia Ostrander, Joey Dahl, Kate Lieberman

Department: Biomolecular Engineering

Home Institution: Cabrillo College

Summer Program: ACCESS

DNA Polymerases (DNAPs) are highly conserved enzymes tasked with faithful replication of the genome. Synthesis and nucleotide incorporation resides in the Polymerase active site. DNAPs with the ability to proofread excise incorrect base pairs in an Exonuclease active site. Our collaborators tested the balance between the two active sites in conserved mutant residues K383R and K498R from Bacteriophage ϕ 29 DNAP, showing the residues to have a direct role in DNAP functionality. Later research determined the specific contacts of the residues in DNA-DNAP complexes in high crystal structures. The ability to describe the biophysical mechanisms that gave rise to the phenotypes in the established mutants is conducted by capturing individual complexes of mutant phi-29 DNAP bound to DNA atop a nanopore with high temporal and spatial precision, determining the kinetic mechanisms at the branch point between DNA polymerase and exonuclease activities. Preliminary data supports previous publications observing decreased polymerase activity, specifically K383R showing a strong bias in exonuclease activity and K498R a decreased affinity for DNA and shifted equilibrium towards pre-translocation state.

POSTER 50

RNAi Screen of Potential Factors Required for Germline Mediated Lifespan Extension

Hugo Padilla, Andrew Knutson, Susan Strome

Department: Molecular, Cell and Developmental Biology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - MARC

In *C. elegans*, multiple molecular pathways are known to contribute to lifespan extension including the insulin-like signaling pathway. Reducing the activity of the insulin-like receptor gene, *daf-2*, promotes an increased lifespan by controlling the nuclear-cytoplasmic distribution of the FOXO transcription factor, DAF-16. In addition to *daf-2* signaling, removal of the germline also leads to lifespan extension. Interestingly the *daf-2* pathway and removal of the germline work synergistically, resulting in animals that live approximately five times longer than wild type animals. This suggests that *daf-2* signaling and germline removal partly work in two different pathways to extend lifespan. We chose to understand the mechanism of extreme lifespan extension by studying the maternal effect sterile mutant, *mes-4*. Compared to sterile *mes-4* single mutants, sterile *daf-2*; *mes-4* double mutants experience extreme longevity. This increase in lifespan is much more pronounced than the lifespan extension observed between *daf*-single mutants and wild type worms, highlighting the additive effects of removing the germline from *daf-2* worms. We performed transcriptome profiling of *mes-4* single mutants versus *daf-2*; *mes-4* double mutants and found significant differences in the levels of transcripts involved in metal detoxification, dauer formation, and embryonic development. We are currently assessing the contribution of these gene candidates for their role in extreme longevity.

POSTER 51

Comparative Genomic Analysis of Human Naïve and Memory B-Cell Immunoglobulin Switch Regions

Theron Palmer, Roger Volden, Henry Hinton, Chris Vollmers

Department: Biomolecular Engineering

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - IMSD

Isotype class switching must occur in order to adapt to the various biological elements of pathogens. The constant regions of b-cells' immunoglobulin heavy chain locus contain several repetitive elements, called switch regions, which are located upstream from the isotype exons. These switch regions are used as recombination sites that save isotype genetic information from being lost due to the DNA cleavage induced by the RAG protein complex during isotype class switching. Improper recombination of b-cell switch regions could result in the loss of isotype information, which will prevent further isotype class switching necessary for the body to adapt to the biological components of pathogens. Now, the recombination of these repeating switch regions that occurs during isotype class switching has yet to have been analyzed genetically. In order to better understand the nature of isotype class switching in relation to switch regions, we created a novel assay that amplified the naïve b-cell constant region and the alpha, and gamma memory b-cell isotype-switched constant regions. Next we will sequence the constant region amplicons using the Oxford Nanopore MinIon sequencer in collaboration with the lab of Dr. Akesson. By computational analysis we can then infer the switch regions of both

naïve and memory (before and after isotype class switching) b-cells looking for switch region recombination patterns during isotype class switching.

POSTER 52

Finding Potent *Wolbachia* Strains to Deter Viral Infection in Mosquitoes

Ivette Perez, Michael Yxcot, William Sullivan

Department: Molecular, Cell and Developmental Biology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRI - CUSP-HLLC

Every year there are millions of cases insect-borne viral infections. Dengue fever is a mosquito-borne viral infection that is endemic to millions of people every year that travel or live in tropical regions such as the Americas, Africa and Asia. Currently, there is no cure for the disease but one unsuspecting microbe, *Wolbachia*, a potential candidate for reducing the transmission of Dengue and other insect-borne viral infections. *Wolbachia* is a gram-negative bacterial infection that can be transmitted via the female germ line of numerous arthropods. The bacteria can form a mutualistic symbiotic relationship with its host that is beneficial for both the bacteria and insects. The host provides the obligate conditions for the growth and survival of *Wolbachia*. Additionally, certain strains of *Wolbachia* give resistance to viral infections in arthropods, which could be used as an effective tool to reduce virus-infected insect carriers. Using *Drosophila melanogaster* and various other arthropods gathered from UC's Big Creek Reserve, the presence of *Wolbachia* was tested within the insect population. The results indicate that about 12% of the wild-type *D. melanogaster* collected was infected with *Wolbachia*. Arthropods such as spiders, pillbugs, moths and turnip bugs were also tested positive for the infection. Future research will involve analyzing the mechanism behind viral resistance caused by potent strains of *Wolbachia* to design potential model treatments against Dengue and other insect-borne viral diseases.

POSTER 53

Functional Studies on a Human Astrovirus-Neutralizing Antibody

Edmundo Perez, Walter Bogdanoff, Rebecca Dubois

Department: Biomolecular engineering

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - CUSP-HLLC

POSTER 54

Quartz Nanopipette for Intracellular Superoxide Sensing

Joanna Perez, Rifat Emrah Ozel, Nader Pourmand

Department: Biomolecular Engineering

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - CAMP

It is well understood that reactive oxygen species (ROS), including superoxide anions, are generated as byproducts in a wide variety of physiological pathways and controlled by cellular antioxidant mechanisms. However, their overproduction can inflict oxidative damage to proteins, cells, and tissues, responses that are all known to be associated in the pathogenesis of a range of neurodegenerative disorders. Understanding the relationship between these disorders and superoxide can hold the key to the development of innovative therapies for combating neural degeneration in the cell. Previous used methods have been indirect, ambiguous, and incapable of performing real-time measurements. We have developed a novel technique for sensing superoxide radical anions using functionalized nanopipettes fabricated from single barrel quartz capillaries. The nanopipette undergoes a series of modifications on its inner surface, including the immobilization of cytochrome c. Cytochrome c allows for the direct measurement of superoxide levels in the cell based on the redox reaction between cytochrome c and the generated superoxide radical anions. These electrochemical biosensors not only enables for the quantitative analysis of superoxide levels in a single cell, but also the monitoring of these levels over a period of time.

POSTER 55

Evidence for Decadal and Century Scale Climate and Oceanic Variability in the Guaymas Basin, Gulf of California, Over the Last Millennium

Linda Pineda, Ana Christina Ravelo, Ivano Aiello, Zach Stewart, Wilson Sauthoff

Department: Ocean Sciences

Home Institution: UC Santa Cruz

Summer Program: No Program Affiliation

Natural climate change affects coastal water resources, human land use, and marine biological productivity. In particular, the seasonal migration of the Intertropical Convergence Zone (ITCZ) is influenced by changes in global-scale temperature and pressure gradients and is responsible for spatial changes in summertime rainfall in Mesoamerica impacting regional water resources and the strength of upwelling. In October 2014, aboard the Research Vessel El Puma, a 3.9 meter long core (G14-P12) was recovered from the Northeast flank of the Guaymas Basin in the Gulf of California within the oxygen minimum zone (27°52.11'N, 111°41.51'W, water depth of 677m) to investigate changes in seasonal upwelling and Central Mexico rainfall over the last ~1000 years. The age model was developed using Pb210, C14 and lamination counting. The time interval includes the Little Ice Age and the Medieval Warm Period. Biological productivity and precipitation proxy records were produced using an X-Ray Fluorescence (XRF) core-scanner and a color line scanner to generate a record of bulk chemistry and color reflectance. The records indicate marked decadal and centennial scale variability in the lithologic composition of the sediment superimposed on millimeter-scale variability that reflects the presence of seasonally laminated sediments. Nitrogen isotopic and nitrogen weight % measurements were used, in combination with the scanned data, to interpret changes in nitrate utilization and biological productivity. These new records will have broad implications on the link

between regional coastal environmental conditions in the Gulf of California and global climate change.

POSTER 6

Designing Smart Demand for Frequency Regulation in a Micro-Grid Test Bed

Justin Pinson, Andres Aranda, Zachary W. Graham, Tela Favalaro, Michael Isaacson

Department: Electrical Engineering

Home Institution: Hartnell College

Summer Program: CUSP-HLLC STEM Internship

One challenge of integrating renewable energy generation into the electric grid is that it may induce deviations in the frequency of power resulting in instability in the electrical service quality. This has the potential to damage equipment and lead to power outages. We propose a method that uses frequency as a signifier of the current state of the grid and regulates this quantity by way of deferrable 'smart' loads employed at the residential level. These loads can be directly controlled to mediate the frequency excursion by deferring consumption whilst preserving their respective duty cycles. Here, we discuss the characterization of potential 'smart' loads as well as the design and implementation of embedded systems that perform the logic to control load behavior and sense frequency in a home-built test micro grid. Thermal loads, refrigerators and water heaters, were selected for their energy storage and their regulation will not cause a noticeable disruption in service. We measure frequency of the mains power using a microcontroller that transmits data wirelessly to a single-board computer for processing. Once data are analyzed, an ancillary algorithm rooted at the specified deferrable load responds to queries and commands from the computer to advance or postpone power usage. This manner of demand regulation allows the test bed to successfully stabilize frequency and improve the state of the power delivered with no disturbance to the consumer. Furthermore, this test bed can be modified for other investigations when direct implementation into the grid is neither practical nor an available resource.

POSTER 56

Factors in Nuclear Extract that Contribute to their Activity and Splicing Efficiency

Mayra Rios, Veronica Urabe, Melissa Jurica

Department: Molecular, Cell and Developmental Biology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - MARC

Nuclear extract is an important key player in research. Specific components in the nuclear extract are used for further study, for instance in labs that focus their work on Ribonucleic Acid (RNA) and understanding the structure and function of the spliceosome. Spliceosomes are molecules important for gene expression. Spliceosomes do splicing, which is the editing mechanism consisting on excision of the intron or noncoding regions of the RNA and ligation of the exons, the coding regions of the RNA. Spliceosomes are composed of many components, proteins and RNAs. All the components of spliceosomes are present in the nucleus of

eukaryotic cells. We can generate spliceosomes and study splicing using nuclear extract. Specifically, we put a synthetic RNA splicing substrate into the nuclear extract, and measure splicing by looking for the products of splicing on a denaturing gel. We can also look at spliceosome assembly by native gel analysis. Our lab makes nuclear extract from Hela cells, however; is not well understood why some extract preparations have good splicing activity while others do not. This is an issue that if resolved could benefit our lab as well as others in the field that encounters the same problem. My project is to determine the factors in the nuclear extracts that contribute to splicing efficiency. My goal is to establish a protocol to rescue inactive extracts. There are two models for inactivity: 1) the inactive extracts lack a component required for splicing and 2) inactive extracts contain an inhibitor of splicing. I tested these models by mixing varying concentrations of active vs inactive extract and measuring splicing efficiency and spliceosome assembly. My preliminary results indicate that inactive extract lack a component required for the very early steps of spliceosome assembly. Currently, I am testing whether U1 snRNP is the missing component. My results will help us identify important splicing components that vary between nuclear extract preparations. With this knowledge, we will improve our protocols to make nuclear extract that is very active for splicing.

POSTER 47

***In vivo* Heterodimeric Transcription Elongation of Spt4 & Spt5**

Anthony Rodriguez, Khahn Nguyen, Chelsea Stewart, Grant Hartzog

Department: Molecular, Cell and Developmental Biology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRI - IMSD

Spt4/5 is a multi-domain protein complex that regulates transcription elongation and processing of pre-mRNAs and is essential for life in eukaryotes. Spt4 is universally conserved throughout all organisms - archaea, bacteria, and eukaryotes-suggesting that it is an ancient regulator of gene expression. We previously showed that Spt4/5 binds RNA Polymerase II and many proteins involved in transcription elongation and RNA processing. Our objective here is construct tools that will allow us to determine what proteins specifically interact with Spt5's KOW4 and KOW5 domains. This will help us understand the individual the individual functions of these two domains of Spt5. We hypothesize that the KOW4 and KOW4 domains are protein-protein interaction domains that interact with and recruit other factors to the RNAPII elongation complex. Our ultimate goal is to perform protein-affinity chromatography with forms of Spt5 that lack the KOW4 or KOW5 domains. We predict that a subset of proteins that interact with full-length Spt5 will not co-purify with forms of Spt5 that lack KOW4 or KOW5 domains. In this experiment, we cloned particular regions of the KOW plasmid and inserted it into pGH231. We know that these sites are compatible because they both have the Bgl II and Eag I restriction digest sites. The clones then must be cultivate in *E. coli* to grow the plasmid and eventually be expressed in the recombinant plasmid yeast. We ultimately hope to find a temperature regulant mutation to observe cell activity fully before and after the introduction of the Spt 4/5 protein.

POSTER 57

MEMS-based Adaptive Optics Multi-photon Microscopy for Deep Tissue Imaging

Ramiro Rodriguez, Xiaodong Tao, Emina Ibrahimovic, Joel Kubby

Department: Molecular, Cell, and Developmental Biology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - CAMP

The purpose of this project is to modify a commercial multi-photon microscope by adding an adaptive optics system for *in vivo* high-resolution deep tissue biological imaging, and to develop a user interface for biologists. The project includes the integration of two-photon and three-photon microscopes in the adaptive optics system. Deeper tissue imaging is expected to be achieved from the longer excitation wavelengths of the microscope systems which penetrate deeper into the tissue and account for aberrations and scattering image distortions introduced by the specimen under observation.

POSTER 58

Climate Change Associated Sea Level-rise in Marshall Islands

Thooba Samimi, Peter Swarzenski, Slawek Tulaczyk

Department: Earth and Planetary Sciences United States Geologic Survey

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - Packard

Fluctuations in global sea level play an important role in the formation and viability of atoll islands. The Republic of the Marshall Islands consist of a series of low-lying carbonate atolls located near the equator in the Pacific Ocean. Roi-Namur is a small, northward-facing islet located in the northern part of Kwajalein Atoll and is where this research was conducted. Prolonged human settlement of these low-lying atolls is risky for several reasons, including very scarce freshwater resources with no significant surface waters (e.g. rivers, streams, or lakes). In Roi-Namur, precipitation recharges a very shallow fresh groundwater lens that floats on top of a seawater intrusion. Water table elevations on these atoll islands fluctuate in response to oceanic tides. A hydrogeological assessment of this freshwater lens was developed to investigate possible impacts caused by recent and future sea level fluctuations and strong storms. Time series surveys of groundwater elevations in a suite of shallow wells and piezometers were used to assess the vulnerability of the freshwater lens to oceanic forcings.

POSTER 59

Assessing Cyclophilin Activity On the Regulation of a Circadian Clock Protein

Marisol Sanchez, Hande Asimgil, Carrie Partch

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: ACCESS

Mammalian molecular clocks coordinate behavioral and physiological processes into circadian rhythms that coincide with the 24-hour solar day. BMAL1 is one of the core clock proteins responsible for our bodies' circadian entrainment. BMAL1 is a transcription factor that has a disordered C-terminus, referred to as the transactivation domain (TAD), which is necessary for circadian cycling. The last 7 residues of TAD play a critical role in the molecular clock by interacting with transcriptional regulators; the absence of this region creates a circadian clock that runs with abnormally short periods. A proline in the last 7 residues of TAD causes the protein backbone to undergo a slow conformational change from cis to trans, which we hypothesize may act as a switch to control the timing of biological processes. Cyclophilins function as prolyl cis-trans isomerases that decrease the activation energy of this slow interconversion to increase the rate of isomerization. This research uses biophysical and biochemical tools to identify cyclophilins that exert regulatory function on BMAL1. Elucidating how prolyl isomerases modulate BMAL1 structure to control circadian rhythms could provide new avenues for therapeutic regulation of the clock that would aid in the treatment of maladies such as diabetes and cancer.

POSTER 60

Finding Site of Pre-mRNA and snRNA Binding to Splicing Proteins CUS2, HSH49, HSH155, PRP5, and PRP9 During Spliceosome Assembly and Splicing

Santiago Sanchez, Britney Martinez, W. Samuel Fagg, Manuel Ares, Jr.

Department: Molecular, Cell & Developmental Biology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - Packard

During gene expression, splicing matures pre-mRNAs into mRNAs that carry protein coding information. The splicing process is controlled by the spliceosome, which assembles on a pre-mRNA, removes the intron, ligates the exons, and releases the mRNA. Five small nuclear ribonucleoproteins (snRNPs), each composed of one snRNA and several proteins, are essential subunits of the spliceosome. An outstanding question is how spliceosome proteins interact with each other, with snRNAs, and with pre-mRNA in three-dimensional space, and how these interactions behave as the spliceosome functions. Using budding yeast *Saccharomyces cerevisiae*, we focus on five spliceosomal proteins: Cus2, Prp5, Prp9, Hsh49, and Hsh155, which operate as part of the U2 snRNP. The yeast strains used contain protein tags encoding six histidines (metal-chelate purification) and a biotinylation site (detection and protein conjugate purification). We have confirmed expression of each tagged protein, and prepared active splicing extracts.

POSTER 61

Soybean Lipoxygenase as a Model for the Human Lipoxygenase Enzyme

Michael Sanchez, Jesus Valdez, Theodore R. Holman

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRI - IMSD

The Mammalian Lipoxygenase enzymes are a non-heme iron containing dioxygenases that have been implicated in heart disease. By using soybean lipoxygenase (SLO) as a model for human lipoxygenase, the substrate-inhibition kinetics of SLO with nordihydroguaiaretic acid (NDGA) can help to gain a better understanding of lipoxygenase behavior. These results can be applied to human lipoxygenase, which can then be used to design effective therapeutics for treatment of heart disease. A Shimadzu UV-Visible Spectrometer was used to measure the rate of product formation at 234 nm of SLO with varying substrate concentrations. The rate data were analyzed by computational methods using the Michaelis-Menten (MM) equation, which confirmed published kinetic parameters. Subsequently, the rate of SLO was measured with increasing amounts of inhibitor. These data were fit to a standard IC₅₀ equation, which produced an IC₅₀ of 0.8 +/- .0025. This IC₅₀ value is consistent with the value found in the literature. In conclusion, we successfully reproduced the literature potency of NDGA and are now poised to investigate unknown inhibitors of SLO and HLO.

POSTER 9

Structural Analysis of pUC19 in NEB 5-alpha Competent *E. coli* Cells Treated with BamHI and Topoisomerase I Enzymes

Nancy Sanchez, Daniela Bolaños, Shankar Shastry, Michael D. Stone

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRI - IMSD

DNA is widely known for its double helix structure, but rarely recognized for the properties it harbors. The goal of this experiment was to understand DNA in its structure through the use of competent *E. coli* cells and pUC19 plasmid. DNA transformation was used to introduce pUC19 into AMPR *E. coli* cell cultures. Purified pUC19 DNA was treated with a restriction endonuclease digest, BamHI, and Topoisomerase I. The enzyme BamHI allowed us to cut the DNA resulting in linear structures. Topoisomerase I gave us control of relaxing the DNA into a circle. With the use of gel electrophoresis, and 1kb ladder, we were able to analyze the different structures in DNA: supercoiled, relaxed, nicked, and linear. An overview of magnetic tweezers was seen to demonstrate how DNA supercoiling relates to its DNA function. For example, DNA supercoiling allows for RNA/DNA synthesis and compacting DNA. Understanding the structural properties of DNA can lead to a better understand of DNA regulation.

POSTER 62

Resistance to the Antibiotics Ampicillin and Kanamycin in *Escherichia coli*

Chad Santo Tomas, Ivette Torres, Victoria Auerbuch Stone

Department: Microbiology and Environmental Toxicology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRI - IMSD

Bacteria's beneficial role in human health is often overshadowed by pathogenic bacteria that give rise to serious public health concerns. Using *E. coli* as the model, we sought to measure the rate of bacterial growth in the presence or absence of the aminoglycoside antibiotic kanamycin and the penicillin family member ampicillin. We used an *E. coli* strain resistant to ampicillin but susceptible to kanamycin as well as a different strain resistant to kanamycin but susceptible to ampicillin. By measuring bacterial cell density using a spectrophotometer or by measuring the number of viable bacteria by growing colony forming units on Luria broth plates, we compared *E. coli* growth over a five hour period to determine bacterial generation time. In addition, we performed a Kirby-Bauer test to examine the level of resistance of both *E. coli* strains to ampicillin using a disc soaked in the antibiotic. The zone of clearing around the VA228 (ampicillin resistant) strain was 0 mm, while that of VA264 (kanamycin resistant) was 20 mm. This means that the VA228 strain was fully resistant to ampicillin, while VA264 was susceptible. With increased use of antibiotics, more treatments must be discovered before our current antibiotics become ineffective towards resistant bacteria.

POSTER 27

The Design and Overexpression of Aldehyde/Alcohol Dehydrogenase Genes in *Haloferox volcanii* for the Conversion of Butyryl-CoA to Butanol

Dominic Schenone, Jazel Hernandez, Alonzo Lee, Sanusha Bijj, Derek Brekke, Jackson DeKloe, Vijay Jayant, Megana Kunda, Isabel Madau, Kendal Prokopakis, David Bernick

Department: Biomolecular Engineering

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - IMSD

Using fossil fuels as the world's dominant source of energy is no longer sustainable and has led to lasting negative effects on the environment and irreversible changes to our climate. As a result, the development of energy-dense carbon neutral biofuels has gained increased research interest. Butanol, a four carbon alcohol that can be metabolized from glucose and from cellulose, a glucose polymer is one possible solution. Continuing previous work done to engineer a glucose to butyryl-CoA pathway in the halophilic archaeon *Haloferox volcanii*, research is now being done to quantify the presence of butyryl-CoA and butanol in the engineered mutant and at the same time aldehyde-alcohol fusion and single genes are being designed to convert butyryl-CoA to butanol. Several approaches are being developed for the design and quantification of the of the genes. These include the identification, optimization and overexpression of fusion and single genes found in other halophilic organisms and the creation of fusion genes using native aldehyde and alcohol dehydrogenase genes(aldy3, aldy5 and adh2) from *H. volcanii*. At the same time, there is evidence that *H. volcanii* under acidogenic conditions activates these same native genes and work is being done to detect the existence of butanol under those conditions. The plasmid constructs are currently being designed using a overexpression plasmid via gibson assembly and will soon be transformed into *H. volcanii*.

Once successful transformants are found, an *in vitro* protein assay will be performed on the expressed proteins to quantify their activity with butyryl-CoA as the substrate.

POSTER 63

Analysis of the Effects of Amyloid- β on Axonal Transport of Mitochondria in *Drosophila* Motor Neurons

Maria V. Serrano, Adrienne M. Maguire, Jeremy Lee

Department: Molecular, Cell and Developmental Biology

Home Institution: Gavilan College

Summer Program: ACCESS

Transport of fluorescently tagged mitochondria in the neurons of *Drosophila melanogaster* was tracked in order to see the effects of genetically induced amyloid beta ($A\beta$) (a hallmark of Alzheimer's disease (AD) in humans) on microtubule-based transport in the motor neurons of flies.

POSTER 64

Autophagosome Transport in *Drosophila* Motor Neurons

Masuda Sharifi, Angeline Lim, William Saxton

Department: Molecular, Cell and Developmental Biology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - UC LEADS

Autophagy is a bulk degradation process in which a double membrane vesicle, autophagosome, forms around cytoplasmic components that need to be broken down. This process is essential in most cells, especially in neurons. Neurons are highly asymmetric cells with long axonal extensions that help transmit essential signals throughout the whole body. Because most biosynthesis occurs in the cell body, anterograde transport away from the cell body in the axons is important for the distribution of freshly synthesized components throughout the neuron. Old damaged components are returned retrograde, towards the cell body to be degraded and recycled. Despite bulk degradation via autophagy mechanisms in axons being unknown, this process is still likely dependent on axonal transport which will target autophagosomes to damaged organelles. In order to gain better insight into autophagosome transport, we utilized *Drosophila melanogaster* as our model organism. We expressed the autophagosome marker ATG8::mCherry in motor neurons and observed their distribution and transport in whole live drosophila larvae. We found more ATG8::mCherry expression in the motor neuron cell bodies compared to the axon and terminals. ATG8::mCherry labeled vesicles moved in both direction in the axons and preliminary observation indicates that autophagosomes occur less frequently than other transport vesicles (dense core vesicles) in axons. Our results suggest that autophagy is maintained at low levels in healthy axons and future work will focus on autophagy in degenerating axons.

POSTER 65

Laminar Fate Determination of Neocortical Progenitor Cells

Georgia Sheppard, Ton Nguyen, Alyssa Perry, Kendy Huang, Bin Chen

Department: Molecular, Cell and Developmental Biology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - UC LEADS

There are currently two opposing theories regarding how the neocortex develops. The classical lineage restriction theory posited that the neocortex develops in an inside out mechanism, and that neuronal laminar fate depends on cell birth date. Contending with this theory is the cell-intrinsic model, that posits that progenitors are fate restricted from an early time point. Experiments performed under Gil-Sanz supports this model as they contend that RGCs expressing Cux2 (Cut-like homeobox 2) produced progeny found mostly in the upper layers. They concluded that the progenitors expressing Cux2 were lineage restricted. Our lab does not support this conclusion because using a constitutive-expressing Cux2-Cre is not a good method for lineage analysis. With a tamoxifen-inducible CreER, we found that E10.5 Cux2-CreER+ RGCs produced progeny that reside through all cortical layers. We compared Cux2 results with Fezf2 (Zinc-finger protein 2), which are expressed on dorsal RGCs (Guo 2013). We also performed population and clonal analysis of E10.5 RGCs and obtained similar results of multipotency throughout the neocortex. The significance of clonal analysis is examining the progeny produced from a single RGC, which demonstrates the lineage is not fate restricted. We are now continuing this research by examining Tbr2+ intermediate progenitor cells that are given a tamoxifen injection between embryonic days 11.5-18.5. The brains are dissected on post-natal day 21 and examined via clonal and population level analysis. We are hoping to further understand the potential of neocortical progenitors and the lineage restriction theory, particularly the determination of laminar cell fate.

POSTER 32

Isolation of Salt Tolerant Cellulase Producing Halophiles for Biobutanol Production in *Haloferax volcanii*

Jocelyn Simlick, Adriana Landeros, Sofia Menendez, Tina DeLeon, Andre Baxter, Raymond Bryan, Henry Vilas, David L. Bernick

Department: Biomolecular Engineering

Home Institution: Hartnell College

Summer Program: iGEM - CUSP-HLLC

Production of butanol via microbiological metabolic processes is being investigated as an alternative for fossil fuels. *Haloferax volcanii* is an ideal microbe that can be utilized in breakdown and fermentation of saline treated plant matter [cellulose rich biomass] for butanol biofuel production. Our study will focus on finding halophiles with cellulases that can fold and work in high saline environments. We (iGEM field team) have collected samples from the Salt Ponds near Fremont, California and performed single species isolations from colonies that have shown robust growth. The inoculation and enrichment process was performed to select for cells that will produce a cellulase using microcrystalline cellulose as the sole carbon source in their growth media. Next, we will test for glucose abundance, in order to select for high activity cellulases. From there, we will identify the species by using its small subunit rRNA and performing PCR [polymerase chain reaction] to amplify regions that are specific for archaea. The amplified DNA will be sequenced to identify species. If species have previously been

identified we will use BLAST [a database that compares and correlates similar sequences] to identify target cellulase enzymes and attempt to transform *H. volcanii*. If we find a novel organism, we can then use whole genome sequencing to produce a draft sequence of its genome, and learn about its cellulose and carbohydrate metabolizing capabilities.

POSTER 47

***In vivo* Heterodimeric Transcription Elongation of Spt4 & Spt5**

Chelsea Stewart, Anthony Rodriguez, Khahn Nguyen, Grant Hartzog

Department: Molecular, Cell and Developmental Biology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRI - Packard

Spt4/5 is a multi-domain protein complex that regulates transcription elongation and processing of pre-mRNAs and is essential for life in eukaryotes. Spt4 is universally conserved throughout all organisms - archaea, bacteria, and eukaryotes-suggesting that it is an ancient regulator of gene expression. We previously showed that Spt4/5 binds RNA Polymerase II and many proteins involved in transcription elongation and RNA processing. Our objective here is to construct tools that will allow us to determine what proteins specifically interact with Spt5's KOW4 and KOW5 domains. This will help us understand the individual functions of these two domains of Spt5. We hypothesize that the KOW4 and KOW5 domains are protein-protein interaction domains that interact with and recruit other factors to the RNAPII elongation complex. Our ultimate goal is to perform protein-affinity chromatography with forms of Spt5 that lack the KOW4 or KOW5 domains. We predict that a subset of proteins that interact with full-length Spt5 will not co-purify with forms of Spt5 that lack KOW4 or KOW5 domains. In this experiment, we cloned particular regions of the KOW plasmid and inserted it into pGH231. We know that these sites are compatible because they both have the Bgl II and Eag I restriction digest sites. The clones then must be cultivated in *E. coli* to grow the plasmid and eventually be expressed in the recombinant plasmid yeast. We ultimately hope to find a temperature regulant mutation to observe cell activity fully before and after the introduction of the Spt 4/5 protein.

POSTER 66

The Regulations of How Cln3 is Made Proportional to Growth

Raymond Tan, Robert Sommers, Doug Kellogg

Department: Molecular, Cell and Developmental Biology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - Packard

Size and shape abnormalities have remained a significant trademark for cancerous cells. Cln3 is a known activator of start and has been shown to be regulated in proportion to some aspect of growth. Cln3 protein levels, and the critical cell size threshold itself, are responsive to nutrient availability. By inhibiting Ypk1 in G1, which halts plasma membrane growth, we observe degradation of Cln3 protein. This raised the question of how Cln3 is being regulated. By adding a CUP1 promoter in front of CLN3, we observe similar Cln3 levels compared to cells with the endogenous CLN3 promoter intact, suggesting that endogenous CLN3 transcriptional regulation

is not required for degradation of Cln3 protein after Ypk1-as inhibition or shifting from rich to poor nutrients.

POSTER 67

Synthesis of Rhenium Carbonyl Complexes as photoCORMs: Contrast in Denticity Depending on the Flexibility of the Ligand

Jennyfer Tena, Indranil Chakraborty, Pradip K. Mascharak

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRE - CAMP

Although CO (carbon monoxide) has been known as the “silent killer”, our body naturally produces CO in small amounts during the degradation of heme by the enzyme heme oxygenase (HO). This has prompted researchers to utilize CO in various therapeutic settings. However, application of CO in gaseous form suffers from difficulties providing controlled and safe delivery. Therefore, certain metal-carbonyl complexes have been proposed as carbon monoxide releasing molecules (CORMs), which are expected to release CO in a more controlled manner to the biological targets. However, the the major downside of CORMs is associated with sustainable delivery. Thus, the photoCORMs (photo induced carbon monoxide releasing molecules) have emerged as credible alternatives where the CO release process can be triggered upon light illumination. In the Mascharak Lab we are interested in the synthesis of photoCORMs with suitable design principle. Herein we have synthesized and characterized a rhenium carbonyl complexes, $[\text{ReCl}(\text{CO})_3(\text{qmtpm})]$ incorporating qmtpm ligand (qmtpm =2-quinoline-N-(2'-methylthiophenyl)-methyleneimine). This complex is structurally characterized. The next step in this project is to reduce the qmtpm ligand with NaBH_4 to obtain to corresponding amine (qmtpa). The main aim is to determine whether the flexibility of qmtpa ligand (compare to qmtpm) can lead to a tridentate binding mode in contrary to the qmtpm which shows a bidentate chelation with a -SMe appendage. All the complexes synthesized are (or will be) characterized by ^1H NMR, IR, UV-Vis spectroscopy and wherever possible with single crystal X-ray crystallography.

POSTER 62

Resistance to the Antibiotics Ampicillin and Kanamycin in *Escherichia coli*

Ivette Torres, Chad Santo Tomas, Victoria Auerbuch Stone

Department: Microbiology and Environmental Toxicology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRI - Packard

Bacteria's beneficial role in human health is often overshadowed by pathogenic bacteria that give rise to serious public health concerns. Using *E. coli* as the model, we sought to measure the rate of bacterial growth in the presence or absence of the aminoglycoside antibiotic kanamycin and the penicillin family member ampicillin. We used an *E. coli* strain resistant to ampicillin but susceptible to kanamycin as well as a different strain resistant to kanamycin but susceptible to ampicillin. By measuring bacterial cell density using a spectrophotometer or by measuring the number of viable bacteria by growing colony forming units on Luria broth plates,

we compared *E. coli* growth over a five hour period to determine bacterial generation time. In addition, we performed a Kirby-Bauer test to examine the level of resistance of both *E. coli* strains to ampicillin using a disc soaked in the antibiotic. The zone of clearing around the VA228 (ampicillin resistant) strain was 0 mm, while that of VA264 (kanamycin resistant) was 20 mm. This means that the VA228 strain was fully resistant to ampicillin, while VA264 was susceptible. With increased use of antibiotics, more treatments must be discovered before our current antibiotics become ineffective towards resistant bacteria.

POSTER 61

Soybean Lipoxygenase as a Model for the Human Lipoxygenase Enzyme

Jesus Valdez, Michael Sanchez, Theodore R. Holman

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRI - IMSD

The Mammalian Lipoxygenase enzymes are a non-heme iron containing dioxygenases that have been implicated in heart disease. By using soybean lipoxygenase (SLO) as a model for human lipoxygenase, the substrate-inhibition kinetics of SLO with nordihydroguaiaretic acid (NDGA) can help to gain a better understanding of lipoxygenase behavior. These results can be applied to human lipoxygenase, which can then be used to design effective therapeutics for treatment of heart disease. A Shimadzu UV-Visible Spectrometer was used to measure the rate of product formation at 234 nm of SLO with varying substrate concentrations. The rate data were analyzed by computational methods using the Michaelis-Menten (MM) equation, which confirmed published kinetic parameters. Subsequently, the rate of SLO was measured with increasing amounts of inhibitor. These data were fit to a standard IC50 equation, which produced an IC50 of 0.8 +/- .0025. This IC50 value is consistent with the value found in the literature. In conclusion, we successfully reproduced the literature potency of NDGA and are now poised to investigate unknown inhibitors of SLO and HLO.

POSTER 68

Simulating Accretion Disk and Stream Interaction in Exoplanetary System

WASP-12/b

Ian Weaver, Philip Macias, Enrico Ramirez-Ruiz

Department: Astronomy and Astrophysics

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - LAMAT– California Space Grant

WASP-12b is a hot Jupiter that orbits dangerously close to its parent star WASP-12 at a proximity of about 1/44th the distance the Earth stands from the Sun, or roughly 16 times closer than Mercury. Due to tidal forces from the gravitational influence of WASP-12 and their incredibly close proximity, WASP-12b gets distorted into an egg-like shape causing it to expand beyond its Roche lobe, allowing mass to be transferred onto its host star through the first Lagrangian Point (the point between two binary objects where the net force is zero) at a rate of 270 million metric tonnes per second. This mass transferring stream forms an accretion disk that transits the parent star, which aids sensitive instruments such as the Kepler spacecraft

whose role is to examine the periodic dimming of main sequence stars in order to detect ones with orbiting planets. By implementing the hydrodynamical code, FLASH, we apply a comprehensive fluid treatment of the behavior of mass transfer under the influence of the system's Roche Potential in a non-inertial reference frame and subsequent disk formation. We hope to use this model in the future to generate virtual spectroscopy signatures to compare to collected light curve data from the Hubble space telescope's Cosmic Origins Spectrograph (COS).

POSTER 33

Design, Construction, and Implementation of a Renewable Energy Integrated Test Bed to Regulate Frequency Deviation

Zachary Wedel, Jbenjamin Lara, Zachary Graham, Tela Favaloro, Michael Isaacson

Department: Electrical Engineering

Home Institution: Hartnell College

Summer Program: CUSP-HLLC STEM Internship

With the increase in renewable energy generation contributing to the production of power in the grid, over or underproduction of power due to fluctuations of environmental conditions induce instability in the frequency of the AC power within the grid. A potential solution that would ensure electrical service quality is by direct control of load behavior in response to the frequency deviation. Thus, power consumption can be deferred to stabilize the frequency using devices that have the ability to convert electrical energy into thermal energy for storage. To implement these "smart" loads, we have designed and constructed a Test Bed that models a residential electrical system. The Test Bed integrates solar energy generation with a grid tie-in and/or generator, while a mounted single board computer senses frequency through a smart meter and modifies the load power usage. The Test Bed was built to National Electric Code to accommodate safety standards; which includes accounting for maximum current-draw by selecting appropriately sized circuit breakers and wire gauges. By creating a model grid that incorporates renewable sources, we can identify and test different types of deferrable loads on a small scale and then use these results for replication on a larger scale.

POSTER 52

Finding Potent *Wolbachia* Strains to Deter Viral Infection in Mosquitoes

Michael Yxcot, Ivette Perez, William Sullivan

Department: Molecular, Cell and Developmental Biology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - SRI - IMSD

Every year there are millions of cases insect-borne viral infections. Dengue fever is a mosquito-borne viral infection that is endemic to millions of people every year that travel or live in tropical regions such as the Americas, Africa and Asia. Currently, there is no cure for the disease but one unsuspecting microbe, *Wolbachia*, a potential candidate for reducing the transmission of Dengue and other insect-borne viral infections. *Wolbachia* is a gram-negative bacterial infection that can be transmitted via the female germ line of numerous arthropods. The bacteria can form a mutualistic symbiotic relationship with its host that is beneficial for both the bacteria and

insects. The host provides the obligate conditions for the growth and survival of *Wolbachia*. Additionally, certain strains of *Wolbachia* give resistance to viral infections in arthropods, which could be used as an effective tool to reduce virus-infected insect carriers. Using *Drosophila melanogaster* and various other arthropods gathered from UC's Big Creek Reserve, the presence of *Wolbachia* was tested within the insect population. The results indicate that about 12% of the wild-type *D. melanogaster* collected was infected with *Wolbachia*. Arthropods such as spiders, pillbugs, moths and turnip bugs were also tested positive for the infection. Future research will involve analyzing the mechanism behind viral resistance caused by potent strains of *Wolbachia* to design potential model treatments against Dengue and other insect-borne viral diseases.

POSTER 69

Saturn as an Exoplanet

Alvaro Zamora, Michael Line, Jonathan Fortney

Department: Physics

Home Institution: Brown University

Summer Program: STEM Diversity - LAMAT

In this investigation, we test the currently accepted jovian atmospheric models used to study exoplanets. Saturn is treated as an unknown planet and Markov Chain Monte Carlo methods are employed to analyze the infrared transmission spectrum of Saturn from data gathered using the Cassini spacecraft]. The presence of haze is probed and constraints are placed on the temperature/pressure profile, cloud pressure and on the concentrations of CH₄, CO, C₂H₂ and CO₂. The well known mysterious ~3.3 micron feature present in Saturn's spectrum was ignored for this investigation.

POSTER 70

Enhancing the Stability of an Appetite Stimulating Peptide

Alfonso Zavala-Chavez, Rafael Palomino, Valerie Chen, Glenn Millhauser

Department: Chemistry and Biochemistry

Home Institution: UC Santa Cruz

Summer Program: ACCESS

The central melanocortin (MC3/4R) system plays an integral role in energy homeostasis. Agouti-related protein (AgRP 83-132) is an endogenous antagonist of the MC3/MC4 receptor subtypes and has been shown by previous studies to play a very important role in energy homeostasis. Mutations in the MC4 receptor subtype have been linked to uncontrolled eating (hyperphagia), obesity, and adult onset diabetes. Due to AgRP's ability to stimulate appetite, it has potential therapeutic use for people with wasting diseases such as cachexia. Previous studies show evidence of AgRP's rapid decay by proteolytic enzymes in *in vivo* testing which warrants improvement in AgRP's stability. We are currently performing studies on several variants of AgRP in order to increase its chemical stability, thermal stability, and proteolytic resistance using head to tail cyclization by means of native chemical ligation. We propose that joining the N and C-terminal ends via a 6 residue amino acid linker will increase AgRP's stability without disrupting its conformation or its biological properties. Fmoc-solid phase peptide

synthesis (SPPS) and native chemical ligation were implemented in order to cyclize mini-AgRP (83-120 C105A). The protein will be folded using an oxidative method to form its disulfide bonds and take on its final conformation. It is expected that the resulting, final conformation of mini-AgRP (83-120 C105A) will be more stable than the wild type and the un-cyclized variant.



UNIVERSITY OF CALIFORNIA SANTA CRUZ

Thank you to the sponsors of this event:

Division of Physical and Biological Sciences

UC Office of the President (UCOP)

National Institutes of Health (NIH)

National Science Foundation (NSF)

STEM Diversity Programs

Julie Packard

Research Mentoring Institute (RMI)

College-to-University Success Program-Hartnell Living

Learning Community (CUSPP-HLLC)

ACCESS

