



CALIFORNIA STATE UNIVERSITY

LONG BEACH

College of Natural Sciences
& Mathematics

Laura Kingsford CNSM Student Research Symposium



Book of Abstracts

Friday, October 16, 2026

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Welcome Letter

Dear Students, Colleagues, and Friends,

Welcome to the 2026 Laura Kingsford CNSM Student Research Symposium! Each fall, the College of Natural Sciences and Mathematics Jensen Student Access to Science and Mathematics Center (SAS) hosts this celebration of student research and faculty mentorship. This is the first symposium named in honor of former CNSM Dean Laura Kingsford, a steadfast champion of the transformative power of student research. We gratefully recognize John E. Clark, whose generosity established the Laura Kingsford CNSM Student Research Symposium Endowment, providing lasting support for this annual event.

Research is central to our vision of student success. Through original inquiry with faculty mentors and peers, students create new knowledge, build resilience, and gain confidence as scientists and mathematicians. They join a community that values their contributions. Our commitment to inclusive excellence means expanding access to these experiences so that students from every background can develop their talents and envision their futures in STEM.

Connecting these experiences to career opportunities is a CNSM priority. Research develops the technical expertise, critical thinking, teamwork, and communication skills students need to succeed in the workplace and further study. We welcome our local industry partners and invite them to meet our student researchers, explore their work, and discover the talent and fresh perspectives they can bring to their organizations.

We thank our faculty mentors, Jensen SAS Center staff, and supporters for their investment in student success. To our presenters: congratulations on your accomplishments! To students exploring research: ask questions, connect with our community, and imagine where your curiosity might lead.

Go Beach!

Kris Slowinski, PhD
Associate Dean for Academic Programs & Professor of Chemistry

Deepali Bhandari, PhD
Interim Associate Dean for Research & Grad Studies & Professor of Biochemistry

Cheyenne Ramon, MS
Research Programs Coordinator, Jensen Student Access to Science Center

About Dr. Laura Kingsford



Laura Kingsford earned a B.S. in biology, with a minor in chemistry, from Boise State University in 1971, followed by a Ph.D. in microbiology from the University of Utah in 1977. After completing postdoctoral training in molecular virology at the University of Virginia, she joined California State University, Long Beach (CSULB), in 1980 as an assistant professor of microbiology. She became an associate professor in 1984 and a professor in 1991.

Her research focused on negative-strand RNA viruses, viral glycoprotein structure and function, virus–host cell interactions, and the molecular mechanisms of antibody-mediated viral neutralization. She also developed marine crustacean and molluscan cell-culture systems for studying viral pathogens. Supported by NIH, NSF, and California Sea Grant funding, she published peer-reviewed research, presented at national and international conferences, and provided antibodies and related materials to research and public-health laboratories.

At CSULB, Kingsford taught undergraduate and graduate courses in microbiology, virology, cell culture, and molecular biology. She supervised undergraduate researchers and fourteen graduate theses and developed major research opportunities for students and faculty. She directed the Beckman Scholars Program for six years, helped establish the

Honors in Biological Sciences Program through a \$1.6 million Howard Hughes Medical Institute award, and served as principal investigator (PI) and program director for the NIH MBRS SCORE program. Under her leadership, SCORE brought more than \$12 million to CSULB for faculty research, institutional infrastructure, and opportunities for underrepresented students.

In 2014, Kingsford and Guido Urizar (multiple PIs) and a team of program directors and staff began working on a 5-year \$24.7 million NIH-funded BUILD award to CSULB. This award focused on developing infrastructure for research, undergraduate research inclusive mentoring, graduate-school pathways, and diversifying the biomedical and behavior research workforce. Faculty and students from four CSULB colleges (Engineering, Liberal Arts, Health and Human Services, and Natural Sciences and Mathematics) participated in these programs.

CSULB BUILD also worked as a consortium with NIH and nine other BUILD awardees nationwide as well as with two regional campuses (UCI and USC). In 2019, CSULB received a competitive renewal (2019-2024) of their BUILD award (for another \$19.8 million). Kingsford then stepped down as PI and served as a senior director to help transition the BUILD program to a new leadership team. A major mandate of NIH for BUILD campuses was to institutionalize the programs for students and faculty developed during the 10-year award. With support of the CSULB president, provost, and other leadership, the core programs now continue with CSULB funding.

Kingsford served as chair of CSULB's Department of Biological Sciences from 1997 to 2003, then became interim dean of the College of Natural Sciences and Mathematics in 2003 and dean in 2004. Until 2017, she led a college encompassing six academic departments, supported faculty and student research, and helped plan and complete two major science facilities—the Molecular and Life Sciences Building in 2004 and the Hall of Science in 2011.

Kingsford stepped down as dean in 2017 to work full time with the BUILD program and retired in 2020. Since then, she has devoted much of her time to her grandson and to birding trips in the United States and around the world, including Brazil, Japan, Panama, Canada, and Belize. She has also enjoyed trips to South America, Antarctica, New Zealand, Australia, Fiji, Italy, Greece, Turkey, Iceland, Alaska, and the Baltic countries. She has visited all seven continents, with Antarctica being her favorite.

Symposium Booklet and Event

The College of Natural Sciences and Mathematics (CNSM) is excited to host the inaugural Laura Kingsford CNSM Student Research Symposium at the CSULB LBS Financial Credit Union Pyramid on October 16, 2026. Inspired by CNSM faculty and their work with students, friend of the University, Mr. John E. Clark, endowed a gift to CNSM in honor of his late wife, Elizabeth Clark, who obtained two degrees from CNSM, a BS in 1980 in Medical Microbiology and MPH in 1985 in Nurse Epidemiology.

This event, hosted by CNSM, is open to both undergraduate and graduate students and showcases research conducted on campus and through summer research experiences at other universities. The symposium provides students with opportunities to write abstracts, prepare posters, and present their research findings in an inclusive environment that welcomes diverse voices and perspectives. Bringing together students, staff, faculty, administrators, and community members, the event fosters a sense of belonging and invites everyone to engage with scientific ideas and discoveries, enriching the experience for all participants.

We encourage attendees to walk around, explore the posters, and engage with students about their research and experiences. Whether this is your first research symposium or you have attended many, we welcome your questions and curiosity. No question is too small, and we hope you enjoy learning about the exciting research being presented today.

Thank you for attending and supporting our students as they share their research and discoveries!

Funding Acknowledgements

Funding support for this event provided in part by:

The Laura Kingsford CNSM Student Research Symposium Endowment established through the generosity of John E. Clark; CSULB College of Natural Sciences and Mathematics; and Jensen SAS Center and G2 Lab.

A Special Thanks to:

Our Faculty Research Mentors, Jensen SAS Center, CNSM Academic Advising Center, Peer Mentors, CNSM Tech Friendly, Dr. Deepali Bhandari (CNSM Associate Dean), Dr. Krzysztof Slowinski (CNSM Associate Dean), and Dr. Curtis Bennett (Richard D. Green Dean of the College of Natural Sciences and Mathematics).

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

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1. Quantum Geometry and Plasmon Spectrum in the Theta Model

Kaeden W. Russell* and Andreas Bill, Ph.D.

Department of Physics & Astronomy, California State University, Long Beach, CA
90840

Electronic collective modes (plasmons) play an important role in condensed matter physics. We show that the dispersion relation of these collective modes is determined by two quantities: the band structure, and the wave function of electrons. This latter contribution is related to the quantum geometry of the underlying Hilbert space. We apply the theory to a one-parameter model where the parameter only affects quantum geometry and leaves the band structure unchanged. We demonstrate that quantum geometry affects the dispersion relation of plasmons.

We gratefully acknowledge support from the CSULB-OSU Partnership for Research and Education in Topological Materials, NSF PREM program under grant 2425133.

2. Optical Conductivity and Quantum Geometry in the Massive Dirac Model

Timothy Van Hoommissen*, Felipe Kosareff, and Andreas Bill

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90840

Optical conductivity characterizes a material's response to an oscillating electric field, and related optical measurements are often used to probe features of the electronic band structure. While the energies of allowed optical transitions are determined by a material's band structure, the transition strengths depend in part on the geometric structure of Bloch states across the Brillouin zone. The quantum geometric tensor (QGT) describes this geometry, with its real part defining the quantum metric and its imaginary part being proportional to the Berry curvature. In this work, we investigate the effects of quantum geometry on optical conductivity using the two-dimensional massive Dirac model, which extends the massless Dirac description of graphene's band structure near the K and K' points. We derive analytical expressions for the Berry connection and Berry curvature of the massive Dirac model and calculate the Berry phase of the conduction and valence bands along a closed path in momentum space. We then show that the current operator matrix elements in the Kubo formula for the optical conductivity can be expressed in terms of the interband Berry connection matrix elements. Using the Kubo formula

with the analytical expressions of the interband Berry connection, we numerically calculate the optical conductivity of the massive Dirac model over a range of mass values.

We gratefully acknowledge support from the Office of Research and Economic Development (ORED) Summer Research Assistantship and support from the CSULB-OSU Partnership for Research and Education in Topological Materials, NSF PREM program under grant 2425133.

3. Morphological Evolution of Copper Phthalocyanine Thin Films Studied by In-situ Heated Atomic Force Microscopy

Mark Serrata*, Alexander Goytia-Fajardo, Thomas Gredig

Department of Physics and Astronomy, California State Long Beach University, Long Beach, CA 90840

Interest in molecular thin films has grown because of their novel applications in flexible photovoltaics, gas sensing and towards quantum sensing. Phthalocyanines are a model family of thermally stable and chemically tunable small molecules that exhibit structural phase transitions depending on substrate temperature, annealing, and templating conditions. Although annealing-induced changes in nanoscale surface morphology have been reported, these changes have not previously been observed in situ. Here, we use atomic force microscopy with a heated stage to directly monitor structural changes in phthalocyanine thin films at elevated temperatures under an argon atmosphere. The correlation length increases abruptly near 100 °C, from approximately 11 to 23 nm, while the surface roughness decreases. These changes persist after cooling to room temperature, indicating that the thermally induced structural reorganization is largely irreversible. Future measurements with smaller temperature increments will investigate more subtle changes with a focus on tracking of individual grains.

This work was funded through the California State University, Long Beach and the Ohio State University Partnership for Education and Research in Topological Materials, a National Science Foundation PREM, Grant No. 2425133.

4. Toward Topological Superconductivity in Flat-Band Systems: A Self-Consistent BdG Framework

Anna Domjan^{1*}, Sarah Grefe¹, Chris Lane²

¹Department of Physics and Astronomy, California State University, Long Beach, Long Beach, CA 90840 and

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Unconventional superconductivity in flat-band systems such as magic-angle twisted bilayer graphene remains poorly understood, with the pairing symmetry and possible topological character still open questions. As a step toward addressing this, we are developing a computational framework to solve the self-consistent Bogoliubov–de Gennes (BdG) gap equation for lattice models with spin–orbit coupling and attractive interactions. We apply this framework to a Kagome lattice as a testbed, where we compute the normal-state band structure, Fermi surface, and the momentum-dependent superconducting gap as functions of interaction strength and chemical potential. We will present preliminary results for the self-consistent gap, the BdG quasiparticle spectrum, and the phase diagram, and we will discuss how this approach can be extended to topological heavy fermion models of twisted bilayer graphene. This work establishes a foundation for identifying pairing symmetries and topological invariants in correlated flat-band superconductors.

This work was supported by the Daniel and Grace Lim and Kueng Luke Undergraduate Summer Assistantship and was funded through the Cal. State. Long Beach and the Ohio State University Partnership for Education and Research in Topological Materials, a National Science Foundation PREM, under Grant No. 2425133. The work at Los Alamos National Laboratory was carried out under the auspices of the U.S. Department of Energy (DOE) National Nuclear Security Administration (NNSA) under Contract No. 89233218CNA000001. It was supported by the LANL LDRD program.

5. Circularly Polarized Light-Induced Topological Phase Transitions in Weyl-Kondo Semimetals

Emma R. Samaniego^{1*}, Sarah E. Grefe¹

¹Department of Physics and Astronomy, California State University, Long Beach, Long Beach, CA 90840

Weyl-Kondo semimetals (WKSMs) are strongly correlated topological materials that combine Weyl nodes with Kondo physics arising from the hybridization of conduction electrons with localized f-electrons. An important theoretical result for WKSMs is that an applied Zeeman field can tune their topology by moving Weyl nodes in momentum space. As the field increases, Weyl nodes of opposite chirality can be driven together and be annihilated. This results in a topological transition of a WKSM to a Kondo-insulator. This Weyl-node annihilation occurs before the collapse of Kondo coherence, showing that the topological phase can be controlled without first destroying the Kondo physics. This work investigates if circularly polarized light can provide an optical mechanism to this control. The proposed mechanism is based on

optical spin injection. Circularly polarized light carries a specific helicity, producing an unbalanced motion/excitation/flow of electronic states through the coupling between the electric field and the electronic velocity. There is spin-momentum locking of the electrons in a Weyl semimetal system which connects the direction of electronic motion with spin and can generate net spin polarization. The resulting photoinduced spin magnetization provides an effective magnetic perturbation to the system. For circular polarization, the injected spin produces a magnetization that is proportional to the optical response coefficient and the square electric-field amplitude. This mechanism provides a potential connection between the optical field and the magnetic coupling that controls the topology of a WKSM.

6. High-Harmonic Generation as an All-Optical Probe of Weyl-Node Annihilation in a Weyl-Kondo Semimetal

Jason Spada* and Sarah Grede, Ph.D.

We investigate high-harmonic generation (HHG) as a contactless probe of the topological transition in a Weyl-Kondo semimetal, modeled as an Anderson lattice on the diamond structure and treated within slave-boson mean-field theory at quarter filling. Driving with an intense few-cycle circularly polarized pulse, we propagate the time-dependent current via the Peierls substitution and compute harmonic spectra across the inversion-breaking staggered mass, spanning both the gapless Weyl phase and the trivial gapped phase. We find the harmonic yield is enhanced roughly fivefold in the Weyl phase relative to the trivial phase. The enhancement is not a discontinuity at the transition: it decays continuously as the Weyl nodes migrate toward pairwise annihilation, identifying HHG as a probe of nodal proximity rather than of the gap itself. We further show the total emitted power exhibits no circular dichroism, an exact consequence of a twofold rotational symmetry of the driven system, while the helicity-resolved emission obeys a period-four rule in harmonic order. Finally, elliptically polarized driving reveals that circular polarization roughly doubles the contrast between the two phases, and the nonlinear response is tied to the renormalized heavy quasiparticle velocity.

Acknowledgement: Cal. State. Long Beach and the Ohio State University Partnership for Education and Research in Topological Materials, a National Science Foundation PREM, under Grant No. 2425133.

7. Investigation of the Magnetic Switching Behavior of Nanocap Samples using the Magneto-Optical Kerr Effect

Brianna Christensen*, Jiyeong Gu, Ph.D.

The Magneto-Optical Kerr Effect (MOKE) uses the reflection of a laser beam from the magnetic material to characterize the magnetic switching behavior of it. The rotation of the reflected light's polarization depends on the magnetization and is observable with the use of an analyzer's optical filtration. The MOKE measurement is local and a non-contact, effective for a wide range of samples, like flat and nanocap thin films. This study investigates the geometry-driven magnetic behavior and switching mechanism of magnetic nanocaps of varying thickness and diameter size. These caps, which are formed when a thin magnetic layer is deposited onto a hexagonally close-packed nanosphere or microsphere template, introduce curvature in the single layer. The curvatures in Permalloy (Py) samples are altered by varying the diameters of the Silica nanosphere (166 nm, 507 nm, and 890 nm), or by varying layer thicknesses (20 nm – 150 nm). We performed the longitudinal hysteresis loop measurements to study how the changes of curvature affect the switching behavior of the Py samples. Increasing the sphere diameter for 20nm thick Py samples decreases the coercivity slightly. Remanence magnetization value grows as the diameter grows, showing that a flatter sample retain more of the longitudinal magnetization. The permalloy nanocap samples on a fixed 890 nm diameter show a trend toward increasing the coercivity as the layers get thicker. However, the longitudinal remanence magnetization is minorly affected. Additionally, Samarium Cobalt (SmCo) nanocaps of the same diameter were measured as a comparison for different materials. Though SmCo has a larger coercivity than permalloy to begin with, increasing the thickness also produces an increase in coercivity. Due to the finite skin-depth penetration of the laser beam, the effect captured by the MOKE focuses mostly on the thin layer at the tips of the nanocaps. Dissimilarly, hysteresis loops that measure across the entire sample, surface and depth, are scanned by the Vibrating Sample Magnetometer (VSM). Differences and similarities are noted.

This work was partially funded through the California State Long Beach and the Ohio State University Partnership for Education and Research in Topological Materials, a National Science Foundation PREM, under Grant No. 2425133.

Brianna would like to acknowledge the Gisela and Wilfried Eckhardt Endowment for Physics and Astronomy award through the College of Natural Science and Mathematics at CSULB.

8. Implementing a Dipole Electromagnet to a Magneto-optical Kerr Microscope

Andy Le Blanc*, Christopher Perez, Jiyeong Gu

The magneto-optical Kerr effect (MOKE) magnetometry method using a laser is an effective characterization tool capable of measuring local magnetic hysteresis loops of magnetic samples in sub-micron size. Therefore, we developed a dedicated MOKE microscope by modifying a regular polarizing microscope for the purpose of imaging magnetic domains of patterned magnetic thin film structures, nanometer/sub-micron-size samples. Py and SmCo nanocaps were fabricated on nano/microsphere templates using a pioneering fabrication method of nanosphere lithography. By implementing an electromagnet to our setup and applying through focus scanning we utilize the direct control over the magnetic field to allow through focus imaging to improve magnetic contrasts. By using the MOKE method on our samples we hope to observed contrasts that reflect the presence of magnetic domains of the micrometer scale. By measuring both hysteresis loops and magnetic domains we expect to provide an understanding of the magnetic characteristics of three-dimensional magnetic nanostructures such as our nanocap thin films.

We acknowledge support from the APS Bridge Program. This work was funded through the Cal. State. Long Beach and the Ohio State University Partnership for Education and Research in Topological Materials, a National Science Foundation PREM, under Grant No. 2425133. We also acknowledge support from the Keck Undergraduate Research Experiences (KURE) Incubator.

9. Curvature Induced Magnetic Switching Behavior in Permalloy Nanocap Thin Films

Alan Mejia*, Angel Gomez, and Jiyeong Gu Ph.D.

Department of Physics and Astronomy, California State University Long Beach, Long Beach, CA 90840

Thin magnetic layers deposited on hexagonally close-packed single-layer nanosphere templates form nanocap thin films. Permalloy (Py) nanocap thin films are prepared to investigate geometry-driven magnetic behavior and switching mechanisms that may enable unconventional spin manipulation in emerging spintronic devices. Several techniques exist for creating close-packed single layers of sphere templates. A manual rubbing method using a polydimethylsiloxane (PDMS) stamp was used to quickly achieve hexagonal packing in large areas. Scanning electron microscope (SEM) images showed that dry rubbing method is effective to obtain a closely packed monolayer sphere template with a uniform coverage of 80 – 90% of the substrate across the area of $\sim 10 \times 10 \text{ mm}^2$. Experimentally measured magnetic hysteresis

loops showed that the variation in sphere size and nanocap thickness altered the overall hysteresis loops and the values of coercivity and remanence in-plane magnetization. Varying thickness on a fixed size diameter showed more noticeable changes in the hysteresis loops. Micromagnetic simulations performed for chosen thicknesses and diameters show similar shapes as the experimentally measured ones although absolute magnitude of coercivity and remnant magnetization were different.

This work was supported by the Partnership for Research and Education in Materials (PREM) program between California State University, Long Beach and The Ohio State through a grant from the National Science Foundation under Grant No. 2425133.

10. 'They Just Get the Answer': Secondary Mathematics Teachers' Concerns About AI and Mathematical Reasoning

Jenna Ersheid^{1*}, Deon Nguyen², Pavneet Kaur Bharaj²

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This qualitative study examined beliefs about mathematics, personal mathematics ability, and mathematics teaching expressed in the mathematics autobiographies of 59 preservice elementary teachers (PSTs). Autobiographies were coded using a thematic coding approach, and belief subcodes were summarized across participants. Findings showed that PSTs held varied beliefs about mathematics: some emphasized rules, procedures, and correct answers, while others described mathematics as involving reasoning, connections, and multiple solution pathways. Beliefs about personal mathematics ability were often complex, with many PSTs expressing both confidence and self-doubt. PSTs also frequently described mathematical competence as something developed through help from others and continued effort. Nearly all participants articulated positive characteristics of an ideal mathematics teacher, while some also identified practices effective teachers should avoid. Findings suggest that mathematics autobiographies can provide a useful way to surface PSTs' beliefs early in teacher preparation and create opportunities for reflection on mathematics, ability, and teaching.

11. Mathematics, Self, and Teaching: Beliefs Revealed Through Preservice Teachers' Mathematics Autobiographies

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Artificial intelligence (AI) is becoming increasingly present in mathematics education, raising questions about how teachers perceive its role in teaching and learning. This qualitative study examined the perceptions of 11 in-service secondary mathematics teachers in Southern California regarding AI use in mathematics classrooms. Participants were recruited through convenience sampling and participated in individual Zoom interviews. Interview transcripts were analyzed using an inductive approach. Findings showed that teachers' perceptions of AI were conditional rather than uniformly positive or negative. Teachers valued AI for lesson planning, generating instructional materials, differentiation, and assessment development, while expressing greater concern about students using AI to obtain answers without engaging in mathematical reasoning. Participants emphasized the importance of preserving reasoning, justification, conceptual understanding, and the mathematical process. Teachers also suggest that productive AI integration in secondary mathematics may depend on whether AI supports rather than replaces mathematical thinking. They also point to the need for mathematics-specific guidance and professional learning that helps teachers use AI while maintaining students' responsibility for reasoning and sense making.

12. How Mathematical Experiences Shape Emotions: Insights from Preservice Teachers' Autobiographies

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Preservice elementary teachers (PSTs) enter mathematics courses with emotional histories shaped by prior experiences as learners. This qualitative study examined the mathematics-related emotions of 59 PSTs enrolled in a geometry and measurement course and the experiences they associated with those emotions. At the beginning of the semester, participants completed mathematics autobiographies that were

analyzed using a thematic coding approach. Findings showed that PSTs expressed complex and overlapping emotional relationships with mathematics, including positive, negative, neutral, and blended emotions. Emotions were commonly connected to experiences with teachers, experiences as mathematics learners, and particular mathematical topics. Negative emotions were especially evident in accounts of struggle, confusion, and perceived lack of success, while enjoyment and confidence were often conditional on understanding. Consistent with appraisal theory, the findings suggest that PSTs' emotions reflect how they interpret and make meaning of mathematical experiences. Implications highlight the value of autobiographical reflection in mathematics teacher preparation courses.

13. Mathematics Teacher Identity: Competence, Performance, and Recognition Across Three Secondary School Cases

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Professional identity is central to mathematics teacher development, shaping teachers' commitment, instructional decision making, and interpretations of their professional experiences. Although there has been substantial research addressing teacher identity, there are continued gaps in how mathematics teacher identity is defined and studied. This study contributes to the broader mathematics education literature by considering a theoretical lens not widely used in mathematics education to define teacher identity and by focusing on mathematics teachers in the secondary school context. The purpose of this study is to explore secondary mathematics teachers' professional identity through the theoretical framework of competence, performance, and recognition. Specifically this study asks: How do secondary mathematics teachers describe their professional identities in relation to competence, performance, and recognition? This study used a qualitative multiple-case interview design to explore the professional identities of three secondary mathematics teachers in California. Participants represented three career stages based on years of experience: early career (1st year), mid-career (6th year), and later-career (14th year). Data was collected through semi-structured interviews. Interview transcripts were initially analyzed using a deductive coding approach. After deductive coding, each participant's interview was read individually, followed by cross-case analysis to examine similarities and differences across career stages. Next, the interview transcripts were coded inductively to identify recurring ideas within and across the three framework dimensions. Preliminary findings indicate that all three teachers placed greater value on recognition from people who knew them and their teaching, expressed a lack of confidence with statistics and probability, and

described time constraints as creating a misalignment between their stated beliefs and instructional practice. The participants differed in how they described their relationship between competence and performance. The two participants with more experience expressed greater alignment between their stated beliefs and practice, whereas the participant with the least experience expressed uncertainty, especially when her instructional decisions did not lead to the student outcomes she expected. Finally, the participant with the most experience described how the significance of recognition had changed over the course of her career. These findings highlight the importance of career-stage responsive support that strengthens teachers' confidence, connects instructional beliefs with practice, and underscores the importance of meaningful recognition of teachers' professional expertise.

14. Efficient Detection of Borromean Links in Ellipses

Jonathan Strange*, Ryan Blair, Alex Klotz

Topological links occur in many physical systems. In dense solutions or melts of polymers, higher-order multi-polymer interactions analogous to Borromean linking may influence material properties. Previous detection of Borromean links relied on knot invariants. In practice however, few of these have been successfully implemented as algorithms that can take space curves as input and yield a topological classification as output. We describe a method by which the number of intersections one ellipse makes inside the plane of another can be determined. The method is based on applying a transformation that maps one ellipse to the unit circle and examining the intersection points of the transformed second ellipse with the unit circle. This may be used to efficiently determine Hopf linking between two ellipses, or Borromean linking between three ellipses. Notably, our algorithm is 150x faster than using the popular Python package Topoly to determine Borromean linking.

All three authors are partially supported by NSF PREM grant DMR-2425133.

15. Optimization of the Cubic Spline Error

Celeste Reynoso*, Astrid Oppen, Judy Rodriguez

This research project examines the optimization of the error bound between the function $f(x) = x^4$ and its cubic spline $s(x)$ on an arbitrary interval $[a, b]$ with evenly and unevenly spaced partitions. The function $f(x) = x^4$ was chosen to be optimized because the error bound will then apply to any quartic function. The error bound sought to be optimized was $|f - s|_\infty \leq \left(\frac{5}{384}\right) \|\Delta\|^4 \|f^{(4)}\|_\infty$. This bound is helpful to optimize software involving data points without a known function and can be applied

across many disciplines of engineering. For mathematics, this research can be used to calculate the distance between $f(x)$ and a vector space of functions.

Incorporating the data analyzed across different cubic splines, this research shows that there is an optimization for the function $f(x) = x^4$ and its cubic spline $s(x)$ on evenly spaced partitions and an arbitrary interval $[a, b]$. Using a chart of general spline data on evenly spaced partitions and an interval $[a, b]$, computation yielded four equations $d_3^i, d_2^i, d_1^i, d_0^i$ that determine the coefficients of our cubic spline such that for sub intervals $\frac{b-a}{n}$, $s_i^n(x) = d_3^i x^3 + d_2^i x^2 + d_1^i x + d_0^i$. Through simplification and applying these equations to $|f - s|_\infty$, results yielded that the lowest error bound is $|f - s|_\infty \leq (\frac{1}{384})||\Delta||^4||f^{(4)}||_\infty$. There was not sufficient data to optimize the error bound for unevenly spaced partitions on an arbitrary interval, but the data that was collected suggests a constant between $\frac{1}{384}$ and $\frac{5}{384}$.

16. Early Detection of Ovarian Cancer Using miRNA Biomarkers via Machine Learning Methods

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Ovarian cancer is rarely detected while still surgically curable, and the serum marker in routine use lacks both the early-stage sensitivity and the specificity against benign pelvic disease that screening would require. Serum microRNA (miRNA) profiles are a proposed alternative, but that literature often selects features on the full sample before partitioning, so reported discrimination carries an optimistic bias of unknown size. We hypothesized that a feature set defined by selection stability across several criteria would discriminate better than any single criterion's selection, and that performance would depend strongly on disease stage.

We analyzed the public GSE94533 serum miRNA dataset (174 samples: 92 invasive ovarian carcinomas and 82 non-cancers, including 45 benign lesions, 22 borderline tumors, and 15 healthy controls). A detection filter retained 194 miRNAs, log-transformed and ComBat-adjusted for cohort batch effects. Performance was estimated by 7 repeats of 10-fold outer cross-validation with 5-fold inner tuning, with selection, tuning, and fitting confined to the training portion of every fold, and metrics pooled over all 174 out-of-fold predictions per repeat. Five selection methods (Mann-Whitney test, ElasticNet, random forest importance, XGBoost gain, and the Classification Ensemble of Random Partitions, CERP) were applied across the 70 outer training partitions, and consensus tiers retained the miRNAs reaching a

threshold selection frequency under at least one method. Each tier was evaluated with ten classifiers, including stacked ensembles and CERP.

Performance followed an inverted-U pattern across tier size, and 7 of the 10 classifiers peaked at the 32-miRNA tier. That tier with a random forest achieved an AUC of 0.837 (SD 0.012), accuracy 0.765, sensitivity 0.750, specificity 0.782, and an absolute sensitivity-specificity difference of 0.032. No ensemble surpassed the best single classifier at any tier. Because the tiers were consolidated across the resampling partitions rather than within them, 0.837 is not directly comparable with the 0.770 obtained under fold-internal selection; their difference of 0.067 bounds the benefit of consensus selection rather than measuring it. Stage dependence was sharp: AUC fell from 0.880 in late-stage disease to 0.716 at Stage I, where sensitivity was 0.534 for random forest and 0.603 for CERP, the highest of any model.

Discrimination was carried by a compact, reproducibly selected feature set rather than by the breadth of the feature space. Stage stratification answers the early-detection question directly: no model detected Stage I disease at a level supporting clinical use, which identifies early-stage sensitivity rather than overall discrimination as the binding constraint on serum miRNA classification. External validation in an independent cohort is required.

17. Updating Listing's List: Topological Linking Asteroid Orbits

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The research we conducted explores the orbits of asteroids in our solar system and the likelihood of orbits topologically linking with one another. Our aim is to update the 1847 investigation into this topic and see if the asteroids are part of linked chains of orbits throughout the solar system. Linked orbits are defined by any two orbits that loop into one another, like rings in a chain. With this, we can get a better understanding about the overall structure of the Solar System. We used NASA's Small-Body Object database (a list of every known asteroid in our solar system separated by categories of distance) to obtain orbital parameters. Using a newly developed method that can determine ellipse linking faster than the Gauss linking integral, determine how many times each asteroid's orbit passes through another asteroid's orbit. We use that information to calculate the likelihood that asteroids within and between groups such as the Main Belt are linked with one another. From our findings, we learned that asteroids within certain groups can have a greater than 50% probability of being linked. These probabilities are higher than in "control" orbits

with randomized parameters. Not only that, but we also found that neighboring asteroid groups are likely to be interlinked with one another; except for the Inner Mainbelt, Mainbelt, and Outer Mainbelt asteroid groups. Lastly, we got 1000 asteroids from each asteroid group and combined them all into one group. We found that their interlinking probability was 9.68%. Not only that, but there is also a small possibility that there could be a long chain of asteroids spanning throughout the solar system.

This work was supported by a CSULB Student Summer Research Award. We acknowledge the METRIC2 program (NSF- DUE-2322416) for additional support.

18. A Comparison of Analytical Methods for the Simulated Untying Process of Polymer Knots

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Knots in proteins and DNA molecules occur naturally in biological systems, where they are known to provide mechanical stability and influence molecular workflows. However, analyzing how these topologies untie under physical perturbations is often restricted by complex computational demands or over-simplifications. This research addresses this challenge by performing coarse-grained molecular dynamics simulations of a polymer chain initialized as a 5_2 twist knot to systematically compare five analytical methods: radius of gyration (R_g), minimal closure, stochastic closure, automated planar projection m and the knotoid spectrum. The rationale behind this comparison is to establish a more accessible, yet rigorous, topological analysis framework that implements foundational hallmarks of knot theory (such as the Alexander polynomial, skein relations, and the Jones polynomial) without relying on heavy computational geometry. Our results reveal a systematic relaxation lag following a controlled chain-cleavage event; while topological tools verify unknotting rapidly, global dimensional metrics like R_g consistently overestimate the untying timeline for more complex unknotting pathways. Concurrently, all three stochastic projection methods demonstrated loose alignment with each other, showing topological transitions around the same timestep. These findings imply that the radius of gyration cannot capture the nuances of complex unknotting pathways due to the delay between unknot and expansion. Furthermore, implementing multi-method stochastic and knotoid tracking provides a significantly more high-resolution, reliable capture of transient topological phases.

This project is supported in part by the Gisela and Wilfried Eckhardt Endowment for Physics and Astronomy Award

19. Molecular Dynamic Investigation of Percolating Membranes

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Thermalized tethered membranes are known to have a flat phase, but random perforations may lead to a transition to a crumpled state. This situation arises both in the study of graphene-like materials and in kinetoplast DNA networks that have had minicircles removed by enzymes. Here, we use molecular dynamics simulations to explore the equilibrium properties of randomly perforated tethered membranes at their percolation threshold. We examine the equilibrium radius of gyration as a function of molecular weight and compare it to a generalized Flory theory based on the spectral dimension of percolation clusters. While percolation clusters are predicted to have a scaling exponent of $1/2$, in between linear polymers and crumpled sheets, our results indicate that their behavior is more sheet-like than polymer-like, consistent with earlier results. We also examine the loss of global surface normal, characterized by an orientational order parameter, as the degree of perforation increases from a pristine sheet to a percolating network. Our results indicate that orientational order is lost before the geometric percolation threshold is reached.

20. (no longer presenting)

Narith Chan*, Michelle McKenzie, Eric Corona-Oceguera, Joshua Luna, Esteban Mack-Flores, Joshua Paras, Chenchu Yakasiri Saravanan, Archibald J. Williams, Joshua Goldberger and Claudia Ojeda-Aristizabal

21. Fabrication of Graphene and Hexagonal Boron Nitride (h-BN) Heterostructures

Said Ortega*, Narith Chan, Chenchu Yakasiri, Eric Corona, Kenji watanabe, Takashi Taniguchi, Claudia Ojeda-Aristizabal

Graphene and hexagonal boron nitride (h-BN) are two-dimensional materials with unique structural and electronic properties. For graphene, I will outline two methods of exfoliation, a mechanical method using a specialized tape, and liquid phase exfoliation (LPE) which uses a liquid solvent. Due to its thinness, monolayer graphene looks nearly transparent and requires careful inspection of a wafer through an optical microscope and further characterization using Raman Spectroscopy and/or Energy Dispersive X-Ray Spectroscopy (EDS). This approach enables the successful isolation of monolayer graphene, which is subsequently stacked onto h-BN to create devices that leverage the heterostructure's unique properties, such as a high electron mobility.

The primary funding for this work was provided by the U.S Department of Energy, Office of Science, Office of Basic Energy Sciences under contract DE-SC0018154 for sample fabrication. Raman characterization was funded by the California State UNiversity, Long Beach and the Ohio State University Partnership for Education and Research in Topological Materials and the National Science Foundation PREM under Grant No. 2425133. E.C. -O acknowledges support from the APS Bridge Program

22. Fabrication, AFM, and EDS analysis of Platinum Ditelluride (PtTe₂)

Joshua Paras*, Narith Chan, Eric Corona, Joshua Luna, Esteban Mack-Flores, Chenchu Yakasiri Saravanan, Pranathi Ramesh, Claudia Ojeda-Aristizabal, Archibald Williams, Joshua Goldberger

Platinum ditelluride (PtTe₂) is a layered material with unique properties that makes it interesting for research and possible applications in electronic devices. In this project, thin flakes of PtTe₂ were prepared through mechanical exfoliation, in which adhesive tape was used to separate thin flakes from a bulk crystal and transfer them onto a silicon substrate. The samples are then studied using atomic force microscopy (AFM) and energy-dispersive X-ray spectroscopy (EDS). AFM is used to examine the surface of the flakes and determine their thickness, while EDS is used to identify the elements present in the sample. These methods allow us to study both the physical structure and composition of the PtTe₂ flakes. The goal of this work is to better understand the fabrication and characterization of thin PtTe₂ and prepare samples that can be used for further study.

23. Molecular Arrangement of a Phthalocyanine Thin Film on Graphene Probed Through Transmission Electron Microscopy

Pranathi Ramesh*, Eric Corona-Oceguera, Narith Chan, Joshua Luna, Chenchu Yakasiri Saravanan, Esteban Mack-Flores, Joshua Paras, Alexander Goytia Fajardo, Thomas Gredig and Claudia Ojeda-Aristizabal

California State University, Long Beach

This project aims to use 4D scanning electron transmission microscopy to investigate the role of the molecular arrangement of a phthalocyanine thin film on the restoration of weak localization in graphene. Our previous work has shown that depositing copper phthalocyanine on bilayer graphene restores weak localization, which is a quantum correction of the conductance. In that work, phthalocyanines were deposited on samples held at room temperature, which produced grain sizes much smaller than our transport coherence lengths. I will discuss our new project in which we will deposit the phthalocyanine molecules while holding the substrate, graphene,

at elevated temperatures, which is expected to significantly increase the grain sizes in the molecular thin film. Using electron transmission microscopy, we will be able to gather more information on how the molecular arrangement of the grains impact weak localization and other phenomena characteristic of graphene such as trigonal warping.

24. Band structure characterization of the antiferromagnet $\text{Fe}_2\text{Ga}_2\text{S}_5$ through photoemission experiments

Tianfei Zhang^{1*}, Connor Krucek⁴, Bowen Yu³, William Arch⁴ Mahfuzun Nabi¹, Ryan Rios¹, Jonathan D Denlinger², Wolfgang E Windl³, Joshua E Goldberger⁴, and Claudia Ojeda-Aristizabal¹

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Angle-resolved photoemission spectroscopy (ARPES) is a powerful tool for probing the band structure and the orbital character in two-dimensional van der Waals materials. Previous works have shown that $\text{Fe}_2\text{Ga}_2\text{S}_5$ is an antiferromagnetic semiconducting material with a narrow band gap of 5 meV and a Néel temperature of 110 K. However, the electronic structure of this material has not been studied in depth yet. Interestingly, it has a crystalline structure that is very similar to the one of $\text{Mn}_2\text{Ga}_2\text{S}_5$, known to be a spin glass.

Here, we use ARPES to reveal the band structure of $\text{Fe}_2\text{Ga}_2\text{S}_5$ and the symmetry of its Fermi surface, which we contrast with first-principles calculations. We acquired photoemission data at various light polarizations to analyze the linear and circular dichroism in search of insight into the orbital character of the $\text{Fe}_2\text{Ga}_2\text{S}_5$'s electronic states and the proper band identification to contrast with our density functional theory (DFT) calculations. Temperature series were also conducted around the Néel Temperature (TN) of $\text{Fe}_2\text{Ga}_2\text{S}_5$ to investigate the change of the band structure in the paramagnetic and antiferromagnetic regimes.

25. Atomic Force Microscopy of Thin Quantum Materials

Esteban Mack-Flores*, Joshua Paras, Chenchu Yakasiri, Eric Corona-Ocegura, Narith Chan, Pranathi Ramesh, et al.

Atomic Force Microscopy (AFM) is a crucial step in the fabrication and characterization of electronic devices made of certain 2D materials. Without AFM, it is oftentimes challenging to determine whether we have a desired crystal thickness.

More specifically with PtTe_2 , an optical image of a thin crystal can give us a general idea of certain thickness ranges, but not its precise thickness. Additionally, at a thickness range of 50nm to 150nm, PtTe_2 presents the same contrast under an optical microscope, which leaves us uninformed about the quality of the crystal for our electronic transport, resistance, conductivity, and quantum hall effect measurements. I will present the principle behind AFM, and how the use of this tool informs us on the thickness and quality of our crystals, and help us to be efficient at fabricating devices that will have only crystals that will provide good results in electronic transport experiments.

26. A Geometric Algebra Formulation of Rotational Optimization for Autonomous Underwater Robots

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This research investigates geometric algebra as a representation for transportation in autonomous underwater vehicles (AUVs). The approach represents vehicle orientation, commanded orientation, and orientation error with geometric algebra rotors, providing a unified framework for describing underwater robotic motion.

The work reformulates an existing quaternion-based rotational optimization process in geometric algebra, preserving orientation-error bounds, control masks, and dynamic behavior. Quaternions provide an efficient representation of three-dimensional rotation and avoid the gimbal-lock singularities associated with Euler angles. However, difficulties can arise constantly converting rotational errors into quantities for constraint handling, controller tuning, or interpretation. Such conversions depend on a selected reference frame and can complicate the analysis of large, coupled rotations, while geometric algebra makes what frame you are working in apparent.

Geometric algebra offers an alternative formulation in which rotations, rotational errors, and spatial relationships are expressed through rotors and multivectors. This retains decomposition along selected principal axes for direct comparison with axis-based quantities, while making the geometric relationship and reference frame of each rotation explicit. Comparing this formulation with the existing quaternion method as vehicle orientations change over time will evaluate whether geometric algebra improves the clarity and structure of rotational constraints and optimization in AUVs.

27. Local Modifications In Planar Hypohamiltonian Graphs

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A graph is hypohamiltonian if it has no Hamiltonian cycle but deleting any single vertex produces a graph that does. Planar hypohamiltonian graphs are known to exist for orders 34, 37, 38, and all orders $n \geq 40$, while no examples are known of order less than 34 or of orders 35, 36, and 39. This work proves that a planar hypohamiltonian graph exists for every order $n \geq 36$ by constructing the first examples of orders 36 and 39. The proof uses local modifications that replace a subgraph with a larger one while preserving hypohamiltonicity. Two of these modifications are new. The plus two modification replaces a configuration of five 4-gon faces with seven, and the plus three modification replaces three 5-gon faces with five. Both new modifications can also be applied in reverse to remove two or three vertices, although the resulting graph is not guaranteed to be hypohamiltonian. Applied to Wiener's almost hypohamiltonian graph of order 31, plus three recovers Tsai's graphs of orders 34 and 37 and produces new examples of order 37. Applying plus two to Tsai's order 34 graphs yields order 36, and applying plus three to those graphs yields order 39. Thomassen's plus four modification, which can be repeated indefinitely, then extends the consecutive orders 36 through 39 to every larger order. Order 35 remains open, and Tsai's graphs of order 34 are conjectured to be the smallest planar hypohamiltonian graphs. In conclusion, these results lower the threshold which planar hypohamiltonian graphs are known to exist for every order from 40 to 36, and the modifications provide a general tool for constructing new examples.

28. Fentanyl-related Harm Reduction Strategies for Music Festivals: Results from a Pre/Post Study among University Students

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Fentanyl-related overdoses remain a significant public health concern in the United States among young adults who encounter illicitly manufactured fentanyl through counterfeit pills and other substances. Music festivals are environments where

substance use may occur, highlighting the importance of harm reduction education and resources such as fentanyl test strips and naloxone. We hypothesized that a campus-based harm reduction intervention would improve university students' awareness, confidence, and willingness to use fentanyl harm reduction strategies for music festivals. A pre/post survey was conducted among students attending a fentanyl-focused harm reduction event at California State University, Long Beach (CSULB) between December 2025 and March 2026. Surveys assessed participants' awareness, knowledge, confidence, and willingness regarding the use of harm reduction resources at music festivals. Using R, descriptive statistics were calculated to summarize survey responses and Chi-square tests were conducted to compare pre- and post-intervention awareness of free naloxone and fentanyl test strip availability through the CSULB Student Health Center (SHC). Our sample included 76 pre-survey respondents and 73 post-survey respondents. The pre-survey sample was diverse, with participants identifying primarily as female (52.6%), Hispanic/Latino (50.0%), and first-generation students (58.3%). Prior to the intervention, most participants indicated they would bring naloxone (94.7%) and use fentanyl test strips (92.1%) if these resources were freely available at music festivals. However, many participants had never received fentanyl test strips (71.2%) or tested substances for fentanyl (84.9%), despite concerns about fentanyl lacing (85.2%) and barriers to accessing and using harm reduction resources. Following the intervention, awareness that the SHC provides free naloxone ($\chi^2=4.45$, $p=0.035$) and free fentanyl test strips ($\chi^2=6.86$, $p=0.009$) increased significantly. Participants reported strong interest in learning how to administer naloxone (73.9%) and strong support for continued access to free harm reduction education and supplies through the university (80.8%). Universities may serve as important settings for expanding access to overdose prevention education and resources among young adults who attend music festivals. Continued efforts to improve awareness and accessibility may strengthen students' engagement with harm reduction resources.

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29. Comparing Assistive Technology Modalities: Preliminary Findings on Performance and Wellbeing

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Environmental control units (ECUs) are assistive devices intended to increase independence by helping physically limited individuals (e.g., those with spinal cord injuries or disorders (SCI/D)) perform everyday tasks and facilitate social support. Despite these intended benefits, previous research revealed that ECUs can be frustrating and effortful to use due to both technology and user-related issues. ECUs offer multiple control modalities, but research comparing these modalities and their effects on usability and performance is limited. This project aims to investigate the differences in task performance and psychological well-being between the touchscreen (direct) and eye-tracking (indirect) control modalities. It is hypothesized that participants in the touchscreen modality will complete tasks more quickly and successfully, report lower cognitive workload, experience greater perceived fulfillment of psychological needs, and rate the system as more usable than eye-tracking users. Participants ($N = 60$) will be randomly assigned to the touchscreen or eye-tracking condition. Participants will complete five tasks that simulate everyday ECU use, then complete three post-test surveys. An ANOVA on preliminary findings ($n = 30$) indicates that modality type has a significant main effect on average task completion time, $F(1,17) = 6.633, p = .020, \eta_p^2 = .281$. There was no significant effect of modality on perceived satisfaction of psychological needs (Autonomy: $F(1,17) = 1.763, p = .202$; Competence: $F(1,17) = .557, p = .466$; Relatedness: $F(1,17) = .214, p = .650$). This research may contribute to advancements in universal design and human factors by identifying how ECUs improve user performance and support psychological needs. The findings may also inform the development of more intuitive and effective interfaces and promote greater accessibility in technology design.

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30. Design of spore-embedded living materials for controlled activation

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Living polymer-based coatings embedded with bacterial spores have demonstrated significant potential as reliable materials for applications like bioactive adhesives, self-healing surfaces and environmentally responsive coatings. However, the understanding of the ability of bacterial spores to preserve viability within polymer matrices and to be efficiently released after drying remains limited. The aim of this study is to investigate the recovery, release and viability of *Bacillus subtilis* spores

from aqueous polymer suspensions that emulates adhesive formulations. Lyophilized spores are dispersed in phosphate-buffered saline to generate the stock solution and are subjected to dilutions before incorporating it into polymer suspensions. Standard microbiological methods are employed such as formulation of Luria-Bertani media and agar, colony-forming unit analysis, and optical density measurements to quantify spore viability and recovery. The spores are embedded in polymer matrices like alginate and polyvinyl alcohol. The influence and effects of formulation composition, drying, rehydration, and polymer matrix characteristics and properties are analyzed and evaluated by the comparative analysis of viable spore recovery under multiple experimental conditions. Initial experiments optimized the experimental workflow and generated preliminary bacterial growth, CFU, electron microscopy imaging and rheology data. Beyond enabling controlled microbial release, this platform establishes the foundation for spore-mediated polymer biodegradation directly from aqueous coating formulations, eliminating the need for high-temperature melt extrusion required in conventional living polymer composites. Results showed that *Bacillus subtilis* spores remained viable in both PVA and alginate matrices, demonstrated by bacterial colony growth. CFU analysis could not be completed because plate smearing and excess salts prevented accurate colony counting. Rheological comparisons showed that alginate was stiffer and more viscous than PVA. Future work will optimize CFU procedures and use a 3D-printed mold to drop-cast the matrices and evaluate shape retention. This approach expands the range of compatible polymers, including those that cannot readily undergo melt processing, while providing design guidelines for engineering living coatings, adhesives, and biofunctional materials with regulated microbial delivery and on-demand biodegradation.

This project is sponsored by the UC San Diego Materials Research Science and Engineering Center (UCSD MRSEC), supported by the National Science Foundation (Grant DMR-2011924)

31. Identifying the Computational Characteristics of Generalized Paroxysmal Fast Activity for the Improved Diagnosis of Lennox-Gastaut Syndrome

Bill Dai*, Derek Hu

Lennox–Gastaut syndrome (LGS) is a severe developmental and epileptic encephalopathy characterized by treatment-resistant seizures and impaired neurodevelopment. Because seizures occur during critical periods of cognitive and social development, delayed diagnosis and treatment can result in lifelong neurological disability. One diagnostic feature of LGS includes the identification of generalized paroxysmal fast activity (GPFA), a characteristic electroencephalogram (EEG) waveform associated with LGS. However, this process is time-consuming,

requiring hours of manual review and thousands of waveform annotations for a single study. GPFAs also lack an objective framework for identification, often relying on subjective, visual review of EEG by specialists. These limitations in GPFA characterization contribute to poor interrater reliability, leading to delayed treatment timelines and variability in diagnostic decision-making. The use of computational approaches to identify and characterize GPFA could improve the consistency of EEG review while reducing the burden and variability associated with specialist review. Here, we use an unsupervised, automated approach to characterize the computational EEG characteristics of GPFA.

32. A Review of Freely Available Science Programming and How They Represent Ethnic, Racial, and Gender Diversity in Science

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Non-commercial television programming is an accessible medium through which educators can shape the viewer's relationship with science. It is a multimedia technology that, while widely used for entertainment purposes, is part of the free choice learning sector. Educational science programming can nurture and establish science identity, literacy, and familiarity. Factors which influence a child's science performance and persistence. Research in the field has revealed that just as crucial as the content material, is the ethnic, racial, and gender representation of the science expert. Children tend to admire and identify with individuals who look like them. When science experts are humanized, listeners are more engaged and view such individuals as reliable sources. In light of such findings, this project investigated the question: how are scientists (science experts) portrayed in children's programming on freely accessible TV? To do this, a review of television programs publicly broadcast on non-commercial networks, namely PBS, were analyzed against the following criteria. The host(s) had to be real people (humans) doing/teaching science and be of an underrepresented group in STEM. The program itself had to be publicly broadcast and not entirely animated.

The review found only one show, SciGirls, from the catalog of PBS Kids that fit the criteria. The vast majority of the programs assessed were entirely animated and led by ambiguous and/or non-human hosts. Despite research into the importance of representation in children's educational TV, freely accessible programming does not

reflect this. While this review concentrated solely on non-commercial shows, similar studies that included cable, commercial channels found the same representational inconsistencies. In turn, this signifies a need to invest in such shows, especially in terms of accessibility since programs that align with the criteria listed do exist but are contained behind a paywall. If this persists, then only a select few children get to see themselves represented in science. To have a diverse scientific community that is reflective of all members of society, such must be first displayed in the TV programs tailored to the education of children. After all, it is this programming that forms children's first impressions of science, the individuals who carry out its processes, and allows them to see what is attainable.

33. Understanding how secondary preservice science teachers think about supporting Multilingual learners from video analysis

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Currently, science instructional practice in the US is heavily dependent on English language understanding. However, English dependency in the classroom can be an obstacle for multilingual learners (MLs) because it limits how they can communicate their understandings and their engagement with science learning. One area of growth is helping pre-service teachers (PSTs) to notice and leverage multimodal and multilingual communication to increase MLs' opportunities to engage in science learning. Video analysis of classroom instruction is a helpful tool to critically examine representations of instructional practice aligned with equitable science teaching. So, the second author developed a video analysis task that used an 8th-grade multilingual classroom within a science teaching methods course. In our study, PSTs analyzed video to reflect on instructional practices that used multimodality and multilingualism to decrease English dependency for MLs. We analyzed data from 13 PSTs' video analysis papers to examine how credential students think about supporting MLs when teaching science. We used a hybrid inductive-deductive thematic coding process. The first author developed an initial code book focused on instructional strategies to support MLs. Their inclusion criteria required the responses to mention "MLs", what instructional strategy was named, and how they perceived the instructional strategy supported MLs science learning. The second author then reviewed the codebook and codes to adjudicate any disagreements or for clarity issues. Our emergent findings were that gesturing and native language use are the most frequently described instructional strategies when credential students think about supporting MLs when teaching science. Two out of the thirteen PSTs did not mention MLs at all in their video analysis reflections. We found that out of 44 total

codes across 13 PST responses, 19/44 (43.2% of total codes) referenced gestures (10/44) and native language use (9/44). Upon further analysis of those PST responses, PSTs discussed gestures as a tool and native language use as valid to communicate science concepts without depending on English. They connected both instructional strategies as a way to create more access and connected it to equitable teaching for MLs. Our emergent findings tells us that this video analysis activity did surface productive conversations that encouraged PSTs to question English-only practices. Overall there is promising data that PSTs may intend to enact these more equitable instructional practices for their own classrooms.

34. Finite Temperature Effects on g-Modes of Warm Neutron Stars

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We study the effect of temperature on composition-driven g-modes in the cores of warm neutron stars. Using a chiral SU(2) sigma model, we construct isentropic equations of state and stellar configurations for hot and dense matter. Weak-interaction rates are incorporated into a complex, frequency-dependent dynamical sound speed that approaches the frozen-composition limit for slow reactions and the beta-equilibrated limit for fast reactions. We solve self-consistently for the complex g-mode eigenfrequency and find that its real part depends non-monotonically on the nuclear symmetry-energy slope parameter L , reaching its largest values near $L \sim 100$ -110 MeV. Increasing the entropy per baryon accelerates chemical re-equilibration and suppresses the oscillation frequency. The associated damping rate reaches a maximum when the weak-interaction relaxation and mode timescales become comparable, signifying that dissipative effects also depend on L . Our results demonstrate that the thermal weak-interaction response and the density dependence of the symmetry energy jointly determine the g-mode spectrum of warm neutron stars.

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35. Characterizing Sun-like stars in the Mount Wilson Observatory HK Project

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The Sun has unusually low photometric variability for its magnetic activity (Lockwood et al. 2007; Radick et al. 2018; Reinhold et al. 2020; Santos et al. 2023). Using the 155 MWO "Next Generation" dwarfs (curated to be Sun-like) and overlapping TESS dwarfs, we investigate relationships between R'HK variability and photometric variability in Sun-like stars over their lifetimes. Through this, we can determine whether the Sun remains an outlier in photometric variability and magnetic activity compared with MWO dwarfs and trace the evolution of the Sun's past photometric variability using Sun-like stars to better understand terrestrial climate evolution and inform exoplanet searches. Here we select a sample from MWO database that has spectroscopy that is consistent with sun-like metallicities. We also describe a method to recover the stellar mass and age using Kiauhoku in combination with stellar models from Modules for Experiments in Stellar Astrophysics (MESA) to create a grid of stars and Kiauhoku to recover the mass and ages from the samples. Future work intends to integrate MESA and MWO database into a single grid for use in Kiauhoku to recover the ages and masses of stars in this database.

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36. Magnetic Cycle Variability Classification Using Gaussian Processes

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There exists a broad spectrum of variability in stellar magnetic activity, driven by the operation of the internal dynamo. Current literature typically classifies magnetic activity into three qualitative categories: flat, erratic, and periodic. Here we use a sample of stars from the Mount Wilson Observatory HK Project to explore a quantitative measure of periodicity. We model the S-index time series using a quasi-periodic Gaussian process (GP) to infer magnetic cycle periods, decoherence timescales, and amplitudes. The GP model includes a linear trend component and physically motivated priors. We find agreement between our inferred cycle periods and those with literature values, where available. We also define a periodicity metric for the sample, defined by the ratio of the decoherence timescale to the cycle period,

as a quantitative metric for assessing the stability of stellar magnetic cycles. The resulting periodicity metric demonstrates the potential of GP modeling as a useful framework for studying magnetic variability and stellar dynamo behavior.

37. How Common is the Milky Way? Stellar Actions in APO-K2 and NIHAO Milky Way–Mass Galaxies

Victoria Grajeda*, Joel Zinn

Previous work has established that the NIHAO cosmological simulations can reproduce the Milky Way's chemical-abundance patterns in $[\text{Fe}/\text{H}]$ – $[\alpha/\text{Fe}]$ space through merger-driven evolution (Buck 2020; I. Boiko et al., in prep.). Here we test to what extent these simulations reproduce Milky Way–like kinematics at fixed chemical abundance. Using a new catalog of orbital actions (J_r , J_z , J_ϕ) for $\sim 7,600$ APO-K2 red giants built from Gaia DR3 astrometry and APOGEE spectroscopy, we define a χ^2_v metric comparing observed and simulated median actions binned in $[\text{Fe}/\text{H}]$ – $[\text{O}/\text{Fe}]$ space, across 33 Milky Way–mass NIHAO galaxies. Three galaxies are not inconsistent with the Milky Way at the 0.1% level in J_z ; the radial action J_r and angular momentum J_ϕ are statistically inconsistent across all NIHAO Milky Way–mass galaxies. The galaxies most Milky Way–like in kinematics are also the most Milky Way–like in stellar ages (I. Boiko et al., in prep.): both metrics independently identify the halos closest to the Milky Way's mass as the most Milky Way–like.

38. Detecting Rotation Periods in Mount Wilson Observatory Data using Gaussian Processes

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The magnetic variability of main-sequence dwarf stars has been extensively documented, notably in studies by Baliunas et al. (1995). However, evolved stars which have structures, rotation periods, and convection patterns that differ from main-sequence stars, have limited existing studies. We use a data set of post-main-sequence red giants monitored over decades by the Mount Wilson Observatory (MWO) data HK project (Baliunas et al. 1998). Using the MWO S-index, an instrumental flux scale taking the ratio in fluxes of the Ca II H and K emission lines, we

model the stellar time series using a quasi-periodic Gaussian process to recover stellar rotation periods (P_{rot}) and magnetic decoherence time scales. We obtain periods for 315 evolved stars and 35 main sequence stars. Discrepancies between our results and existing documentation such as Olsperg et al. (2018) highlight potential new magnetic cycles and opportunity to improve on existing period-search methodologies. Additionally, we perform an independent check for rotation periods using TESS (Transiting Exoplanet Survey Satellite) photometric data. Synthetic light curves are generated by injecting a rotation period into TESS targets with little to no variability and are then processed through a pipeline proposed by Coleman et al. (2024) to test and confirm rotation period recovery.

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39. Impact of Quantum Statistics on Cosmological Matter Creation

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For several decades, attempts to explain the late-time acceleration of the Universe without a Cosmological Constant have resulted in a class of cosmological models called Creation Cold Dark Matter Models (CCDMs). These models suggest a mechanism for the continual creation of dark matter at the expense of energy from the expanding gravitational field. This matter-creation mechanism introduces a particle creation rate, Γ , and associated creation pressure. [1] shows that, for a single-fluid ideal Boltzmann gas model and a particular creation pressure ansatz, an initial decelerated expansion period followed by late-time accelerated expansion can be achieved. The goal of the work presented here is to explore the sensitivity of expansion and thermodynamic evolution in this model to underlying equation of state assumptions. We replace the Boltzmann gas assumption of [1] with an ideal relativistic Fermi gas with and without a bag condensate which introduces the effect of a background condensate. In comparing these evolution parameters, we explore the role of microscopic thermodynamics in CCDM cosmology. The equation-of-state choice has a relatively small influence on the early expansion history, while producing more significant differences during the later evolution. For the parameter choices considered, the matter-creation models exhibit earlier and more rapid expansion than the reference Λ CDM evolution. Thus, the macroscopic expansion history in the Ivanov and Prodanov CCDM model retains sensitivity to underlying microscopic equation of state assumptions.

40. Multiplicity Corrections to Nuclear Matter

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Hadron resonance gas (HRG) models provide an effective description of confined QCD matter below the crossover. Short-range repulsive interactions are commonly modeled through excluded-volume (EV) corrections. Although successful in the low-temperature, low-density regime, the EV approach fails naturally in dense matter, at the latest when particles occupy all available volume. We address this issue in a thermodynamically consistent phenomenological framework where interactions depend on the usual (relativistic mean-field) vector interaction channel, which couples to the baryon number density. We then introduce a corresponding multiplicity-dependent interaction that remains nonzero at nearly vanishing net baryon density. By construction, the framework reproduces conventional relativistic mean-field behavior in cold and dense baryonic matter. At low density, we compare our results with ideal HRG, EV-HRG, and lattice QCD results.

41. Late-time X-ray and Optical Spectroscopy of AT2019fdr

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X-ray transients (XRTs) are sources of X-rays that increase significantly in brightness or appear where no X-ray source has been seen before. XRTs can be caused by a variety of astronomical events such as Tidal Disruption Events (TDEs), which occur when a star passes too close to a supermassive black hole and gets accreted, leading to a flare of emission across the electromagnetic spectrum. We set out to find and classify recent previously unknown XRTs in Swift data by searching through the living Swift X-ray Point Source Catalog. We identified LSXPS J170906.9+265122 as a new Swift X-ray detection and it appears likely to be associated with AT2019fdr, a cosmic event surrounded by much debate. Due to its unique characteristics, AT2019fdr has been categorized as a Type IIIn Superluminous Supernova (SLSN), AGN flare, and a TDE. We obtained a NuSTAR observation of LSXPS J170906.9+265122 in 2026 July and

confirmed its ongoing X-ray activity. These X-ray detections disfavor a SLSN, as late-time X-ray emissions are rare for Type II SLSN and are not consistent with an AGN flare due to a lack of counterpart optical flaring. Therefore, we find that AT2019fdr was most likely a TDE that occurred in an AGN, and that LSXPS J170906.9+265122 represents X-ray emission delayed by 6-7 years, the longest such delay yet observed by a TDE.

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42. From 331 to Pfaffian: Antisymmetrization Across the Excitation Spectrum at $\nu = 5/2$

Juan Robles*, Michael Peterson

Topologically ordered quantum phases of matter that can support exotic fractionalized excitations are of particular interest for the development of quantum computing. The Fractional Quantum Hall Effect (FQHE) at filling factor $\nu = 5/2$ is believed to be described by a paired state of composite fermions (Moore-Read Pfaffian), whose ground state is the antisymmetrization of a bilayer state (Halperin 331). Prior work showed that at a layer separation distance ($d \approx 2.4$) the Pfaffian and bilayer ground state are close to being identical. We're exploring whether a similar value exists for the excited states of the system by treating the separation distance as a parameter and sweeping across each angular momentum sector and excitation level. We're finding that there isn't a single separation distance that reproduces this behavior for excited states, but rather, different (L,d) combinations each give good overlap independently. This raises the question of whether this is a finite-size effect or reflects real physics distinguishing the excited-state correlations. Next, we plan to increase the system size (to $N=8$) to check whether the same behavior persists.

43. Apolipoprotein E Isoform Specific Effect on the Inflammatory Response of Brain Microvasculature Endothelial Cells at the Neurovascular Junction

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Apolipoprotein E (ApoE; 34 kDa, 299 amino acids) is a lipid transport protein essential for cholesterol homeostasis in the plasma and brain. It also plays a critical role in regulating inflammatory responses in the central nervous system. In humans, APOE is polymorphic, with three major alleles—APOE $\epsilon 2$, APOE $\epsilon 3$, and APOE $\epsilon 4$ —that encode the apoE2, apoE3, and apoE4 isoforms, respectively. Among these, APOE $\epsilon 4$ is the strongest genetic risk factor for late-onset Alzheimer's disease (AD), which is

characterized by amyloid plaque and neurofibrillary tangle formation, as well as chronic neuroinflammation. We hypothesize that apoE differentially regulates the inflammatory response of blood–brain barrier (BBB) at the neurovascular junction in an isoform-specific manner. To test this hypothesis, recombinant human apoE2, apoE3, and apoE4 containing an N-terminal hexa-His tag was overexpressed and isolated from a bacterial expression system using optimized codon usage. ApoE was purified by nickel-based immobilized metal affinity chromatography followed by size-exclusion chromatography. Purified apoE was reconstituted with 1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine (POPC) and cholesterol at a 9:1 (w/w) ratio by the cholate dialysis method. The resulting reconstituted high-density lipoprotein (rHDL) was isolated by density-gradient ultracentrifugation. Nondenaturing polyacrylamide gel electrophoresis revealed rHDL complexes of approximately 440 and 660 kDa for all three isoforms, like that reported for nascent HDL generated in vivo. rHDL containing apoE2, apoE3, or apoE4 was applied to mouse brain microvascular endothelial (bEnd.3) cells at 10 µg/mL for 2 h to stimulate cytokine production. In parallel, cells were treated with vehicle control consisting of 20 mM sodium phosphate, pH 7.4, containing 150 mM NaCl (phosphate buffered saline, PBS), under identical conditions. IL-6, TNF-α, IL-1β, and IL-10 concentrations were quantified using a multiplex assay. Preliminary results indicate that rHDL/apoE4 significantly increased the production of IL-6, a pro-inflammatory cytokine to 46.7 ± 22.7 pg/mL compared with 2.79 ± 0.40 pg/mL in the PBS control ($n = 4$, $P = 0.002$). Additional studies are underway to confirm these findings with more biological replicates and to quantify cellular cytokine mRNA levels by qPCR. We will also stimulate a pro-inflammatory response in bEnd.3 cells using lipopolysaccharide and assess the relative abilities of the apoE isoforms to attenuate inflammation. Together, these findings suggest isoform-specific roles for apoE in regulating inflammation at the neurovascular junction and bear the potential to provide insight into the role of apoE4 as a risk factor in AD.

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44. Role of Cholesterol and Apolipoproteins in Maintaining the Blood-Brain Barrier Integrity

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The blood–brain barrier (BBB) protects the brain by tightly regulating the movement of molecules between the blood and the central nervous system (CNS). It is formed by

tight junctions (TJs) between brain endothelial cells, with cholesterol being essential for maintaining junctional stability. Cholesterol can be provided from de novo synthesis or by the diet; it is transported between cells by lipoproteins such as very low-density lipoproteins and high-density lipoproteins (HDL), the latter being the predominant form of lipoprotein in the CNS. Apolipoprotein E (apoE), a major component of HDL and a critical factor in cholesterol homeostasis and transport, exists in three isoforms (E2, E3, E4), with apoE4 being the strongest genetic risk factor for late-onset Alzheimer's disease (AD). We hypothesize that apoE facilitates cholesterol delivery to TJs and plays a role in maintaining the TJ integrity in an isoform dependent manner. To test this hypothesis, we determined the levels of TJ marker proteins and cholesterol levels in mouse brain endothelial cells that were exposed to apoE isoforms. In parallel, we propose to visualize location and levels of externally supplied cholesterol by apoE isoforms. Recombinant apoE2, apoE3, and apoE4 were expressed in a bacterial system, and then purified by nickel affinity and size exclusion chromatography. The purified proteins were reconstituted with commercially available phospholipids (POPC), fluorescently tagged cholesterol* (BODIPY), and unlabeled cholesterol to generate reconstituted HDL (rHDL*), which was isolated by density gradient ultracentrifugation. Non-denaturing PAGE revealed formation of lipoprotein complexes of ~ 440 and 670 kDa. Fluorescence spectroscopy revealed presence of BODIPY in the lipoprotein fraction of the ultracentrifugation fractions. In parallel rHDL with POPC and unlabeled cholesterol, and apoE2, apoE3 or apoE4 was generated. The rHDL were then applied to bEnd.3 endothelial cells. Western blot analysis demonstrated that apoE/rHDL upregulates TJ marker proteins in an isoform-specific manner (apoE3 > apoE2 > apoE4) based on band intensities normalized to β -actin. ApoE2-treated cells showed significantly higher levels of cholesterol compared to those treated with PBS ($p = 0.02$), apoE3/rHDLc ($p = 0.0004$) and apoE4/rHDLc ($p=0.0004$). Future studies will involve exposure of endothelial cells to rHDL* and determine if BODIPY-cholesterol colocalizes with TJ markers in an isoform-specific manner by confocal microscopy and quantified by flow cytometry. By investigating how cholesterol reaches TJs and how apoE isoforms influence this process, our research aims to fill a critical knowledge gap in BBB maintenance. Understanding isoform-specific differences in cholesterol transport could provide insight into why apoE4 carriers are more susceptible to AD and may inform therapeutic strategies to strengthen BBB integrity.

45. Oxidative Modification by 4-Hydroxynonenal and Methylglyoxal Impair Lipid Binding of Apolipoprotein E

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Apolipoprotein E (apoE) mediates lipid and cholesterol transport, with major isoforms apoE2, apoE3, and apoE4 differing in disease associations. ApoE4 shows increased risk cardiovascular disease (CVD) and Alzheimer's disease (AD). Studies in apoE knockout mice revealed an increase in blood-brain barrier (BBB) permeability with age, which was further exacerbated by apoE deficiency, implicating the importance of apoE and age in BBB integrity. We investigated two age related biomolecules that are generated endogenously: i) 4-hydroxynonenal (HNE), a reactive aldehyde derived from lipid peroxidation, detected on proteins from postmortem tissues of AD subjects, and, ii) methylglyoxal (MGO), a reactive 1,2-dicarbonyl that is generated during normal cellular breakdown of glucose, and found in high levels in brain tissues and cerebrospinal fluid of AD patients. We hypothesize that HNE and MGO modify apoE isoforms and compromise their structure and function.

To test this hypothesis, recombinant human apoE2, apoE3, and apoE4 bearing a hexa-His tag at the N-terminal end were expressed in *E. coli* with optimized codon usage and purified by nickel-affinity and size-exclusion chromatography. The purified proteins (~95% pure) were treated with HNE (5:1 molar ratio of HNE: apoE) for 2 hours at 37 °C and unreacted HNE was dialyzed out. Unmodified and HNE-modified apoE isoforms were subjected to immunoblot analysis with anti-HNE antibody, which revealed a band ~36 kDa for the HNE-modified but not the unmodified apoE. In parallel, immunoblot analysis with anti-apoE antibody revealed a band ~ 36 kDa for both unmodified and HNE-modified apoE. This confirms modification of apoE by HNE. In a similar manner, apoE was modified by 10 mM MGO for 24 hours at 37 °C followed by dialysis to remove excess MGO. Immunoblot analysis with anti-MGO antibody revealed a band ~ 36 kDa for MGO-modified but not for unmodified apoE. In parallel, BSA modified with HNE or MGO was detected by anti-HNE and anti-MGO antibodies, respectively, confirming the specificity of the antibodies for the respective modifications. Further, our preliminary analysis revealed that compared to unmodified apoE, both HNE- and MGO-modification notably altered the ability of apoE to bind and convert multilamellar vesicles of dimyristoylphosphatidylcholine (DMPC) (~200 nm diameter) to smaller discoidal lipoprotein complexes (~20 nm) as determined by changes in sample turbidity at 320 nm as a function of time. Future studies will assess the changes to the secondary and tertiary structure of apoE as a result of modification and the functional ability of oxidatively modified apoE to be

internalized by cells. Taken together, our findings indicate that oxidative modification alter the major lipid binding function of apoE, which has direct implications in its role in mediating cholesterol homeostasis in CVD and AD.

46. The Roles of Leu-163, Gly-217, and Lys-226 in ApoA-I Self-Association

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Reverse cholesterol transport is a process that removes excess cholesterol from peripheral tissues to the liver and is mediated by high-density lipoprotein (HDL). Apolipoprotein A-I (apoA-I) is the major protein component of HDL and consists of an N-terminal (NT) and C-terminal domain (CT). While the NT domain structure has been resolved recently, the CT domain molecular structure is largely unknown. The CT domain facilitates self-association of apoA-I into dimers at physiological protein concentrations, but the intermolecular interactions are not understood. Lys-226 has been identified as a crucial residue, as mutation into Gln resulted in a large shift towards the monomeric state. It has been proposed that Lys-226 forms a cluster with Leu-163 and Gly-217, raising the possibility that these residues contribute to the apoA-I dimer interface. Therefore, L163A- and G217Q-apoA-I mutants were generated by site-directed mutagenesis. Wild-type (WT) apoA-I and the mutants were expressed in *E. coli* and purified using nickel-affinity and size-exclusion chromatography. The mutant proteins were analyzed for secondary structure with far-UV circular dichroism (CD), and guanidine HCl-induced denaturation. Far-UV CD showed α -helical contents of $71.5 \pm 1.6\%$ for WT, $59.1 \pm 1.5\%$ for L163A-apoA-I, and $67.9 \pm 0.7\%$ for G217Q-apoA-I ($n = 3$). Guanidine-HCl denaturation yielded denaturation midpoints of 1.07 M for WT-, 0.641 M for L163A-, and 0.996 M for G217Q-apoA-I. Self-association was studied by dimethyl suberimidate crosslinking followed by SDS-PAGE. ImageJ analysis of crosslinking gels showed an increased monomer population for L163A-apoA-I ($72.1 \pm 3.7\%$) compared with WT-apoA-I ($47.7 \pm 0.4\%$), whereas G217Q-apoA-I displayed a lower monomer population ($29.3 \pm 2.1\%$, $n = 3$). Lipid-binding function was assessed by monitoring the solubilization of 1,2-dimyristoyl-sn-glycero-3-phosphocholine (DMPC) vesicles at 325 nm. L163A-apoA-I showed an increased solubilization rate ($6.52 \pm 0.12 \times 10^{-3} \text{ s}^{-1}$) compared with WT ($3.51 \pm 0.02 \times 10^{-3} \text{ s}^{-1}$), whereas G217Q-apoA-I showed a decreased rate ($1.56 \pm 0.04 \times 10^{-3} \text{ s}^{-1}$). Thus, structural studies show a decrease in apoA-I α -helical content and conformational stability upon the L163A mutation. Leu-163 is buried in the four-helix bundle of the N-terminal domain, and replacement with the smaller Ala residue may have disrupted the hydrophobic packing. The decrease in self-association indicates a change in the interactions between the NT and CT domain. The G217Q mutation did not alter the

structural integrity of the protein while it increased the extent of self-association. Thus, Gly217 may contribute to molecular interactions inside the CT domain, thereby affecting apoA-I self-association. The increased DMPC solubilization by L163A and decreased solubilization by G217Q suggest that changes in apoA-I self-association may influence lipid-binding function.

47. The Role of the Non-polar Face of Helix 10 of ApoA-I in the Formation of Discoidal HDL

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High density lipoprotein (HDL) plays an essential role in the transport of cholesterol from peripheral tissues to the liver for processing. The protective role of HDL against cardiovascular disease is well documented, and apolipoprotein A-I (apoA-I) is the main protein of HDL. ApoA-I (243 amino acid residues) contains a 4-helix bundle N-terminal domain, and a small C-terminal (CT) domain (residues 180-243) which is largely unstructured. Mediated by the CT domain, apoA-I binds to phospholipid membranes forming discoidal HDL. When discoidal HDL is enriched in cholesterol esters, it develops into spherical HDL, which deposits the cholesterol load at the liver. The CT domain of apoA-I consists of three putative α -helices, but their molecular organization remains largely unknown. Pyrene fluorescence analysis indicated that the last helix (H10) is more exposed, and could act as a lipid sensor, initiating formation of discoidal HDL. H10 is an amphipathic α -helix with a non-polar face rich in leucine and aromatic residues. It is hypothesized that H10 initiates phospholipid binding with its non-polar face to form discoidal HDL. To test this, the non-polar face was disrupted by mutating leucine residues into serine. Single mutations L222S, L233S, and L240S were introduced in apoA-I, and the recombinant proteins were overexpressed and purified by Ni-affinity and size-exclusion chromatography. Far UV circular dichroism was performed to measure the α -helical content, yielding 59.8% for WT-apoA-I, 53.7% for L222S-apoA-I, and 62.4% for L240S-apoA-I. Thus, the mutations did not lead to major changes in α -helical content, and indicate the structural integrity was not compromised. To analyze the ability of apoA-I to form discoidal HDL, dimyristoylphosphatidylcholine (DMPC) was used. At the lipid transition temperature of 24 °C, DMPC vesicles were spontaneously transformed into discoidal HDL by WT-apoA-I, as measured by a decrease in light scatter at 325 nm, with a rate constant of $1.6 \times 10^{-3} \text{ s}^{-1}$. The rate constants of transformation for L222S- and L240S-apoA-I were 1.9×10^{-3} and $3.7 \times 10^{-3} \text{ s}^{-1}$, respectively. This result showed that the mutations did not decrease phospholipid binding, likely because the single mutations were insufficient to disrupt the non-polar face of the amphipathic α -helix.

While L233S-apoA-I remains to be analyzed, a triple mutant will be designed that includes all three mutations and will be analyzed for phospholipid binding.

48. Optimization of Fragment-Based Crystallographic Screening Using IRF3

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Interferon Regulatory Factor 3 (IRF3) is a key transcription factor in the innate immune response and is a prime target for fragment screening as it allows us to visualize potential binding sites for drug-based discovery. IRF3 was expressed, purified, and crystallized under varying protein and mother liquor concentrations, as well as seed amounts. Optimized crystals were subsequently soaked in 11 benzoic-acid derived fragments and visualized in electron density maps obtained from X-ray diffraction data. Crystals grown in 12 mg/mL protein, 1.50 M mother liquor, and 1:4 seed dilution produced sufficiently large crystals for X-ray diffraction. However, analysis of S7-soaked crystals did not reveal clear binding sites with the protein. Further evaluation of the collected data is needed to provide insight into potential fragment-binding sites. Nonetheless, the results establish optimal crystal conditions, and a foundation for potential fragment-binding sites that can support further drug development.

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49. Synthesis and Characterization of Fmoc-Amino Acid Phenyl Esters as Potential Selective Inhibitors of Butyrylcholinesterase for Alzheimer's Disease

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Alzheimer's disease (AD) is a progressive neurodegenerative disorder characterized by declining cognitive functions and reduced acetylcholine levels in the brain. While acetylcholinesterase (AChE) activity remains relatively constant or decreases during disease progression, butyrylcholinesterase (BChE) activity has been shown to increase, making BChE an attractive therapeutic target. Previous studies in our

laboratory identified Fmoc-amino acids as selective BChE inhibitors, providing a scaffold for the development of more potent and selective compounds. An attractive feature of the Fmoc-amino acid scaffold is the ability to readily incorporate varied substituents. In this study, we first focus on a series of phenyl esters and later on phenyl esters bearing halogen substituents. Fmoc-amino esters were found to be effective inhibitors, providing the foundation for evaluating additional esters. The aromatic phenyl group is proposed to make favorable interactions with aromatic groups in the enzyme active site, leading to better inhibitors. The phenyl esters are synthesized from an Fmoc-amino acid and phenol, purified, and characterized by NMR. Following synthesis, biochemical assays are conducted to determine the IC₅₀ value (potency), reversibility, and selectivity. Computational docking studies are also being conducted to identify potential interactions between the amino acid compounds and the enzyme. Future studies involving halogenated groups are aimed at investigating whether electron-donating or electron-withdrawing groups lead to better inhibitors, potentially by affecting π - π interactions with the enzyme. Together, these studies are aimed at furthering our understanding of the relative importance of features involved in cholinesterase inhibition and to help guide the design of more potent inhibitors.

This project is supported by the CSULB Building Infrastructure Leading to Diversity Program in the Office of Undergraduate Research Services.

50. Analysis of Butyrylcholinesterase Inhibition Using Benzyloxycarbonyl Amino Acid Derivatives as a Potential Therapy for Alzheimer's Disease

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Alzheimer's Disease (AD) is a neurodegenerative disorder characterized by memory loss, behavioral and psychological changes, and a reduction in cognitive function. Although no cure has been found for AD due to its complexity as a disease, hypotheses suggest cholinesterases and their activity as an area of investigation to slow the progress of the disease and increase cognitive function.

Acetylcholinesterase (AChE) and butyrylcholinesterase (BChE) have been a target of inhibition and the development of pharmaceuticals to combat neurodegenerative disorders. These enzymes break down the neurotransmitter acetylcholine, which is directly connected to one's memory and learning ability. Typically, a reduction in acetylcholine is connected to individuals affected by AD, AChE activity remaining similar or reduced and BChE increasing. It is possible that BChE is linked to acetylcholine depletion, which makes it a target for inhibition with the goal to increase the pool of available neurotransmitter. Previously, BChE inhibitors utilizing amino acid analogs bearing 9-fluorenylmethoxycarbonyl (Fmoc) groups have shown promise as selective BChE inhibitors. The results suggest that utilizing aromatic

protecting groups linked to amino acids could be an approach to increasing BChE-specific inhibition. This study focused on analyzing the inhibitory activity of benzyloxycarbonyl (CBZ) protecting the amino acid. CBZ-methionine and analogs were investigated due to compounds bearing the methionine side chain showing effective BChE inhibition. It is hypothesized that by introducing differing aromatic groups and longer alkyl chains, inhibitory activity can increase. By increasing inhibitor potency, more enzyme-specific drugs can be designed, leading to a wider array of therapeutics for neurodegenerative disorders.

51. Investigating Fmoc-Amino Acid Derivatives as Prospective Butyrylcholinesterase Inhibitors to Combat Alzheimer's Disease

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Alzheimer's Disease (AD) is a severe neurodegenerative disorder that affects 1 in 9 people aged 65 and older in the United States. Progression of AD has been shown to be associated with the depletion of the neurotransmitter acetylcholine in connection to overactive levels of cholinesterases, leading to decreased cognitive abilities and neurological functioning. Two major cholinesterases show two different patterns in patients with AD: acetylcholinesterase (AChE) levels remain stable, while butyrylcholinesterase (BChE) levels increase, suggesting a detrimental relationship between heightened BChE activity and acetylcholine availability. This pattern exposes a biological target that can be exploited therapeutically through the development of BChE specific inhibitory molecules that work to replenish acetylcholine levels and aid in the restoration of neurological functioning. Previously, we have shown that several Fmoc-amino acids function well as BChE inhibitors. The amino acid-based scaffold allows for the addition of various modifications that can be readily investigated to build more potent and selective compounds. A potential limitation in the original study is that the Fmoc-amino acids bear a negatively charged carboxylate group and the enzyme binds and hydrolyzes a positively charged substrate, acetylcholine. In this study, a series of methyl esters were synthesized and biochemically evaluated to investigate the effect of removing the charged group on inhibitor binding. Variations of the side chain groups were evaluated including Fmoc-Leu and Fmoc-His analogs, as the compounds were two of the more potent inhibitors in the original study. The Fmoc-Leu and Fmoc-His methyl esters were synthesized and characterized by NMR. Relative inhibitory activity was measured using UV-Vis

activity assays and quantified by determining IC₅₀ values. While the IC₅₀ values for the carboxylate compounds were ~30-50 mM, the IC₅₀ values for Fmoc-Leu-OMe and Fmoc-His-OMe were 1.3 mM and 8.1 mM, respectively. The results suggest the methyl ester derivatives are more potent BChE inhibition compared to the corresponding carboxylates and provide the foundation to explore ester-based compounds as inhibitors. Current biochemical studies to evaluate selectivity and computational docking are underway to investigate potential interactions with the enzyme. Overall, this study is aimed at identifying more potent BChE inhibitors and furthering our understanding of the enzyme-small molecule interactions important for inhibitor binding.

This work is supported by the CSULB BUILD Program in the Office of Undergraduate Research Services and CSULB College of Natural Sciences & Mathematics.

52. Surface-First Kondo Meltdown in Driven Topological and Trivial Kondo Insulator Slabs

Jaime Zendejas* and Sarah Grefe

With the recent surge in use of laser pulses as a method of inspecting condensed matter system dynamics, we ask how this pulse may itself alter the system state. Specifically, we examine how a Kondo insulator responds to variable pulse amplitude in the driving laser pulse.

On a 3D primitive cubic lattice, we derived an auxiliary-boson mean-field slab Hamiltonian with k-dependent hybridization, applied a Peierls substitution, and developed a self-consistency solver to determine values of the auxiliary-boson amplitude and constraint Lagrange multiplier per layer, and the global chemical potential. We then time-evolve the system under an applied pulse and a post-pulse free-evolution window. The time-dependent auxiliary-boson amplitudes are recorded and plotted across multiple runs using varying field strengths of the pulse. This process is completed for the Kondo insulator in both strong and trivial topologically insulating phases.

We find a surface-first Kondo meltdown as a function of pulse-amplitude, without regard to topological phase. This result is measured as a decay in the auxiliary-boson amplitude over time, per layer, for each run.

53. Phenomenological Density-Functional Modeling of Strange Quark Stars

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The equation of state of cold, dense quark matter remains uncertain at densities relevant to compact stars, and commonly used effective models do not necessarily recover the asymptotic behavior expected from quantum chromodynamics. We study electrically neutral, beta-equilibrated three-flavor quark matter using a phenomenological density-functional framework. The interaction pressure is represented by Padé parametrizations constrained to remain finite and to become negligible relative to the free-quark pressure at high baryon density. We calculate the equation of state and speed of sound and solve the Tolman-Oppenheimer-Volkoff (TOV) equations to obtain mass-radius sequences of the strange stars. By construction, the models recover the conformal limit for the squared speed of sound at high density. Across the parameter space considered, maximum masses range from 1.92 to 2.30 solar masses, with corresponding radii from 10.54 to 12.70 km; the upper end satisfies the observational two-solar-mass constraint. By comparing Padé orders, interaction parameters, and bag-pressure values, we assess the sensitivity of the predicted stellar properties to the assumed interaction functional.

54. Expanding Heterometallic Cluster Chemistry through Nickel-Gallium Trimer-Based MOFs

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Nickel and gallium are well known to form intermetallic compounds with useful properties. However, metal-organic frameworks based on Ni-Ga clusters remain essentially unexplored despite the tremendous expansion of heterometallic MOF chemistry over the past decade. Here, we report the synthetic design of a family of heterometallic Ni-Ga MOFs based on Ni(II)/Ga(III) trimeric nodes. Using the modular pore-space-partition strategy, Ni-Ga trimers were formed and incorporated into crystalline frameworks constructed from three dicarboxylate linkers (bdc, bcp, and bco) and three multitopic pyridyl partitioning ligands (tpt, tppy, and tpbz), yielding seven crystalline NiGa-pacs materials. Systematic structural analysis reveals pronounced linker-dependent effects on framework formation, geometry, phase purity, and stability. The representative NiGa-bdc-tpt framework displays permanent microporosity and preferential C₂H₂ adsorption over CO₂, with a high C₂H₂ uptake of 136.69 cm³ g⁻¹, an equimolar C₂H₂/CO₂ IAST selectivity of 4.83, and a separation potential of 3.10 mmol g⁻¹ at 298 K. Dynamic breakthrough experiments further demonstrate reproducible C₂H₂/CO₂ separation over multiple cycles. These results establish heterometallic Ni-Ga trimers as viable building units for MOF construction

and demonstrate the utility of modular pore-space partitioning for accessing chemically challenging mixed-metal framework compositions.

This work was supported by National Science Foundation, Division of Materials Research, under Award # 2105961 and by CSULB RSCA award for 3-unit teaching release time.

55. Enterobactin directed host-guest interactions based on side-chain design

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Enterobactin – the ubiquitously known sequestrator of iron, found in nature from organisms that evolved to harvest iron from low iron environments – it serves as a quintessential example not only of host-guest binding, but provides an example of a metal-organic complex with a breathtaking Association Constant (K_A) of 10^{52} M^{-1} !! Few things in nature like each other this much. The deceptively simple scaffold (shown below) is tripodal, and with nature evolving to use three catechol ligands to catch iron; modern synthetic techniques provide opportunity of new applications in host-guest science. Our work aims to explore the utility of heteroaromatic side-chains of varying polarity to trap metals, organic ions and molecules of biological importance. Success in these endeavors would result in the creation of new knowledge in medicine, sensing and the development of molecular machines. differences, phase of the light cycle, aging, and functional AR modulate locomotion, drinking, and feeding in mice.

56. Modeling Heterogenous Disease Trajectories in Chronic Neurodegenerative Disease: A Case Study of ALS

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Amyotrophic lateral sclerosis or ALS is an age-related neurodegenerative disease that is prevalent among 6-8/100,000 Americans and remains a significant risk for the aging populations worldwide. The Amyotrophic Lateral Sclerosis Functional Rating Scale (ALS-FRS) is a standard, questionnaire-based clinical tool that tracks the progression of ALS by measuring a patient's ability to perform everyday physical functions and was revised into the ALS-FRS-R scale, now including functional area sub scores and expanding the range of tracked functions. The objective of the present study is to

characterize the clinical development of ALS using multifaceted clinical outcome measures, prognostic indicators from patient trials, and patient demographics to model and predict the heterogeneous disease trajectories. Using a subset of patient data from the comprehensive Pooled Resource Open-Access ALS Clinical Trials (PRO-ACT) Database, curated by the Neurological Clinical Research Institute, Massachusetts General Hospital, our study has two specific aims: (1) To classify patients into groups based on similar prognostic markers and modeling their disease progression trajectories, (2) Using a suitable supervised machine-learning method, classify patients into the previously-identified common patient profiles and extract the dominant deciding features. The investigation of aim (1) was conducted by first creating smoothed representations of our longitudinal prognostic data, with numeric features modeled using Locally Estimated Scatterplot Smoothing (LOESS). These functional representations of the various prognostic indicators were then clustered using the *clustcurv* package in R; the labels from which were then used to group patients into prognostic-indicator-spanning patient profiles. These profiles were then examined using semiparametric regression for significant differences in the patients' ALS-FRS-R score trajectories over time and whether these trajectories were linear. For aim (2), we built a random-forest multinomial classification model to predict the patient's profile grouping based on their cluster membership in the features studied and identify the principal indicators used to create the patient profiles. We found nine distinct patient profiles, of which, four had statistically significant parametric terms at the 0.05 level, indicating significant differences of ALSFRS-R score trajectories between them. We also found that six profiles had statistically significant smoothing terms at the 0.05 level, indicating that the rate of disease progression was nonlinear. These preliminary results validated the foundations of project's aims and will enable our planned expansion of this project's scope and scale.

57. Exploring a Multilayer Network Framework for Multiscale, Multifunctional Interactions in Neuroscience

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Neuroscience literature contains functional relationships that span biological scales, cell types, experimental contexts, and interacting physiological processes. However, these findings are often fragmented across primary research articles, making it difficult to represent and analyze their interconnected structure. TRACK-Neuro is a workflow developed in the Venugopal laboratory for transforming experimentally supported findings into structured Scientific Meta Summaries and directed network graphs of functional relationships in neural systems [1]. This study explores

multilayer network theory [2] to provide an analytical framework for the TRACK-Neuro network. We evaluate alternative layer schemas based on node and edge attributes, including biological scale, cell type, functional process, and experimental context. We demonstrate how TRACK-Neuro network components can be mapped onto multilayer and multiplex network structures, and we visualize these representations to examine patterns of within-layer and between-layer connectivity. We further identify analytical strategies for investigating scientifically relevant features, including cross-scale relationships, cell-type-specific interactions, multifunctional nodes, interlayer connectivity, and the convergence or divergence of functional pathways. Ongoing work is evaluating suitable multilayer network metrics, community structure, cross-layer motifs, and other computational approaches for generating biologically interpretable insights from structured neuroscience knowledge.

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58. Regional Astrocytic Reactivity Associated with Early Feeding-Related Behavioral Changes in the SOD1G93A Mouse Model for Amyotrophic Lateral Sclerosis

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Amyotrophic lateral sclerosis (ALS) is a progressive neurodegenerative disease characterized by motor neuron (MN) loss, muscle weakness, paralysis, and atrophy. ALS-vulnerable motor neurons are cholinergic and can be identified by choline acetyltransferase (ChAT) expression. Besides MNs, cortical and subcortical regions also have a distributed cholinergic system which modulates attention, arousal, and other cognitive and behavioral functions. Astrocyte reactivity, commonly assessed by glial fibrillary acidic protein (GFAP) immunoreactivity, is widely used as an indicator of astrocyte activation. ALS affects motor nuclei selectively in the brain and spinal cord. While the brainstem trigeminal and facial motor nuclei are vulnerable, extraocular motor nuclei, including the abducens nucleus, are relatively resilient. Comparing

these spatially separated vulnerable and resilient regions may help identify cellular features associated with disease susceptibility and resistance.

This study examined early feeding-related behavior and regional astrocyte reactivity in SOD1G93A mice and wild-type (WT) controls, prior to onset of significant motor symptoms. A novelty-suppressed feeding assay was used as a conflict-based measure in which hunger-driven feeding motivation competes with avoidance of a novel open environment. Histological analyses assessed GFAP immunoreactivity and ChAT-positive cholinergic neuronal populations in vulnerable and resilient brainstem motor nuclei, as well as motor cortical and subcortical regions. Early SOD1G93A mice generally approached the food pellet more rapidly than age-matched WT mice, suggesting an altered feeding-related behavioral response in the SOD1G93A model. Pellet consumption did not show an obvious relationship with body weight in either genotype. Preliminary histological analyses showed prominent GFAP immunoreactivity in ALS-vulnerable brainstem motor regions, including the trigeminal and facial motor nuclei, but limited GFAP immunoreactivity in relatively ALS-resilient extraocular and abducens motor nuclei. Ongoing analyses are evaluating the distribution of GFAP immunoreactivity in motor cortical and subcortical regions and its spatial relationship to ChAT-positive cholinergic neurons. Together, these observations support further investigation of altered feeding-related behavior and region-specific astrocyte pathophysiology as potential early nonmotor features of ALS.

59. GFAP-Defined Astrocyte Reactivity in the Feeding Neuroaxis After High-Energy Diet Exposure

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High-energy diets can alter feeding behavior and disrupt neural systems that integrate energy status, reward, and bodily homeostasis. This study examines whether short-term exposure to a high-energy diet modulates neuronal activity and astrocyte reactivity within key feeding-related brain regions. A cohort of 19 rats was assigned to alternate-day fasting with access to chow and a high-energy diet (ADF), alternate-day

fasting with chow only (ADFc), ad libitum access to chow and a high-energy diet (ADLIB), or ad libitum chow access (CON). Animals underwent 10 cycles of diet-specific feeding conditions to assess food-directed and hedonic behavioral responses. Body weight, food intake, and water intake were measured daily, and additional physiological measures, including gastric emptying and stomach and liver weights, were recorded. On the final test day, all animals received 4 g of high-energy diet for 15 minutes and were euthanized 30 minutes after the meal for brain collection. To investigate the neural and glial correlates of these behavioral phenotypes, ongoing immunofluorescence histochemistry is assessing cFOS expression as an indicator of recent neuronal activity and GFAP immunoreactivity as a measure of astrocyte reactivity. Analyses focus on the ventromedial hypothalamus and arcuate nucleus, which integrate metabolic and hormonal signals, and the medullary caudal nucleus of the solitary tract, a primary hindbrain relay for visceral and satiation-related information. Preliminary histological observations indicate diet- and feeding-history-associated changes in both cFOS and GFAP expression. Notably, the observed pattern of GFAP labeling suggests that astrocytic plasticity may be comparable to, or in some regions more pronounced than, neuronal activation. These findings support a model in which high-energy diet exposure rapidly remodels the feeding neuroaxis through coordinated neuronal and astrocytic responses. Astrocytes may therefore contribute actively to the integration of hedonic feeding signals with metabolic and visceral information, potentially serving as an important cellular mechanism linking dietary experience to altered feeding behavior and homeostatic regulation.

60. Investigating Enantioselectivity of Newly Synthesized Bisoxazoline Ligands in Fe-Catalyzed Kumada Cross-Couplings

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Transition metal-catalyzed cross-coupling reactions are essential in pharmaceutical and industrial synthesis. While nickel catalysts are well-studied, their toxicity and cost limit large-scale use. Iron offers a cheaper, less toxic alternative, but its potential in asymmetric transformations remains underexplored. Our laboratory investigates iron-catalyzed Kumada cross-couplings of α -haloesters with bisoxazoline (BOX) ligands to evaluate their ability to promote enantioselectivity. Optimization studies revealed that selectivity is highly sensitive to reagent purity, reaction scale, and catalyst loading. Under optimized conditions, PhBOX ligands achieved up to 68% ee at the 0.25 mmol scale, with a 1:2 iron-to-ligand ratio critical for consistent results. Systematic ligand screening highlighted the importance of

ligand-specific reaction environments, while stability studies suggested that PhBOX degradation contributed to plateauing enantioselectivity during optimization. To expand our ligand library beyond natural amino acid-derived structures and incorporate ligands that have shown promising activity in other catalytic systems, we are synthesizing a novel BOX ligand through a nine-step route starting from a commercially available ester. The synthesis proceeds through TBS protection, DIBAL-H reduction, ABNO-catalyzed Stahl oxidation to the aldehyde, and diastereoselective sulfinimine formation using (R)-(+)-tert-butylsulfinamide. The first four steps have been completed with optimized yields and successful chromatographic purification. The finished ligand will be incorporated into future screening efforts, contributing to a deeper understanding of how BOX ligand structure influences enantioselectivity in iron-catalyzed cross-coupling reactions and supporting the development of sustainable asymmetric catalysis.

61. Ni-Catalyzed C-H Functionalization of Amides with Alkenyl Bromides

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Synthetic strategies for the C-H functionalization of amides are emerging because they enable the direct transformation of chemically inert C(sp³)-H bonds into C-C bonds. This strategy is typically reported to occur photochemically or with noble-metal catalysis; however, non-photochemical activation with earth-abundant metals is not well established. We are developing a novel method for the Ni-catalyzed functionalization of amides using dimethylacetamide (DMA) as the amide substrate and an alkenyl bromide as the primary electrophile coupling partner. The reaction also incorporates an alkyl halide that acts as a radical acceptor. We screened a wide range of conditions and found the optimal conditions to include TMSCl as an additive, an excess of alkyl halide, -10 °C, and a reaction concentration of 0.25 M. Overall, these results demonstrate the potential of nickel catalysis for the non-photochemical C-H functionalization of amides using earth-abundant metals.

This project is supported in part by CNSM Faculty Start-Up Funds.

62. Diastereoselective Synthesis of cis- and trans-2,3-Tetrahydrofurans from Chiral Allylic Silanes

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Polysubstituted tetrahydrofurans are common motifs found in various bioactive natural products; however, methods that offer stereochemical control in the synthesis of these motifs are limited. We developed a divergent synthetic strategy to utilize chiral allyl silanes to prepare *cis*- and *trans*-2,3-disubstituted tetrahydrofurans with excellent diastereocontrol and near-perfect transfer of chirality. The *cis* tetrahydrofurans are prepared using an allyl silane containing a pendant alcohol. TMSOTf acts as a Lewis acid to catalyze a Prins cyclization through an oxocarbenium intermediate. In contrast, the *trans* tetrahydrofurans are prepared using an allyl silane with a pendant chloride. A tandem Sakurai allylation using TiCl₄ sets the relative stereochemistry through an open transition state, and a subsequent base-catalyzed cyclization affords the tetrahydrofuran ring. A variety of aldehydes were used to afford fifteen substrates for each pathway, providing up to 99% yield, >20:1 dr, and 98% ee for the *cis* pathway, and up to 92% yield, >20:1 dr, and 98% ee for the *trans* pathway.

63. Ni-Catalyzed Cross-Coupling of Aryl Iodides and Benzylic BMIDA NHP Esters Towards the Synthesis of Enantioenriched Diarylalkanes and Triarylmethanes

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Ni-catalyzed reductive cross-couplings are useful in synthetic organic chemistry because they form carbon–carbon bonds from bench-stable electrophiles. Ambiphilic substrates containing both nucleophilic and electrophilic sites could provide access to cross-coupling products that can be further functionalized in downstream synthesis. Our laboratory is investigating the use of ambiphilic substrates in reductive cross-coupling. We have obtained promising results showing that NHP esters containing α -boronates can undergo reductive cross-coupling to provide arylation and alkenylation products, such as diarylboronates and allylic boronates. These products could be further functionalized to prepare bioactive compounds, including diarylalkanes and triarylmethanes. We will discuss the current results of this reaction and ongoing progress toward optimizing enantioselective variants.

64. Investigating Catalytic Asymmetric epoxidation to enable simplified downstream purification

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Dihydrobenzofurans are an important structural motif found in numerous biologically active natural products. Maceneolignan A and similar dihydrobenzofuran-containing natural product isolated from nutmeg, have been reported to exhibit anti-inflammatory, anticancer, antiviral, and antifungal activity, however, its medicinal properties remain relatively unexplored. Developing a reliable synthetic route to Maceneolignan A would provide access to material for further biological investigation and enable the preparation of related analogs. Our previous developed synthesis of Maceneolignan A provides racemic product, resulting in at 1:1 mixture of enantiomers which requires chiral HPLC separation to prepare enantiopure product. Because this type of purification can be costly and difficult to scale, we are investigating whether the use of a catalytic asymmetric epoxidation can prepare enantiopure diastereomers, which are more amenable to purification by standard column chromatography techniques. Selective formation of the desired epoxide stereoisomer could simplify downstream purification and improve the overall efficiency and scalability of the synthesis. We are in the process of testing two asymmetric Shi epoxidation catalyst, an asymmetric Berkessel-Katsuki epoxidation catalyst and the Jacobsen Hydrolytic Kinetic Resolution. These studies aim to establish an asymmetric epoxidation-based approach for the synthesis of Maceneolignan A and analogs and provide a more practical route for future medicinal studies.

65. Ligand Screen of Ni-Catalyzed Reductive Cross-Coupling with NHP Esters and Vinyl Bromides

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Metal-catalyzed cross-coupling is a crucial technique for the synthesis of complex, bioactive molecules through carbon-carbon bond formation. Compounds containing dihydrobenzofuran cores are of great interest due to their demonstrated anti-inflammatory, anticancer, and antibiotic bioactive properties. While traditional palladium-catalyzed methods are effective, their high cost and safety risks warrant the development of sustainable approaches utilizing earth-abundant metals such as nickel. This project explores nickel-catalyzed reductive cross-coupling as a strategy to create dihydrobenzofuran derivatives for therapeutic applications. A consistent 50% product yield was determined through reaction optimization of conditions such as temperature, solvent ratio, and reductants, establishing a reliable baseline. We later screened 53 asymmetrical ligands to observe enantioselective cross-coupling between vinyl bromides and NHP esters. While our objective was to achieve high enantiomeric excess (EE >80%), the highest EE attained was 41.2% with 11% yield.

Due to the limited enantioselectivity observed with asymmetrical ligands, we have shifted our focus to the synthesis of racemic natural products. This strategy allows us to produce specific bioactive derivatives and assess their functional efficacy as racemic mixtures or isolated enantiomers. This work provides critical insights into the mechanistic challenges of nickel-catalyzed cross-coupling and informs future strategies for the efficient, sustainable production of therapeutic candidates.

This project is funded by faculty start-up funds provided by CSULB College of Natural Science and Mathematics.

66. Hyaluronic Acid Expression in Electrically Stimulated Human Keratinocytes

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Electrical stimulation (ES) has been shown to promote the expression of collagen and other extracellular matrix (ECM) components involved in wound repair. It also influences the proliferation of human keratinocytes (HaCaT) in the epidermis and the migration of human dermal fibroblasts (HDFs) in the dermis, both of which are essential for wound healing. It has been hypothesized that ES may mimic the endogenous transepithelial potential (TEP) generated following skin injury, which helps direct HDF migration toward the wound site. Both cell types contribute to tissue regeneration by producing connective-tissue components, secreting growth factors into the wound environment, and communicating with one another. Hyaluronic acid (HA), a polysaccharide present in the ECM, plays an important role in regulating tissue repair and is elevated during wound healing. In this study, we found that ES increased HA expression in HaCaT cells. These findings suggest that ES may enhance the wound-healing response by modulating HA production in keratinocytes.

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67. Does Electric Field stimulate Human Dermal Lymphatic Endothelial Cells?

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Human dermal lymphatic endothelial cells (HDLECs) play important roles in cutaneous inflammation, lymphatic transport, and fluid clearance during wound healing. This study investigated whether electrical stimulation activates HDLECs, as determined by changes in cellular proliferation and vascular endothelial growth factor receptor 3 (VEGFR3) expression. Standardized cell-culture, stimulation, imaging, and analysis procedures were necessary to minimize experimental variability and reduce the influence of human error. Cell proliferation was evaluated using imaging-based measurements, while VEGFR3 expression was quantified by flow cytometry using a fluorescently labeled antibody. Together, these complementary assays enabled assessment of HDLEC activation in response to electrical stimulation and provided a more reliable approach for characterizing cellular responses.

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68. Electrostatically Controlled DNA-Peptide Assemblies

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Protein–DNA interactions provide a useful strategy for designing materials that organize across multiple length scales. The assembly of plasmid DNA (pDNA) with arginine-functionalized collagen-like peptides (CLPs) was studied to determine how peptide structure influences DNA organization. C-terminal arginine domains interact with the DNA phosphate backbone, while the collagen triple helix provides a rigid framework that controls these interactions. Peptide-to-DNA ratio strongly affects the resulting morphology: selected ratios produce ordered lamellar structures, whereas higher peptide content favors compact, disordered assemblies. Spectroscopic data support an important role for phosphate–guanidinium interactions in assembly. Temperature also influences structural organization. Heating near the collagen melting transition promotes assembly rearrangement and growth, while heating above the transition disrupts ordered structures and produces condensed DNA–peptide complexes. Circular dichroism measurements indicate that this transition is accompanied by changes in DNA organization. Cryo-TEM and three-dimensional electron diffraction show that the ordered assemblies are thin and exhibit long-range in-plane organization. These findings suggest that the geometry and rigidity of the collagen triple helix direct lateral growth, enabling controlled annealing to produce larger, organized DNA-based materials without sequence-programmed assembly.

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69. Determining Uplift Rates of Marine Terraces in the San Luis Obispo Bay Using Luminescence Dating

Brandon Rapozo* & Nate Onderdonk, Ph.D.

Between Morro Bay and the Santa Maria Valley, Quaternary marine terraces are present along the south-central coastline, with the presence of these emergent marine terraces indicating a topography formed because of regional uplift and local deformation (Lettis and Hanson, 1994; Tutterow, 2021). The late Quaternary California coastal range front landscape development is driven by tectonics, climatic shifts, and sea-level change, but the deformation across the San Luis Obispo Bay remains poorly understood. (Stokes and Garcia 2009). A more developed understanding of uplift rates is essential for ensuring the safety of nearby communities and critical infrastructure in this region.

Numeric dating of the marine terraces in the San Luis Bay area has been limited to Uranium-series (U-series) dating of coral samples along the lowest two terraces, with the age ranges then inferred to marine terraces south of the Santa Maria Valley (Hanson et. al. 1994). Recent quaternary geologic mapping and geochronology using luminescence dating along the coast, south of the Santa Maria Valley, has shown that emergent marine terraces are much younger than previously interpreted, suggesting higher uplift rates akin to deformation rates of the Western Transverse Ranges (Tutterow, 2021).

To test these dating methods, I will use infrared stimulated luminescence dating (IRSL) of feldspar crystals sampled from the two lowest Quaternary marine terraces between Pismo Beach and Point San Luis near the San Luis Obispo Bay area (Figure 2). Numerical ages of marine terrace deposits determined from IRSL in this study will be compared to previous age determinations of the marine terrace deposits using U-series dating of corals within San Luis Bay. Luminescence dating measures the ionized radiation of a crystal to determine its date of burial, which is the inferred time of the date of deposition (Mahan et al 2022). Because the Santa Maria River Valley acts as a boundary between the areas of high and low uplift rates within the Southern Coast Ranges and Western Transverse Ranges, I hypothesis that luminescence dating will validate U-series dating of the lowest marine terraces in the San Luis Obispo Bay area indicating a change in local structures north and south of the basin.

70. Evaluation of Multi-Frequency Electromagnetic Induction Methods for Fractured-Bedrock Aquifer Characterization

Lena Wilson* and Alyssa Abbey, Ph.D.

Frequency-domain electromagnetic (FDEM) methods provide a rapid, non-invasive way to image subsurface conductivity variations related to lithology, saturation, and pore-fluid properties. However, their ability to resolve directional conductivity contrasts associated with fracture-controlled groundwater flow in crystalline bedrock remains poorly constrained, particularly when using multi-component magnetic-field measurements. This study evaluates the IRIS PROMIS multi-component FDEM system at Edwards Air Force Base, where thin alluvium overlies weathered and fractured granitic bedrock associated with the Kramer Hills Fault Zone and shallow groundwater occurs within weathered bedrock and fracture networks. Data were collected along transects co-located with electrical resistivity tomography, towed time-domain electromagnetic, and seismic profiles for comparison across methods. Processing included frequency filtering, tilt correction, and station averaging, followed by 1D layered and smooth inversions to produce pseudo-2D resistivity sections. Interpretation focuses on depth of investigation, spatial resolution, and component-dependent conductivity contrasts associated with fracture zones and structural fabric. The results are used to assess whether multi-component FDEM can improve identification of preferential groundwater-flow pathways in fractured crystalline bedrock.

71. Apatite (U-Th)/He Thermochronology Reveals Variable Cooling in the Eastern Precordillera, Argentina

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Active fold-thrust belts generate spatially variable burial, heating, uplift, and erosion, yet resolving the thermal histories associated with individual thrust structures remains challenging. The eastern Precordillera, Argentina, is an active fold-thrust belt in which complex deformation provides an opportunity to examine how thrust faulting controls cooling and exhumation. We apply apatite (U-Th)/He (AHe) thermochronology, a low-temperature method sensitive to shallow-crustal thermal histories, to assess spatial variability in burial and cooling across the thrust system. Euhedral, inclusion-free apatite grains were separated from sediment samples and analyzed as individual crystals.

AHe ages show substantial variation both within and among samples, spanning young ages to ages exceeding 100 Ma. The data do not record a single uniform cooling

event or complete resetting across the study area. Instead, ages generally become younger toward the south, a pattern that may reflect southward fault propagation and/or greater burial in the southern part of the system. The broad age dispersion further suggests partial age resetting and heterogeneous thermal histories. Younger grains likely record localized reheating or enhanced exhumation, whereas older grains preserve partially reset ages.

Together, these results indicate that burial and cooling in the eastern Precordillera were strongly influenced by spatially variable deformation. The findings are consistent with complex thrust-fault evolution, including differential burial and possible out-of-sequence thrusting, and demonstrate the value of single-grain AHe data for resolving thermal heterogeneity in active fold-thrust belts.

72. Characterization and Enzyme Loading of Highly Boron-Doped Porous Silicon

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Porous silicon exhibits a tunable pore size, a large surface area, and biocompatibility, suggesting it could be used for in vivo applications such as drug delivery and biosensing. In this study, silicon chips were electrochemically anodized to prepare the porous silicon material as a thin layer on top of the chip. The current density used was varied to change the porosity of the thin layer. After characterization of porosity and thickness using the spectroscopic liquid infiltration method (SLIM), the samples were thermally oxidized and loaded with a protein. Mass loading of the protein was determined using a bicinchoninic acid (BCA) assay. It was predicted that greater current density would lead to greater porosity, which in turn would result in a greater protein loading capacity. This system provides insight into how etching conditions can be optimized to maximize protein loading for chemical sensing, bioresponsive deliveries, and protein immobilization.

73. Optimization of Nucleofection Protocols for Megakaryocytic Cell Lines for the Purpose of CRISPR/Cas9 Editing of Platelet Specific Loci

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The CRISPR/Cas9 system offers a promising platform to deliver therapeutic transgenes at targeted genomic safe harbors to treat monogenic diseases. By utilizing

a programmable single-guide RNA (sgRNA) to direct the Cas9 endonuclease, this system can be used to induce a site-specific double strand break (DSB) in DNA that is endogenously repaired via two competing cellular repair pathways: non-homologous end joining (NHEJ) and homology directed repair (HDR). NHEJ is an error-prone pathway that introduces insertions and deletions (INDELs) at the cleavage site, causing frameshift mutations useful for targeted gene disruptions. Conversely, HDR is an error-free pathway that can accomplish targeted gene addition by co-delivering an exogenous DNA repair template. A valuable application of CRISPR/Cas9-mediated HDR would be providing a safer, site-specific alternative to potentially disruptive lentiviral methods currently used to achieve platelet-specific FVIII expression in megakaryocytes for Hemophilia A patients with inhibitors. Specifically, instead of relying on randomly integrating lentiviruses, we hypothesized that CRISPR/Cas9 could be used to target a F8 transgene to the vWF or PF4 locus, capitalizing on their active expression within this cell lineage to produce FVIII while preserving native gene function. However, while the components needed for CRISPR/Cas9-mediated gene addition could be delivered to megakaryocytes via nucleofection, no pre-established electroporation programs for these cells are currently available. Therefore, we evaluated several candidate programs within the 4D Lonza Nucleofector® system using a GFP expression plasmid to assess the most optimal electrical pulse parameters that could be used for two megakaryocytic cell models: DAMI and KU812. Through fluorescence microscopy and flow cytometry analysis, we identified programs capable of achieving robust transfection efficiencies: the DN-100 program yielded 89% GFP-positive DAMI cells while the DS-104 program yielded 77% in KU812 cells. Both programs maximized post-nucleofection cell survival as indicated by high visual confluency with a minimal gating shift in dead cell/debris population relative to untreated controls. Using these newly established optimized protocols, subsequent nucleofections will co-deliver a Cas9 expression plasmid and a GFP DNA repair template corresponding to either the vWF or PF4 loci to validate integration feasibility before therapeutic F8 knock-in.

74. Mapping RGS Interactions in *Neurospora crassa* via a Yeast Two-Hybrid Screen: A Course-Based Undergraduate Research Experience (CURE)

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G-protein signaling is an important pathway that allows eukaryotic cells to sense external stimuli and coordinate intracellular processes involved in growth, differentiation, and metabolism. Regulators of G-protein Signaling (RGS) help terminate G-protein signaling by accelerating GTP hydrolysis on the G α subunit. Although the role of RGS proteins in regulating G α activity is well established, the protein interaction networks through which they regulate specific cellular and developmental processes remain poorly understood. In this study, we use *Neurospora crassa*, a haploid, genetically tractable, and fast-growing model filamentous fungus with a sequenced genome and available knockout mutant collection, to investigate proteins that potentially interact with RGS proteins. During Spring 2025, students in BIOL 440L used a yeast two-hybrid (Y2H) library screen to identify potential protein interactors of RGS-1 and RGS-2. Preliminary screening identified six positive hits with RGS-1 and three with RGS-2, including proteins associated with transcriptional regulation, protein turnover, metabolism, and proteins of unknown function. Two preliminary interactors were further investigated through functional analysis of their corresponding *N. crassa* knockout strains. Deletion of NCU09812, a predicted LIM-domain-containing protein, resulted in reduced linear hyphal growth and a trend toward increased aerial hyphae formation compared with wild-type strains, while sexual development and protoperithecia formation were largely unaffected. Analysis of NCU00480, which encodes a predicted ubiquitin C-terminal hydrolase, showed increased hyphal growth and altered conidial morphology compared with wild-type strains. Together, these preliminary phenotypes suggest that candidate RGS-interacting proteins may contribute to distinct aspects of fungal growth and development. This project will continue in Spring 2027 as BIOL 490: Special Topics in Fungal Functional Genomics. Students will validate candidate RGS-1 and RGS-2 interactors, characterize their corresponding knockout mutants, and integrate molecular, phenotypic, and bioinformatic analyses to begin defining the protein interaction network associated with RGS-mediated G-protein signaling in *N. crassa*.

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75. Radiation-Induced Myeloid Inflammation Drives Immunotherapy Resistance by Promoting Immune Cell Dysfunction in Breast and Prostate Cancer

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Immunotherapy has demonstrated limited activity in breast and prostate cancer, which are the two most common cancers. Inflammation is a hallmark of therapeutic resistance and is associated with worse oncologic outcomes. Although radiotherapy (RT) can synergize with immunotherapy, we have shown that this combination generates significant myeloid inflammation that can potentially antagonize a productive T cell response. We hypothesize that secreted thrombospondin-1 (TSP-1) promotes immunotherapy resistance by driving T cell exhaustion and promoting immune cell dysfunction. We performed scRNA-seq on CD45⁺ immune cells from the EO771 and RM9 murine models. We analyzed gene expression data using Seurat and inferred intercellular signaling using CellChat. Magnetically enriched CD4⁺/CD8⁺ splenic lymphocytes from *Thbs1*^{-/-} mice or bone marrow-derived macrophages (BMDMs) from wild-type mice were activated and treated with recombinant TSP-1. Functional analyses were performed by multiparametric flow cytometry and ELISA. Our results reveal that RT is a potent inducer of *Thbs1* expression in polymorphonuclear myeloid-derived suppressor cells and tumor-associated macrophages (TAMs) in both tumor models. Further, we identified inferred *Thbs1*-CD47 signaling from these cells into TAMs and T cells by CellChat. To recapitulate these effects, we found that recombinant TSP-1 drives CD8⁺ T cells into a terminally exhausted PD1⁺LAG3⁺ state. TSP-1 was also associated with reduced CD8⁺ T cell activation by downregulation of CD44 and TCF1 and was associated with increased CD25⁺Foxp3⁺ Treg differentiation. Lastly, TSP-1 drove the production of CXCL1 by bone marrow derived macrophages (BMDM). These results suggest that myeloid inflammation, via TSP-1 signaling, promotes T cell and macrophage dysfunction, which may contribute to immunotherapy resistance in multiple cancers.

This project is supported by 2024 Tower Cancer Research Foundation Career Development Award, NIH/NCATS KL2 Translational Science Award (KL2TR001882) and the Cedars-Sinai Donna and Jesse Garber Award for Cancer Research.

76. The Synergistic Effect of Valproic Acid and Metformin for the Enhancement of the CRISPR/Cas9 system

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Recently, the CRISPR/Cas9 system has been approved by the FDA for the treatment of sickle cell disease by gene disruption in hematopoietic stem cells. Despite this significant progress, the efficiency of gene addition using the CRISPR/Cas9 system in hematopoietic stem cells is not yet optimal. Previous experimentation originating from the Johnston lab have indicated that the efficiency of CRISPR/Cas9 improves when hematopoietic cell lines are treated with either a histone deacetylase inhibitor such as valproic acid (VPA) or the diabetic drug metformin (Met) (Rollins J.L. et. al, 2023) (Björnson Y. et. al, 2023). Given that the mechanism of action of these two compounds are distinct, we evaluated the effect of a combination treatment in which both are utilized simultaneously. We treated the K562 myeloid-erythroid leukemic cell line and the Jurkat T lymphocyte cell line with various concentrations of both drugs and compared the growth curve to that of untreated cells. There was no statistical significance between the dual treatment conditions when ranging from 1 to 0.001 mM of Met and 0.5 to 0.005 mM of VPA (p values ranged from 0.70 to 0.99). However, a dose response was observed in that when the cells were treated with much higher doses (100 mM) a significant impact on the growth of K562 cells ($6.9\text{E-}04$ for 100 mM Met and $5.9\text{E-}04$ for 100 mM VPA) and Jurkat cells ($p = 2.9\text{E-}04$ for 100 mM Met and $2.9\text{E-}04$ for 100 mM VPA) was noted. We decided to move forward with our investigation using two dosing regimens: (1) a higher treatment condition with 1mM Met and 0.5 mM VPA simultaneously and (2) a lower treatment condition at 0.001mM Met and 0.005mM VPA. The effect of these two dosing regimens will first be evaluated regarding the ability of the CRISPR/Cas9 system to produce a double strand break (DSB). Towards this aim, single guide RNAs (sgRNA) specific to a genomic location will be delivered to K562 cells via electroporation. Genomic DNA will be isolated and the region surrounding the target site was PCR amplified. PCR products will be sequenced, and a TIDE analysis will be performed to identify the frequency of insertions or deletions (INDELs) at the target site compared to that of no sgRNA negative control. INDELs are produced following a DSB because of the nonhomologous end joining endogenous repair pathway and serve as identifier of CRISPR/Cas9 cutting activity. In addition, the effect of the dual treatment on editing efficiency will be evaluated.

77. Proton Shuttling Across Synthetic DPPC Modified Monolayer: Liquid-Liquid Interfaces Using PEIS

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Proton shuttling across liquid–liquid interfaces is important for understanding proton transport in biological and biomimetic systems. In this study, Potentiostatic Electrochemical Impedance Spectroscopy (PEIS) was used to investigate how the pH of the aqueous-phase and presence of phospholipid layers at the interface influence the electrochemical behavior of decorated liquid–liquid interface. The aqueous phase consisted of phosphate buffer solutions with variable pH, while the organic phase consisted of 1,2-dichloroethane (DCE) containing 5 mM tetrabutylammonium tetraphenylborate (TBATB). The interface was decorated using varying concentrations of 1,2-dipalmitoyl-sn-glycero-3-phosphocholine (DPPC). Changing the pH of the aqueous phase resulted in characteristic variation of impedance response, correlating with solution pH and interfacial concentration of the phospholipid layer. In particular, presence of DPPC influences the interfacial tension as evident in optical images of the interface. DPPC presence also changes the electrochemical impedance response of the interface, most significantly by showing features corresponding to limited interfacial mobility. This observation may point to an interplay between phospholipid organization and interfacial dynamics. These initial studies will guide how we incorporate interfacial molecular assemblies with known proton mobility interactions to control DPPC interactions at model chemical interfaces.

This project is supported in part by Department of Chemistry and Biochemistry, California State University.

78. Investigating Chemomechanical Evolution of Cu Surface Interfaces during Zn Deposition in Aqueous Media

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The relationship between electrochemical deposition and chemomechanical changes is important for improving the stability and performance of electrochemical systems. This study investigates the chemomechanical evolution of copper (Cu) surface interfaces during zinc (Zn) deposition in aqueous media. The hypothesis

proposed that Zn deposition on Cu would produce electrochemical and mechanical changes that may be unstable due to hydrogen evolution, pH changes, and stress at the Cu/Zn interface. The stability of Cu substrates in aqueous battery applications is important because repeated cycling and more acidic conditions may increase interfacial instability and mechanical stress. Electrochemical measurements were conducted in 1.0 M zinc sulfate (ZnSO_4) to observe the current response at different applied potentials and scan rates. Surface stress measurements were used to observe tensile and compressive stress changes at the Cu/Zn interface during Zn deposition. These measurements link electrochemical behavior and mechanical changes at the Cu/Zn interface. The results showed that electrochemical responses varied depending on the applied potential, while mechanical stress developed during Zn deposition. These findings motivate future work under more acidic and neutral conditions to better understand Cu/Zn stability for aqueous battery development.

This project is supported by California State University, Long Beach (Department of Chemistry).

79. Chemomechanics of Charged Species at Ideal Solid Interfaces

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The structure and dynamics of interfaces between ideal solid surfaces and electrolyte solutions, known as electrical double layers, are key to controlling many processes in industry and nature. In particular, electrical double layers at transition-metal surfaces in aqueous electrolyte solutions govern advanced electrochemical systems, such as aqueous batteries and electrolyzers. Charged species at surfaces initiate a cascade of coupled chemo-electro-chemical events. While the Gouy-Chapman model provides a basic estimate of the electrical response at double-layer interfaces, the effects of ion adsorption at different concentrations on the overall structure and dynamics are still unknown. Here we use electrochemical stress measurements under controlled solution conditions and salt concentrations to monitor interfacial charge interactions and adsorption. Electrochemical stress analysis of gold thin films in electrolyte solutions of sodium sulfate (Na_2SO_4) and sulfuric acid (H_2SO_4) reveals substantial estimated film-stress changes on the order of 1–5 GPa as electrolyte concentration changes. We assign these changes to diffusion and rate limited charge interactions at model Au surfaces. Our analysis also reveals processes with distinct relaxation times that are assigned to diffusion and (co)adsorption of (bi)sulfate and sodium ions with interfacial water and protons.

These studies will eventually enable us to construct a holistic view of the electrical double layer across a wider range of electrolyte conditions and interfacial dynamics.

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80. Langmuir-Blodgett Techniques and their Applications Towards Semiconductive MOF Thin-Films

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Metal-organic frameworks (MOFs) are a class of highly porous materials composed of metal ions and organic linkers. Porphyrin-based MOFs are particularly important as some porphyrin MOFs exhibit semiconductive properties that are ideal for applications in clean energy, photocatalysis, and redox reactions. However, porphyrin-based MOFs can suffer from aggregation due to π - π interactions, which can limit the material's properties and potential applications. This study investigates how aggregation in porphyrin-based MOF can be prevented through the use of Langmuir-Blodgett techniques. Langmuir-Blodgett techniques allow precise control over thin film formation at the air-liquid interface. Using Langmuir-Blodgett techniques, thin films were formed of the three porphyrin MOFs: Cu-PPF-1, Cu-PPF-2, and Cu-HHTP. Cu-PPF-1 produces a surface pressure isotherm which begins to increase at about 3 Å, maximizing at 38 mN/m with a surface potential maximizing at 0.914 V. Cu-PPF-2 surface pressure isotherm raises more steadily in comparison to Cu-PPF-1. Cu-HHTP required the use of stearic acid to help coordinate the MOF, resulting in a sharper more prominent surface pressure isotherm in comparison to only Cu-HHTP. The resulting films demonstrate how Langmuir-Blodgett techniques improve the uniformity of porphyrin-based MOFs by minimizing areas of aggregation. This work may contribute to the development of more uniform thin films and help evaluate the full potential of various materials when aggregation is minimized.

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81. Targeted Delivery of Salt Inducible Kinase Inhibitors with Zoledronate Coated ZIF-8

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Metal-organic frameworks (MOFs) are highly porous, crystalline materials composed of metal ions connected by organic linkers, offering remarkable potential for drug delivery applications due to their large surface area, low toxicity, and biocompatibility. Zeolitic Imidazolate Framework-8 (ZIF-8) stands out as a well-regarded MOF known for its solvo and thermal stability, easily synthesized at room temperature through the self-assembly of zinc ions and 2-methylimidazole linkers. We explored the drug loading capacity of ZIF-8 for salt-inducible kinase (SIK) inhibitors — molecules with potential therapeutic relevance in managing osteoporosis, a condition characterized by weakened bones and increased fracture risk. To enhance the framework's performance and biocompatibility, we applied a bisphosphonate coating, specifically using zoledronate, known for its strong affinity to bone tissue and ability to inhibit bone resorption. 2-tert-Butyl-910-di(naphth-2-yl)anthracene (Proxy Molecule 1) and 5-Amino-1,3-dimethylpyrimido[4,5-d]pyrimidine-2,4(1H,3H)-dione (Proxy Molecule 2) were used to mimic SIK inhibitor 1 (HG-9-91-01) and SIK Inhibitor 2 (YKL-05-099), respectively. Thermogravimetric analysis (TGA) and Infrared spectroscopy were used to confirm the encapsulation of the proxy molecules and to ensure zoledronate coating on the surface of ZIF-8. High-Performance Liquid Chromatography (HPLC) was performed to measure the concentration of proxy being eluted from ZIF-8 when in an experimental environment mimicking blood pH, temperature, and movement. Additionally, X-ray diffraction (XRD) was used to confirm ZIF-8 structure and chemical composition remained. This research aims to optimize MOF-based drug delivery systems for bone-targeted therapies.

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82. Investigation of Hydroxyl Radicals During Photocatalysis of Carbon Quantum Dots

Diego De Luna* and Young Seok Shon PhD

Heavy metal quantum dots, such as CdSe and ZnS, have been widely used in photocatalysis and bioimaging; however, their toxicity, environmental persistence, and regulatory restrictions have driven the search for safer alternatives. Carbon quantum dots (CQDs) are carbon-based nanoparticles under 10 nm that are biocompatible, non-toxic in their degradation products, and possess tunable fluorescence, making them promising candidates for sustainable photocatalytic applications. This study investigates the photocatalytic activity of hydrothermally

synthesized CQDs, with a specific focus on their capacity to generate hydroxyl radicals ($\bullet\text{OH}$) under 365 nm UV irradiation. CQDs were synthesized hydrothermally using citric acid and water, then purified through filtration, dialysis, and rotary evaporation. The photocatalytic mechanism proceeds through light-driven electron-hole pair generation, where oxidative holes react with water to produce hydroxyl radicals, and reductive electrons reduce dissolved oxygen into superoxide species that further yield $\bullet\text{OH}$.

Styrene was selected as a hydroxyl radical probe due to its well-characterized oxidation products, industrial relevance as a wastewater pollutant, and biological significance as a genotoxic metabolic precursor. Following a 3-hour irradiation experiment, ^1H NMR and ^{13}C NMR analysis revealed no styrene conversion in the initial trial, suggesting insufficient CQD concentration or deactivated by charge recombination. Future work will incorporate palladium nanoparticles as co-catalysts to suppress charge recombination and enhance hydroxyl radical yield, alongside expanded biomedical applications including antimicrobial testing and photodynamic therapy simulations.

Thank you to the NIH URISE program for funding and support.

83. Investigating the Role of the Unfolded Protein Response in Aspirin-Mediated Chemoprevention Using *Drosophila melanogaster* as a Model System

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Colorectal cancer is the second leading cause of cancer-related death in the United States, and its increasing incidence among younger individuals highlights the need for effective prevention strategies. Long-term aspirin use is associated with a reduced risk of colorectal cancer, but the biological mechanisms underlying this protective effect remain poorly understood. Studies from our laboratory and others using cultured cells suggest that aspirin targets the unfolded protein response, a cellular stress pathway that helps cells cope with damaged or improperly folded proteins. One key component of this pathway is protein kinase R-like endoplasmic reticulum kinase (PERK).

The goal of this project is to determine whether PERK contributes to the cancer-preventive effects of aspirin in a living organism. We use a genetically engineered fruit

fly (*Drosophila melanogaster*) model in which an activated form of the cancer-promoting human Ras protein is produced in intestinal stem cells of the flies in a temperature-controlled manner, leading to tumor cell formation in the gut. These cells also express green fluorescent protein, allowing them to be visualized by fluorescence microscopy. Actively dividing cells are identified by staining the gut with anti-phospho-Histone H3 antibody, a marker of cell division. Preliminary results indicate that aspirin-fed control flies have fewer actively dividing tumor cells. Reducing PERK expression through gene silencing appears to antagonize aspirin-mediated suppression of tumor cell proliferation.

These findings suggest that aspirin-induced PERK activation may provide a mechanistic basis for aspirin's cancer-preventive effects. Ongoing studies are focused on completing the necessary experimental replicates and quantitative analyses of how aspirin dose and treatment duration influence tumor cell proliferation in control flies and PERK knock-down flies. Future studies will investigate the molecular mechanisms by which aspirin may activate the PERK pathway. Together, this work may provide new insight into how aspirin helps prevent colorectal cancer and identify cellular pathways that could be targeted for future cancer prevention strategies.

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84. Effects of Manganese on Insulin Signaling and Glucose Transporter Localization in Skeletal Muscle Cells

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Insulin signaling plays a central role in maintaining glucose homeostasis by promoting glucose uptake in skeletal muscle and other insulin-responsive tissues. A key component of this pathway is Akt, also known as protein kinase B, a family of serine-threonine protein kinases that regulates numerous cellular processes, including metabolism and glucose homeostasis. Of the three Akt isoforms, Akt2 plays a particularly important role in insulin-stimulated glucose uptake by promoting the translocation of glucose transporter 4 (GLUT4) from intracellular storage vesicles to the plasma membrane. Although magnesium is generally considered the primary

divalent cation required for Akt activity, our in vitro kinase studies revealed that Akt2 exhibits greater activity with manganese than with magnesium, whereas Akt1 functions similarly with either cation. This isoform-specific difference led us to hypothesize that manganese may enhance Akt2 signaling and influence GLUT4 trafficking in insulin-responsive cells.

To investigate this possibility, we examined the effects of manganese on Akt signaling in L6 rat skeletal muscle cells, an established model for studying glucose metabolism. L6 cells were treated with manganese chloride with and without insulin, and Akt signaling was evaluated by immunoblotting. GLUT4 localization and cellular actin organization were examined in insulin treated L6 myocytes by immunofluorescence microscopy. Preliminary results demonstrate that Mn^{2+} pre-treatment did not make a statistically significant difference in level of Akt signaling in response to insulin treatment in L6 myocytes. Insulin treatment of L6 myocytes led to a punctate distribution of GLUT4 and actin along the cellular periphery. Ongoing studies are focused on completing the necessary experimental replicates and quantitative analyses to determine the concentration- and time-dependent effects of manganese on Akt signaling and GLUT4 localization in L6 myocytes vs myotubes. Future experiments will assess whether these changes translate into increased glucose uptake and enhanced insulin responsiveness. Together, these studies may reveal a role for Mn^{2+} cations in regulating insulin signaling and provide new insight into mechanisms controlling glucose homeostasis.

85. Phylogeny Builds, Environment Fine-Tunes: Glycoside Hydrolase Architecture

Alison Hughes*, Andrea Castillo Sevilla, and Renaud Berlemont, Ph.D.

Glycoside hydrolases (GHs) are central to microbial carbohydrate degradation and frequently occur as multidomain proteins containing accessory domains involved in substrate binding, localization, and retention. However, the extent to which GH multidomain architectures are shaped by phylogeny versus environmental adaptation remains poorly understood. Here, we analyzed 158,829 GH-containing proteins from 17,108 high-quality metagenome-assembled genomes (MAGs) in the GEM catalog, focusing on major GH families involved in polysaccharide and oligosaccharide degradation. We developed domain–domain adjacency networks (DANs) to quantify multidomain organization and compared network weighted architectural similarity across bacterial genera and environments. GH architectures were highly conserved within genera, with bootstrapped DANs displaying stable network properties and distinct lineage-specific architectural similarities, indicating strong phylogenetic constraints on domain organization. Accessory domains associated with substrate targeting and enzyme retention represented approximately 61% of non-catalytic partner domains, highlighting their importance in GH evolution. Although phylogeny

was the dominant determinant of multidomain architecture, environmental effects were detected in cosmopolitan genera. Environmental variation had a limited and lineage-dependent influence on GH abundance but more consistently affected the prevalence of multidomain GHs, particularly within GH3, GH13, and GH18 families. These results support a hierarchical model in which phylogeny establishes a conserved framework of GH organization, while environmental pressures fine-tune multidomain architectures. Our study demonstrates that protein domain architecture represents an important and previously underappreciated dimension of microbial functional adaptation and provides a scalable network-based framework for linking enzyme organization to ecological function.

86. Conservation and Diversification of CAZyme Repertoires Across Bacterial Lineages

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Carbohydrate-active enzymes (CAZymes) are central to microbial interactions with polysaccharides and contribute substantially to carbon transformation across ecosystems. Building on previous studies showing that the distribution of glycoside hydrolases are phylogenetically structured, we investigated the distribution and evolution of the entire CAZyme repertoires across ~300,000 bacterial genomes. We first quantified CAZyme abundance, prevalence, and family-level diversity across major bacterial lineages, identifying clades with different potential for carbohydrate degradation, modification, and biosynthesis. We then evaluated how conserved (or variable) CAZyme repertoires are across taxonomic levels, from species to phylum, testing whether closely related bacteria share stable CAZome signatures or exhibit substantial lineage-specific turnover. Finally, we examined how protein architecture (i.e., precise domain composition) relates to CAZyme abundance and repertoire diversity. This framework distinguished conservation of catalytic potential from diversification of enzyme organization and substrate-targeting strategies. Together, the project provides a comprehensive view of how bacterial classification and protein architecture shape CAZyme distributions, revealing whether CAZome evolution is primarily governed by lineage inheritance, recurrent innovation, or the interaction between both processes.

87. Determining the Role of AnnexinA2 in SARS-CoV-2 Replication

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Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), the causative agent of COVID-19, has resulted in over 7 million deaths worldwide. Although vaccines are available, few antivirals to treat infection remain limited. The SARS-CoV-2 Spike protein mediates viral entry into host cells and serves as the primary antigen in current mRNA vaccines. Thus, identifying host factors that support viral replication and regulate intracellular trafficking of Spike is critical. Annexin A2 (AnxA2) is a calcium- and phospholipid-binding host protein implicated in several viral infections, but its role in SARS-CoV-2 replication remains unclear. Knockdown of AnxA2 reduced SC2-VLP infectivity by ~50% compared to siRNA-scrambled control cells (non-targeting siRNA), which indicate AnxA2 enhances SARS-CoV-2 assembly. We used Bimolecular Fluorescence Complementation (BiFC) to explore whether the SARS-CoV-2 Spike protein interacts with AnxA2. BiFC involves fusing complementary fragments of a fluorescent protein to two proteins of interest; interaction restores fluorescence. HEK293T cells co-transfected with Spike-VN and AnxA2-VC or with the control pair Spike-VN/Moesin-VC showed a 15-20-fold increase in fluorescence compared to cells expressing a single BiFC construct, suggesting Spike associated near AnxA2. Future experiments are aimed at determining whether AnxA2 directs the incorporation of Spike into viral particles and validating the Spike/AnxA2 interaction through co-immunoprecipitation (Co-IP) analyses. Collectively, these studies will yield new models of coronavirus biology and may reveal AnxA2 as a potential antiviral target.

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88. Defining the Role of Long Non-Coding RNA PVT1 in HIV-1 Latency Reversal

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Despite advances in antiretroviral therapy (ART), HIV-1 remains a significant global health concern. Worldwide, more than 40 million people are living with HIV (PLWH),

including over 1 million in the United States. HIV-1 persists in infected individuals because it can hide within CD4+ T cells in a dormant state. These latent viral reservoirs represent the major barrier to an HIV-1 cure. The "shock and kill" approach is a popular strategy aimed to reactivate and eliminate HIV-1. This method requires latency reversing agents (LRAs) potent enough to induce reactivation without causing systemic immune activation. Long noncoding RNAs (lncRNAs) consist of RNA molecules greater than 200 nucleotides that do not encode protein. They act as molecular scaffolds, binding proteins, often transcription factors, to regulate gene expression. Due to their cell, tissue, and disease-specific expression, lncRNAs are attractive LRA targets. RNA sequencing identified that the lncRNA Plasmacytoma Variant Translocation 1 (PVT1), an oncogene and cancer biomarker, was upregulated in two T cell models of HIV-1 latency. Because PVT1 binds and recruits the HIV-1 transcriptional repressor Enhancer of Zeste Homolog 2 (EZH2), we hypothesize that reducing PVT1 expression will promote HIV-1 reactivation. To test this, we used a T cell line harboring a latent replication-incompetent HIV-1 genome that expresses green fluorescent protein (GFP) upon reactivation. JLat cells treated with PMA, a validated in vitro LRA, induced robust GFP expression in a dose-dependent manner, confirming the model's suitability for latency reversal studies. Interestingly, four different siRNA's targeting PVT1 yielded a 4–8-fold increase in GFP expression relative to control. We are currently validating PVT-1 knockdown using qPCR. These preliminary findings support our hypothesis that reducing PVT1 expression promotes HIV-1 reactivation, identifying PVT1 as a candidate for LRA and providing proof-of-concept for targeting lncRNAs as a strategy for HIV-1 latency reversal.

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89. Determining the role of AnnexinA2 in HIV-1 infection

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Annexin A2 (AnxA2) is a calcium and lipid-binding host protein that plays essential roles in endocytosis, exocytosis, membrane dynamics, membrane fusion, and cytoskeletal organization. Several enveloped and nonenveloped viruses hijack AnxA2 to support their replication. However, whether HIV-1 requires AnxA2 for efficient infection remains unclear. Here, we used CRISPR/Cas9 to knockout AnxA2 in HeLa cells, a cervical cancer cell line. Loss of AnxA2 reduced HIV-1 infection, suggesting that AnxA2 supports viral replication. Interestingly, we observed higher levels of phosphorylated AnxA2 incorporated into HIV-1 particles. Furthermore, we established nucleofection as an effective method for delivering CRISPR/Cas9

components into T cells, with CXCR4-targeting guide RNAs reducing CXCR4 expression by approximately 70–90% in a CD4+ T cell line (CEM). Future studies will validate the presence and phosphorylation state of AnxA2 in virions, perform rescue experiments using plasmids encoding a wildtype AnxA2 or a nonphosphorylatable mutant (Y23A), and use CRISPR ribonucleoproteins (RNPs) to knockout AnxA2 in primary CD4+ T cells to assess its role in HIV-1 target cells. These studies will enhance our understanding of retrovirus biology and may identify potential novel therapeutic targets.

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90. Validating the Interaction Between HIV-1 Nef and Annexin A2 (AnxA2)

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Human Immunodeficiency Virus type 1 (HIV-1), the infective agent responsible for the development of AIDS, is a retrovirus that consists of a positive sense single stranded RNA (+ssRNA) genome. The surface of the virus contains Nef proteins that are small, nonenzymatic proteins that aid in HIV-1 viral pathogenesis. Nef uses Src and Tec kinases to modulate signaling and AP-1/AP-2 complexes to hijack and use for MHC-1, CD4, SERINC5 downregulation. These proteins specifically interact with AnnexinA2 (AnxA2), a membrane-binding protein found in host cells, and is believed help HIV to enter and assemble.

To further investigate the interaction between HIV-1 Nef and AnxA2, we used HeLa cells to first optimize conditions to detect endogenous AnxA2 via immunofluorescence. This was accomplished using different antibodies, specifically CD71 and Flotillin-2. We used Goat-Anti Mouse Alexa Fluor 488 and Goat-Anti Mouse Alexa Fluor 555 as secondary antibodies for these trials. In a more recent trial, we used directly conjugated antibodies that utilized RFP. We hypothesized that HIV-1 Nef will interact and localize with endogenous AnnexinA2 within a membrane compartment. After the trials imaging was conducted to observe the effectivity of the different antibodies. Additionally, we are developing a new AnxA2 clone that includes a 5 amino acid linker between AnxA2 and the HA epitope tag. We utilized Npnl and Not1 primers on the insert and pcDNA3.1(+) backbone.

With dilutions of 1:100, 1:250, and 1:500, the directly conjugated antibodies presented us with a more prominent signal, allowing us to visualize the location of AnxA2 within the HeLa cells. The 1:100 dilution allowed for the best visualization of the locality of AnxA2 in host cells. Future work aims to test different AnxA2 primary antibodies and to validate HIV-1 Nef and AnnexinA2 interaction via Co-IP and efficacy of AnxA2 clone with IF and Co-IP.

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91. Defining the Roles of Interferon Priming and Metabolic State on SARS-CoV-2 Infection

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Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), the causative agent of the COVID-19 pandemic, manipulates host-cell metabolism to support infection. Comorbidities such as obesity and diabetes are associated with altered cellular metabolism and an increased risk of severe COVID-19; however, the molecular mechanisms underlying this relationship remain unclear. Although glycolysis can support viral production, metabolic conditions that favor oxidative phosphorylation (OXPHOS) have been associated with reduced SARS-CoV-2 infection. Interferon (IFN) signaling can also restrict SARS-CoV-2 entry through induction of antiviral proteins such as interferon-induced transmembrane protein 3 (IFITM3). Interestingly, metabolic reprogramming led to differential expression of the antiviral factors IFITM3 and interferon regulatory factor 1 (IRF1), resulting in contrasting infection outcomes with poxviruses. Whether metabolic reprogramming alters susceptibility to SARS-CoV-2 remain unresolved.

Here, we investigated whether reprogramming human lung cancer A549 cells expressing ACE2 and TMPRSS2 toward glycolytic or OXPHOS-favoring states, in combination with IFN priming, alters susceptibility to SARS-CoV-2 virus-like particles (SC2-VLPs) entry. We observed reduced SC2-VLP entry in IFN- α and IFN- γ primed A549 cells under both glycolytic and OXPHOS-favoring conditions. Both IRF-1 and IFITM3 expression increased with both IFNs and in both glycolytic and OXPHOS-favoring treatments, although there was minimal change in expression between metabolic states.

We also investigated whether reprogramming A549 cells with IFN priming would alter the assembly and release of SC2-VLPs. We observed greater reductions in SC2-VLP infectivity with IFN priming in both metabolic states. Furthermore, infectivity in OXPHOS conditions were reduced both with and without IFN priming compared to glycolytic conditions. Western blot analysis will be used to assess IRF-1 and IFITM3 protein levels across treatment conditions and determine whether their induction is associated with reduced SC2-VLP assembly and release. These findings may clarify how cellular metabolic state and IFN signaling interact to regulate SARS-CoV-2 entry and may identify IFITM3 as a potential host therapeutic target.

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92. Generating a SARS-CoV-2 Spike Expression Plasmid for Interaction & Immunofluorescence Studies

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The SARS-CoV-2 Spike protein mediates viral entry and remains a central target for studies of viral infectivity and antibody neutralization. Spike variants carrying the D614G and N501Y substitutions have been widely used to model enhanced transmissibility and receptor binding. However, studying Spike protein trafficking, expression, and interactions in mammalian cells requires an epitope-tagged expression construct that can be readily detected by immunoblotting and immunofluorescence. Here, we report the subcloning of a C-terminally FLAG-tagged SARS-CoV-2 Spike (Wu-1) open reading frame into the mammalian expression vector pcDNA3.1(+) using KpnI and NotI restriction sites. The 3822 bp Spike-FLAG insert was PCR-amplified from a donor plasmid (CoV2-Spike-EF1a-D614G-N501Y) with Q5 Hot Start polymerase (63°C annealing, 30 cycles), producing a band of the expected size on a 1% agarose gel. Following purification, both Spike-FLAG and pcDNA3.1(+) were digested with KpnI-HF and NotI-HF. Dephosphorylation was performed to prevent vector self-ligation. Gel extraction recovered the insert at 20.0 and 146.6 ng/μL, while the backbone required a second extraction attempt, yielding 13.8 to 50.5 ng/μL, although spectrophotometric purity ratios (A260/280 of 1.02 to 1.26) indicated residual buffer contamination in both fractions. Ligation and bacterial transformation yielded no colonies. Current attempts are aimed at achieving higher purity of vector and insert. Generation of a Spike-FLAG expression plasmid will aid in conducting

molecular and cellular assays to monitor Spike localization and identify Spike interaction partners.

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93. Identifying Linoleic Acid Reactive B-Cells as Potential Targets for Inflammation in Type 2 Diabetes

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Type 2 diabetes (T2D) is a chronic metabolic disorder characterized by chronic inflammation and insulin resistance, driven in part by altered lipid metabolism. These changes create a cycle that promotes immune dysregulation and drives the progression of T2D; however, the underlying immune mechanisms are not completely understood. While most research has been done in T cells in this context, B cells remain understudied. B cells contribute to inflammation through mechanisms such as antibody production, cytokine secretion, and antigen presentation. While B cells are well established for their role in protein antigen recognition, previous research has identified lipid-reactive IgG antibodies in human serum that bind to palmitic acid, suggesting that B cells may be capable of directly recognizing lipid antigens. To further investigate this possibility, we hypothesized that human B cells would recognize linoleic acid, a polyunsaturated omega-6 fatty acid, as a lipid antigen. To investigate this hypothesis, PBMCs were isolated from healthy donor blood and B cells were enriched using magnetic separation. The isolated B cells were then incubated with linoleic acid-conjugated beads, and flow cytometry was used to detect lipid-reactive B cell populations. We did not detect a distinct population of linoleic acid-reactive B cells. These preliminary results may reflect technical limitations, including insufficient cell counts or suboptimal gating, rather than a true absence of linoleic acid reactivity in B cells.

Future directions include optimizing detection protocols, confirming B cell enrichment, and comparing linoleic acid reactivity between healthy donors and T2D donors. Demonstrating that B cells recognize lipid antigens would identify a novel immune mechanism linking altered lipid metabolism to chronic inflammation in T2D,

establishing B cells as a potential therapeutic target for interventions aimed at reducing inflammation in this disease.

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94. Aposematic Signal Variability and Müllerian Mimicry in North American Skunks

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The hooded skunk (*Mephitis macroura*), the striped skunk (*Mephitis mephitis*), and the American hog-nosed skunk (*Conepatus leuconotus*) are three species of skunk found in North America with strong aposematic coloration that have overlapping ranges, fill similar ecological niches, and face similar predation risks. The aposematic coat patterns of hooded skunks are highly variable, being caped or striped or a combination of the two, while striped skunks are usually striped and hog-nosed skunks are black with a white cape. I am interested in understanding the factors behind this variable coat pattern in the hooded skunk. There may be a Müllerian mimicry ring occurring in which hooded skunk pelage patterns are similar to sympatric Mephitinae skunks to reduce predator learning costs. I plan to analyze images of preserved skunk skins and compare the dimensions of skunk pelage patterns against various biotic and abiotic factors for the area where the specimen was collected. These factors include congener presence, humidity, and predation risk from both avian and mammalian predators. I expect that there will be less variability in aposematic patterns in areas with Mephitinae skunk presence and high predation risk. Literature also suggests that there will be a greater proportion of black fur in areas with higher humidity. If there is interspecies aposematic signal conformity in areas where congener skunks are sympatric, this would be the first evidence of a Mullerian mimicry ring in mammals. In the future, it may be worthwhile to compare the pelage patterns of the four species of spotted skunk (*Spilogale* spp.) also found in North America.

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95. The Influence of Black-and-White Pet Models on Aposematic Color Generalization in Urban Coyotes

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Coyotes have been expanding their range since the beginning of the 19th century; currently, every major continental US city is home to populations of urban coyotes. With this urbanization comes the potential for human/wildlife conflict. One form this conflict takes is coyote predation on domestic pets, as urban coyotes readily predate cats and small dogs. Interestingly, preliminary research indicates domestic pets sporting black-and-white coat colorations may be better protected from coyote attack. These lucky pets may owe this protective effect to yet another urbanized animal: the striped skunk. Striped skunks are aposematic – they advertise their noxious chemical defenses with conspicuous black-and-white pelage. The Stankowich lab has conducted research indicating that captive coyotes may have a predisposition to fear black and white coloration and can learn to generalize this coloration to an extent. Additionally, wild coyotes are more cautious of contrasting coloration and skunk-like body shapes. Furthermore, domestic dogs with skunk-like pelage have less severe interactions with coyotes. These studies indicate pets with more contrasting coloration may be better protected from coyotes than their monochromatic counterparts. To study this potentially protective coloration, I placed highly realistic pet statues at six different sites in LA and Orange County, with trials starting on July 3, 2024 and stopping August 13, 2026. These statues consisted of a cat, small dog, large dog, and striped skunk for a control. The statues were painted in both monochromatic and black-and-white colorations and rotated out on a weekly basis. Each station had a camera trap set up to record coyote behaviors with the models. Coyotes demonstrate a high and continuing interest in the models, which resulted in a large data set for the project. Initial data analyses show that coyotes do exhibit a preference for interacting with monochromatic pet models. If my research proves a strong link between skunk-like coloration and survivability of domestic pets, I may be able to develop protective tools such as black-and-white pet sweaters. Such tools can aid in alleviating human/wildlife conflict, especially in urban environments in LA County where urban coyotes have become a charged topic. Additionally, there is scant research on aposematic learning among mammalian carnivores, and my study will add to that body of knowledge.

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96. Is Tooth Morphology an Indicator of Dietary Ecology in Mammals?

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Mammals exhibit diverse dental morphologies that are associated with their diets, particularly in the structure of their molars. Different dietary adaptations are reflected in the shape, size, number, and arrangement of cusps and ridges on molars. In this study, we will examine whether molar morphology differs among mammals with different dietary specializations. We hypothesize that cusp and tooth number are greater in carnivorous and insectivorous mammals, while ridge number is greater in herbivorous mammals. We also expect mammals that specialize in consuming ants and termites to have fewer teeth and cusps. Molar diagrams from *Mammal Teeth* by Peter S. Ungar will be used to examine cusp, ridge, and point morphology across Mammalia. One representative species will be selected for each Order, Family, and Genus based on the species represented in the diagrams in the book. To accurately scale the diagrams, the largest molar of each species will be measured using digital calipers when skull specimens are available. Specimens will be obtained from the CSULB Vertebrate Collection and the Natural History Museum of Los Angeles County. For species that are not available in these collections, photographs of the upper and lower teeth with scale bars will be obtained from the American Museum of Natural History, Canadian Museum of Nature, Field Museum of Natural History, and Smithsonian National Museum of Natural History. ImageJ will be used to measure the largest molar from photographs containing scale bars. The measured molar dimensions will then be used to scale the corresponding diagrams from Ungar's book in ImageJ. Once the diagrams are accurately scaled, the lengths and numbers of cusps and ridges, as well as the number of points on each molar, will be recorded. The mean cusp and ridge lengths will then be calculated for each molar. The resulting morphological data will be analyzed using phylogenetic methods to account for evolutionary relationships among species and to evaluate associations between dental morphology and dietary specialization. We expect carnivorous and insectivorous mammals to exhibit greater cusp and tooth numbers, while herbivorous mammals are expected to exhibit greater ridge numbers. Mammals specializing in ant and termite consumption are expected to exhibit reduced cusp and tooth numbers compared with mammals with other dietary specializations.

97. Facial Contrast Markings Versus Bite Force and Defensive Ability in Carnivores

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The order Carnivora is a highly diverse group of mammals, categorized by their specialized, meat-shearing teeth known as the carnassial pair. They have also evolved to possess visual signaling patterns, such as stripes, masks, and patches as a warning sign against predators. This project aims to examine the role that facial contrast markings play in various carnivore species relative to their respective bite force, and additionally to other defensive abilities they possess. We used ImageJ to take measurements of twelve distinct facial regions on a representative from each carnivore family to look at the size and border length of adjacent sections. Using supplemental data on bite force (Christiansen and Wroe, 2007) and skull length (Harano and Asahara, 2022), we were able to construct a dataset to use in future phylogenetic analyses on the relationship between these variables and the maximum difference in shades on the face. The next steps involve looking into tooth morphology of each family, designating a representative to scale each group and categorize 1) if they truly possess secodont teeth and 2) how strong of a carnassial pair they have (very strong, moderate, weak/none). This will establish the experimental framework to test bite force, diet type, tooth morphology, the size of the mouth, thickness of skin and fur, and mating/social group systems against facial contrast markings to determine whether they act as a signal of danger to predators or prey. We anticipate that individuals with a higher proportion of contrast signal that they have better defensive abilities against their predators. This study aims to bridge the gap in knowledge between evolutionary signaling and functional morphology in carnivore species.

98. Data Acquisition and Assumption Testing for Developing a Larval-Specific Dynamic Energy Budget in *Dendraster excentricus*

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In response to food availability, larvae of the sand dollar *Dendraster excentricus* exhibit morphological and physiological plasticity, yet no mechanistic model exists to describe the underlying energy dynamics. Dynamic Energy Budget (DEB) theory provides a unifying framework for comparing metabolic strategies across species by

representing shared processes with species-specific values. The DEB framework can be used for *D. excentricus* to create a holistic view of the diverging strategies between low- and high-fed larvae, answering questions about the relationship between food availability, structure as a reverse energy source, and metamorphic competency. The goal is to address knowledge gaps in plasticity/growth responses in sand dollar larvae necessary for the creation of a Dynamic Energy Budget (DEB) model, which will be accomplished in a series of four specific aims. (1) To model protein biomass growth rates as a function of food availability, and correct parameters at intermediate feeding levels. Protein biomass measurements are taken across a range of feeding levels. (2) To verify isomorphy, morphological measurements are taken across a range of feeding levels. (3) To quantify structural reabsorption under starvation and assess the need to model multiple reserves, measurements for the change in rudiment, post-oral arm length, and midline body length are taken. (4) Ultimately, new data will be incorporated with published data to create a DEB model that can mechanistically describe larval energy dynamics. Preliminary results show that protein biomass does not increase linearly with increasing food availability, and the ratio of post-oral arms to midline body length decreases non-linearly with increasing food availability. This motivates further testing of isomorphy and multiple shape coefficients for the DEB model. Preliminary results regarding structure under starvation show that a well developed rudiment will be maintained under starvation, but other structures, such as the post-oral arms, will shrink. It is concluded that rudiment protein appears to be a structural element that is unavailable as an energy reserve. Commitment to rudiment growth and development may be non-reversible, which would explain why protein biomass is not used as an energy reserve even under nutrient stress.

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99. β -arrestin-mediated dopamine receptor D1 signaling acts through Src kinase in the ARH to regulate sexual receptivity in female rats

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Progesterone rapidly facilitates lordosis in ovariectomized rats primed with 17 β -estradiol benzoate (EB; 2 μ g) via activation of progesterone receptor-B (PR-B) in the arcuate nucleus of the hypothalamus (ARH). Progesterone inhibits ARH β -endorphin neurons that project to the medial preoptic nucleus (MPN) to facilitate lordosis. Although PR-B are nuclear transcription factors, membrane-associated PR-B mediate

progesterone rapid facilitation of lordosis. Like progesterone, activation of either Src kinase (Src) or dopamine receptor-1 (D1) in the ARH facilitates lordosis. Antagonism of either PR-B, Src, or D1 blocks the facilitation of lordosis by the other two. Previous studies from our laboratory demonstrated that PR-B, Src, and D1 signaling converge in ARH β -endorphin neurons that project to the MPN. Co-immunoprecipitation findings indicate that PR-B forms complexes with Src. However, we failed to detect direct interactions between D1 receptors and PR-Src complexes, suggesting the involvement of an intermediary protein. The D1 being a GPCR suggested a G-protein mediated D1 receptor interaction with Src. Yet, double-label immunohistochemistry revealed minimal Src and Gas-protein colocalization. D1 can also signal through β -Arrestin 2, and β -Arrestin 2 can activate Src. Therefore, we tested the hypothesis that β -Arrestin 2 mediates D1 receptor signaling with PR-Src complexes to regulate sexual receptivity. Double-label immunohistochemistry was used to assess colocalization of Src and β -Arrestin 2, and D1 and β -Arrestin 2 in the ARH. We observed subpopulations of ARH neurons that were immunopositive for Src and β -Arrestin 2 as well as D1 and β -Arrestin 2, indicating the potential of D1, β -Arrestin 2, Src interactions and complex formation. Additionally, EB-primed ovariectomized rats received sequential ARH infusions of the β -Arrestin inhibitor, barbadin, followed 15 min later by a Src activator (47.5 h after EB priming). Sexual receptivity was assessed 30 min later by lordosis quotient (LQ). Barbadin significantly attenuated Src activator-induced sexual receptivity ($LQ = 10.0 \pm 0$) compared with saline-treated controls (70.0 ± 10.8 ; $p = 0.012$, paired t-test). These findings support the hypothesis that D1 signaling through β -Arrestin 2 associates with the D1-PR-Src signaling complex in ARH β -endorphin neurons to facilitate sexual receptivity.

100. Potential progesterone regulated dopaminergic neurons in the anteroventral periventricular nucleus

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The luteinizing hormone (LH) surge initiates ovulation in rats and humans alike. Rising estradiol levels induces both neuroprogesterone produced by hypothalamic astrocytes and progesterone receptors (PR) receptors in kisspeptin neurons of the anteroventral periventricular nucleus (AVPV) of female Long-Evans rats. This neuroprogesterone acts through PR to induce the release of kisspeptin that signals the surge release of gonadotropin releasing hormone (GnRH) into the hypophyseal portal system. This GnRH then triggers the surge release of LH from the anterior pituitary and to act on the ovary to induce ovulation and luteinization of the corpus luteum. Previous studies indicate that progesterone also alters mesolimbic and

nigrostriatal dopamine release (Lonstein, 2004). Further, when the D2-R was stimulated in anestrus ewes, GnRH and LH production was attenuated (Goodman, 2012). This inspires the question of whether dopamine has a stimulatory effect on GnRH and LH during estrus. Our lab observed that that D1, PGR complex with and signal through Src to facilitate lordosis in females rats in the arcuate nucleus of the hypothalamus (ARH). Our lab also demonstrated that PR signals through a Src in the AVPV as well as the ARH (Choun, 2021), suggesting that a D1-PGR-Src complex could be present in the AVPV as well. Therefore, we hypothesized that progesterone may be regulating dopamine release that may act on AVPV kisspeptin neurons to trigger the LH surge. To test this hypothesis, we used double labeled immunohistochemistry for PR and tyrosine hydroxylase (TH; a precursor for dopamine). Ovariectomized (OVX) rats were all injected subcutaneously with 2 ug estradiol benzoate followed by either of progesterone (500 ug) or vehicle (safflower oil) 26 hours after the EB injection. Four hours after the final steroid treatment, brains were prepared for immunohistochemistry, post-fixed, cryoprotected and then sectioned (20 μ m) on a cryostat. Double label immunohistochemistry revealed a subset of AVPV neurons that had colocalization of TH (extranuclear staining) and PR (nuclear staining) immunostaining. This colocalization demonstrates the possibility that dopaminergic neurons in the AVPV may be regulated by progesterone to facilitate the LH surge via kisspeptin neurons in the AVPV.

Keywords: Anteroventral Periventricular Nucleus (AVPV), Dopamine, Progesterone Receptor (PR), Tyrosine Hydroxylase (TH)

101. Potential co-transmission of dopamine and orphanin FQ in the arcuate nucleus neurons that is modulated by progesterone and regulates sexual receptivity in female rats

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Progesterone facilitates female reproductive behavior through progesterone receptors (PGR) located in β -endorphin (β -end) neurons and β -end presynaptic neurons. Two neuronal types that facilitate lordosis and synapse onto β -end neurons are dopamine (a small molecule neurotransmitter) and nociceptin/orphanin FQ (OFQ/N), a neuropeptide. These neurotransmitters act at the β -end neuron through their perspective receptors: OFQ/N - nociceptin receptor (ORL-1) and dopamine – dopamine receptor-1 (D1) to inhibit the β -end neuron and facilitate lordosis. Previous studies have identified PGR in OFQ/N-containing neurons as well as dopaminergic neurons of the arcuate nucleus of the hypothalamus (ARH), suggesting progesterone regulates the release of OFQ/N and dopamine to facilitate lordosis. However, it is unclear whether OFQ/N and dopamine are released from the same neuron or are two

separate neurons that converge on β -end neurons. Presynaptically, we hypothesized that OFQ/N and dopamine are co-localized in ARH neurons. Postsynaptically, we hypothesized that PGR and ORL-1 are co-localized. Brains from adult ovariectomized (OVX) female rats treated with estradiol benzoate and oil (EB/O) or oil and oil (Oil) were fixed, sectioned and stained using double-label immunohistochemistry. Primary antibodies against PGR, ORL-1, tyrosine hydroxylase (TH, a marker for ARH dopaminergic neurons), and OFQ/N were used to identify the distribution of each receptor, followed by fluorescent secondary antibody labeling. Fluorescent microscopy was used to examine the ARH for presynaptic neurons expressing TH and OFQ/N and postsynaptic neurons expressing PR and ORL-1. We observed a subpopulation of ARH neurons that expressed TH and OFQ/N, as well as a subpopulation with PR and ORL-1 co-localization. The preliminary findings indicate that a single presynaptic OFQ/N-dopaminergic neuron could be regulated by progesterone and synapses onto β -end neurons. The subpopulation of neurons that express both PGR and ORL-1 are likely expressed in β -end neurons. Thus, progesterone appears to be acting both presynaptically at the OFQ/N-dopaminergic neurons and postsynaptically in the β -end neuron that expresses ORL-1-D1 and PGR. These findings will provide further insight into the neural mechanisms through which progesterone and nociceptin signaling interact within the hypothalamus to facilitate female reproductive behavior.

102. Estradiol Levels Predict Alzheimer's Disease Pathology in Female apoE ϵ 4 Carriers

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Alzheimer's disease (AD) disproportionately affects women (~2:1 compared to men), even after accounting for women's longevity. This female-specific risk is thought to be linked to the neuroendocrine transition into menopause, correlating with a drop in estrogen levels and thus the loss of estrogen's neuroprotective properties.

Apolipoprotein E (apoE) genotype is a reliable predictor for the development of AD pathology, particularly carriers of the ϵ 4 isoform allele. Estrogens like estradiol (E2) are known to interact with apoE, suggesting a potential moderating relationship. However, it remains unclear if there is any interaction between E2 and apoE genotype on the development of AD pathology like β -amyloid deposition, and whether this estrogen effect can be linked to memory decline, another prevalent AD marker. To test this, 142 cognitively unimpaired individuals ages 60+ from the BEACoN neuroimaging study at UC Irvine provided saliva samples for E2 and apoE genotype data, and amyloid pathology was quantified using 18F-florbetapir PET. Standardized

uptake value ratios (SUVRs) were calculated in the entorhinal cortex and posterior cingulate cortex. Memory data were collected using the Temporal Mnemonic Discrimination Task (MDTT). This task evaluates the ability to discriminate between highly similar objects/events, and deficits in this type of task is one of the earliest detectable signs of memory decline. Linear regression models tested the interaction between E2 levels and apoE genotype on amyloid SUVRs, and a moderated mediation model estimated the indirect effect of estradiol on cognition through amyloid pathology. The initial regression models showed that in the left entorhinal cortex, higher E2 levels predicted lower amyloid pathology in female $\epsilon 4$ carriers but not in non-carriers. Using a 95% bootstrap confidence interval, the moderated mediation model revealed a significant indirect effect of estradiol on cognition (via left entorhinal amyloid SUVR) that is present only in female $\epsilon 4$ carriers. These findings suggest an apoE-estradiol mechanism that influences amyloid burden which differs between $\epsilon 4$ carriers and non-carriers. This mechanism is an important topic for further research.

103. Assessing the Role of the Heat Shock Protein (HSP) Response in Food-Induced Phenotypic Plasticity During Sand Dollar Larval Development

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Dendraster excentricus larvae display food induced phenotypic plasticity, which allows larvae to change their morphology depending on food availability: low food produces longer feeding arms, while high food produces shorter arms and faster growth. Heat shock proteins (HSPs) are molecular chaperones used as biomarkers of cellular stress, and HSP70 expression increases with thermal stress in many species, including *D. excentricus*. We hypothesize that HSPs contribute to the plasticity response induced by feeding and we will test this by comparing HSP70 abundance between larvae grown under constant high food (10,000 cells mL⁻¹) and constant low food (1,000 cells mL⁻¹). Larvae will be sampled at multiple days post fertilization, and total protein will be separated by SDS-PAGE; HSP70 will be detected and quantified by Western blot using a human anti-HSP70 antibody. Before testing this hypothesis, we set a pilot culture to confirm that our culturing and measurement methods could be trusted and show the expected plasticity response. Larval morphology (post-oral arm length and midline body length) was tracked from 5 to 15 days post fertilization, and the post-oral arm to midline body length (PO:MBL) ratio increased steadily with age (1.68 to 2.13), closely matching patterns reported in a recent study of this species. These results confirmed that our culturing and measurement methods reliably reproduce known plasticity responses, making it safe to proceed with the

planned feeding treatments and HSP70 comparison to identify the role HSP70 plays in this response. It would also connect the cellular stress pathway to the developmental plasticity of *D. excentricus*. Ultimately this would give us new insight into how marine invertebrate larvae physiologically deal with variable food availability, connecting this work to the real-world threat that climate change poses to food availability in marine ecosystems.

This work is supported by the CSULB BUILD Program in the Office of Undergraduate Research Services.

104. Assessing the Efficacy and Biochemical Underpinnings of Reversible Phenotypic Plasticity in Larvae of the Pacific Sand Dollar, *Dendraster excentricus*

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Food availability induces distinct phenotypes in larvae of the Pacific sand dollar, *Dendraster excentricus*. Under low-food conditions, larvae develop longer arms and grow more slowly, whereas high-food conditions produce shorter arms and faster development. This study examined whether larvae can reverse these phenotypic responses throughout development and identified the biochemical reserves that support morphological remodeling. Larvae were maintained under constant high-food or low-food conditions using *Rhodomonas* sp. as a food source. Additional groups were switched from high-food to low-food conditions at 4, 8, or 12 days post-fertilization. Phenotypic responses were assessed by measuring post-oral arm length and midline body length. A second experiment examined changes in protein and lipid reserves after larvae were switched from high- to low-food conditions at 8 days post-fertilization. High-food larvae successfully reversed their phenotype at all developmental stages examined, with the strongest response occurring at 8 days post-fertilization. Changes in protein biomass did not support protein use as the primary energy source for remodeling. In contrast, triglyceride depletion following the food switch corresponded to an estimated energy expenditure of 3.8 mJ, suggesting that triglycerides provide a major fuel source for morphological change. These results demonstrate that *D. excentricus* larvae retain substantial phenotypic flexibility during development. The capacity for reversal may depend on both developmental timing and the lipid content of available food.

This project is supported by Los Angeles Rod and Reel Grant, Donald Reish Student Research Fellowship, Alan and Della Wells Assistantship, and Southern California Tuna Club.

105. Fact or Artifact? Testing Starvation Tolerance in Marine Invertebrates

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Marine larvae are a vulnerable developmental stage between embryos and adults. During this stage, they face challenges such as predation and transport away from suitable habitats. Feeding larvae also face inconsistent food availability, making periods of starvation an additional, significant challenge. Studies examining larval starvation have found surprising results: larvae can survive far beyond expected energy limits, suggesting unique physiological adaptations or alternative energy sources, such as dissolved organic matter (DOM). However, laboratory conditions may not reflect natural environments, particularly because larvae are reared at unnaturally high densities (e.g., >1 larva per mL). We hypothesize that high larval densities elevate DOM concentrations due to mortality of other larvae in the culture vessel. This extra energy from larval mortality therefore artificially extends survival in laboratory settings. Our experiment used a novel culturing approach in which larvae were reared in 20 mL scintillation vials mixed with a fast-food "hot dog roller" in a temperature-controlled room (16 °C). Larvae were reared under starvation conditions at low and high density (1 and 0.05 larvae per mL, respectively). We assessed growth, development, and survivorship at 7 and 14 days post-fertilization. Preliminary results support our hypothesis, demonstrating increased survivability in larvae reared at higher density. These results improve understanding of larval physiological tolerance to starvation during development at more natural densities. These data are crucial for modeling larval growth and predicting how changes in environmental conditions will affect juvenile recruitment and adult population stability.

The project is supported by the Undergraduate Research Training Institute for Student Enhancement (U-RISE) Program, funded by the National Institutes of Health (NIH).

106. A Tale of Tails: Round Stingray (*Urobatis halleri*) Tail Muscle Anatomy

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Round stingrays (*Urobatis halleri*) are abundant in sandy nearshore habitats along the southern California coast. This species uses its strong, barbed tail for defense and stabilization, as exhibited during tail strike and sand burial behaviors, respectively. The goal of this study is to describe the tail musculature which will inform future

investigations of the motor patterns responsible for the aforementioned behaviors. We collected round stingrays across Southern California and made transverse cross sections of tails at four standardized regions: base of tail, base of barb, central point relative to these two positions, and central point between base of barb and caudal fin. We analyzed the cross sections in order to describe the muscle compartments and their positioning in relation to the vertebral column and along the length of the tail. Findings indicated that tail musculature was composed of 10 muscle compartments. These muscle compartments were bilaterally symmetrical, with 5 on each side: 3 dorsally oriented and 2 ventrally oriented. Compartment proportions changed at each tail cross sectional region. Describing the basic tail anatomy of *U. halleri* will facilitate future investigations into the function of individual muscles and their motor patterns across various behaviors, notably the tail strike, sand burial, and escape responses.

107. An Inducible Genome-Engineering Platform for Synthetic Virus Production

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Viruses are the most abundant entities on the planet and a major driver of mortality, yet most cannot be cultured or experimentally characterized. Moreover, the rapid proliferation of metagenomic sequencing has revealed massive diversity of viral genomes for which no corresponding virus has been isolated. Here, we are developing a sequence-to-virus approach that uses synthetic biology to produce viruses directly from known genome sequences to accelerate their discovery and characterization without the requirement for compatible host cultivation. We are engineering *Phaeodactylum tricornutum*, an ecologically important and genetically tractable model diatom, to produce a single-stranded DNA virus from a poorly characterized family that infects diatoms, the *Bacilladnaviridae*. First, the 5.6kb viral genome was synthetically redesigned to include a modular control mechanism in which selectable marker genes (antibiotic resistance and green fluorescent protein) are inserted into an essential virus replication gene (vRep) to prevent viral replication. This module can be excised using a nitrate-inducible Cre-loxP system to control virus production. Genetic transformation and the CRISPR/Cas9 system were then optimized for the delivery of the synthetic virus genome to the diatom. Transformation via electroporation was achieved across a range of pulse numbers and DNA concentrations (1-16 pulses; 0.5-5 µg DNA), with an average transformation efficiency of 6.9×10^{-5} cfu µg⁻¹ at 500 ng DNA and a single 50 µF pulse. Four single guide RNAs targeting an intergenic region on chromosome 1 of *P. tricornutum* were cloned and confirmed by sequencing, and Cas9 codon usage was computationally tuned for optimal expression in the diatom. Together, these results demonstrate the

host can be genetically transformed with the components needed for synthetic viral production. Upon final assembly and integration of the complete viral construct, we will evaluate virus production by measuring viral gene expression, host cell lysis, and release of morphologically consistent viral particles, comparing these to established diatom-virus systems. This approach provides a potential route for experimentally recovering and characterizing sequenced but uncultured viruses. More broadly, it could create a high throughput method to tap the massive reservoir of genomic potential in the global virome.

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108. Quantification of Macroalgal-infecting Phaeoviruses in Coastal Seawater

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Phaeoviruses are large dsDNA viruses of the phylum *Nucleocytoviricota* that infect multicellular brown algae. Viral infection of these habitat-forming primary producers is widespread, often exceeding 50% of sampled hosts, and can impair host reproduction and photosynthetic performance. However, the abundances of phaeoviruses in the water column are unknown, and this reservoir may be an important pathway for transmission of these viruses, affecting coastal ecosystem productivity and structure. Here, we developed a single-virus molecular approach, the polony method, to quantify the four major lineages of phaeoviruses, subgroups A-D. We redesigned major capsid protein primers and developed a new phaeovirus-specific probe using publicly available sequences from isolated phaeoviruses, proviruses from macroalgal genomes, and environmental sequences. We then validated the approach, showing that the method can detect all four phaeovirus subgroups at an average detection efficiency of 44.5% with a detection limit of 10 viruses mL⁻¹ seawater. We then applied this to a weekly timeseries in Newport Beach, California, located 7 km from a *Macrocystis pyrifera* bed. Phaeoviruses were detected at an average of 1045 viruses mL⁻¹ in the water column with increasing abundances in late spring and early summer and decreasing abundances in early fall. These measurements provide the first quantitative estimates of water-column phaeovirus abundance and reveal a seasonally dynamic extracellular reservoir of viruses with the potential to mediate transmission among brown algal hosts.

109. Inducing Morphological Changes in a Model Diatom to Enhance Genetic Engineering

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Diatoms are one of the major groups of oceanic phytoplankton, which produce 20% of the world's oxygen, and are important to biotechnology applications such as biofuel and therapeutics. Genetic engineering approaches are increasingly enabling new technologies to be developed using diatoms. One of the model diatom systems is *Phaeodactylum tricornutum* for which several engineering tools, such as CRISPR/Cas9, currently exist. One challenge is that *Phaeodactylum tricornutum*, like most diatoms, has a silica shell, which makes it difficult to insert foreign DNA into the cell, a requirement for efficient genetic engineering. Here, our focus is to develop an approach to reduce the silica content and change the cell morphology of *Phaeodactylum tricornutum* from the typical highly silicified tridate and fusiform shapes to the less silicified oval and protoplast shapes, which may enhance DNA delivery. We used two different approaches in which the cell medium was altered, and cell morphotypes were observed over time using microscopy. First, cultures were exposed to a gradient of decreasing salinity (100%, 50%, 25%, 5% seawater). Decreasing salinity increased the relative abundance of oval morphotypes with maximum numbers of oval cells observed at <10% salinity after 48 hours. However, these oval diatoms were overtaken by fusiform morphotypes within seven days of the initial transfer to the lower salinity medium. Second, alcalase, a serine protease which degrades cell walls to produce spheroplast cells, was added to the medium at concentrations of 0, 0.3, 0.6, 1.0, 1.5 microAnson Units. Adding alcalase at 1.5 microAnson produced the most abundance of protoplast cells, but the highest number of cells were observed at 24 hours. This suggests *Phaeodactylum tricornutum*'s morphology can be precisely controlled and provides a means to test DNA delivery to this model diatom in the future.

This project is supported in part by a CSULB ORED Multidisciplinary Grant and a CSUBiotech Research Development Grant.

110. Parasite Infection and Phytoplankton Abundance in Southern California

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Diatoms are photosynthetic bacteria in the ocean that are major producers of oxygen and are the base of the marine food web. They go through periods of high mortality that are caused by infections from an increased number of parasites. There is not much information about the frequency of these parasite blooms and the loss of diatoms specifically in the Southern California region. Here, we aim to quantify the abundance of diatoms throughout the year along with the number of diatoms that have been infected by parasites by looking at ocean samples from the Long Beach coast under a microscope and recording the number of infected and non-infected diatoms from various genres. Samples were collected as two 25-ml replicates that were fixed and stained and then poured into a utermohl chamber to settle for 24 hours before being examined under a microscope. From the data collected throughout the year, there was higher parasite infection when diatom numbers were lower. Looking at the parasite infection, there were two distinct peaks that occurred at around the same time a year apart, in October 2024 with a 2.58% infection and in October 2025 with an 8.40% infection. These were also the highest peaks of infection observed throughout the year with ~121 diatom cells per milliliter in October 2024 and ~41 diatom cells per milliliter in October 2025. Additional data from a one-day cruise going from the Long Beach to open ocean showed the highest peak of percent infection, 25.58%, with a diatom count of ~7 cells per milliliter. The data suggests that parasites can be a significant source of mortality for diatoms in the marine ecosystem. Our single-day additional data supports this finding across an open water transect. It also shows that there is an annual parasite bloom in Southern California waters. Weekly diatom counts will continue to be sampled and recorded to see if there the parasite bloom is consistent or if there are other times of the year where it occurs.

This project is supported by the Sloan Pathways Program at COAST.

111. Targeting C5a Peptidase of Streptococcal Bacteria as a Target for Vaccine Development

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Group B *Streptococcus* (GBS, *Streptococcus agalactiae*) is an opportunistic, gram-positive pathogen that is often fatal in neonates and closely associated with maternal GBS vaginal colonization associated with numerous infections such as meningitis and sepsis. The current standard for preventing mother-to-newborn transmission during delivery is intrapartum antibiotic prophylaxis, such as penicillin. However, this approach significantly disrupts neonatal microbiome diversity and reduces the

abundance of essential bacteria, such as *Bifidobacterium*. Given the high global prevalence of maternal GBS colonization and the adverse impacts of antibiotic prophylaxis, there is an urgent need for nonantibiotic and vaccine-based interventions. To address this, our research aims to identify and validate such remedial strategies. Studies conducted with GBS WT and CRISPRi mutants show the importance of C5a peptidase in biofilm formation, host signals, immune evasion, and gene regulation. Further understanding of GBS pathogenesis and mechanistic insights will provide more insight on the potential of certain bacterial proteins that can be used to develop other preventative biomedical strategies for GBS colonization.

This project is supported in part by CSULB Department of Biological Sciences startup funds.

112. Testicular Development and Hepatic Oxidative Stress Assessment in Adult and Juvenile Male Cooper's Hawks (*Astur cooperii*)

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Cooper's hawks (*Astur cooperii*) are woodland-associated raptors that inhabit riparian and urbanized areas throughout Southern California. Exposure to anthropogenic and natural environmental stressors may increase hepatic oxidative stress indices in Cooper's hawks when reactive oxygen species exceed antioxidant defenses. Because environmental damage may accumulate with age, we hypothesized that indices of oxidative stress would differ between adult and juvenile hawks. Male Cooper's hawk carcasses were collected opportunistically from a local wildlife care center between October 2025-July 2026. At necropsy, male hawks were aged and categorized as adults or juveniles, and testes were removed and processed for histological analysis of seminiferous tubule size and development. Antioxidant defense and lipid peroxidation were measured in liver tissue using glutathione (GSH), superoxide dismutase (SOD), and TBARS assays. Paired testicular mass and gonadosomatic index were significantly higher in adult as compared to juvenile hawks ($p < 0.05$). The average seminiferous tubule area was $394\mu\text{m}^2$ in juveniles and $1593\mu\text{m}^2$ in adults. Body mass, wingspan, and feather length did not differ between age groups ($p > 0.05$). Similarly, levels of TBARS, GSH, and SOD activity did not differ between adults and juveniles ($p > 0.05$). Our findings suggest that variation in liver antioxidant responses and lipid peroxidation may be driven by factors other than age and testicular activity in wild Cooper's hawks.

This project was supported in part by the Dr. Theresa M. Rohr-Kirchgraber & Dr. Paul R.N. Kirchgraber Health Professions Advising Award.

113. Seasonal Changes in Ovarian Follicular Composition is Not Mirrored by Changes in Oxidative Stress Biomarkers in Female Red-tailed Hawks (*Buteo jamaicensis*)

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Red-tailed Hawks (*Buteo jamaicensis*; RTHA) are apex predators that may be vulnerable to biomagnifying impacts of environmental toxins. We hypothesized female RTHAs would show seasonal changes in ovarian function which might correlate with changes in oxidative stress. Wild hawk carcasses were collected opportunistically (7/25-6/26) from a local wildlife center, and ovarian/liver samples were collected during necropsy. Females were classified according to the historical breeding season in Southern California as collected during the reproductive (R; mid-Jan to late May) or non-reproductive (NR; June to early Jan) season. Gonadal and body mass, wingspan, feather lengths, and size of largest ovarian follicle did not differ between groups ($p > 0.05$). However, the ratio of growing follicles to non-growing ovarian follicles was higher in R compared to NR females ($p < 0.05$), and the growing follicle density trended higher in R females ($p = 0.06$). Ovaries of R hawks had lower numbers of non-growing follicles and total follicle counts ($p < 0.05$), although variation in this group was substantial and did not align with collection date, suggesting historical breeding season alone may not always accurately reflect ovarian activity. Finally, hepatic measures of oxidative stress, including lipid peroxidation, superoxide dismutase, and glutathione did not differ between group ($p > 0.05$), suggesting that seasonal changes in ovarian function may occur without corresponding changes in oxidative stress.

114. Crab population density as an indicator of condition in southern California estuaries

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Estuaries are among the most productive ecosystems in southern California and provide habitat for a range of species. Crabs as one of those wetlands species; they burrow in sediment as protection from predators and to prevent desiccation, while altering sedimentation and nutrient cycling as ecosystem engineers. We investigated

the abundance and distribution of burrowing crab species across eight southern California estuaries from 2021-2024 and evaluated the correlation between multiple abiotic and biotic factors and crab abundance. Results showed that presence of burrows was a strong indicator of crab abundance and that crabs are generally found near burrows. Crab abundance ranged widely among estuaries; the highest recorded average was 17 crabs per 1m² at Seal Beach in 2024 while two of the eight estuaries had no crabs recorded throughout all sampling seasons. To investigate correlates of population differences among estuaries, we examined habitat type, vegetation cover, presence of *Cerithidea californica* (a key prey item), sediment grain size, and the amount of time an estuary is open to the ocean. While vegetation cover and presence of *Cerithidea californica* were not correlated with crab presence, habitat type (low marsh) and sediment grain size (sandier areas) were both strong indicators of where crabs would be in the marsh. Ultimately, all abiotic and biotic factors varied greatly among estuaries, so site-specific burrow presence, sediment grain size, and the amount of time an estuary is open to the ocean should all be taken in strong consideration when evaluating crab abundance as an indicator of estuarine health. Monitoring crab population dynamics in estuaries is key to understanding estuarine condition and how they vary with time and stressors.

115. Applying Passive Acoustic Monitoring to Study Estuarine Bird Communities

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Estuaries are transitional and dynamic ecotones which support a variety of marine and terrestrial organisms. In addition to providing habitat, estuarine ecosystems yield critical infrastructure which protect coastlines as well as capture carbon, filter pollutants, and provide recreational opportunities. As coastal development, climate change, and sea level rise continue to jeopardize functional wetland systems, only a select few estuaries remain as refugia for southern California's migratory shorebird and waterfowl populations. This study examines the application of passive acoustic monitoring (PAM) and BirdNET audio processing software to monitor estuarine birds. We compared traditional bird observation techniques with PAM data, and we investigated how BirdNET confidence score thresholds affected the PAM results. We expected congruence between ground-truthed observations and PAM detections to increase with predetermined confidence score. We found that the most accurate BirdNET detections occurred between a confidence score minimum range of 0.7-0.9. Using these methods, we investigated how species composition changed over spring migration at three different estuaries. We predicted site-specific variation to drive temporal variation in species presence, with long-term migrants demonstrating the greatest variability in arrival date. We found that community composition varied

significantly across site and date, highlighting unique migratory species-site relationships. Understanding demographic variation in site usage by threatened birds can provide insight into how different population cohorts are actively reacting to changing ecosystems, allowing for informed management strategies. The results of this study provide an overview of the capabilities of PAM and a benchmark for accurately interpreting BirdNET data in southern California.

116. Automated Classification of Tail Visibility and Substrate Use of Lizards in iNaturalist Photos Using Convolutional Neural Networks

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Tail autotomy and substrate use in lizards are measurable indicators of predation risk and habitat adaptation. Studying these traits jointly across large image datasets may reveal ecological patterns and potential relationships with modern environmental changes, helping us understand animal responses in the Anthropocene. Citizen science platforms such as iNaturalist could enable such large-scale studies, but manual image labeling creates a labor-intensive bottleneck. We developed and evaluated convolutional neural network (CNN) workflows to automate two labeling tasks using iNaturalist lizard photographs: binary classification of tail usability and three-class classification of the substrate type used by lizards. Tail usability was based on its quality of visibility for assessing evidence of tail autotomy, or the voluntary loss of the tail which is an antipredator defense in lizards. It was classified as 1 when the tail was visible and of use and as 0 when the tail was not discernible. Substrate type was classified as wild/natural, artificial (human-made/alterd), or not discernible. We packaged the resulting pipeline into a browser-based application enabling researchers without programming expertise to apply the model to their own image datasets, improving accessibility and scalability. Using transfer learning with EfficientNetV2-S and DenseNet121 backbones, we compared multitask and task-specific architectures across 6 training runs, refining preprocessing, class weighting, and decision thresholds. Tail-usability class 1 F1 scores ranged from 0.47 to 0.54, and accuracy alone proved misleading, reaching 74.7% test accuracy in one run despite a class 1 F1 score near 0.41. Substrate classification was consistently stronger, reaching a final test accuracy of 87.7% and a validation macro-F1 score of 0.857. Per-class test F1 scores were 0.922 for wild/natural substrate, 0.808 for

artificial substrate, and 0.733 for not discernible substrate. Substrate classification proved reliable enough to label approximately 13,000 previously unannotated images, whereas tail-usability classification remained constrained by strict criteria, limited data, and severe class imbalance. The resulting model and web application provide a scalable approach for labeling ecological trait data from citizen-science imagery.

117. Investigating the Role of Androgen Receptors in Mouse Olfactory Preference

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Olfactory cues play an important role in regulating social behaviors in mice, and androgen receptor (AR) signaling contributes to the sexual differentiation of responses to olfactory stimuli. The testicular feminization mutation (Tfm) results in a nonfunctional AR protein, providing a model to investigate the contribution of AR signaling to sex-specific olfactory behavior. This study examined olfactory preference in middle-aged wild-type females (WTF; $n = 5$), wild-type males (WTM; $n = 8$), heterozygous females (Het; $n = 7$), and Tfm mice ($n = 3$). Mice were exposed to female-soiled (FS), male-soiled (MS), and clean bedding (CS) during an olfactory preference test. Behavioral activity was recorded and analyzed with our video tracking software (Ethovision) using distance traveled, number of visits, time spent investigating each bedding stimulus, and female-soil preference indices. Behavioral data were analyzed using two-way ANOVA with appropriate post hoc tests, while preference indices were compared against a 0.5 preference threshold. No significant differences in total distance traveled across the entire arena were observed; however, mice made more trips within activity zones containing soiled bedding than the clean-bedding zone. Tfm mice also traveled farther within activity zones than WTF and WTM mice. In the activity zones, mice visited FS more frequently than CS, while Het mice showed a preference for MS over FS. Within the bowl zones, Het and Tfm mice made more visits to MS than CS, and Tfm mice spent more time investigating FS than CS. Preference indices further revealed that Tfm mice preferred FS, whereas Het mice preferred MS. These findings demonstrate genotype-dependent differences in olfactory investigation and suggest that AR signaling contributes to sex-specific responses to social olfactory cues in middle-aged mice.

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118. Optimizing the Novel Object Recognition Test: Evaluation of Object Preferences and Preliminary Recognition Memory Performance in Mice

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To establish the novel object recognition (NOR) test in our laboratory, we first evaluated mice's preferences for candidate objects to identify suitable stimuli for this behavioral paradigm. Mice ($n = 24$), middle-aged (12.69 months), were habituated to a 30 cm $\times$ 30 cm arena for 15 min and then exposed to either two, three, or four objects positioned in the corners of the arena for 10 min. Four distinct objects were tested: a metal bottle, a glass bottle, a LEGO cat, and a LEGO dog. Mouse behavior was video-recorded and analyzed using EthoVision software, and the percentage of time spent in each corner zone was quantified. A one-sample t-test was used to determine whether the percentage of time spent in each corner zone differed from the expected value of 25%, assuming equal exploration of all four corner zones. When two objects were present, mice spent more than the expected 25% of their time in the corner zones containing the LEGO cat (32.0%) and LEGO dog (31.4%). In trials comparing a metal bottle and a glass bottle, mice showed a preference for the glass bottle (31.2%) and spent less time than expected near the metal bottle (19.5%). Time spent in the two empty corners was either consistent with the expected value or significantly lower. When all four objects were present, mice continued to show reduced interest in the metal bottle (19.5%), exhibiting greater preference for the LEGO cat, LEGO dog, and glass bottle. Similarly, with three objects present, mice spent more time than expected near the LEGO cat, LEGO dog, and glass bottle, while spending less time in the empty corner (21.3%). These findings indicate that object identity influences exploratory behavior and should be considered when selecting stimuli for NOR testing.

Based on these results, we selected two LEGO dogs and one LEGO cat for a preliminary NOR experiment. Following habituation, mice were exposed to two identical objects (LEGO dogs) during a 15-min training phase. One LEGO dog was then replaced with a LEGO cat, and mice were reintroduced to the arena for a 15-min test phase. A total of 17 mice were tested. During the training phase, 8 of 17 mice spent more than 50% of their object-investigation time exploring the two identical objects rather than the two empty corners, with an average of 66.3% of investigation time directed toward the objects. Among these mice, object investigation during the test phase accounted for 57.6% of total investigation time. Furthermore, mice spent a greater proportion of their object-investigation time exploring the novel object (63.5%) than the familiar object (36.5%).

These preliminary findings suggest that the selected objects and testing paradigm can elicit novelty preference and may be suitable for assessing recognition memory in mice. However, because only a subset of mice met the criterion for adequate object exploration during the training phase, additional testing with a larger sample size will be required to confirm the reliability and robustness of these findings and to further optimize the NOR protocol for use in our laboratory.

119. Kappa Opioid Receptor Activation Reduces Pavlovian Motivation in Adaptive Reward Seeking.

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Opioid use disorder is a chronic relapsing disorder characterized by uncontrolled drug use and reduced interest in normally rewarding activities. Opioid withdrawal is associated with reduced motivation for non-drug rewards, which might contribute to continuation of drug use. Recruitment of the dynorphin/kappa opioid receptor (KOR) system may contribute to negative affect associated with withdrawal. The Pavlovian-to-instrumental transfer (PIT) test is a behavioral procedure best suited to measure how reward-predictive cues can activate reward seeking, a measure of motivation. The exact mechanisms that contribute to withdrawal-associated changes in motivation, and the potential neural mechanisms underlying these impairments still need to be fully elucidated. We hypothesize that activating KOR, by using the selective KOR agonist U50,488, would reduce motivation measured during the PIT test, by reducing lever pressing during a reward-paired cue (CS+) relative to the pre-cue baseline. Adult Sprague Dawley rats (N = 60; 31 female, 29 male) completed Pavlovian conditioning (CS+ paired with grain pellets; CS- unpaired), and instrumental training (lever pressing for pellets, thinned from continuous reinforcement to random-interval schedules). Rats were randomly assigned to two groups, U50,488 high dose (5 mg/kg; n = 30) or low dose (1 mg/kg; n = 30), counterbalanced for sex and cue type. Rats were tested both following vehicle or U50,488 treatment. Cue-triggered lever pressing and magazine entries were measured as the change from the pre-cue baseline. U50,488 dose-dependently reduced cue-induced motivation (presses) and reward retrieval (entries), with significant effects at the high dose only. Those effects could be attributable to general suppression of activity. No sex differences were detected. Overall, these findings suggest that KOR signaling regulates cue-driven reward seeking and may contribute to reduced motivation during opioid withdrawal.

120. Self-Pollination Frequency in *Justicia sonorae* (Acanthaceae)

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Plants can self-pollinate in the wild if they have a way to move their own pollen to their stigmas and if there are no genetic barriers to self-pollination. To better understand self-pollination, we investigated *Justicia sonorae*, which grows wild in the Sonoran Desert of the United States and Mexico. Our goal was to measure the rate of self-pollination. We did so by applying different treatments to *J. sonorae* plants grown in pots at the CSULB greenhouse. We measured fruit production and seed production among the different pollination treatments. After conducting our data analyses, we found that there was no significant difference in the quantity of seeds in plants that were self-fertilized and those that were outcrossed. This suggests that *J. sonorae* may have a mixed mating system in which it is capable of producing viable fruits and seeds through either self-fertilization or outcrossing. Flowers can self either by a hummingbird transferring pollen from the same plant or corolla abscission.

121. Early Leaf Senescence Observed in the *pen1pen3* Double Mutant is not Dependent on *HIR2*, a Protein that Physically Interacts with *PEN1*

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The *pen1pen3* double mutant displays early leaf senescence that depends on salicylic acid (SA) biosynthesis, a phytohormone associated with defense and leaf senescence. *PEN1*, a Qa SNARE, physically interacts with *HIR2*, a protein that tethers immune receptors to plasma membrane nanodomains. We hypothesized that *PEN1* binding to *HIR2* may prevent immune receptor localization. Consistent with this hypothesis is the expectation that *pen1pen3hir2* mutants would show reduced early leaf senescence when compared to *pen1pen3*. We constructed the triple mutant, quantified leaf senescence, and observed early leaf senescence that was not significantly different than *pen1pen3*. This result does not support our hypothesis.

This project is supported by the CSULB Research and Scholarly Activities Award (RSCA).

122. Overexpressing *ERF54* in *Arabidopsis thaliana* Accelerates Leaf Senescence

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Leaf Senescence (LS) is a programmed degenerative process that recycles nutrients in older leaves to growing and storage tissues. The molecular process begins with the degeneration of the protein-rich chloroplasts, followed by nutrient export and eventual cell death. The *ERF54* gene, encoding a transcription factor, is predicted to be a central regulatory hub in a gene regulatory network (GRN) proposed by our lab for LS. To test the validity of the GRN, I generated *ERF54* overexpression transgenic lines. These were made via the floral dip method using *Agrobacterium tumefaciens* to insert T-DNA randomly into the *Arabidopsis thaliana* genome. The vector used was pEGG20 which includes a Ubiquitin-10 (Ubi10) constitutively-active promoter driving expression of the *ERF54* gene. The highest expression transgenic lines are OX-7 and OX-18 with about a 150 fold-increased *ERF54* expression when compared to wild type (WT). LS phenotype was tested by quantifying chlorophyll level decrease and increased expression of *SGR1*. Chlorophyll is degraded during LS while *SGR1* expression is induced. *Arabidopsis* was harvested on the day of bolting (T0) or 12 days after bolting (T12). The LS phenotype was tested using these two lines along with a WT control in plants that are kept in low light (LL) conditions or transferred to higher light (HL) intensity conditions prior to bolting. In LL OX-18 showed a significant decrease in chlorophyll compared to WT. The *SGR1* data supports this with a significant increase in expression in the T12 group. Both OX-7 and OX-18 had significantly higher *ERF54* expression when compared to WT. Both lines showed a significant decrease in chlorophyll when transferred into the HL conditions.

123. Investigating the Roles of TET8-Associated and PEN1-Associated Extracellular Vesicles During Leaf Senescence in *Arabidopsis thaliana*

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Leaf senescence (LS) is the final phase of leaf development, during which cells in older leaves undergo metabolic and structural changes that result in nutrient recycling followed by cell death. Published findings from our laboratory implicate

tetraspanin (TET) proteins, abundant residents of extracellular vesicles (EVs), as important regulators of LS in *Arabidopsis thaliana*. EVs are secreted into the leaf apoplast and comprise two characterized populations: TET8-associated EVs and PEN1-associated EVs. Zimmerman et al. (2024) demonstrated that apoplast-localized TET8, with TET3, acts as a positive regulator of LS, highlighting a potential role for TET8-associated EVs in coordinating LS. In contrast, *pen1* and *pen1pen3* mutants exhibit early LS, suggesting that PEN1-associated EVs act as negative regulators of LS. We hypothesized that overexpression (OE) of *TET8* would promote LS in *Arabidopsis thaliana*. Additionally, we hypothesized that the early senescence phenotype of *pen1pen3* would be partially reversed by the delayed senescence phenotype associated with *tet3tet8*. LS was assessed in developmentally equivalent leaves by measuring chlorophyll concentration and *SGR1* transcript abundance, normalized to *ACT2*. *TET8* transcript levels were measured to verify OE, and TET8 protein abundance in the apoplast fluid was assessed by Western blotting. *pen1pen3tet3tet8* quadruple mutants were identified by genotyping and subjected to LS phenotype analysis, alongside *pen1pen3*, *tet3tet8*, and WT plants. We observed increased *SGR1* expression and reduced chlorophyll concentration in the TET8 OE line compared with WT. The increase in *TET8* mRNA levels corresponded with increased apoplast TET8. Accelerated leaf senescence observed in the *TET8* OE line and high abundance of apoplast TET8 supports the role of TET8-associated EVs positively regulating LS. The quadruple mutant line showed a partial reversal of the early senescencing *pen1pen3* mutant by the delayed senescencing *tet3tet8* mutant. These genetic results are consistent with opposing roles for TET8- and PEN1-associated EVs in the regulation of LS.

124. The Role of NADPH Oxidases during Early and Rapid Leaf Senescence in *Arabidopsis thaliana*

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Leaf senescence (LS) is the regulated degradation process when older leaves remobilize nitrogen to developing tissues. *RbohD* (AT5G47910) and *RbohF* (AT1G64060) are plasma-membrane localized NADPH oxidases that synthesize superoxide anion ($O_2^{\bullet-}$) in the apoplast, the fluid and gas-filled space surrounding the cell wall components. The $O_2^{\bullet-}$ is then rapidly converted into H_2O_2 . Accumulation of H_2O_2 is suggested to mediate the transition into LS (Zentgraf et al., 2022), and the T-DNA insertion loss-of-function mutants *rbohD* (SALK_070610) and *rbohF* (SALK_059888) are predicted to significantly reduce apoplastic H_2O_2 production, resulting in delayed LS. The double mutant *rbohDrbohF* was predicted to delay LS

further; however, to our surprise, these plants display early and rapid LS after approximately 6 weeks of growth. The goal of this study is to determine how *RbohD* and *RbohF* protect aging leaves, and the role of H_2O_2 during LS. Chlorophyll degradation and LS-related *StayGreen1* (*SGR1*) expression analyses will be performed on WT (Col 0) and *rbohDrbohF* plants aged 36-44 days to quantify LS just before and during the rapid LS stage. Dark-induced LS (DILS) has shown that chlorophyll loss occurs at similar rates in both WT and *rbohDrbohF*, demonstrating that dark-induced LS of detached leaves is independent of *RbohD* and *RbohF*. We have obtained Arabidopsis lines containing the redox-sensitive H_2O_2 biosensor roGFP2-Orp1 localized to the apoplast (Ingelfinger et al., 2026) that allow for visualization of the apoplast under both reducing (DTT) and oxidizing (H_2O_2) conditions. We have generated roGFP2-Orp1 lines in the *rbohD* and *rbohF* single mutant backgrounds, and these will be crossed to produce *rbohDrbohF* containing the biosensor, to compare apoplastic H_2O_2 accumulation during rapid LS. These results will confirm whether apoplastic H_2O_2 is decreased in the *rbohDrbohF* mutants. A genetic approach will also be taken, resulting in three triple mutants: *rbohDrbohFore1*, *rbohDrbohFsid2*, and *rbohDrbohFein3*, to identify the hormonal and transcriptional pathways regulating rapid and early LS. SID2 (AT1G74710) is required for salicylic acid synthesis, EIN3 (AT3G20770) is needed for ethylene signaling, and ORE1 (AT5G39610) is a transcription factor that is a master regulator of LS. The *ore1* mutant has been used by a previous graduate student, and I have sequenced the insertion sites for *sid2* and *ein3* mutants, and I'm verifying reduced expression in these mutant alleles.

125. Tetraspanins and Leaf Senescence in *Arabidopsis thaliana*

Anthony Aldana* and Judy Brusslan, Ph.D.

Tetraspanins (TET) are membrane-bound, non-soluble proteins named by their four transmembrane helices. Previous studies in *Arabidopsis thaliana* have shown that TET proteins localize to the plasma membrane and extracellular vesicles (EVs) and that TET3 and TET8 promote leaf senescence (LS). TET3, TET7, and TET8 are closely related through their shared GCCK/RP motif, and EV proteomes contain TET3, TET7, TET8, and as well as the more divergent TET18 (Rutter and Innes, 2017, Koch Rutter Innes, 2020). Supporting their role in promoting LS, *myb59* mutants that display early LS have increased levels of TET8 protein in the extracellular liquid surrounding the cell wall, the apoplast, and *tet3tet8* double mutants show delayed LS (Zimmerman et al., 2024).

Higher-order tetraspanin triple mutants were created to test if a further delay of LS would be observed. *tet3tet7tet8* and *tet3tet8tet18* triple mutants were grown in high and low light conditions. Stronger LS induction is observed under high light, which

induces mild stress. We expected delayed LS in the triple mutants in both high and low light since these lines were expected to have a reduced number of EVs. LS was quantified by measuring chlorophyll loss from leaf 3 and *SGR1* mRNA induction from leaves 4 and 5. A one-way ANOVA with Tukey's HSD was used to determine significant differences. We expected delayed LS in triple *tet* mutants. We found that both triple *tet* mutants showed significantly lower *SGR1* levels and higher chlorophyll levels than WT when grown in low light indicating delayed leaf senescence. High variability in high light confounded the analysis.

126. Investigating the Role of C1q in Programming Macrophage Responses

George Alkomous* and Deborah Fraser, Ph.D.

Macrophages are innate immune cells that perform essential immune functions. C1q, a complement protein produced by macrophages, binds apoptotic cells and pathogens to initiate phagocytosis and has been shown to polarize macrophages toward an anti inflammatory M2 phenotype. This study tested whether endogenous C1q affects macrophage gene expression. Bone marrow-derived macrophages (BMDM) were isolated from wild type and C1q deficient mice, RNA was extracted and converted to cDNA, and gene expression was measured using quantitative RT PCR. *Cdh1*, a gene encoding E cadherin and associated with M2 macrophages, was reduced in C1q deficient macrophages. These findings support the hypothesis that C1q influences macrophage responses and may contribute to understanding inflammatory disease mechanisms.

127. Investigating Innate Immune Protein C1q activation of Liver X Receptor via modulation of 25-Hydroxycholesterol in macrophage foam cells

Enidh Padron* and Deborah Fraser, Ph.D.

Atherosclerosis is a chronic inflammatory disease that damages the endothelium that can lead to infiltration of monocytes/macrophages and low-density lipoproteins (LDL) into the arterial wall becoming oxidized also known as oxLDL, which is pro-inflammatory. Macrophages migrate to arterial walls, ingest oxLDL, store cholesterol as lipid droplets forming foam cells. C1q binds oxLDL in atherosclerotic lesions. Earlier studies in the lab have shown that C1q increases production of bioactive lipid, 25-hydroxycholesterol in macrophage foam cells. This is a known ligand for the liver X receptor (LXR), however the effect of C1q on LXR activation via 25-Hydroxycholesterol is not well understood. The aim of our study was to test if C1q activates the LXR through production of 25 hydroxycholesterol (25-OHC) in inflammatory macrophage foam cells. We will test the hypothesis that C1q bound to oxLDL will increase 25-OHC leading to LXR activation and improve survival in inflammatory THP-1 macrophage

foam cells. To test this, cells will be treated with different concentrations of oxLDL with and without C1q. Gene expression of LXR subunits (LXR α and LXR β) and cholesterol modifying enzyme cholesterol 25-hydroxylase (CH25H) will be measured by QPCR. LXR activation will be measured by luciferase gene reporter assay. THP-1 deficient in CH25H will be produced by CRISPR/Cas9 gene editing, and LXR activation assays will be repeated to determine the role of 25-OHC in programming macrophage responses. We predict C1q increases in 25-OHC leading to LXR activation and improved survival in inflammatory THP-1 macrophage foam cells will be absent in CH25H.

128. Global Analysis of Cancer Trends in Highly Developed Countries: Identifying Epidemiologic Outliers

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We compared incidence, prevalence, and mortality across 52 countries (reduced number on poster) for 16 cancers. We obtained cancer data from 2022 through World Health Organization's Global Cancer Observatory (GLOBOCAN). The countries were chosen based on information regarding population size, human development index (HDI), and methods used for retrieving values for mortality and incidence.

To estimate treatment effectiveness, we divided mortality by incidence (M/I) for each country. These values allow us to compare nations across cancer types. Countries that display high or low outliers in cancer rates differ in treatment effectiveness compared to countries with typical outcomes.

Our findings revealed several countries that stood out in terms of population health outcomes. For example, Japan and South Korea were the two countries that displayed a low M/I ratio in esophageal cancer compared to other areas.

Additionally, we analyzed the differences observed for the treatment effectiveness values in females versus males. For example, males appeared to be treated less effectively than females for thyroid cancer in the European region as shown by their higher M/I ratios.

Identifying good treatment effectiveness values (i.e., low values) highlight nations using practices that should be studied and possibly emulated. Identifying poor treatment effectiveness values (i.e., high values) highlight nations using non-ideal practices that should potentially be changed. Recognizing large discrepancies between female and male rates suggest the presence of sex bias which should be

investigated to identify if this arises from biological factors or societal ones (i.e., sexism).

129. Gel Conditions and Temperature Highlight Individual Variation in Bisphenol A Genotoxicity in Male Mice

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Bisphenol A (BPA)-induced stress is known to disrupt the hydrogen bonding framework of chromosomal DNA, yet the precise in vitro kinetics of strand denaturation and subsequent reannealing in specialized mammalian tissues remain difficult to isolate without optimized matrix conditions. This study investigated the structural impacts of thermal stress on genomic DNA extracted from male mice pancreatic tissues (C57BL/6J strain) using optimized agarose gel electrophoresis. To assess denaturation and reannealing dynamics, two mice DNA samples were heated to 100°C for strand separation and rapidly cooled to 0°C across varying durations. Methodological optimization was conducted over three separate trials to refine agarose concentration, voltage, and running time. Initial trials yielded poor resolution and fragile matrices due to low agarose concentrations, uneven sample loading, and outdated reagents. Methodological troubleshooting resolved these limitations, establishing an optimized protocol utilizing a stable 1% agarose gel run at 50V for four hours. The optimized gel run provided enhanced clarity, revealing distinct differences between control and experimental samples. Untreated controls consistently exhibited prominent, high-molecular-weight bands near the top of the gel, indicating that the baseline chromosomal DNA remained intact and that extensive fragmentation did not occur during extraction. In contrast, temperature-treated samples demonstrated inconsistent variations in band intensity and migration patterns. Current data we collected will be used to solidify the standard measurements and conversions for future sexual dimorphism projects in DNA damage detection.

This project was supported by the UROP/BUILD program, CSULB Mini-Grants and Summer Stipends (MGSS) Grant and the KURE program.

130. A Portable, Low-Cost Smartphone-Optimized Paper Device for Colorimetric Bisphenol A Detection

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Bisphenol A (BPA) is a molecule found in various plastics, including water bottles, food containers, thermal paper, and more. BPA can enter the human body through several factors, such as physical contact, ingestion, and inhalation. This molecule has a negative effect on the human body, affecting organs such as the liver, heart, and male/female reproductive systems. Due to the research on the effects of BPA, detection methods for this molecule have grown increasingly popular. Our goal for this project is to create a low-cost, accessible, and portable device that can detect BPA. To do so, we have created a wax-printed microfluidic paper-based device coupled with the Emerson reaction to detect the molecule. The Emerson reaction is a colorimetric detection method and was used to visualize whether a sample contained any amount of BPA. This reaction occurs when BPA is oxidized by potassium ferricyanide and then bonded to 4-aminoantipyrine (4-AAP), turning from a faint yellow color to an orange/red hue. So far, four prototypes have been made to see which one would show the color change the best. The devices were first designed in Adobe Illustrator, then printed using a wax printer. All four devices were able to detect BPA at a concentration of 100ppm, but two out of the four showed the color change better. New device (ND) 1 and ND 2 particularly showed the orange color better and were easier to capture on a smartphone camera for analysis. Runtimes of each experiment were recorded, and the mean grey value of each run was obtained via ImageJ. We successfully developed a brand-new BPA-detection device and hope that in the future, this device will become accessible to the public as a tool to detect BPA in their daily lives.

This project was supported by the UROP/BUILD program, CSULB Mini-Grants and Summer Stipends (MGSS) Grant.

131. Deciphering Domain-Specific Interactions of Endocrine disruptor Bisphenol A with the Human Androgen Receptor

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Bisphenol A (BPA) is a ubiquitous environmental contaminant and well-documented endocrine-disrupting chemical (EDC) capable of interfering with human androgen receptor (AR) signaling pathways. Despite its known toxicological profile, most computational investigations into BPA-AR binding dynamics restrict their analysis exclusively to the canonical ligand-binding domain (LBD), a widespread limitation that stems primarily from the historic absence of an experimentally resolved, high-resolution structural model for the full-length human androgen receptor (hAR). Because hAR operates as a complex, multi-domain protein—comprising a variable N-terminal domain (NTD), a conserved DNA-binding domain (DBD), and the C-terminal LBD—intricate inter-domain and intra-domain interactions are structurally critical to its overall conformation, stability, and functional activation. To overcome this structural data gap, this study leveraged the state-of-the-art machine learning algorithm AlphaFold3 to predict a high-fidelity, full-length tertiary structure of hAR, enabling comprehensive, comparative molecular docking simulations of BPA across both the full architectural context and its isolated individual domains. In silico docking trials were executed utilizing AutoDock Vina to evaluate binding affinities and spatial configurations, followed by detailed structural analysis and visualization within UCSF Chimera. Comparative binding energy calculations revealed that BPA binds with significantly higher affinity and greater structural stability to the full-length hAR complex than to any of its isolated, truncated domains, suggesting that the broader intra-domain environment and global structural context play an indispensable role in stabilizing non-canonical ligand interactions. Ultimately, these findings underscore the limitations of conventional single-domain docking paradigms and highlight the necessity of implementing full-length receptor models to accurately capture the nuanced molecular mechanisms driving environmental endocrine disruption.

This project was supported by the UROP/BUILD program, CSULB Mini-Grants and Summer Stipends (MGSS) Grant and the KURE program.

132. Exploring Novel Bisphenol A Interactions with Full-Length Human Estrogen Receptor Alpha Using Molecular Docking

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Bisphenol A (BPA) is an endocrine-disrupting chemical that can interfere with normal estrogen signaling. Human estrogen receptor alpha (ERα) regulates estrogen-dependent gene expression and is one of the receptors that BPA can interact with.

Many experimental ER α structures only represent specific regions of the protein, such as the ligand-binding domain (LBD). This project investigated whether using a full-length ER α model could help identify potential BPA interactions other than the known LBD binding sites. The full-length human ER α structure was predicted by using AlphaFold 3 and the known LBD was compared with the experimental ER α structure PDB 1A52 for validation. UCSF ChimeraX and Meeko were used to prepare the receptor and ligands, and molecular docking was performed using AutoDock Vina. Estradiol was used as a reference ligand and had a best predicted binding affinity, and BPA had a relative strong affinity within the LBD as well. Additional docking using the full-length ER α model identified a potential BPA interaction near the DNA-binding domain/hinge region with a mid-range of affinity and in the C-terminal region. These results suggest that using a full-length ER α model may help identify potential BPA interaction sites other than the known LBD. This full-length docking approach may help future studies explore how BPA interacts with regions outside the known ligand-binding domain and better understand its potential effects on estrogen receptor signaling.

This project was supported by the UROP/BUILD program, CSULB Mini-Grants and Summer Stipends (MGSS) Grant and the KURE program.

133. Investigating the roles of specific cyclins in the dissemination of Ras^{V12}-driven tumor cells in *Drosophila melanogaster*

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Tumor cell dissemination is the initial step of cancer metastasis, which is responsible for the majority of cancer-related deaths. However, the molecular mechanisms that drive dissemination remain poorly understood. To study this process in vivo, we induced oncogenic Ras^{V12} in *Drosophila* intestinal stem cells, which undergo morphological changes to breach the extracellular matrix and visceral muscle to disseminate. Cyclins, best known for regulating the cell cycle through Cyclin-dependent kinases (Cdks), can also regulate other processes, such as transcription. Through a candidate-based RNAi screen of cell-cycle and transcription controlling cyclins, we found that knockdown of cell-cycle cyclins (Cyclin D and Cyclin E) did not noticeably alter tumor dissemination, whereas knockdown of the transcription controlling cyclins (Cyclin T and Cyclin K) resulted in cell retention in Ras^{V12}-induced tumors. These findings indicate that specific cyclins may differentially regulate Ras^{V12} tumor behavior compared to cell-cycle cyclins, highlighting an underappreciated role of transcriptional cyclins in tumor progression.

134. Metabolic and Epigenetic Control *Ras*^{V12} Tumor Cell Dissemination Through Methionine Cycle Regulation

Sema Hammoudeh*, Alan Vu, and Dr. Jiae Lee

Dissemination is the first critical step in the progression of cancer to a metastatic state, causing the majority of cancer deaths. However, the basic cellular activities responsible for tumor cell migration remain undefined. To understand the cellular mechanism, we drive oncogenic *Ras*^{V12} in *Drosophila* intestinal stem cells (ISCs) to examine these early events in a genetically modifiable in vivo system, and observe directly how malignant cells break through the extracellular matrix and the visceral muscle, and subsequently disseminate throughout the organism. Adenosine kinase is a phosphotransferase that converts adenosine into AMP, linking the adenosine cycle to methionine cycle balance. We have found that Adk3 knockdown by RNA interference reduced dissemination of tumor cells. SAME is a methyl donor commonly used as a dietary supplement and contributes methyl groups to DNA. We fed SAME to flies expressing *Ras*^{V12} with Adk3 knockdown in tumor cells to determine whether tumor cells can overcome the knockdown phenotype. We also supplemented flies with adenosine to clarify the role of extracellular adenosine in tumor cell dissemination, and performed adenosine receptor knockdown to further assess how extracellular adenosine might function as an epigenetic signal during dissemination. Collectively, our study highlights how Adk3, Adenosine-Receptor transcription, SAME availability, and extracellular adenosine influence tumor cell dissemination, paving a path toward genetic strategies that can drive the next generation of cancer therapeutics.

135. IRE1-Dependent Unfolded Protein Response Signaling Contributes to Sodium Salicylate Chemoprevention in a *Drosophila* Model of Colorectal Cancer

Hiep Vu Hoang Nguyen*, Amber Peek, Jiae Lee Ph.D., Deepali Bhandari Ph.D.

Colorectal cancer (CRC) remains a major cause of cancer-related mortality, highlighting the need for effective chemopreventive strategies. Epidemiological studies have associated aspirin use with reduced CRC incidence, but the mechanisms underlying this protective effect remain incompletely understood. To investigate salicylate-mediated chemoprevention in vivo, we used a *Drosophila* model in which oncogenic *Ras*^{V12} is expressed in intestinal stem cells, inducing rapid tumor-like proliferation. Flies were treated with sodium salicylate (NaSal) at varying doses and durations before *Ras*^{V12} induction. NaSal pretreatment significantly reduced intestinal tumor proliferation and helped preserve the integrity of the visceral muscle layer, which is disrupted during tumor progression. To determine whether the unfolded protein response (UPR) contributes to this effect, we depleted IRE1—the

most evolutionarily conserved UPR sensor—using RNA interference. IRE1 knockdown substantially reduced the protective effects of NaSal, resulting in less suppression of tumor proliferation and tissue damage. Together, these findings demonstrate that NaSal has chemopreventive activity in a *Drosophila* model of CRC and suggest that this activity depends, at least in part, on IRE1-mediated UPR signaling. These results provide new insight into a potential mechanism by which salicylate-based compounds may suppress early intestinal tumor development.

Thanks to Our Industry Guests

We extend our sincere gratitude to our invited industry guests for joining us at this year's symposium. Thank you for investing your time to interact with our students and faculty, and we look forward to the career opportunities and collaborations that lie ahead.

California Air Resources Board (CARB)

CARB's mission is to promote and protect public health, welfare, and ecological resources through effective reduction of air pollutants while recognizing and considering effects on the economy. CARB is the lead agency for climate change programs and oversees all air pollution control efforts in California to attain and maintain health-based air quality standards.

City of Long Beach

Long Beach boasts a thriving economy supported by industries such as aerospace, education, health services, manufacturing, and professional services. With over 500 diverse job opportunities across 23 departments, we offer a wide range of career paths for every passion and skill set—whether you're starting your journey or advancing your profession. We're committed to helping you grow through career pathways, mentoring, and development programs so you can build a meaningful career while making a real impact on our community.

Maglut Heavy Industries

Maglut Heavy Industries is a Long Beach-based advanced manufacturing start-up developing a sustainable processing engine for rare earth elements. The company adapts biotech-inspired chromatography and proprietary resins to produce 99.9%+ pure rare earth oxides at scale. By utilizing a water-based system that eliminates toxic solvents, Maglut provides clean, resilient supply chains for defense, semiconductors, and energy infrastructure.

Mako Advanced Materials / PTM&W Industries Inc.

MAKO Advanced Materials and PTM&W Industries Inc. create a unified U.S. network for high-performance composite materials, resins, and tooling. This integration enhances PTM&W's ability to serve key industries such as aerospace, defense, automotive, marine, sporting goods, and industrial applications, while also expanding R&D, production efficiency, and technical support.

RTX

RTX is a team of explorers united in the goal to push the boundaries of known science – and solve the world's most complex problems. They are advancing aviation, building smarter defense systems and creating innovations to take us deeper into space.

Support Our College

Support for the [Laura Kingsford CNSM Student Research Symposium](#) was made possible by the thoughtful generosity of John E. Clark, friend of the university.

To celebrate today's event, individuals and organizations can make a tax-deductible contribution to the [Laura Kingsford CNSM Student Research Symposium Endowment](#)— or any of the college's funds or initiatives by visiting [Give to CSULB](#). Supporting CNSM enables the success of its student-centered, community-focused, discovery-driven model.

Join us in our mission is to nurture a vital pipeline of diverse scientists and mathematicians who will contribute to major advances in medicine, technology, and solutions to society's most pressing problems. As a donor you play a crucial role in every student's success.

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If you have any questions about how you can support our students or would like to speak about making a gift, please email me at Christina.Hall@csulb.edu or call 562-985-1780 (voice only).

Thank you,

Christina Hall
Director of Development

P.S. For more information about how to send a gift, please visit csulb.edu/give.