THURSDAY AFTERNOON **SORTED BY NUMBER**

Poster #	Presenter	Topic	Title	Author(s)	Abstract
1	Jianying Zhang, PhD	Basic Life Science	Stem Cell Mechanobiology in Relation to Tendon and Plantar Fascia Disorder	Jianying Zhang, PhD; Feng Li, PhD; Daibang Nie, PhD; Kelly Williamson, PhD; James H-C. Wang, PhD	Tendinopathy, a prevalent tendon disorder, affects millions of Americans and costs billions of health care dollars every year. Current clinical treatments for tendinopathy are largely palliative because the precise cellular and molecular mechanisms of the tendon disorder are not clear. It is known that stem cells play an important role in tissue repair and regeneration. Histological analysis found some bony, fatty, and cartilage tissues in the tendinopathy tendon tissues. However, whether the aberrant differentiation of tendon stem/progenitor cells (TSCs) into non-tenocytes caused tendinopathy is unclear. A mouse model of tendinopathy was set up by removing the native tendon cells with irradiation, injecting GFP-TSCs, and treating with intensive treadmill running (ITR) for four weeks. Non-tenocytes were determined by histological analysis. The results showed that intensive mechanical loading induced TSCs to differentiate into adipocytes, osteocytes, and chondrocytes; however, moderate mechanical loading didn't cause non-tenocyte differentiation of TSCs. Human plantar fascia (PF) contains membrane-like tissue formed sheath part (PF-S) and ligament-like tissue formed core part (PF-C). PF-S cells grow faster, formed larger colony, express more stemness, collagen IV, CD31 and CD34, multi-differentiation potential, and less collagen I than PF-C cells. ITR induced PF-S cells to produce more IL-6 and PGE2 than PF-C cells.
2	William Barrington, MS	Basic Life Science	Determining the Mechanisms and Biological Effects of Ultrasound Targeted Microbubble Cavitation on Endothelial Cell Permeability in the Blood Brain Barrier	William Barrington; Jianhui Zhu; Xucai Chen; Flordeliza S. Villanueva	
3	Yuzhao Huang	Basic Life Science	Enhancing Regenerative Potential of Chondrocytes by Selectively Removing Senescent Cells via Apoptosis	Yuzhao Huang, MD; Rocky S. Tuan, PhD; Hang Lin, PhD	Nowadays the clinical outcome of autologous chondrocyte implantation(ACI) is variable, and the quality of chondrocytes may account for one of the major reasons. In order to collect a sufficient number for transplantation, healthy chondrocytes from patient will undergo a long time *in vitro* expansion, which would lead to a increasing number of senescent cells, and may adversely affect the quality of chondrocyte. FOXO4-DRI, a FOXO4 peptide, was reported to selectively kill the senescent cells. Therefore, we hypothesized that FOXO-DRI could selectively remove the senescent cells in chondrocytes and enhance the regenerative potential of chondrocytes. In this study, chondrocytes were isolated from healthy donors with IRB approval. To simulate *in vitro* expansion for ACI, cells were expanded to population doubling level (PDL)3 (early passage) and PDL9 (ready for implantation), and then treated with FOXO4-DRI (at 25μM) for 5 days. Followed by analysis of chondrocytes function and senescence. Our results showed that chondrocytes for ACI exhibited a higher level of cellular senescence as a result of replication during *in vitro* expansion, and the treatment of FOXO4-DRI was able to selectively kill senescent cells in PDL9, which reduced the SASP in chondrocytes, enhanced their proliferation capacity, and led a cartilage formation with superior quality.
4	Zixuan Lin	Basic Life Science	Human iPSCs-Derived Osteochondral Tissue Chip to Model the Pathology of Osteoarthritis	Zixuan Lin, MD; Zhong Li, PhD; Xinyu Li; Hang Lin, PhD	Osteoarthritis (OA) is a common joint disease, which causes pain and immobility. To date, there are no efficacious treatments able to retard the progression of OA. The lack of disease modifying OA drugs (DMOADs) may be the function of incongruence between *in vitro* models of OA and the pathogenesis *in vivo* , and between disease mechanisms in humans and model animals. To overcome these issues, we developed tissue chips *in vitro* that functionally represented the osteochondral tissue directly affected by OA. Compared with MSCs, induced pluripotent stem cells (iPSCs) are a better source of cells, since they exhibit an almost unlimited proliferative capacity in culture and maintain their pluripotent potential to differentiate into all MSC lineages. In this study, iPSCs were first differentiated into MSC-like cells (iMPCs) and then differentiated into cartilage and bone tissues in customized bioreactors. Chondrogenic medium was perfused onto the construct through the top flow, and osteogenic medium was perfused on the bottom. After 28 days, bi-phase osteochondral tissues were successfully created, which were confirmed by real-time PCR and histology. Osteoarthritic osteochondral tissue will be generated to simulate the pathological process, which provides a good platform to examine the efficacy of several potential DMOADs under disease-like condition.
5	Michelle Elise Spicer, MS	Basic Life Science	Seeing Beyond the Trees: A Comparison of Tropical and Temperate Plant Life Forms and Their Vertical Distributions	Michelle Elise Spicer, MS; Hannah Mellor, BS; Walter P. Carson, PhD	Structural traits of forests can drive major differences in ecological functioning, as well as create nuanced implications for biodiversity conservation among biomes. However, large-scale comparative studies in forest diversity rarely encompass the entire vascular plant community (they focus only on woody species) or have any three-dimensional component. Here, we demonstrate the importance of including these physiognomic data (the type and heights of plants) in forest diversity studies by rigorously quantifying the distribution of vascular plant species among five major growth forms (trees, shrubs, lianas, herbs, and epiphytes) and five vertical forest strata (forest floor, understory, subcanopy, canopy, and emergent). Our physiognomic comparison of nine tropical and nine temperate forests from the New World clearly illustrates a previously unquantified fundamental difference between these two forest biomes: where in the vertical forest profile plants become reproductive, and what life forms are most speciose. Overwhelmingly, our data from >3,400 species show that herbs on the forest floor make up the vast majority (80%) of eastern deciduous forest species, whereas Neotropical forest plant species are more evenly distributed among life forms and vertical strata. We suggest that herbaceous plants, whether terrestrial or aerial (epiphytes), have been understudied relative to their contribution to forest diversity.
6	Ray Bowman	Basic Life Science	Alpha-Arrestin Regulation of Autophagy Identified Through Screening of the *Saccharomyces cerevisiae* Ubiquitin Interactome (Scubi) Library	Ray Wesley Bowman; Karandeep Chera; Allyson F. O'Donnell	Cells respond to cues in their extracellular environment by selectively redistributing proteins. This reorganization is imperative for cell survival and is regulated, in part, by alpha-arrestins. How, then, is alpha-arrestin-mediated trafficking controlled? We know that modification by ubiquitination plays a role in modifying alpha-arrestin function. To help us identify specific alpha-arrestin regulators, we generated and utilized a unique yeast gene deletion library called the Saccharomyces cerevisiae Ubiquitin Interactome (ScUbI) library. ScUbI contains all the nonessential genes annotated as important for ubiquitination/ubiquitin interaction. The ScUbI library was transformed with plasmids over-expressing alpha-arrestins Aly1 and Aly2, then assessed for gene deletions that either increased or decreased cells' sensitivity to rapamycin, an inhibitor of TORC1 function that mimics nitrogen starvation. Students initially chose Atg7 for follow up analysis and demonstrated that in atg7Δ cells Aly1 and Aly2 electrophoretic mobility is altered. This mobility shift is due to hyper-phosphorylation of the alpha-arrestins in the absence of Atg7 and our preliminary data suggest that Atg1, the kinase needed to initiate autophagy, is required for this alpha-arrestin phosphorylation. These and additional data support an exciting novel role for alpha-arrestins as regulators of autophagy, which expands on their known function in sensing and responding to nutrient stress.

Poster #	Presenter	Topic	Title	Author(s)	Abstract
7	Mairobys Socorro, DDS, PhD	Basic Life Science	Opposing Effects of Inorganic Phosphate and Trps1 Transcription Factor on Expression of SerpinB2 in Bone and Tooth	Mairobys Socorro, DDS, PhD; Apurva Shinde; Daisy Monier; Sana Khalid, BDS, MSc, PhD; Victoria Smethurst, MS; Dobrawa Napierala, PhD	Inorganic Phosphate (Pi) is essential for normal skeletal and dental mineralization. This function is accomplished, in part, by regulating expression of genes involved in this process. Besides the classic Pi-responsive genes to be upregulated in osteogenic cells, we identified SerpinB2 as one of the novel genes vastly upregulated by Pi. Interestingly, this gene has never been implicated in formation nor homeostasis of mineralized tissues. SerpinB2 gene codes for plasminogen activator inhibitor-2 (PAI-2), a protein that is widely studied in the context of immunity and cancer. Moreover, SerpinB2 is one of the most upregulated proteins following cellular stress. In this study, we analyzed *in vivo* expression of SerpinB2 in bone and tooth. Additionally, we compared expression of SerpinB2 in WT and transgenic mice overexpressing Trps1 specifically in osteoblasts and odontoblasts (Col1a1-Trps1 mice). To accomplish this, skeletal and dental tissues were analyzed at different developmental stages. Immunohistochemical detection of SerpinB2 in alveolar bone and tooth uncovered that this protein is highly expressed not only in endothelial cells, but also in cells producing mineralized ECM. In summary, we identified that SerpinB2 is highly and specifically expressed by cells producing mineralized ECM, and showed that SerpinB2 is upregulated by Pi and repressed by Trps1.
8	Murugesan Velayutham, PhD	Basic Life Science	Generation of Superoxide Radical by Human Cytochrome b5 Reductase Is Modulated by Cytochrome b5	Murugesan Velayutham, PhD; Eric Cecco, BS; Sruti Shiva, PhD; Mark Gladwin, MD; Courtney Sparacino-Watkins, PhD	Previous studies have demonstrated that NO production by the NADH, cytochrome b5 reductase (CYB5R), cytochrome b5 (CYB5), and mitochondrial amidoxime reducing component system is quenched by oxygen (O2) and suggested that superoxide radical production was involved. However, the direct formation of superoxide radical by human CYB5R had not been studied. Here, electron paramagnetic resonance (EPR) spin trapping studies using 5,5-dimethyl-1-pyrroline-N-oxide (DMPO) were performed with CYB5R and NADH. An EPR spectrum corresponding to the superoxide radical adduct of DMPO (DMPO-OOH) was obtained. The amount of DMPO-OOH formed from the oxidation of NADH by the CYB5R increased with NADH concentration. This EPR signal was quenched by the addition of the SOD1 or CYB5. Further, the NADH consumption was observed in the absence of O2 using UV-Vis spectroscopic technique. The rate of NADH consumption increased with increasing concentrations of CYB5R. Our results demonstrate that human CYB5R catalyzes the O2 dependent oxidation of NADH to generate superoxide radical. Additionally, CYB5 can possibly protect biological targets from oxidative damage, by inhibiting superoxide radical production by CYB5R. This study shows that the ability of CYB5R to catalyze superoxide radical production has potential pathophysiological implications for the ischemia/reperfusion induced damages, endothelial dysfunction, and cardiovascular and neurological diseases.
9	Ryan Phillips, PhD	Basic Life Science	Simulating Pharmacological Blockade of Persistent Sodium Currents in Respiratory Circuits	Ryan Phillips, Jonathan Rubin	The mechanism(s) of action of most commonly used pharmacological blockers of voltage-gated ion channels are well understood; however, this knowledge is rarely considered when interpreting experimental data. Effects of blockade are often assumed to be equivalent, regardless of the mechanism of action of the blocker involved. Using computer simulations, we demonstrate that this assumption may not always be correct. We simulate the blockade of persistent sodium current (INaP), thought to be central for rhythm generation in pre-Bötzinger complex (pre-BötC) respiratory neurons, via two distinct pharmacological mechanisms: (1) pore obstruction mediated by tetrodotoxin and (2) altered inactivation dynamics mediated by riluzole. Our simulations predict that *in vivo* , riluzole but not tetrodotoxin will fail to effectively block INaP in the pre-BötC and to stop respiratory rhythm generation. These simulations support a critical role for INaP in respiratory rhythmogenesis *in vivo* and illustrate the importance of mechanism when interpreting and simulating data relating to pharmacological blockade.
10	David Macar, MA	Basic Life Science	Alpha-Arrestin Regulation of Protein Trafficking: Leveraging Evolutionary Rate Covariation to Define Protein Trafficking Regulatory Networks	David A. Macar; Tova Finkelstein; Abdullah Malik; Alexiy Nikiforov; Hilary Serbin; Zelia Ferreria, PhD; Nathan Clark, PhD; Allyson F. O'Donnell, PhD	The trafficking of membrane proteins is widely regulated by ubiquitination, which can stimulate trafficking. Many membrane proteins lack the binding motifs needed to interact with ubiquitin ligases. Instead, protein trafficking adaptors, like the alpha-arrestins, serve as bridges between ligase and membrane cargo proteins to control trafficking. What dictates the alpha-arrestin and membrane protein interaction and what classes of membrane proteins are controlled by alpha-arrestins? The answers are unclear, as few membrane cargos are known to be controlled by the alpha-arrestins. To expand the repertoire of alpha-arrestins-membrane cargo protein associations, we took a computational approach called Evolutionary Rate Covariation(ERC). Proteins that share a common function likely share a selective pressure and evolve at similar rates. We performed ERC analyses on the yeast alpha-arrestins, filtering our data for transmembrane domain proteins. Changes in abundance or localization of GFP-tagged cargos between wild type cells or cells lacking alpha-arrestins are indicators the trafficking of these cargos is alpha-arrestin-dependent. Using this approach, we have confirmed 46 new cargos controlled by the alpha-arrestins. We are currently using bimolecular fluorescence complementation to assess *in vivo* association of alpha-arrestins with cargo proteins. ERC is a powerful tool to define networks, undoubtedly of interest to the cell biology community.
11	Chia-Hsin Liu, MD	Basic Life Science	LPS Mediated Chronic Inflammation Promotes Cigarette Carcinogen NNK-Induced Lung Tumorigenesis Associated with Th1/IL17A Signaling Pathway	Chia-Hsin Liu, MD; Kong Chen; Y. Peter Di, PhD	Chronic obstructive pulmonary disease (COPD) is an independent risk factor for lung cancer that is characterized by chronic airway inflammation. However, the mechanisms in linking chronic lung inflammation and tumorigenesis remain unknown. We have established a murine lung cancer model to elucidate this mechanism by treating mice with or without recurrent lipopolysaccharides (LPS) in combination with nitrosamine 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone (NNK). The LPS/NNK combined treatment significantly increased lung tumor number, tumor incidence, and tumor burden compared to NNK treatment alone. In addition, the inflammatory cell counts in the bronchoalveolar lavage (BAL), especially those of the lymphocytes and neutrophils, significantly increased in the LPS/NNK treatment group. The BAL fluid of chemokines/cytokines, as analyzed by luminex assays, revealed higher levels of GM-CSF, G-CSF, MIP-1□, IL1-□, IL-6, CXCL10, IL-17A, and KC in LPS/NNK than in NNK treatment. Flow cytometry analysis of the mouse lung tissue revealed significantly increased CD4+Th1, Th17, Treg, M-MDSC, and G-MDSC expression in LPS/NNK treatment compared to NNK treatment alone. Ingenuity pathway analysis of differential genes between LPS/NNK and NNK treatment showed upregulated Th1 and IL-17A signaling pathway. Our results suggest that LPS-induced chronic inflammation likley promote NNK-induced lung tumorigenesis through Th1- and IL17A-mediated inflammation with immune suppression in the tumor microenvironment.
12	Jonathan Florentin, PhD	Basic Life Science	Interleukin-6 Mediated Mobilization of Neutrophils in Pulmonary Hypertension Depends Upon CX3CR1 Expression	Jonathan Florentin, PhD; Jingsi Zhao; Yi-Yin Tai; Stephen Y. Chan, MD, PhD; Partha Dutta, DVM, PhD	Myeloid cells, such as neutrophils, are important in disease pathogenesis. Neutrophils are produced in the bone marrow (BM) in high quantity in vascular diseases like pulmonary hypertension (PH). Egress of newly generated neutrophils into the lungs results in inflammation and remodeling of pulmonary arterioles. However, the mechanisms of neutrophil egress from the BM in disease conditions are poorly understood. Using multicolor flow cytometry, we observed an increased number of neutrophils in the lungs of hypoxic mice and PH patients. Concomitantly, the lungs and blood of PH patients contained high levels of IL-6. Transgenic mice overexpressing IL-6 (Tg(+)) had exaggerated recruitment of neutrophils in the lungs. Additionally, these mice had exacerbated lung remodeling and right ventricular systolic pressure (RVSP), which are features of PH pathogenesis. To investigate how IL-6 increases egress of neutrophils from the BM, we discovered that this cytokine increases CX3CR1 expression in neutrophil. BM chimeric mice deficient of CX3CR1 in hematopoietic cells had significantly reduced number of circulating and lung neutrophils but increased neutrophil retention in the BM, indicating the importance of CX3CR1 in neutrophil egress. Additionally, Tg(+) mice lacking CX3CR1 had fewer neutrophils in the blood and lungs and had significantly diminished pulmonary remodeling and RVSP.

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13	Weiqi Zhang	Basic Life Science	Differential *In Vivo* Effects Of Hepatoblastoma-Associated Beta-Catenin Mutations	Weiqi Zhang, MDc; Huabo Wang, PhD; Jennifer Meyfeldt, MD; Sucheta Kulkarni, PhD; Jie Lu, MS; Edward V. Prochownik, MD, PhD	
14	Sarah Sokol	Basic Life Science	Stress Sensitivity in *Toxoplasma gondii* is Linked to its Uniquely Flexible Life Cycle	Sarah L. Sokol; Zhee Sheen Wong; J.P. Dubey; Jon P. Boyle	*Toxoplasma gondii* , a highly successful and globally ubiquitous pathogen, possesses a uniquely flexible two-host life cycle that differs from the obligate two-host life cycle employed by many eukaryotic parasites. *T. gondii* 's success can be attributed to these flexibilities because it enables transmission between multiple intermediate hosts (via asexual reproduction), creating a bypass for sexual reproduction. To better understand this phenomenon, we compared life stage progression and stress induced development in *T. gondii* and its closest relative, *Hammondia hammondi* , with which it shares ~97% of its genes in perfect synteny. We found that *H. hammondi* followed a strictly regulated developmental progression with unique life stages. Furthermore, we found that early life stages of a *H. hammondi* infection were refractory to stressors that induce tissue cyst formation in *T. gondii* . However, when we applied stressors later in development, *H. hammondi* displayed susceptibility resulting in approximately ~20% tissue cyst formation. Together, these data suggest that a link exists between life stages and the ability to respond to specific stressors. Our future work will investigate transcriptional differences between *T. gondii* and *H. hammondi* at critical developmental time points and will be used to elucidate genetic factors contributing to life cycle flexibility in *T. gondii* .
15	John Goté, MS	Basic Life Science	Solutions to the Extreme Miniaturization of a Visual System in Jumping Spiders	John Goté, MS; Patrick Butler, BS; Daniel Zurek, PhD; Annette Stowasser, PhD; Elke Buschbeck, PhD; Nathan Morehouse, PhD	While adult jumping spiders rely on their visual abilities to analyze complex courtship displays, avoid predators, and stalk prey, it's not well understood how juveniles cope with structural modifications of their visual system as they mature. These growing animals are orders of magnitude smaller than their adult counterparts, but display many of the same visually guided behaviors. We are specifically interested in how these eyes adapt across a lifespan to deal with size limitations in youth while maintaining high visual performance. We investigate developing eye morphology in the jumping spider *Phidippus audax* through various methodologies. Focusing on the lens structure, maturing jumping spiders display proportionally larger eyes, indicating negative allometric growth. Novel ophthalmoscopic imaging techniques reveal that anterior lateral eyes contain near constant photoreceptor cell numbers across development, and these cells differentiate growth based on their location within the retina, as shown through histological sectioning. Measures of visual performance are surprisingly retained, with no significant changes between field of view or spatial acuity across lifespans. This is hypothesized to be maintained by changes to optical function. As the lens and retinal structures move away during morphological development, focal length also increases and appears to correct for these structural changes.
16	Deepa Kumari, MSc	Basic Life Science	Investigating the Roles of Molecular Chaperones During the Endoplasmic Reticulum Associated Degradation of a Cholesterol Transporting Lipoprotein	Deepa Kumari; Jeffrey L. Brodsky, PhD	Coronary artery disease (CAD) kills 17.3 million people worldwide every year, and elevated levels of apolipoprotein B (ApoB) are a major risk factor for CAD. ApoB is the primary component of atherogenic lipoprotein particles and is regulated by Endoplasmic Reticulum Associated Degradation (ERAD). Current CAD treatments include statins and a drug that directly targets ApoB, but side effects and/or the cost limit their efficacy and availability. We propose that a better understanding of the mechanism of ApoB regulation will lead to the isolation of new therapeutics to help combat CAD. To better define the mechanism of ApoB regulation and degradation in the ER, we investigated if Hsp40 chaperones regulate the ERAD of ApoB. In yeast and mammalian cells, we discovered that Ydj1/DNAJA1, a cytosolic Hsp40, associates with ApoB and facilitates its degradation. Furthermore, knockdown of DNAJA1 in a rodent cell line causes the accumulation of ubiquitinated ApoB, which resides in a membrane-associated fraction. We, therefore, hypothesize that DNAJA1 binds and maintains the solubility of ApoB prior to degradation. Elucidation of novel regulators of ApoB biogenesis, such as DNAJA1, broadens the avenue for the development of better therapeutic targets to treat CAD.
17	Anne Beethe, MA	Basic Life Science	Lower Extremity Motor Evoked Potential Latency as a Biomarker for Warfighter Fatigue: Preliminary Data	Anne Z. Beethe, MA; Felix Proessl, MS; Adam J. Sterczala, PhD; Courtenay Dunn-Lewis, PhD; Christopher Connaboy, PhD; Bradley Nindl, PhD; Shawn D. Flanagan, PhD	Transcranial magnetic stimulation (TMS) noninvasively characterizes corticospinal system function, inducing successive excitatory volleys observed as motor evoked potentials (MEP). MEP latency is a relatively stable measure, providing evidence of differences in direct and transcallosal pathways, with longer latencies indicative of stress. Differences between target (T) and nontarget (NT) muscles may provide insight into MEP latency as a biomarker for fatigue. PURPOSE: To analyze preliminary observations of MEP latency as a biomarker for fatigue. METHODS: Three warfighters were recruited to identify markers of cognitive degradation during operational stressors. During an isometric squat at 15%, 40 stimuli were delivered to the dominant vastus lateralis (VL), at varying intensities. Subjects were limited to half of normal sleep and calories Days 2 and 3. The difference between T and NT MEP were analyzed across days. RESULTS: The differences in VL T and NT MEP latencies were as follows: day 0 (2.63±1.3ms); day 1 (1.58±0.7ms); day 2 (3.31±0.9ms); day 3 (3.19±0.8ms); day 4 (2.90±0.9ms). CONCLUSION: Task familiarization may explain increases on Day 0, and increased latency during days 2 and 3 due to interhemispheric signaling, as fatigue stresses the transcallosal pathways. More trials are necessary to assess difference of MEP latency as a fatigue biomarker.
18	Mingjun Liu, MS	Basic Life Science	Histone Modification H3K4 Di-Methylation (H3K4ME2) Regulates Vascular Smooth Muscle Cell Differentiation Through Interaction with TET2	Mingjun Liu; Sidney Mahan; Anh T. Nguyen, PhD; Gary K. Owens, PhD; Delphine Gomez, PhD	Vascular smooth muscle cells (SMC) are highly specialized cells regulating vascular functions by expressing a specific repertoire of contractile proteins. Remarkably, differentiated SMC can reversibly dedifferentiate under pathological conditions. Chromatin analysis identified the epigenetic signature of SMC lineage, including a histone modificiation, H3K4me2, on promoters of SMC contractile genes. H3K4me2 appears on these genes specifically and uniquely in SMC prior to their activation during development and is stably retained during reversible dedifferentiation. Consequently, H3K4me2 may be a key mechanism driving SMC differentiation and retention of lineage memory. In order to investigate the functional relevant of H3K4me2, we developed an editing system combining Myocardin, a master transcriptional regulator, with H3K4 demethylase LSD1 (Myocd-LSD1) to selectively remove H3K4me2 from SMC-marker genes. We found that Myocd-LSD1 efficiently removed H3K4me2 on SMC-marker genes and markedly reduced expression of the SMC-marker genes *in vitro* and *in vivo* . We also discovered direct interactions between H3K4me2 and Tet methyl-cytosine dioxygenase 2 (TET2), an enzyme mediating DNA demethylation and SMC differentiation. Removal of H3K4me2 effectively abolished TET2 recruitment on the SMC contractile genes. Collectively, our results indicated H3K4me2, residing on promoters of SMC contractile genes, maintains SMC differentiated phenotype by serving as the docking site for TET2 recruitment.

Poster #	Presenter	Topic	Title	Author(s)	Abstract
19	Adrianna Oh	Basic Life Science	Functional Range of Motion of the Cervical Spine in Posterior Cervical Discectomy and Fusion Patients During Activities of Daily Living	Adrianna Oh, BS; Abenezer Alemu, BS; Marcus Allen, PhD; Anna Bailes, BS; Malcolm Dombrowski, MD; Joon Y. Lee, MD; William F. Donaldson, MD; William W. Clark, PhD; Kevin Bell, PhD;	Previous research shows reductions in total cervical range of motion (CROM) in patients having undergone posterior cervical discectomy and fusion (PCDF), which may be associated with worse postoperative pain and functionality. However, total CROM is a limited descriptor of everyday functionality, as most activities of daily living (ADLs) require only a median 19% of full active CROM. This study examines functional CROM in 7 fusion patients compared to 7 controls using a novel telerehabiliation motion tracking device. Motion data in 6 directions (flexion, extension, lateral bending to left and right, axial rotation to left and right) showed statistically significant ($p<0.05$) reduction in functional CROM in at least 1 direction in 6 out of 9 ADLs. In 2 out of 9 ADLs, CROM is correlated with worse scores on neck disability index, fear avoidance behaviors, and pain ($p<0.05$). These findings contribute to a better understanding of cervical fusion's impact on patient-oriented outcomes, and implies future categorization of pathologic motion modification e.g., changes in velocity, acceleration, or jerkiness. Ultimately, our work with this device will enable a cheap, precise, and automated telerehabilitation tool that will aid in diagnosis and rehabilitation of neck fusion patients.
20	Christina Le	Basic Life Science	Identification and Isolation of an Antibiotic Compound Produced by an Unknown Violet Pigmented Strain	Christina Le; Tyler Rohr; Lingfeng Liu, PhD	At least 23,000 people die in the United States each year as a result of infections caused by antibiotic resistant bacteria. If no action is taken, it is estimated that by the year 2050, there will be more deaths caused by antibiotic resistant microbes than are currently caused by cancer. Identified antimicrobial molecules have the potential to be used in cutting-edge infection treatments where antibiotic resistant bacteria previously nullified a cure. We are able to contribute to the discovery of a remedy in the Course-Based Undergraduate Research Experience (CURE) lab, where antibiotics produced from various strains of soil bacteria are isolated in the search for a new treatment. The current bacterial strain under study is an unknown Gram-negative specimen with a strikingly unusual violet pigment. Raw antibiotic compounds were extracted from this strain, purified using multiple chromatography methods, and characterized utilizing various spectroscopy methods. Although spectroscopy methods were unable to definitively determine the molecular structure of the discovered antibiotic, several pieces of evidence suggest the molecule containing antibacterial properties is violacein, a pigmented compound found in certain bacterial species.
21	Aidan Dadey	Basic Life Science	Pharmacological Inhibition of Myocardin-Related Transcription Factor as a Novel Strategy to Inhibit Growth and Migration of Triple-Negative Breast Cancer Cells	Aidan Dadey; Dave Gau; PhD; Partha Roy, PhD	Breast cancer (BC) is the second leading cause of cancer deaths in the United States for women, due to metastasis of the cancer. In particular, triple-negative breast cancer (TNBC) has a higher propensity to metastasize and reoccur post-treatment. Treatment of TNBC is difficult because of the tumor heterogeneity and lack of molecular targets. The five-year survival for patients with TNBC is less than 30% despite adjuvant chemotherapy treatment. Recurrence of metastatic tumors arises from a switch from “dormant” state single cells or non-growing micro-metastasis into an active proliferative state. As such, keeping BC cells in a dormant state and/or slowing the metastatic growth of BC cells should prolong the survival of TNBC patients. Recent studies have highlighted the importance of actin cytoskeleton regulatory proteins and their upstream regulators in promoting metastatic outgrowth of disseminated BC cells. In response to actin polymerization, myocardin-related transcription factor (MRTF) promotes the activation of serum-response factor (SRF), and in turn SRF-mediated transcription initiates for a wide range of actin cytoskeletal and adhesion regulatory proteins in addition to SRF itself. The goal of this study is to investigate the effect of small molecule inhibitor of MRTF on single cell outgrowth and motility of TNBC *in vitro* .
22	Muhammad Feroze	Basic Life Science	The Neuroprotective Effect of Estrogen Receptor Agonists in a Cellular Model of Parkinson’s Disease	Muhammad Feroze; Juliann Jaumotte; Donald DeFranco, PhD	Parkinson’s disease is a neurodegenerative disease which involves a degeneration of midbrain dopaminergic neurons. While current therapies compensate for the decreased dopamine in the nigrostriatal pathway, a therapy that can modify or halt the progression of the disease has yet to be developed. Although the cellular mechanisms involved in initiating the loss of striatal dopaminergic neurons are complex, neuroinflammation has been implicated in the degeneration. Thus, the ability of steroids, such as estrogen receptor beta (ERβ) agonists, to reduce the inflammatory response in the central nervous system after biological insult was of interest. To understand the neuroprotective effect of two ERβ agonists against cytotoxity, experiments were designed to assess the effects of a synthetic and an endogenous ERβ ligand in MN9D cells, a dopaminergic cell line, after toxin exposure. After a pretreatment with varying doses of either ligand, WAY-200070 or 5-Androstene-3beta,17beta-diol (Δ5-diol), the cells were exposed to hydrogen peroxide for 24 hours. Following the toxin exposure, cell viability assays were performed. Results revealed that at certain concentrations of hydrogen peroxide, cells that were pretreated with Δ5-diol experienced less cell death than the vehicle-treated cells. In conclusion, ERβ agonists can potentially improve the resistance of MN9D cells to oxidative stress.
23	Marissa Kaufman	Basic Life Science	*Rhodiola Rosea* Reduces Platelet Driven Endothelial Activation	Marissa Kaufman; Valentina Ochoa; Eileen Bauer, PhD	*Rhodiola rosea* is a plant used in traditional medicine to treat anxiety and depression. Recent studies have demonstrated its protective effect after hypoxia-induced endothelial damage and further reported on its anti-inflammatory properties. We are interested in how platelets contribute to pulmonary arterial hypertension, a fatal disease driven in part by the innate immune system. Platelets are blood cells that continuously interact with the inner-most layer of the blood vessel wall, the endothelium. Here, we report that treatment of platelets with the *Rhodiola rosea* extract during platelet activation leads to decreased release of their inherent inflammatory factors. Co-culture experiments of platelets with endothelial cells in the presence of *Rhodiola rosea* extract showed diminished release of inflammatory cytokines by the endothelial cells. Salidroside is one active compound identified within the Rhodiola extract and has been shown by others to be responsible for the protective effects of the plant. Interestingly we observed that treatment of platelets and endothelial cells with salidroside alone, caused an exaggerated immune response. Thus, *Rhodiola* ’s protective effect operates via a mechanism independent of salidroside. *Rhodiola* is not approved for medicinal treatment within the U.S., but has been successfully used for millennia in other countries.
24	Lillian Leak	Basic Life Science	Identifying the Biotic and Abiotic Drivers of Duckweed Species Composition	Lillian C. Leak; Julie M. Everett; Martin M. Turcotte	Environmental factors have extensive impacts on local biodiversity, but these factors’ relative importance may differ among species. When several species coexist in natural communities, multiple ecological envelopes converge. Duckweed (*Lemnaceae*) is a floating aquatic plant that is easily dispersed, with several species native to Pennsylvania. It is of interest as a model for biodiversity because of the wide range of conditions the various species can tolerate, but despite its widespread prevalence, duckweed species composition varies dramatically from pond to pond. It is unclear what environmental factors, biotic and abiotic, dictate this variance, and how much of the observed variation they explain. We hypothesized that duckweed species composition varies according to specific environmental factors, especially agricultural gradients. We sampled duckweed across Western Pennsylvania to measure species richness and diversity and estimate absolute abundance. We measured environmental factors such as human impact, water chemistry, eutrophication, and physical attributes such as shading and pH. So far, we have observed trends in differing species richness across human impact gradients and different types of water bodies. It would seem that some species have advantages over others in different environments. Studying the factors that determine species composition will help understand the drivers of biodiversity.

Poster #	Presenter	Topic	Title	Author(s)	Abstract
25	Shifan Ma, MS	Basic Life Science	Structure-Based Drug Design and Identification of P62 zz Ligands with Potential Efficacy to Treat Multiple Myeloma by iDSC-Apoptosis Signaling	Shifan Ma, PhD; Liping Wang, PhD; Liyong Zhang, PhD; Min Li, MS;Yuemin Bian, MS; Qin Tong, PhD; Peng Yang, PhD; Zhiwei Feng, PhD; Xiang-Qun Xie, PhD	Multiple myeloma (MM) is a plasma cell cancer, which damages the bones, immune system, kidneys, and red blood cell count. Although great efforts have been made to improve the symptoms and lengthen the lifetime of some MM patients, some subgroups of MM patients cannot benefit from currently available medications and are at high risk of death. More diverse treatment is required for this disease. Our previous studies show our compounds targeting p62/SQSTM1 has beneficial effect in treating multiple myeloma on both *in vitro* MM cell lines and MM animal models. Our lead compound was shown to inhibit the osteoclast formation, against the proliferation of myeloma cells, inhibit the overall bone damage in animal models. To improve the efficacy of our lead compound, here we did chemical modification on our lead compound, and attained 38 analogies. We got one compound with 10-fold anti-proliferation effect compared with lead compound in MM cell lines, and better drug like properties, such as higher solubility, less toxicity on BJ cells, better selectivity with more difference between results from p62-KO cells and normal cells. In this study, we further identified that our p62 compounds killing the myeloma cells through p62-LC3-iDSC-apoptosis signaling using immunofluorescence and Western Blot.
26	Zexin Li	Basic Life Science	Modulation and Characterization of Chip, A Ubiquitin Ligase Involved in CFTR Degradation	Zexin Li; Samuel K. Estabrooks; Sara Sannino; Jeffrey L. Brodsky	The cystic fibrosis transmembrane conductance regulator (CFTR) is an ion channel expressed in lungs and intestines. Defects in CFTR cause accumulation of mucus in lungs, thus instigating bacterial infection, and are the underlying cause of cystic fibrosis (CF). Many disease-causing CFTR mutants are unstable and degraded by a process known as endoplasmic reticulum associated degradation, where a peptide known as ubiquitin is conjugated onto substrate proteins and form a polyubiquitin chain, which marks protein substrates for export into the cytosol and degradation by the proteasome. One ubiquitinating enzyme that targets CFTR is a ubiquitin ligase called CHIP. We suggest that ablation of CHIP activity should reduce degradation of CFTR. We evaluated a compound, BC1685. To test if BC1685 inhibited CHIP, we developed CHIP ubiquitination assays in which CHIP, BC1685, a denatured CHIP substrate, and ubiquitination enzymes are incubated. Preliminary results suggest that BC1685 did not inhibit CHIP, which may be due to the limited sensitivity. In parallel, we generated CHIP variants with a mutated C-terminus since this region is important for CHIP biogenesis. Determining precisely which residues are required for CHIP to mature could reveal new ways in which this enzyme could be specifically targets by small molecule inhibitors.
27	Beverley Kozuch	Basic Life Science	The Role of Multiple LexA Repressor Binding Sites in SOS Response and Autoregulation Kinetics	Beverley C. Kozuch, BS; Matthew J. Culyba, MD, PhD	The bacterial DNA damage repair pathway (also known as the SOS response) has been linked to the acquisition of antibiotic resistance. Bacteria survive and adapt to genotoxic stress, such as that caused by antibiotic therapy, by activation of the SOS response. The pathway contains ~40 genes regulated by the LexA repressor, which undergoes self-cleavage in response to DNA damage, leading to SOS gene transcription. For bacteria to survive, they must rapidly turn-on and shut-off the SOS response. Interestingly, the promoter for the lexA gene, itself, contains multiple LexA binding sites and thus is under negative autoregulation, potentially via a cooperative binding mechanism, which may enhance SOS turn-on and shut-off kinetics. Using a lexA GFP-reporter plasmid and a large dose-range of DNA damage, we are able to parameterize lexA promoter activity and characterize promoter mutants quantitatively. Using site-directed mutagenesis, we show that only two of three putative LexA binding sites are functional on the promoter and find no evidence for cooperative binding from the two functional binding sites. To understand the role of this promoter-motif further, future work will characterize LexA-promoter binding kinetics *in vitro* and test the requirement of two binding sites *in vivo* .
28	Aaron Zheng	Basic Life Science	Exploring Allosteric Binding Sites on Dual Specificity Phosphatases	Aaron Zheng; Cynthia Hinck; Chang-Hyeock Byeon; Andrew P. Hinck; Andreas Vogt	Dual specificity phosphatases (DUSPs) are a subfamily of phosphatases that have important roles in heart development, cancer, and the immune system. The discovery of small molecule inhibitors has been largely unsuccessful because the DUSP active sites are shallow and susceptible to non-selective, irreversible inactivation by oxidation. We have identified one small molecule, (E)-2-benzylidene-3-(cyclohexylamino)-2,3-dihydro-1H-inden-1-one (BCI), which inhibits DUSP6 in zebrafish and mammalian cells but is not a catalytic inhibitor. Computational models predict multiple binding sites on DUSP6 that could explain its non-canonical mechanism of DUSP inhibition. To date, however, there have not been any direct binding studies between BCI and DUSP6. In this study, we aimed to perform physical binding studies using isothermal titration calorimetry (ITC). We improved an existing procedure to produce recombinant DUSP6, resulting in milligram quantities of protein purified to near homogeneity. While preliminary ITC studies with BCI and recombinant DUSP6 have thus far failed to document a direct interaction between BCI and DUPS6, further analysis via differential scanning fluorimetry and enzymatic activity assays suggest that the protein may have denatured. We are currently investigating the causes of the denatured protein within our protein production protocols as well as alternative methods to investigate the BCI-DUSP6 interaction.
29	Eugenio Alvarez	Basic Life Science	PEG-Asparaginase Induces Hepatic Steatosis via Adipose Tissue Lipolysis	Eugenio Alvarez; Sanjay Rathod, PhD; Manda Ramsey; Christian Fernandez, PhD	Background: Asparaginase (ASNase) is a chemotherapeutic agent used for the treatment of pediatric acute lymphoblastic leukemia. However, ASNase is avoided in adult regimens due to its high risk of hepatotoxicity. Nevertheless, the mechanism of ASNase hepatotoxicity remains unknown. Recent studies by our group have suggested that the mechanism may involve hepatic steatosis. Aim: To determine if mice receiving PEG-ASNase develop steatosis due to a dysfunction in de novo lipogenesis, fatty acid oxidation, fatty acid uptake, VLDL secretion, and/or lipid droplet formation. Methods: BALB/c mice receiving 1,500 IU/kg of PEG-ASNase were sacrificed after 8 days, and liver, white adipose tissue (WAT), pancreas, and plasma were collected. Body and tissue weight loss, asparaginase levels, insulin, hepatic triglyceride levels, liver histology, and hepatic gene expression were assessed. Results: PEG-ASNase-treated mice had lower body, liver, and WAT weight relative to controls, and developed microvesicular steatosis with elevated hepatic triglyceride levels and lower insulin compared to controls. The expression of genes involved in hepatic lipid regulation did not explain the development of steatosis. Conclusion: PEG-ASNase-treated mice develop steatosis without the dysregulation of genes involved in hepatic lipid regulation. Rather, it is likely that the observed steatosis is due to drug-induced adipose tissue lipolysis.
30	Swati Banerjee, MS	Basic Life Science	Epidermal Growth Factor Receptor (EGFR) Inhibition Reverses Steatosis and Non-Alcoholic Fatty Liver Disease (NAFLD) Progression in a Murine Dietary Model	S. Banerjee; B. Bhushan; Paranjpe; G.K. Michalopoulos	EGFR is the regulator of hepatocyte proliferation, liver regeneration and lipid metabolism during liver regeneration after liver-resection in mice, along with its several roles in liver injury and fibrosis. Based on these findings, we investigated the function of EGFR in mouse model of NAFLD utilizing pharmacological inhibition strategy. C57BL6/J mice were administered chow diet, fast-food diet (western diet plus high-fructose corn syrup), or Canertinib (a potent EGFR inhibitor) containing fast-food diet for two months. Canertinib treatment completely prevented development of steatosis and liver injury in this model. To study the reversal inhibition, mice were administered fast-food diet for five months, with or without Canertinib treatment for last 5 weeks of the study. Canertinib treatment remarkably decreased liver enlargement, steatosis, liver injury, and fibrosis, and improved glucose tolerance. Microarray analysis reconfirmed the EGFR regulation. Several relevant signaling pathways (like mTOR/AKT, lipid metabolic pathways, and glycolysis), along with some fatty acid synthesizing proteins, which were affected by fast-food diet, were found to be regulated by EGFR. In conclusion, our study revealed a novel role of EGFR in NAFLD and potential of EGFR inhibition or manipulation of its downstream targets as treatment strategy for NAFLD.

Poster #	Presenter	Topic	Title	Author(s)	Abstract
31	Weiwei Lin	Basic Life Science	Molecular Docking and Molecular Dynamics Simulation on Acetaminophen and its Metabolites – An Insight into Acetaminophen Mechanism of Action	Weiwei Lin; Yuanqiang Wang, PhD; Nan Wu, BS; Xibing He, PhD; Junmei Wang, PhD; Zhiwei Feng, PhD; Xiang-Qun Xie, PhD, EMBA	Acetaminophen (APAP), also known as paracetamol, is a commonly used analgesic/antipyretic medication with low risk of adverse effects, dependency, tolerance, and withdrawal symptoms. Acetaminophen is considered a relatively safe drug with a large therapeutic range, however, when administered in large quantities it could be potentially dangerous due to the risk of hepatotoxicity. In the human body, APAP is known to be metabolized into N-(4-hydroxyphenyl)-arachidonamide (AM404) via the action of CYP enzymes, and into N-acetyl-p-benzoquinone-imine (NAPQI) via fatty acid amide hydrolase (FAAH); however, the details of the acetaminophen mechanism of action are still unclear. In present work, we perform molecular docking and molecular dynamics simulation of acetaminophen and its metabolites (AM404 and NAPQI) to try to provide an insight into their relationship. We first carried out a series of molecular docking studies between acetaminophen/AM404/NAQPI with their reported target receptors, including CYP 2E1, FAAH, TRPA1, CB1 and TRPV1. Secondly, we performed Molecular Dynamics Simulation and energy decomposition for CB1-AM404, TRPV1-AM404, and TRPV1-NAPQI for the further investigation of the dynamics of their interactions. Overall, we wish to provide a new insight into the structural and functional roles of APAP and its metabolites for the development of treatments and prevention methods of acetaminophen overdoes.
32	Mireia Perez Verdaguer	Basic Life Science	Cross-Talk between Ligand- and Stress-Kinase-Induced Endocytosis of Endogenous FAP-Tagged EGF Receptor	Mireia Perez-Verdaguer, PhD; Mads B. Larsen, PhD; Marcel P. Bruchez, PhD; Simon C. Watkins, PhD; Alexander Sorkin, PhD	Receptor Tyrosine Kinases (RTK) internalization is no longer seen as a mere attenuation mechanism, but as an integral part of signaling which provides spatiotemporal regulation to the signaling network. Epidermal growth factor receptor (EGFR), an archiotypic RTK, is internalized via: i) canonical ligand-induced receptor-tyrosine-kinase-dependent pathway; and ii) stress-induced non-canonical pathway involving p38-MAPK activation. Both these pathways are mediated by clathrin coated pits (clathrin-mediated endocytosis, CME), although high doses of EGF can also induce substantial clathrin independent endocytosis (CIE). *In vivo* cells are often exposed to multiple stimuli and stress factors at the same time, but how this complex microenvironement influence pathways and patterns of EGFR endocytic trafficking has not been studied. Therefore, in the present study EGFR internalization was compared when endocytosis was induced by ligand (EGF) or by stress p38 mediated signaling (induced by TNFa or anisomycin), or by a combination of both types of factors. To quantitatively examine EGFR endocytosis, fluorogen activating protein (FAP) was inserted into endogenous EGFR gene locus by CRISPR/Cas9 gene-editing in HeLa and human squamous carcinoma HSC3 cells. Control experiments confirmed normal activity and endocytosis of the FAP-EGFR fusion, thus validating the use of gene-edited cells in the analysis of EGFR endocytosis and signaling.
33	Thomas Zhang	Basic Life Science	Uptake of Nitrogen Doped Carbon Nano Materials and its Use in Intracellular Protein Delivery	Thomas Zhang; Amber Griffith; Seth Burkert; Alexander Star, PhD; William Saunders, PhD	Defects in cell division are intimately linked with cancer. However, the specific mechanisms behind certain divisional defects remain unclear. One such divisional defect is the response to lagging chromatin in the formation of anaphase bridges. When a dicentric chromosome is attached to both centrosomes during cell division, certain pathways cause abscission delay and inhibit cytokinesis, sometimes resulting in a tetraploid cancer cell. We believe that AuroraB kinase, which phosphorylates myosin light chain kinase, is activated during anaphase bridge formation and causes furrow regression. However, this has not been proven. Protein conjugated carbon nanotubes can be used to elucidate this mechanism. Nitrogen doped carbon nanocups (NCNC) and nanobowls (NCNB), are multiwalled carbon nanotubes with nitrogen introduced into its structure for greater solubility and biocompatible. To use NCNC as a mechanism for protein delivery and targeting, we must first understand its uptake and cellular biocompatibility. NCNC and NCNB were incubated with HeLa cells and visualized using immunofluorescence and transmission electron microscopy. Here, we report that these nanomaterials were uptaken into the cell and mostly though endocytosis. Alexafluor tagged IgG was conjugated to NCNC and incubated with cells to determine the usability of NCNC as a platform for intracellular protein delivery.
34	Xujie Liu, PhD	Basic Life Science	Drug Discovery and Mechanistic Study of P23H Rhodopsin Clearance for Treatment of Rhodopsin Associated Retinitis Pigmentosa	Xujie Liu, PhD; Yuanyuan Chen, PhD	Retinitis pigmentosa (RP) is the most prevalent inherited blindness among people at working age. The P23H rhodopsin mutation is a typical example of the misfolded rhodopsin that is the most common cause of rod photoreceptor death among RP patients carrying the rhodopsin mutations. To develop an effective treatment for this currently untreatable disease, we are looking for a pharmacological approach to selectively clear the P23H-opsin mutant which will to restore rhodopsin homeostasis and support photoreceptor survival. From a small molecule high-throughput screen (HTS) using a cell-based luciferase reporter assay, we identified a group of novel and potent small molecules which only clear the P23H opsin without affecting the normal opsin which will maintain visual function. Then we followed the degradation of the P23H opsin and discovered small molecules increasing the degradation of this misfolded opsin. We determined the effect of these compounds on the autophagy and proteasome pathways which are involved in P23H opsin degradation. We have identified novel pharmacological tools to destabilize the misfolded rod opsin which are used as drug candidates to be tested in the *in vivo* RP models. Further, the molecular targets of these small molecules will help us identify the drugable targets regulating rhodopsin metabolism.
35	Nan Wu	Basic Life Science	Structural Insight into Serotonin (5-HT) Receptor Family Using System Pharmacology Analysis	Nan Wu; Yuanqiang Wang; Weiwei Lin; Siyi Wang; Zhihua Lin; Xiangqun Xie; Zhiwei Feng	
36	Tarun Bhatia	Basic Life Science	Exogenous Heat Shock Protein 70 Mitigates The Olfactory Deficits and Proteinopathy of Lewy Body Disorders in Aged Mice	Tarun N. Bhatia, BS; Patrick G. Needham, PhD; Daniel M. Mason, PhD; Kristin M. Miner; Elizabeth A. Eckhoff; Catherine M. Navagh; Sara A. Trbojevic; Jeffrey L. Brodsky, PhD; Peter Wipf, PhD; Kelvin C. Luk, PhD; Rehana K. Leak, PhD	The chaperone heat shock protein 70 (Hsp70) refolds misfolded proteins or enables their clearance. Following intranasal delivery, Hsp70 has been shown to improve cognition, reduce neurodegeneration, and extend lifespan in mouse models of aging and dementia, and to improve insulin sensitivity in mouse models of diabetes. However, intranasal Hsp70 has not been tested in Lewy body disorders. We infused Hsp70 into the left nares of 20 month-old male mice daily for 28 days following infusions of preformed α-synuclein fibrils in the left olfactory bulb—the first site to develop α-synucleinopathy in human Lewy body disorders. Daily Hsp70 delivery significantly mitigated fibril-induced α-synucleinopathic inclusions and loss of olfaction. Furthermore, we confirmed that Hsp70 entered the mouse brain from the nares within three hours post-infusion, as demonstrated by immunoblotting on tissue lysates from the olfactory bulb and the caudal recesses of the temporal cortex. Inhibition of Hsp70 activity *in vitro* with the small molecule inhibitors MAL3-101 and/or VER155008 dramatically increased the number of inclusions in primary neurons harvested from the rat sensorimotor neocortex, entorhinal allocortex, and hippocampus, suggesting a generalizable effect. These collective findings support further testing of the ability of intranasal Hsp70 to impede the propagation of Lewy pathology.
37	Bing Feng	Basic Life Science	Pharmacological Profile of Small Molecule Chaperones on the Folding of Class II Rhodopsin Mutants Associated with Retinitis Pigmentosa	Bing Feng; Yuanyuan Chen	Rhodopsin mutations lead to autosomal dominant retinitis pigmentosa (adRP), a progressive retinal degeneration. We have discovered a group of small molecules which rescues transport of the P23H rod opsin (a typical example misfolded rhodopsin mutation) from endoplasmic reticulum (ER) to the plasma membrane using a cell-based high-throughput screening (HTS). Here we want to ask whether these pharmacological chaperones also rescue the folding and transport of other rod opsin mutants located in the extracellular loop that lead to adRP in mammalian cell culture using a high-content imaging analysis. Our results showed that most of these opsin mutants are retained in the ER suggesting they are misfolded. The pan-HDAC inhibitor scriptaid rescues the transport of mutant opsins without directly binding to the rod opsin, whereas a novel non-retinal ligand of rod opsin showed similar efficacy compared to 9-cis-retinal, with lower toxicity, rescuing the transport of 10 rod opsin mutants. Our studies showed a therapeutic potential of pharmacological chaperones of rod opsin for treatment of misfolded rhodopsin associated adRP.

Poster #	Presenter	Topic	Title	Author(s)	Abstract
38	Taylor Zallek	Basic Life Science	Variation in Genetic Diversity, Structure, and Patterns of Hybridization among and within Populations of Invasive Eurasian Watermilfoil (*Myriophyllum spicatum*) in Waterbodies with and without Histories of Herbicide Treatment across Michigan	Taylor Zallek; Casey Huckins; Erika Hersch-Green	Novel selective forces in the form of anthropogenic control agents (such as chemical herbicides) can dramatically influence different evolutionary trajectories among populations of invasive species. Routine exposure to herbicides can lead to the selection for herbicide resistance traits in targeted populations and impact the potential invasibility of these populations through the differential expression of invasive traits between historically targeted populations and non-targeted populations. In this study, we examined whether patterns of genetic diversity and population structure of invasive watermilfoil (Myriophyllum spicatum and M. spicatum x M. sibiricum hybrids) populations differed amongst waterbodies with and without histories of herbicide treatment. We also examined whether histories of herbicide treatment could be impacting the abiotic environment or biotic plant community. We found that genetic diversity within populations is low while genetic variation among populations is high. Invaded waterbodies with histories of herbicide treatment have more admixture than non-herbicide waterbodies. Populations are typically represented by one genetic class and evidence of hybridization is greatest in herbicide treatment waterbodies. Plant communities differ between herbicide treatment waterbodies and non-treatment waterbodies. Invasive watermilfoil populations in their introduced range demonstrate a spectrum in genotypic diversity, admixture, and hybridization among invaded waterbodies with different histories of herbicide application. Routine use of herbicides could be sending populations of invasive watermilfoil, as well as plant communities, on different evolutionary and ecological trajectories.
39	Matthew Rannals	Basic Life Science	Targeted Translatome Profiling Using In Utero Gene Transfer Identifies Ion Channel Pathophysiology in a Brain Development Model of Transcription Factor 4 (TCF4) Function	Matthew D. Rannals; Stephanie Cerceo-Page; Thomas M. Hyde; Joel E. Kleinman; Andrew E. Jaffe; Daniel R. Weinberger; Nathan N. Urban; Brady J. Maher	Healthy brain development is remarkably robust to the genetic differences across individuals. By altering the genetic instructions of a developing brain in our model system in utero, we have found that changes in a gene (TCF4) linked to a rare autism spectrum disorder (Pitt-Hopkins syndrome, PTHS) and schizophrenia results in attenuated neuronal spiking in cortical neurons by increasing the afterhyperpolarization. Using a novel technique called iTRAP that combined in utero electroporation and translating ribosome affinity purification, we have been able to identify the specific signaling problem in these neurons. Through pharmacological rescue and molecular phenocopy we have also shown it is possible to reverse neuronal function back to the level found in a normal healthy brain. Our continued work on CNTNAP2 aims to investigate the hypothesis that this gene shares, with TCF4 and other ASD genes, downstream targets and common molecular pathways controlling critical aspects of normal brain development.
40	Carolina Gorgulho	Basic Life Science	Making a Good Impression: Autophagic Colorectal Cancer Cells for Cross Presentation of Tumor Antigens by DC	Carolina Mendonça Gorgulho; Lin Zhang; Ramon Kaneno; Michael T. Lotze	Treatment of DC with low, noncytotoxic concentrations of chemotherapeutic agents enhances antigen presentation that is partly IL-12 dependent. Low dose chemotherapy-treated tumor cells, up-regulate antigen presenting machinery genes, without apoptosis, rendering them more immunogenic antigenic sources for DC. Autophagy maintains cellular homeostasis, enabling survival postchemotherapy.
41	Luca Calzoni, MD	New Research Tools and Techniques	Design of a Learning EMR: A Qualitative Study of ICU Clinicians' Information Needs	Luca Calzoni, MD; Gilles Clermont, MD, MSc; Gregory F. Cooper, MD, PhD; Shyam Visweswaran, MD, PhD; Harry Hochheiser, PhD	Complex EMRs presenting large amounts of data create risks of cognitive overload. We are designing a data-driven Learning EMR (LEMR) for use in ICUs. The LEMR will utilize recordings of data items accessed by clinicians when reviewing patient cases to develop predictive models capable of suggesting and highlighting the most relevant items for each patient. To inform the design of a user interface capable of prioritizing the presentation of such high-value data, we combined observations with design activities. First, a review of relevant literature provided us with insights on design aspects applicable to a LEMR, including the use of visual attributes and concept-oriented information views to support analytical reasoning. The insights gained guided the creation of paper prototypes, representing how the system might highlight high-value data. Second, we observed ICU physicians interacting with EMRs. The insights gained on their information seeking activities guided the revision of our prototypes. Third, in a focus group we asked clinicians to provide feedback on the LEMR concept and prototypes, and to generate design ideas for the user interface. Study findings led to the creation of final prototypes, which will guide the eventual development of a fully functional user interface.
42	Natalie Hager	New Research Tools and Techniques	A Suite of Fluorogen-Activating Protein (FAP)-Tagged Vectors and Organelle Markers Enables Quantifiable Dye-Activated Selective Imaging of Location-Specific Protein Pools	Natalie A. Hager; Ceara K. McAtee; Justina A. Warnick; Marcel P. Bruchez; Jeffrey L. Brodsky; Allyson F. O'Donnell	Recent advantages of genetically encoded fluorescent probes have led to the development of fluorogen activating proteins (FAPs). This technology has two components: a non-fluorescent single chain antibody (SCA) that can be fused to a protein of interest and fluorogens, which are non-fluorescent dye molecules when free in solution. When the SCA and fluorogen bind, there is a 20,000-fold fluorescent increase relative to unbound dye. This level of fluorescence is comparable to typical fluorescent proteins. However, the FAP-technology has two major advantages; (1) using either a membrane-permeant or impermeant fluorogen dye we are able to selectively label intracellular proteins from proteins at the plasma membrane and (2) since the fluorogen does not fluoresce when it is not bound by SCA, we are able to completely eliminate background fluorescence when imaging in other fluorescent channels. Although developed in yeast, this technology is rarely used in this model organism. In order to make this technology more readily available to the cell biology community, we have first optimized the SCA sequence for expression in yeast, and then created a series of SCA-tagging constructs and organelle markers to be used as tools for the cell biology research community.
43	Ran Sun, MSN	New Research Tools and Techniques	Military Teen App: Engagement, Safety, Commercialization, & Marketing	Ran Sun; Ann Gleeson; Debbie Nichols; David Rivetti; Naveen Khan; Kathy Puskar	Military teens who experience significant life changes such as relocation and parent deployment are vulnerable to certain mental health issues. Limited online resources are available to support coping and promote resilience. Mobile applications hold the potential to connect teens together and provide social support; however, the existing mobile apps for military adolescents are primarily for entertainment and educational purposes, rarely seeking to build a continuous and supportive system. The MilTeenChat™ app was created to provide an online social platform to support the mutual learning of coping and resilience strategies among military teens. The app is a translation of adolescent coping science to the general public of military teens. The purpose of this study is to describe four factors considered during the app development of teen engagement, data security and teen safety, commercialization, and marketing. The app is a new tool and technique using social media to promote resilience in military teens. A heightened awareness of these factors contributes to best practice as healthcare professionals skilled in computer technology develop more mobile apps.
44	Felix Proessl, MS	New Research Tools and Techniques	Corticospinal Excitability as a Potential Biomarker of Neurophysiological Responses to Military Operational Stress	Felix Proessl; Anne Z. Beethe; Shawn R. Eagle; Meaghan E. Beckner; Aaron M. Sinnott; Adam J. Sterczala; Courtenay Dunn-Lewis; Christopher Connaboy; Anne Germain; Bradley C. Nindl; Shawn D. Flanagan	Military personnel are exposed to operational stressors such as physical fatigue, and caloric/sleep restriction. Using transcranial magnetic stimulation (TMS), corticospinal excitability may represent a sensitive biomarker of neurophysiological adaptations to such stressors. METHODS: To date, five male US Army reserves (24.9±3.0 yrs) completed five consecutive days of evaluation: familiarization (D0), baseline assessment (D1), two days of sleep and caloric restriction (D2 & D3), and a recovery day (D4). Stimulus response curves were produced during bilateral contractions of the first dorsal interosseus (FDI). Forty TMS pulses were delivered to the M1 FDI hotspot from 5-100% stimulator output (SO). Motor evoked potentials (MEP) were fit to a Boltzmann sigmoidal curve (BSC), with the slope, maximum, and SO at 50% maximum (V50) determined each day. RESULTS: Measures of corticospinal excitability peaked on D2&D3. On average, BSC slope increased by 25% (3.1±1.9 to 3.9±1.6), max by 24% (5.0±.03 to 6.2±0.3 mV), and V50 by 8% (51.6±2.2 to 55.5±1.8 SO) from baseline to D2. On D4, corticospinal excitability was decreased relative to D2 (BSC slope: 3.6±1.8, Δ: -8%; max: 6.2±0.4 mV, Δ: 0%; V50: 49.4±2.1 SO, Δ: -12%). CONCLUSION: Corticospinal excitability may present an objective means to monitor neurophysiological responses to military operational stressors.

Poster #	Presenter	Topic	Title	Author(s)	Abstract
45	Nicole Shigiltchoff	New Research Tools and Techniques	Allorecognition in *Hydractinia symbiolongicarpus*	Nicole Shigiltchoff; Matthew Nicotra, PhD	Allorecognition, the process of recognizing tissue of self or close kin through genetic similarity, plays an important role in organ and graft transplant success, triggering rejection responses. While the similarity between invertebrate and human allorecognition is unclear, Hydractinia Symbiolongicarpus, a colonial marine invertebrate capable of allorecognition, could become a model organism for studying human transplantation. It was believed that Hydractinia allorecognition was controlled by two genes, Alr1 and Alr2, and the number of matching alleles at these genes determined whether two organisms would fuse, reject, or transitory fuse (when colonies would start fusing, then separate). However, this rule only works for inbred colonies, and not wild-type. It was hypothesized that additional genes could contribute to Hydractinia allorecognition. After sequencing the genome of wild-type Hydractinia, eight new genes sequentially similar to Alr1 were found, potentially playing a part in allorecognition. To test these new Alr-like genes' contribution to allorecognition, siblings were genotyped for molecular markers linked to the new genes. I report results of fusion tests between animals matching at Alr1 and different molecular markers. I found a distinct region on the chromosome controlling allorecognition, containing two Alr-like genes, demonstrating that one or both of those genes likely participate in allorecognition.
46	Carly O'Connor-Terry	New Research Tools and Techniques	Exploring Reproductive Justice Through the Perspectives of Women Experiencing Intimate Partner Violence	Carly O'Connor-Terry; Tejasvi Gowda; Judy Chang, MD, MPH	Recently, women's reproductive health and abortion services provision has been the focus of increasingly restrictive legislative policies, including in Pennsylvania. One policy specific to Pennsylvania legislation regarding abortion services is a 24-hour waiting period and mandatory counseling prior to a women's receipt of abortion services. Another that had been proposed was a provision regarding "spousal notification" for abortion. An argument supporting the rebuke of this policy included concern that this requirement could place an "undue burden" on women experiencing intimate partner violence (IPV). This argument raises the question regarding the potential impact of various reproductive health policies and laws on women experiencing intimate partner violence. There has been limited empiric examination of how women experiencing IPV perceive and experience the impacts of these laws. The purpose of this qualitative study is to specifically identify how women experiencing IPV are affected by reproductive health and abortion policy using semi-structured individual interviews. Women seeking services for IPV will be asked to share their experiences and perceptions of seeking and using reproductive health services and their reactions to, beliefs about, and concerns regarding various currently enacted and proposed reproductive health and abortion policies. Interviews will be transcribed and qualitative coded to identify themes.
47	Zahra Ahmad	New Research Tools and Techniques	FGFR4 as a Prognostic Marker for Endocrine Therapy Resistance in Invasive Lobular Carcinoma	Zahra Ahmad; Kevin Levine, BA; Steffi Oesterreich, MD, PhD	Invasive lobular carcinoma (ILC) is a histological subtype of breast cancer characterized by its linear tumor growth pattern. Almost all ILC tumors are estrogen receptor positive (ER+); they depend on the ER to fuel tumor growth and are treated with drugs that block ER signaling. However, ILC tumors often have de novo or acquired resistance to endocrine therapy. The Lee-Oesterreich Lab has recently shown that ER+ ILC patients with high FGFR4 (fibroblast growth factor receptor 4) RNA expression have an increased risk of developing distant recurrences, suggesting FGFR4's role in de novo resistance. This study aims to understand the correlation between FGFR4 RNA and its protein expression and to see if protein expression is a better predictor of endocrine therapy resistance. FGFR4 antibody was validated for immunohistochemistry using a western blot to detect protein expression difference. IHC was then performed on ER+ ILC patient tumor samples with available FGFR4 RNA expression and clinical data. FGFR4 protein expression in tumor samples was then correlated to the levels of FGFR4 RNA and the clinical outcome of patients. We found a positive correlation between FGFR4 RNA and FGFR4 protein expression, and patients with high protein expression had an increased risk of recurrence.
48	Yankang Jing	New Research Tools and Techniques	DAKB-GPCRs: An Computational Chemogenomics Platform for Drug Abuse	Yankang Jing; Maozi Chen; Lirong Wang; Zhiwei Feng; Xiang-Qun Xie	Drug abuse (DA) is a complex brain illness, which is commonly considered as a neural disorder with genetic and environmental factors that influence its development and manifestation. G protein-coupled receptors (GPCRs) is the largest family of trans-membrane in human genome that targeted by approximate 40% of marketed drugs worldwide and plays important role in DA therapy. However, only 32 crystal structures of GPCRs have been published in the last seventeen years. To overcome the limitation of crystal structure and conformational diversity of GPCRs, we firstly built molecular models sampled different conformations by molecular dynamics (MD) simulation. Subsequently we built a GPCRs drug abuse database implemented with our established chemogenomics tools and algorithms for data visualization and analyses. Our GPCRs drug abuse database provides the following results for a query compound: docking scores via our HTDocking; similarity score via our TargetHunter; target classification via machine learning method that combined both docking scores and similarity score; molecule-proteins network map via our Spider-Plot; and blood brain barrier (BBB) plot via our BBB predictor.
49	Alexis Duray	New Research Tools and Techniques	Single-Cell Transcriptomics of Human Primary Cells Inoculated with BK Polyomavirus	Alexis M. Duray; Connie L. Xu; Wenshan Zheng; Paul G. Cantalupo; Ping An, PhD; Maria Teresa Sáenz Robles, PhD; David A. Weitz, PhD; James M. Pipas, PhD	Single-cell transcriptomics (SCT) allows analysis of RNA expression from a heterogenous population of cells with single cell resolution. We have used the InDrop platform to determine transcriptomic changes in response to BK polyomavirus (BKV) infection in two types of primary human cells, renal proximal tubule epithelial cells (RPTE) and microvascular endothelial cells (HVEC). Upon inoculation with BKV, only a portion of RPTE or HVEC express viral proteins, suggesting that only a subset of cells is susceptible to viral infection. Using Seurat, we analyzed transcript patterns in individual cells and then clustered them based on their gene expression profiles. These clusters indicate not only potential subpopulations of cells within culture, but also various metabolic or replicative states. We quantified variations in viral gene transcription and determined differentially expressed host genes, thereby identifying genes whose expression is altered by viral infection. To verify the classifications of the clusters, we selected marker genes for each cluster and then assessed their expression at the protein level. Successful SCT identification of markers genes for each cluster will allow us to track the fate of those clusters over the course of infection through conventional molecular analysis.
50	Elizabeth Pinto	New Research Tools and Techniques	Chronological Event Recording of Stimuli Using CRISPR/CAS9-Mediated Base Editing	Evan Becker; Vivian Hu; Matthew Greenwald; Tucker Pavelek; Elizabeth Pinto; Zemeng Wei; Cheryl Telmer, PhD; Natasa Miskov-Zivanov, PhD; Jason Lohmueller, PhD; Sanjeev Shroff, PhD; and Alex Deiters, PhD	Timing is important in biology; therefore, there is a critical need to be able to measure and record when a molecular signal changes a cellular state. Previously, recombinases and integrases have enabled scientists to record states directly into the genetic code. Despite these advancements, current systems are limited in that they can only take a "snapshot" of the environment, preventing scientists from understanding event order along with the strength and duration of stimuli. An advancement of CRISPR-Cas9 technology includes a fusion protein known as a base editor consisting of the DNA base modification enzyme cytidine deaminase (CDA), a modified Cas9 (nCas9 or dCas9), and uracil DNA glycosylase inhibitor (ugi). This complex can produce a permanent single nucleotide change while allowing for both high specificity and certainty of mutation. Researchers have previously developed two systems that utilize base editors to record stimuli, however recording capability was limited to logging an average concentration of stimuli over a period of time. Our system, termed CUTSCENE, builds upon these foundations by designing a method of true chronological event recording. By introducing recording plasmids with repeating units of DNA with a two-gRNA and base editor construct, we can achieve temporal resolution of stimuli.

Poster #	Presenter	Topic	Title	Author(s)	Abstract
51	Issam Abushaban	New Research Tools and Techniques	Reevaluating the Calculation of Fetal Head Molding in Finite Element Models of the Second Stage of Labor	Issam Abushaban; Megan Routzong, BS; Steven D. Abramowitch, PhD	During the second stage of labor, the female pelvic floor and fetal head must undergo extreme levels of strain, which can cause injury to the maternal musculature and/or cranial injuries to the fetal head. We turn to finite element modeling to computationally simulate the complex biomechanics and interactions of childbirth, allowing clinicians to better predict maternal and fetal complications without risking fetal or maternal health. This study aims to increase the accuracy of such simulations, particularly the way fetal head molding is calculated, by reevaluating the current standard, developed by Lapeer and Prager. We found that by applying pressures to the skull bones of a finite element fetal head model, we can measure the displacement of each node or any point of interest. Selected nodes can then be fit to an ellipsoid to determine the overall and relative volume changes of the fetal head in response to different amounts of pressure. To date, we have run this test on one fetal head model (26 weeks gestation). By testing this method on various fetal head models, we hope to verify its reliability and standardize it as our method for future analysis of fetal head molding in finite element simulations of childbirth.
52	Shaoming Zheng	New Research Tools and Techniques	Formal Model of Mask-RCNN and Analysis on Street View Segmentation	Shaoming Zheng	Convolutional Neural Network is originally inspired by activation and connection mechanism of biological light receptors. Despite such a successful bionic model, its mathematical backstone is relatively deficient and many issues (e.g. model uniqueness) remain unresolved. Mask-RCNN was shown to be a state-of-the-art machine learning solution on COCO 2017 Object Detection Task for instance-aware semantic image segmentation (pixel-level object detection). In this paper we will give a formal model of Mask-RCNN from formalizing some of its milestone preceedors (i.e. CNN, and Faster-RCNN) (Readers are recommended to acknowledge the general data structure and algorithm of the network prior to this paper). We will define a new operator for convenience in multiple convolutions on multiple input in a convolutional layer We will also analyze the performance of a TensorFlow implementation of this model on street view images, which we have a particular interest on. We will test the precision of semantic segmentation (measured by MSE of segmentation area overlap) with respect to different level of brightness, contrast, and most importantly, noise transformation, which mimics the real world situation in segmentation tasks. We show that the method performs robustly under these artificial alterations as the error shows low relevance to the level of transformations.
53	Upasana Bhattacharyya	New Research Tools and Techniques	Complement C4 Functions as a Secretory Protein in Neural Cells Derived from Human Induced Pluripotent Stem Cells (HIPSC)	Upasana Bhattacharyya; Demers Matthew; D'Aiuto, Leonardo, PhD; Kodavali V. Chowdari, PhD; Konasale M. Prasad, MD; Vishwajit L. Nimgaonkar, DPhil,MRCPsych	Complement C4 protein is a key regulator of complement activation in non-CNS cells. Though it is present in neurons and glial cells, its CNS functions are speculative. Recently, elevated gene copy number (GCN) of C4A, a major C4 isotype was associated with increased risk for schizophrenia (SZ). An ~40% increase in C4 transcript level is seen in SZ patients in post mortem studies. As C4A is not present in rodents, hiPSC-based experimental systems could bridge the gap between genetic association and clinical or brain imaging studies of C4A. We are developing hiPSC-derived neuronal cells (hi-N) in 2D and 3D cultures to study C4 function in human CNS cells. In isogenic 2D bulk cultures, C4 transcripts and protein levels increased in proportion to GCN. Using C4c (Quidel), an antibody that detects C4 protein and C4 fragments, we observed punctate staining in hi-N soma and neurites, similar to reports in human primary neuronal cultures. Using C4c, immunostaining was also observed in the extracellular matrix in specific areas of 3D organoids. C4 was detected in supernatant fluid from astrocyte monocultures and hiPSC-derived 2D bulk cultures. Further studies are needed to link C4A GCN with downstream effects in this experimental system.
54	Tian Yong Foong	Physical Science and Engineering	Who Bears the Load? Characterizing Collagen Fiber Recruitment Over the Corneoscleral Shell	Tian Yong Foong; Yi Hua, PhD; Alexandra Gogola, MS; Ian A. Sigal, PhD	To characterize pressure-induced collagen fiber recruitment across the corneoscleral shell. Methods: Using experimentally-measured collagen fiber crimp we constructed a 3D model of the corneoscleral shell with seven mechanically distinct regions: cornea and limbus, anterior-equator, equator, posterior-equator, posterior, peripapillary. We then simulated an intraocular pressure increase of 50 mmHg and quantified pressure-induced collagen fiber uncrimping and recruitment. Results: All regions exhibited sigmoid recruitment curves, but recruitment rates varied substantially. At low pressures, collagen fibers in the posterior equator were recruited the fastest, such that at a physiologic 15 mmHg over 90% of fibers had been recruited, compared with only a third in the cornea and peripapillary sclera. At an elevated 50 mmHg, collagen fibers in the limbus and anterior/posterior equator had been almost fully recruited (~ 100%), compared with ~ 90% in the cornea and posterior sclera, and ~ 75% in the peripapillary sclera and equator. Conclusions: Collagen fibers across the corneoscleral shell are not recruited simultaneously, indicating region-dependent rate of tissue stiffening with IOP. This information is critical to understand the role of microstructure in eye physiology, aging, and in biomechanics-related ocular diseases, such as glaucoma.
55	Jooli Han	Physical Science and Engineering	Soft Robotic Bi-Ventricular Sleeve for Long-term Cardiac Support	Jooli Han, MS; Dennis R. Trumble, PhD	
56	Beihong Ji, MS	Physical Science and Engineering	Mechanism of Drug-Drug Interaction between Opioids and Benzodiazepines	Beihong Ji, MS ;Ying Xue, PhD; Lirong Wang, PhD; Xiang-Qun Xie, PhD; Junmei Wang, PhD	Recently concurrent use of opioids and benzodiazepines (BZDs) has aroused high attention in the world. Combining opioids and BZDs can be unsafe and lead to severe side effect. Many researchers have attempted to understand the mechanism of the drug-drug interactions between opioids and BZDs but there is not a theory which has been accepted in explaining it. In this work, we attempt to study the mechanism of drug-drug interaction between opioids and BZDs. Our research is divided into two parts: the PK modeling and the pharmacological study. For the first part, we applied PySB and SimBiology to investigate how BZD inhibits the metabolism of opioids. As for physiological part, we used the Schrodinger software to perform docking simulations to predict the binding poses of opioids and BZDs binding to μand κ opioid receptors. We found that there was drug-drug interaction between opioids and BZDs. Our study suggests that both the PK and pharmacological factors contribute to the drug-drug interaction between these two drugs. Although PK is the minor factor for normal use of the two drugs, overdosage of BZDs can significantly increase the drug-drug interaction. The pharmacological factor should contribute more to the interaction between the two types of drugs.
57	William Conkright, MS	Physical Science and Engineering	Mission Profile Characteristics of a Special Forces Deployment in Afghanistan	William R. Conkright, MS; Nicholas D. Barringer, PhD; James P. McClung, PhD	Army Special Operations Forces (SOF) carry heavy loads, resulting in high energy output. Energy expenditure in excess of intake results in weight loss, impaired performance, and increased injury risk. This survey-based study was to determine the energy expenditure of SOF Soldiers conducting missions in the Central Command (CENTCOM) region. Demographics of the participants were as follows: age (yrs) 30±3.5, height (in) 70.65±2.8, weight (lbs) 195.2±24, years in Army 8.3±3.9, and total time deployed during career (yrs) 1.26±1.2. Surveys were collected from 46 personnel operating in eight locations in Afghanistan during February 2018. Surveys revealed the mission energy requirements and difficulty of exertion. Multiple factors surrounding mission intensity were used to calculate energy expenditure estimations using a recently published SOF-specific equation. Ninety percent of respondents reported carrying a load 40% heavier than the recommended fighting load (32.9±8.62 vs. 21.8 kg, respectively). Average estimated energy expenditure (4848±525 kcal/day) exceeded the military dietary reference intake of 3400 kcal/day. Nearly all respondents reported a rate of energy expenditure exceeding the benchmark of 300 kcal/hr necessary to maintain adequate energy reserves upon enemy contact. Attention must be given to pack weights and nutrition strategies aimed at meeting mission demands and recovery from strenuous activity.

Poster #	Presenter	Topic	Title	Author(s)	Abstract
58	Kellen Krajewski, MS	Physical Science and Engineering	Exploratory Analysis of Ground Reaction Forces During Loaded and Unloaded Marching at Different Velocities	Kellen T. Krajewski; Camille C. Johnson; Dennis E. Dever; Alex Rawcliffe; Scott Graham; Richard Simpson; Chris Connaboy	Ground reaction force variability and changes in impulse could be indicative of maladaptive motor control when performing load carriage tasks. Current military load carriage screening involves time to completion tests. Novel methods assessing entire waveform gait variability should be assessed. Purpose: to assess vertical ground reaction force kinetics differences at different loads and velocities for walk/run tasks. Methods: Six healthy adult subjects performed two trials, five minutes each of an unloaded condition (UL) and a loaded condition (LD) with 30% of their body mass. Velocity linearly increased every minute. Descriptive statistics were performed on impulse, GRF waveform plots constructed, and hierarchy cluster analysis conducted for each load condition and stage. Results: Mean impulse for UL at each stage were: stage 1=4.93?0.2NS, stage 2=4.58?0.22 NS, stage 3=4.23?0.21NS, stage 4=3.64?0.33NS. Mean impulse for LD at each stage were: stage 1=4.98?0.3NS, stage 2=4.52?0.22NS, stage 3=4.07?0.32NS, stage 4=3.11?0.45NS. Conclusion: Lower impulse magnitudes for the LD can indicate smaller propulsive forces and greater force absorption and energy dissipation. Variability was greater stride to stride during LD. Greater variability during a linear gait task could portend an injury. Hierarchy clustering identified one individual with more stride variability, that a simple time to completion task would not.
59	Sooraj Sharma	Physical Science and Engineering	Self-Cleaning and Antireflective Nanostructured Glass Substrates for Energy Efficient Solar Cells	Sooraj Sharma, BS; Sajad Haghanifar, MS; Paul Leu, PhD	The poor electrical conversion efficiency of conventional solar cells employed in residential as well as commercial areas has been shown to be directly affected by surface-level phenomena, such as fouling from pollutants and particulates and specular reflection. Existing substrates used in photovoltaics such as low iron tempered glass and fused silica display an inability to prevent energy losses due to these issues, but the introduction of various nanofabrication processes to change the properties of these substrates could eliminate them altogether. Namely, the introduction of nanostructures of varying morphologies onto the surfaces of these substrates through techniques such as reactive ion etching and plasma-enhanced chemical vapor deposition allows for anti-soiling, self-cleaning, and antireflective properties. Our research focused on the synthesis and testing of fused silica with anti-soiling/self-cleaning nanostructures, antireflective subwavelength nanostructures, and hybrid self-cleaning, anti-reflective properties. A Bayesian optimization algorithm was utilized in order to streamline our workflow and reduce dependence on experimental intuition when manipulating multiple experimental parameters. The droplet contact angle of water and various oils, as well as the light transmission of the glasses, was measured and superomniphobicity (WCA: 155.1 OCA: 149.6) and a high degree of antireflection (95.7% transmision) were observed across our samples.
60	Shixiong Jing	Physical Science and Engineering	Parallelization of Eager Prim's Algorithm with Performance Analysis	Shixiong Jing; Evan W. Gretok; Alan D. George	Minimum spanning tree problem, referring to finding a set of edges linking all the vertices in a given graph with minimum total edge weight, has been a fundamental problem faced in different fields. Among all the algorithms developed for minimum spanning tree problem, the Eager Prim's algorithm is one of the most famous and most broadly used approaches. For a given linked graph G(e, v) with v vertices and e edges, the Eager Prim's algorithm reduces the runtime to O(e log(v)) from Lazy Prim's by making the priority queue index-able and eliminating the size of priority queue. Restricted by the fact that the minimum spanning tree can only grow vertex by vertex, the Eager Prim's algorithm appears to be highly sequential and hard to parallelize in the normal way. The objective of this project is to parallelize the Eager Prim's algorithm by building partial spanning tree independently from different start point and analyze its performance in different scenarios.
61	Aria Eppinger	Translational Life Science	Serum Marker of Glyphosate Exposure Associated with Changes in Oral and Gut Microbiome Composition	Aria Eppinger; Alison Morris, MD	The oral cavity and digestive system contain beneficial and harmful bacteria. Imbalance in these microbiomes, called dysbiosis, is linked to diseases such as cancer. Therefore, eliminating causes of dysbiosis represents an important public health issue. Glyphosate, an ingredient in weed killers such as Roundup, is found on common foods and in human urine. It is unknown whether consuming glyphosate-laden foods leads to gut or oral dysbiosis in humans. This study analyzed the association between serum glyphosate levels, measured using a competitive ELISA, and the composition of oral and gut bacteria from 16S rRNA V4 sequencing data in 96 human participants. In the oral and gut microbiomes, higher serum glyphosate levels correlated with abundance changes in two and seven genera, respectively (p=0.01 to p =0.12). Some genera that increased in abundance with higher glyphosate levels are linked to disease. For example, high abundance of Escherichia/Shigella is associated with inflammatory bowel disease. Other genera that decreased in abundance serve beneficial functions for the host, such as Phascolarctobacterium, which produces short-chain fatty acids that may prevent colon cancer, diabetes, heart disease, and obesity. Preventing glyphosate exposure, especially through the food chain, can have important implications for public health.
62	Sarah Hogan	Translational Life Science	Temporal Dynamics of NREM Sleep in Older Adults with and Without Insomnia	Sarah E. Hogan; Gisela M. Delgado Rosado; Martica H. Hall; Daniel J. Buysse; Kristine A. Wilckens	Introduction: Although sleep in older adults with insomnia may be characterized by reduced slow wave sleep and increased high-frequency EEG activity, studies of NREM EEG do not consistently support this notion. Optimally restorative sleep, is thought to depend on the temporal dynamics of slow-wave activity and high frequency activity. Methods: Overnight EEG spectral power from 99 older adults with insomnia and 73 controls was analyzed across all NREM sleep, by NREM period, and by time within the first NREM period in multiple frequency bands using a combination of MANOVA and mixed model analyses. Results: In whole-night NREM, older adults with insomnia had marginally lower slow-oscillation power and significantly higher theta, alpha, sigma and beta power. Insomnia differences were not moderated by NREM period. Within the first NREM period, group differences in slow-oscillation power were significantly moderated by time. Conclusions: In addition to greater overall high frequency power in insomnia, generation of the slow-oscillation may be diminished, with an altered time course within the first NREM period. These findings may be used to target specific NREM sleep oscillation dynamics that contribute to daytime functions in older adults with insomnia.
63	Brady Marburger	Translational Life Science	Predicting Prognosis in Pediatric Liver Cancer: B-Catenin Mutations Drive Differential Survival in Hepatoblastoma	Brady Marburger; Ying Liu; Huabo Wang, PhD; Sucheta Kalkarni, PhD; Jie Lu; Weiqi Zhang; Jordan Mandel; Edward V. Prochownik, MD, PhD	Hepatoblastoma (HB), the most common pediatric liver malignancy, predominantly affects patients < 3 y/o. Survival depends on tumor stage, histology, macrovascular involvement, etc. It is unknown why patients present with differences in these features. 85% of HBs have mutations in b-catenin, a transcription factor with multiple targets involved in cell proliferation and differentiation. Unlike most oncogenes in which mutations tend to be restricted in number, b-catenin mutations are highly variable. We hypothesized that different mutations would impart different properties to tumors in a mouse model of HB, and would be associated with distinct histologic, transcriptional and metabolic features. We therefore induced HBs in groups of mice using 14 different patient-derived b-catenin mutant vectors. All mice developed HBs, and Kaplan-Meier curves indicated stratification of mutants into four groups. Survival outcomes did not correlate with type or location of mutation. Metabolic analysis of pyruvate dehydrogenase activity, fatty-acid b-oxidation, and oxidative phosphorylation indicated a clear difference between normal liver and tumors. Each group of tumors also displayed unique metabolic profiles. Ongoing transcriptomic analysis suggested that survival and metabolic differences were linked to mutant-specific transcriptional profiles. We conclude that b-catenin mutational variability underlies differential tumor growth, survival, and the other clinical behaviors of HB.

Poster #	Presenter	Topic	Title	Author(s)	Abstract
64	Hannah Apfelbaum	Translational Life Science	Social Withdrawal in Early Childhood Is Associated with Greater Activation in the Ventral Striatum During Passive Viewing of Happy Faces	Hannah Apfelbaum, BS; Judith K. Morgan, PhD	Early childhood is a critical period for developing social engagement, or frequent and meaningful interactions with peers. We hypothesized that low social engagement as measured by parent-reported child social withdrawal in preschool and school-age would predict blunted response in the ventral striatum, thalamus, and precuneus, regions involved in social processing, when viewing happy and sad faces at school age. Participants were 24 emotionally healthy children followed longitudinally. Parents completed the Child Behavior Checklist (CBCL) at preschool age and again three years later. We combined the CBCL withdrawn subscales at each age into one score. Children completed an fMRI passive viewing task of adult happy, sad and neutral faces at school age. Unexpectedly, social withdrawal was associated with greater response in the ventral striatum during passive viewing of happy faces relative to neutral faces. There was no association between social withdrawal and neural response to sad faces. Greater responding to unfamiliar happy faces in this neural region involved in affective salience may partially explain why socially withdrawn children disengage in new social situations. Future investigation should follow socially withdrawn children with enhanced ventral striatal response to happy faces to ascertain if it predicts later anxiety disorders and social problems.
65	Joshua Zollman	Translational Life Science	Neural Concordance of Mother-Adolescent Dyads Is Related to Their Agreement on Adolescent Anxiety Symptoms, Depressive Symptoms, and Affect	Joshua W. Zollman, BS; Judith K. Morgan, PhD; Erika E. Forbes, PhD; Jill Cyranowski, PhD; Brittany K. Woods, MA	The development of healthy of parent-adolescent relationships relies on the ability of a parent and child to identify and respond to each other's mental states. The goal of this study was to identify parent-adolescent differences in coordination of neural response to better understand why some dyads have more harmonious relationships than others. We recruited 21 typically developing mother-adolescent dyads to complete questionnaires assessing both mother and adolescent perceptions of shared relationship quality, adolescent anxiety symptoms, and adolescent depressive symptoms. All participants separately underwent fMRI scanning while watching videos of unfamiliar mother-adolescent dyads engaging in positive and comforting interactions. Whole-brain cluster-wise analysis (pFWE< .001) across all participants revealed activation in response to the videos in areas implicated in theory of mind processing, including temporoparietal junction and middle frontal gyrus. Dyadic concordance of right temporoparietal junction activation predicted agreement of child anxiety and depression symptoms (Banxiety=.635, p<.05; Bdepression=.601, p<.05). Additionally, concordance of left middle frontal gyrus activation predicted agreement of child anxiety and affect (Banxiety=.660, p<.05; Baffect=.749, p<.05). Our results indicate that neural similarity of theory of mind-related brain regions may aid parents and offspring in understanding one another's affective states. This in turn could facilitate parental help for adolescent affective problems.
66	Meaghan Beckner, MS	Translational Life Science	Multi-Ingredient Pre-Workout Supplement Improves Cycling Anaerobic Power in Recreationally Active Men	Meaghan E. Beckner, MS; Brian J. Martin, PhD; Alexis A. Pihoker, MA; Matthew D. Darnell, PhD; Alicia L. Kjellsen, BS; Paul J. Arciero, PhD; Mita Lovalekar, PhD; Kim Beals, PhD; Shawn D. Glanagan, PhD; Bradley C. Nindl, PhD	Multi-ingredient pre-workout supplements (MIPS) have become a popular ergogenic aid to improve explosive power. PURPOSE: To examine the effectiveness of MIPS, one with beta-alanine and caffeine (BAC) and one without (NBAC), vs. placebo (PLA) on anaerobic performance. METHODS: Fourteen men (24.6 ± 5.0 years, 179.2 ± 5.9 cm, 84.3 ± 14.3 kg) participated in a randomized trial to assess anaerobic power and capacity. Subjects completed vertical jump (VJ), 30 repeated ballistic squats (RBS), and a 30 second Wingate anaerobic cycle test (WAnT) 30 minutes after ingestion of BAC, NBAC, or PLA. RBS peak power (RBSPP) and mean power (RBSMP) were calculated across the 30 reps. WAnT anaerobic power (WAnTAP) and anaerobic capacity (WAnTAC) was calculated relative to body mass. Comparisons across supplements were determined using one-way repeated measures ANOVA (p<0.05) and Bonferroni adjusted pairwise comparisons. RESULTS: WAnTAP was different across supplements (p=0.019). BAC WAnTAP (11.95 ± 0.85 W/kg) was higher than PLA (11.35 ± 0.66 W/kg, p=0.037), but not NBAC (11.54 ± 0.84 W/kg, p=0.319). There were no significant differences in WAnTAP between NBAC and PLA (p=0.703). No significant differences were observed across supplements in WAnTAC , RBSPP, RBSMP, or VJ. CONCLUSION: A MIPS can improve cycling anaerobic power.
67	Deepa Rajan, MD	Translational Life Science	The Neurogenetics Initiative: Clinical Data	The Neurogenetics Clinical Team at UPMC Children's Hospital of Pittsburgh	Many neurological conditions have a genetic etiology, making genetic testing an essential component of modern neurology practice. However, many probable neurogenetic conditions lack molecular diagnoses, and many known conditions lack treatment options. The Neurogenetics Initiative was established in 2017 to address these issues by promoting cross-disciplinary interactions between clinical and research teams. Our mission is twofold: to improve care for patients with neurogenetic conditions and to advance research on the underlying etiologies for these conditions. The clinical arm of this initiative is the Neurogenetics subspecialty clinic at UPMC Children's Hospital of Pittsburgh. The clinic is staffed by three neurologists, a clinical geneticist, and two genetic counselors. It offers neurological and genetic evaluations with extensive phenotyping, genetic counseling, and follow up care. Here, we highlight recent data from the first year of the Neurogenetics clinic including patient population, categories of testing, and testing outcomes
68	Jinman Cai, MS	Translational Life Science	Attenuation of a Subset of Protective Cytokines and CXC chemokines Correlates with Adverse Outcomes in Severely Injured Patients	Jinman Cai; Isabel Billiar; Yoram Vodovotz; Timothy R. Billiar; Rami A. Namas	Blunt trauma elicits a complex, multi-dimensional inflammatory response that is intertwined with late complications such as nosocomial infection and multiple organ dysfunction. Among multiple presenting factors (age and gender), the magnitude of injury severity appears to have the greatest impact on the inflammatory response which in turn correlates with clinical trajectories in trauma patients. Here, we sought to characterize the time course changes in 31 cytokines and chemokines in a large cohort of 472 blunt trauma patients and analyze the differences as a function of injury severity. The results showed that 21 inflammatory mediators were significantly higher in the severe group upon admission and over time vs the mild and moderate groups. However, 8 inflammatory mediators (IL-22, IL-9, IL-33, IL-21, IL-23, IL-17E/25, IP-10, and MIG) were significantly attenuated during the initial 16 h post-injury in the severe group when compared to the mild and moderate groups. These findings suggest that severe injury is associated with an early suppression of a subset of cytokines known to be involved in tissue protection and regeneration (IL-22, IL-33, IL-25 and IL-9), lymphocyte differentiation (IL-21 and IL-23) and cell trafficking (CXC chemokines) post-injury which in turn correlates with adverse clinical outcomes.
69	Alexander Clark	Translational Life Science	The Implications of Cerebral Vascular Amyloidosis on Blood Brain Barrier Integrity	Alexander Clark; Eric Abrahamson, PhD; Milos Ikonomovic, MD	After brain injury, the Neurovascular unit (NVU) undergoes degenerative changes resulting in increased Blood-Brain Barrier (BBB) permeability. Cerebral amyloid angiopathy (CAA) is the deposition of amyloid-β (Aβ) peptide around the NVU of cortical and meningeal vessels causing spontaneous intracranial hemorrhages. CAA is more prevalent in Alzheimer's disease (AD). Despite this clinical significance, temporal changes in NVU morphology due to CAA-associated vascular Aβ deposition are not characterized sufficiently. We hypothesize that vascular amyloid pathology decreases BBB integrity, resulting in altered PDGFR-β (pericyte), AQP4 (astrocyte end-feet), ZO-1 (endothelial tight-junction), and capillary density in a transgenic (Tg) mouse model of AD. We studied four groups: elderly control, juvenile control, elderly transgenic, and juvenile transgenic. Tg mice were APP/PS1 mutants with Aβ overproduction, compared to non-overproducing C57Bl6 wild-type (Wt). Coronal brain hemi-sections were chosen at hippocampal level and sampled using unbiased stereological principles. We examined 400 sites total using dual- and triple-labeled IHF for capillary density and NVU constituents, respectively. Confocal analysis yielded the following: Tg elderly averaged 13 pericytes per high-power selected regions, Tg juvenile averaged 16, Wt elderly averaged 25, and Wt juvenile averaged 43. The analyses support changes in pericyte number and morphology in normal aging and associated with amyloid pathology.

Poster #	Presenter	Topic	Title	Author(s)	Abstract
70	Mirna Bulatovic, PhD	Translational Life Science	Cisplatin Promotes Intrinsic and Reactive Immune Suppression in an Ovarian Cancer Mouse Model	Mirna Bulatovic, PhD; Shannon Grabosch, MD; Feitianzhi Zeng, MD; Tianzhou Ma, PhD; Lixin Zhang, MD, PhD; Malcolm Ross, MD; Joan Brozick, MS; George Tseng, PhD; Esther Elishaev, MD; Robert. P. Edwards, MD, PhD and Anda M. Vlad, MD, PhD	To assess the effect of chemotherapy on the immune microenvironment in ovarian cancer (OC). Methods: We analyzed in vitro the effect of cisplatin on human and murine OC cell lines with varying susceptibility to the drug. *In vivo* , we tested the effect of cisplatin in combination with PDL1 blockade in two syngeneic OC models that correspond to platinum sensitive and platinum resistant tumors, respectively. Results: *In vitro* and *in vivo* exposure to cisplatin triggers increased expression of tumor PDL1, an immune checkpoint molecule involved in immune suppression. However, at the same time, cisplatin also triggers upregulation of several genes involved in antigen presentation and T cell recognition, suggestion its pro-immunogenic role. Mice with platinum sensitive tumors showed increased survival in response to cisplatin or anti-PDL1 alone. In contrast, cisplatin/anti-PDL1 treatment combination triggered significantly longer survival in mice with moderately resistant tumors. Conclusion: Our results demonstrate that cisplatin exposure triggers dichotomous effects in OC: it increases the potential for recognition by immune cells, while also triggering PD-L1 upregulation. Importantly, these results provide the rationale for cisplatin in combination with PDL1 blockade.
71	Marie Gerges	Translational Life Science	RAR and RXR Agonists as Novel Therapeutic Agents for IDH Mutant Gliomas	Marie Gerges; Aparna Rao, PhD; Nduka Amankulor, MD	70-90% of diffuse gliomas carry a mutation in the isocitrate-dehydrogenase (IDH) gene. IDH mutant gliomas downregulate retinol-binding protein 1 (RBP1), a protein that facilitates the generation of retinoic acid (RA). The binding of RA and its receptor complex (either RAR or RXR) induces the transcription of NKG2D ligands, including ULBP1 and ULBP3. NKG2D ligands interact with NKG2D receptors on Natural Killer (NK) cells, enabling them to recognize and attack target cells. Our previous studies have shown that treating IDH mutant gliomas with All-trans Retinoic Acid (ATRA) induces the upregulation of NKG2D ligands. We sought to compare the therapeutic efficacy of two isoforms of retinoic acid: Bexarotene, a pan-RXR agonist, and AM80, an RARα agonist. We treated IDH mutant cells with either Bexarotene or AM80 at varying doses and timepoints. After treatment, we assessed cell viability and gene expression of ULBP1 and ULBP3. For both Bexarotene and AM80, IDH mutant cell death increased in a dose-dependent and time-dependent manner. As observed via qPCR and luciferase expression studies, expression of ULBP1 and ULBP3 increased one- to four-fold in Bexarotene-treated cells (as compared with controls). In AM80-treated cells, gene expression of ULBP3 increased two-fold at the highest dose (100 uM) tested.
72	Feng Li, MD, PhD	Translational Life Science	Damage Associated Molecular Pattern Molecules (DAMPS) Are Involved in Initiating Tendon Inflammation and Eventual Degeneration	Feng Li; Jianying Zhang; Daibang Nie; Guangyi Zhao; Kelly Williamson; James H-C. Wang	Damage-associated molecular patterns (DAMPs) are endogenous molecules that are released into the extracellular space under conditions of activation, cellular stress, or tissue damage. High mobility group box 1(HMGB1) as a DAMPS plays a critical role at the intersection of the host inflammatory response to sterile threat by tissue damage. Mechanical overloading is considered to cause tendinopathy, but the mechanism underlying the tendinopathy development is unclear. Here we show for the first time that mechanical overloading of tendon cells induces HMGB1 translocation from nucleus to cytoplasm and then releases to extracellular matrix, thereby eliciting inflammatory and catabolic responses in tendon cells as marked by upregulation of COX-2 expression, and PGE2 and MMP3 production. Application of a natural triterpene glycyrrhizin (GL), a specific inhibitor of HMGB1, blocks the inflammatory/catabolic responses in tendon cells. Moreover, intensive treadmill running leads to typical degenerative changes in mouse Achilles tendons, whereas GL administration completely blocks the tendinopathy development. Collectively, our study identifies HMGB1 as a key molecule that is responsible for the induction of tendinopathy due to mechanical overloading placed on the tendon. Blocking HMGB1 with its inhibitor could be a novel therapeutic strategy for preventing tendinopathy development, thus potentially benefiting millions of tendinopathy patients.
73	Ge Yang, MD	Translational Life Science	Serum Cadmium and Lead, Wheezing and Lung Function in a Nationwide Study of Adults in the United States	Ge Yang, MD; Tao Sun, PhD; Yueh-Ying Han, PhD; Franziska Rosser, MD, MPH, FAAP; Erick Forno, MD, MPH; Wei Chen, PhD; Juan C. Celedón, MD, DrPH, FAAAAI	Background: Little is known about heavy metal exposure and respiratory diseases in US adults. Objective: To examine the reaction between serum level of cadmium or lead and current wheeze and lung function in US adults. Methods: Cross-sectional study of 13,898 adults aged 20 to 79 years old in the 2007-2012 National Health and Nutrition Examination Survey. Logistic or linear regression was used for the multivariable analysis of serum cadmium or serum lead and the outcomes of interest. Results: Exposure to the 4th quartile of serum cadmium (odds ratio=2.2, 95% CI = 1.78, 2.73) or serum lead (odds ratio=1.3, 95% CI = 1.03, 1.63) was significantly associated with increased odds of current wheeze. Serum levels of cadmium and lead were significantly and inversely associated with decline in % predicted FEV1, % predicted FEV1/FVC and FENO in all adults, with more pronounced reductions in those who had current wheeze and were current smokers. Conclusion: Our findings suggest that exposure to cadmium or lead is related to current wheeze and worse lung function in US adults.
74	Ned Mitrovich, Jr.	Translational Life Science	Metabolic and Phenotypic Effects of TIM-3 Ligation Inhibition on CD8+ T Cells	Ned Mitrovich, Jr.; Amber G. Huang; Susheel K. Khetarpal; Elizabeth L. McMichael, PhD; Lawrence P. Kane, PhD; Robert L. Ferris, MD, PhD	T cell immunoglobulin and mucin domain (Tim)-3 is a prospective target molecule in reversing T cell exhaustion. Tim-3 is of particular interest, due to its overexpression following anti-PD-1 monotherapy in head and neck cancers, with only 15% of treated patients experiencing a durable response. Pharmaceutical collaborators provided three different monoclonal antibodies (mAbs) specific for Tim-3. While it is established that they bind to this receptor, it is currently unknown if they prevent Tim-3 ligation on CD8+ T cells. Tim-3-specific antibodies will block the inhibitory receptor-ligand interaction, reinstating effector functions. The metabolic and phenotypic effects of Tim-3 receptor ligation in CD8+ T cells were examined using “exhausted” PBMC from healthy donor controls or freshly isolated TIL from HNSCC patients as well as flow cytometry and several *in vitro* assays for cell examination. Each Tim-3 mAb increased IFN-γ secretion above levels of the exhausted cells. Tim-3 mAb 1 increased mitochondrial mass the most during contact with HMGB1, while all of the Tim-3 mAbs in contact with galectin-9 increased mitochondrial mass. Tim-3 mAbs are capable of inhibiting ligation to an extent, leading to select recovery in our studied effector functions. Efforts focused on determining the exact effects of the antibodies are ongoing.
75	Alice LaGoy, MS	Translational Life Science	Action Boundary Perception Across 30-Days in an Isolated, Confined, and Extreme Environment	Alice D. LaGoy, MS; Aaron M. Sinnott, MS; Kellen T. Krajewski, MS; Richard J. Simpson, PhD; Joanne L. Bower, PhD; Candice A. Alfano, PhD; Christopher Connaboy, PhD	The inability to perceive changes in action possibility due to changing action boundaries, the thresholds where an action is possible, may increase the risk adopted during a task. It is unknown how isolated, confined and extreme environments (ICE) affect action boundary perception (ABP). PURPOSE: Investigate ABP changes during 30-day Human Exploration Research Analog (HERA) missions. METHODS: Sixteen subjects completed the perception-action coupling task (PACT), a novel ABP task, on days 3, 10, 17, 24 and 5 days post-mission. PACT presents virtual balls and apertures varying in ball to aperture size ratio (B-AR) about the action boundary. Subjects determined whether balls could fit through apertures, then responded accordingly. 8 (ratio) x 5 (time) ANOVAs were performed assessing response time (RT), accuracy (ACC) and lapse changes. RESULTS: Day 24 RT ($F_{4,60} = 3.631$, $p = 0.010$) was faster (0.738 ± 0.088s) than day 17 (0.768 ± 0.092s). Other timepoints, ACC and lapses did not vary during the mission ($p > 0.05$). RT ($F2.583,38.742 = 42.815$, $p < 0.001$) increased and ACC ($F1.423,21.341 = 42.815$, $p = 0.002$) decreased near the action boundary. CONCLUSION: Minimal change in ABP performance was observed suggesting ABP is not compromised by a 30-day ICE analog assessment.

Poster #	Presenter	Topic	Title	Author(s)	Abstract
76	Eva Chernoff	Translational Life Science	Discrimination and Structural Bias Against Sexual and Gender Minority Medical Trainees: A Qualitative Analysis	Eva Chernoff, BS; Mary Hawk, DrPH; Ron Stall, PhD; David Finegold, MD	Sexual and gender minority (SGM) medical trainees can train and work in environments that are discriminatory towards both SGM patients and as well as medical practitioners. Although some studies have been completed regarding SGM medical trainee discrimination, there remains to be a lack of current and relevant research on the subject of mistreatment of SGM medical trainees. Qualitative research is necessary to understand the social and cultural context from which students and residents are experiencing discrimination, how they feel they should address it, and issues surrounding reporting. The main research question for this project is: What is the experience of medical training for medical trainees who identify as SGM? METHODOLOGY: Several weeks were spent interviewing medical students and residents who identify as SGM. A total of 6 interviews were completed. Interviews are being analyzed qualitatively using Nvivo software to identify and determine common themes among responses. The final themes identified will establish the current professional issues that SGM medical trainees face in today's medical training environment. RESULTS: Results of this study are currently in the process of analysis and all themes identified will be included in the final poster presentation.
77	Will Okoniewski	Translational Life Science	Glucose Control and Lung Function Recovery During Acute Pulmonary Exacerbations in Patients with Cystic Fibrosis-Related Diabetes	Will Okoniewski; Erick Forno, MD, MPH; Kara Hughan, MD; Daniel Weiner, MD	Pulmonary disease remains the most significant determinant of morbidity and mortality in cystic fibrosis (CF). Objective: To determine whether glucose control in patients with CF-related diabetes (CFRD) affects recovery from acute exacerbations. Methods: Retrospective analysis of FEV1 recovery during hospitalizations for pulmonary exacerbation among CFRD patients ages 6-21 years. Main outcome was FEV1 recovery. Glucose control defined as area under the curve (AUC) and hemoglobin A1c. Analysis performed using adjusted longitudinal analysis. Results: A total of 67 hospitalizations were analyzed. Higher glucose AUC was associated with greater FEV1 recovery at discharge: for each log-unit higher AUC, FEV1 recovery was 7.2% higher (95%CI=0.2% to 14.1%, P=0.044). However, among patients who did not stay in the hospital for the full treatment (i.e., completed IV antibiotics at home), AUC was associated with lower FEV1 at follow-up: for each log-unit higher AUC, FEV1 was 27% lower (95%CI=-2.3% to -51.8%, P=0.033). Conclusions: In patients with CFRD, glucose AUC is associated with greater FEV1 acute recovery, but also with further FEV1 decrease at follow-up. Patients with CFRD and poor glucose control may benefit the most from acute hospital treatment, but some may deteriorate again if discharged home early on.
78	Libing Yang, MDc	Translational Life Science	Alterations in Oral and Gut Microbiota in HIV-Infected Individuals Related to Chronic Obstructive Pulmonary Disease (COPD)	Libing Yang, MDc; Adam Fitch, MS; Kelvin Li, MS; Joesph Huwe, BS; S. Mehdi Nouraie, MD, PhD; Rebecca DeSensi, MS; Ken S. Ho, MD, MPH; Jeremy J. Martinson, DPhil; Barbara Methé, PhD; Alison Morris, MD, MS	HIV infection is a risk factor for COPD, but mechanisms involved are poorly understood. Alterations in the microbiome are a possible mechanism of disease development. METHODS: HIV-infected and -uninfected men performed spirometry and diffusing capacity for carbon monoxide per guidelines and had oral and stool samples collected. Sequencing of 16S rRNA gene on Illumina MiSeq was performed to characterize the composition of oral and gut microbiota. RESULTS: In saliva samples, the oral microbiome composition of HIV-infected individuals was significantly different compared to HIV-uninfected individuals (Permanova p-value=0.0002). Microbiome profile alterations (p-value=0.008) and lower alpha diversity (p-value=0.018) were seen in HIV-infected individuals with reduced diffusing capacity for carbon monoxide (DLCO), compared to those with normal DLCO. However, among HIV-uninfected individuals, microbiome communities were taxonomically overlapping between groups with/without an abnormal DLCO. For stool samples, the gut microbiome communities of HIV-infected individuals were different from those of HIV-uninfected (p-value=0.005), but there was no relationship to lung function in either group. CONCLUSIONS: Next-generation sequencing identifies oral and gut microbiota alterations in HIV-infected individuals. The oral microbiome was altered in HIV-infected individuals with abnormal lung function, but not in HIV-uninfected individuals, suggesting a potential unique relationship of the microbiome to lung disease in HIV.
79	Shawn Eagle, MAT	Translational Life Science	Leveraging Machine Learning Techniques to Reveal Relationships Between Neuromuscular Traits in Previously Concussed Warfighters	Shawn R. Eagle, MAT; Qi Mi, PhD; Shawn D. Flanagan, PhD; Bradley C. Nindl, PhD; Kim Beals, PhD; Chris Connaboy, PhD	Recent studies have demonstrated an increased risk of musculoskeletal injury following concussion, but the underlying mechanisms are still unknown. Purpose: To compare military personnel with a concussion history in the previous 2 years (CH) with matched controls (NCH) in physiological, musculoskeletal and biomechanical performance using independent samples statistics (Aim 1) and using a machine learning decision tree algorithm (Aim 2). Methods: Air Force Special Operations Command Operators and Naval Special Warfare Operators self-reported injury history, and completed physiological, musculoskeletal, and biomechanical analysis. A one-way Analysis of Variance (ANOVA) was used to compare CH (n=24) to NCH (n=24; Aim 1), as well as the C5.0 decision tree algorithm (Aim 2). Results: The C5.0 algorithm revealed CH demonstrated quicker time to peak knee flexion angle during the single-leg landing task (<=0.170 secs; CH: n=22 vs. NCH: n=14), longer time to peak torque in knee extension isokinetic strength testing (>500 msecs; CH: n=18 vs. NCH: n=4) and larger knee flexion angle at initial contact (>7.7°; CH: n=18 vs. NCH: n=2). Conclusion: This study revealed differences between Warfighters in neuromuscular traits based on CH using the C5.0 machine learning algorithm. Future research should assess if neuromuscular changes following concussion are related to injury risk.
80	Aaron Sinnott, MS	Translational Life Science	Prolonged Exposure to an Isolated, Confined, and Extreme Environment: Impact On Vigilance and Cognitive Function	Aaron M. Sinnott; Kellen T. Krajewski; Alice D. LaGoy; Richard J. Simpson; Joanne L. Bower; Candice A. Alfano; Christopher Connaboy	Astronauts are required to perform a variety of cognitively demanding tasks in the face of psychosocial stressors occurring throughout extended periods in isolated, confined and extreme (ICE) environments. However, vigilance and cognition have not collectively been studied during a long-duration ICE environment exposure. PURPOSE: Investigate vigilance and cognition during an ICE environment simulation. METHODS: 110 participants were assigned to either inland or coastal Antarctic sites and completed the Psychomotor Vigilance Task (PVT) and Spaceflight Cognitive Assessment Tool for Windows (WinSCAT) each month. A series of 2 (site) X 5 (time) ANCOVAs were conducted to evaluate monthly performances between sites whilst controlling for time of day. RESULTS: A within-subjects' effect was identified for WinSCAT performance (p<.01); post-hoc analysis revealed an improved performance at months 2-4 compared to month 1 (p<.01). Between-subjects' effects were identified for PVT as the coastal site had a longer (worse) RT at month 4 (p=.029), and more lapses at months 1 (p=.03), 3 (p=.02) and 4 (p<.01). No between-site differences in WinSCAT performance or interactions for any outcome were observed. CONCLUSION: Vigilance and cognitive performance were marginally affected during an ICE environmental simulation. Other factors require consideration to comprehensively understand the deleterious effects of ICE environment exposure.
81	Dale Erikson	Translational Life Science	Lead Optimization through Reverse Synthesis Exploration	Dale Erikson; David Koes, PhD	Lead optimization is an important step in the drug discovery process. Before this point, a ligand is found to bind to a protein target and have some druggable effect. However, it has the potential to be enhanced. With lead optimization, the ligand can be modified to improve its solubility, bioavailability, binding affinity and other drug properties. In this project, a synthetic approach is used in order to explore the vast chemical space. Using a large data set of chemical compounds and organic reactions, a subset of molecular structures is chosen for each reaction. These subsets are chosen based on a substructure match to one of the retrosynthetic schemas. From this subset, a fragment library is built and the original lead undergoes an effective fragment substitution at a given reaction site. 3D conformers are then generated and the new in silico compounds are scored. Results have indicated that this process is scalable and the retrosynthetic breakdown can efficiently explore the accessible chemical space while optimizing a lead.

Poster #	Presenter	Topic	Title	Author(s)	Abstract
82	Matthew Demers	Translational Life Science	R430: A Potent Inhibitor of DNA and RNA Viruses	Leonardo D'Aiuto; James McNulty; Caroll Hartline; Matthew Demers; Raj Kalkeri; Joel Wood; Lora McClain; Ansuman Chattopadhyay; Yun Zhi; Jennifer Naciri; Adam Smith; Robert Yolken; Kodavali Chowdari; Carlos Zepeda-Velazquez; Chanti Babu Dok	Acyclovir (ACV) is an effective antiviral agent for treating lytic Herpes Simplex virus, type 1 (HSV-1) infections, and it has dramatically reduced the mortality rate of herpes simplex encephalitis. However, HSV-1 resistance to ACV and its derivatives is being increasingly documented, particularly among immunocompromised individuals. The burgeoning drug resistance compels the search for a new generation of more efficacious anti-herpetic drugs. We have previously shown that trans-dihydrolycoricidine (R430), a lycorane-type alkaloid derivative, effectively inhibits HSV-1 infections in cultured cells. We now report that R430 also inhibits ACV-resistant HSV-1 strains, accompanied by global inhibition of viral gene transcription and enrichment of H3K27me3 methylation on viral gene promoters. Furthermore, we demonstrate that R430 prevents HSV-1 reactivation from latency in an ex vivo rodent model. Finally, we provide evidence that R430 effectively inhibits other DNA viruses as well as RNA viruses, including Zika virus. Its therapeutic index is comparable to standard antiviral drugs, though it has greater toxicity in non-neuronal cells than in neuronal cells. Synthesis of additional derivatives could enable more efficacious antivirals and the identification of active pharmacophores.
83	Kyle Feldman	Translational Life Science	Cardiac Targeting Peptide, A Novel Cardiac Vector: Studies in Biodistribution, Mechanisms of Transduction and Imaging Application	Kyle S. Feldman, BS; Timothy Feinstein, PhD; Maliha Zahid, MD, PhD	Our prior work utilizing a combinatorial approach of *in vitro* followed by in vivo phage display identified a 12-amino acid long, synthetic non-naturally occurring peptide that we termed cardiac targeting peptide (CTP) due to its ability to transduce the murine heart in vivo with peak uptake at 30 minutes following an intravenous injection. We hypothesized that the transduction capability will be localized to either C- or N-terminus. CTP was synthesized in its native full-length form (NH2-APWHLSSQYSRT-COOH), as well as an N-terminus 6 amino acid called CTP-A (NH2-APWHLS-COOH), or as CTP-B (NH2-SQYSRT-COOH). A random, linear, 12-amino acid long peptide (RAN: NH2-STLMKFCYVEQN-COOH) was also synthesized to serve as control. All peptides were fluorescently labeled with Cyanine5.5 (Cy5.5). Confocal and flow cytometry based peptide transduction assays were performed using isolated, beating neonatal mouse cardiomyocytes (CMC) and H9C2 cells, a rat cardiomyoblast cell line. Our results demonstrate that both versions of CTP retained the ability to transduce CMCs but the full-length CTP was superior in its transduction abilities of CMCs and H9C2 cells over truncated 6-amino acid N- or C-terminus versions. Further studies are needed to elucidate the mechanism of transduction that could provide insights into mechanism of cell entry.
84	Adam Smith	Translational Life Science	Generation of 3D Human Neuronal Cultures: Modeling CNS Viral Infections	Adam Smith; Leonardo D'Aiuto, PhD; Jennifer N. Naciri; Matthew Demers; Paul Kinchington, PhD; David C. Bloom, PhD; Vishwajit L. Nimgaonkar, MD, PhD	Human induced pluripotent stem cells (hiPSCs) have revolutionized modeling of neurological disease and CNS neural infections because they can be differentiated into limitless numbers of neuronal cells that follow human neurodevelopmental patterns. We have developed scaffold free 3D cultures to enable more realistic models of infection with herpes simplex virus type 1 (HSV-1). Methods: A prototype of scaffold-free adherent 3D (A-3D) human neuronal cultures in 96-well plates was generated from hiPSCs-derived neural progenitor cells (NPCs). A-3D neuronal cultures were infected with a genetically engineered herpes simplex virus type 1 (HSV-1) construct incorporating enhanced green fluorescent protein (EGFP) and red fluorescent protein (RFP) as reporter genes with or without acyclovir (ACV) and IC50 for ACV determined using flow cytometry (FC) and a confocal based CX7 platform (Fischer Scientific). Results: The IC50 of ACV determined by using FC and CX7 platform were similar showing 3.14 μM and 3.12 μM concentration respectively. Conclusion Our A-3D human neuronal cultures, paired with a novel confocal-based HCS platform (CX7), provide an unprecedented opportunity to develop a rapid and robust drug screening tool for CNS infections. This is the first study demonstrating the feasibility of antiviral drug screening in 3D hiPSC-derived neuronal platforms.
85	Shirley Jiang	Translational Life Science	The Effect of Overexpression of an OCD-Associated Gene On Behavior and Neural Activity	Shirley Jiang; Jared M. Kopelman; Susanne E. Ahmari, MD, PhD	Obsessive-compulsive disorder (OCD) is a neuropsychiatric disorder characterized by obsessive thoughts and compulsive behaviors. The cause of OCD is unknown, but family and twin studies show that genetics play a significant role in the development of OCD. Multiple polymorphisms of the gene SLC1A1 have been associated with OCD, the most common of which increases expression of its protein product, excitatory amino acid transporter-3 (EAAT3). To model the changes caused by this polymorphism, our lab created a mouse line that employs an inducible gene expression system to overexpress EAAT3, with reversal of this overexpression by administration of doxycycline. Our results show that EAAT3-overexpressing (OE) mice are more susceptible to the development of stereotypy, a repetitive behavior, following the administration of amphetamine. To examine the neural activity underlying this behavior, we performed cFos immunohistochemistry in the patch and matrix compartments of the striatum. The administration of amphetamine increased cFos in patch relative to matrix in both wildtype and OE mice, and this increase did not correlate with stereotypy behavior. This indicates that striatal patch to matrix cFos expression may be a marker of amphetamine-induced behavior in general, while different mechanisms may underlie the increased susceptibility to stereotypy seen in OE mice.