

Friday, October 9 – 1:00 p.m. Poster Session

Sorted by Poster Number				
Name	Poster Number	Poster Abstract	Poster Title	Authors
Isabelle Viana	1	HIV-1 vaccine development approaches currently focus on stimulation of pan-neutralizing antibodies (pnAbs). Our goal is to engineer antigenic structures capable of inducing B-cell secretion of HIV-1 pnAbs. These neutralizing epitopes are masked or structurally dynamic, resulting in weak antibody response in natural infections. The Envelope membrane-proximal external region (MPER) is one of those target sites for the pnAbs 2F5, Z13 and 4E10. We postulated that conformationally stable structures are better immunogens and can elicit the production of better antibodies. To test this we have engineered a protein with increased exposure of a stable	Structure-Guided Design of an Affinity-Enhanced Protein Displaying the Broadly Neutralizing HIV-1 2F5 Antibody Epitope: Toward the Next-Generation Vaccines and Implications for Immunogen Design	Isabelle F.T. Viana, PhD; Eduardo Nascimento, PhD; Jodi Craigo, PhD; Marco Krieger, PhD; Robbie Mailliard, PhD; Rafael Dhalia, PhD; Roberto Lins, PhD; Ernesto Marques, MD, PhD

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		<p>conformation of the 2F5 epitope. We grafted the 2F5 epitope into a scaffold protein Top7 (Top7-2F5 chimera) and molecular dynamics (MD) simulations and circular dichroism analysis confirmed the structural stability of Top7-2F5. ELISA and surface plasmon resonance assays showed that the 2F5 pAb exhibits a superior affinity to the Top7-2F5 as compared to the isolated 9-mer and 23-mer MPER peptides. Following, 2F5-specific memory B-cells from patient-derived PBMCs were identified by flow cytometry. The Top7-2F5 ability to activate the identified cells and to induce pAbs secretion in vitro is being evaluated. These results show that MD simulations can help engineer vaccine antigens capable of enhancing protective</p>		
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		antibody responses.		
Madeline Lee	2	<p>Introduction: Acrolein is a highly reactive aldehyde. Lethal doses can be found in smoke from house fires and terrorist attacks causing acute lung injury. Our aim is to characterize acrolein-induced acute lung injury in mice as a model to develop therapies. We performed bronchoalveolar lavages (BAL) in acrolein-exposed mice to assess lung cell composition and protein levels.</p> <p>Methods: Female C57BL/6J mice (6-8wk) were exposed to 45ppm acrolein (35min). BAL was performed 6H or 12H after exposure. The BAL was centrifuged (500g x10min) and the supernatant used for protein assay. The cell pellet was resuspended and used for total cell count and differential cell count. Results: BAL protein concentration</p>	Characterization of Acrolein-Induced Lung Injury	Madeline Lee, Kiflai Bein PhD, Rahel Birru, Natalya Bondarchuk, George Leikauf PhD

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		<p>increased in the acrolein-exposed mice with time. Total BAL cell count was significantly higher in the unexposed than the acrolein-exposed mice. Although macrophages were the main cell type in the BAL, the percentage decreased, as did the total macrophage count. The percent and total count of neutrophils increased with time. Conclusions: Findings suggest that acrolein exposure increased lung membrane permeability and pulmonary edema, resulting in increased protein concentration and increased inflammation, resulting in increased neutrophils – indicative of acute lung injury. Acrolein exposure may also activate macrophage cell adhesion and reduced recovery.</p>		
Rohan Chalasani	3	Background: Plasma cell-rich acute	A Novel Analysis Tool Explores Mechanisms of Graft Rejection	Rohan Chalasani, Thin Maw, Chethan Puttarajappa, Puneet

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		<p>transplant rejection (PCAR) represents a distinct clinicopathologic entity and portends failure of renal and liver transplants. Pathogenesis of PCAR is not well-understood and definitive treatment guidelines are lacking. Current attempts to treat PCAR, based on targeting plasma cells, have been unsuccessful and necessitate better understanding of rejection mechanisms. Methods: Stained biopsies from PCAR and non-PCAR renal transplant rejections were imaged through immunofluorescence microscopy. Application software was developed using MATLAB to distinguish and quantitate infiltrating cells in digital images of the tissue. Data was used to characterize cellular infiltrates in</p>		<p>Sood, Maricella Castillorama, Parmjeet Randhawa, Jake Demetris, Sundaram Hariharan, Geetha Chalasani, Bala Ramaswami</p>
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		<p>PCAR rejections, as these cells are the mediators of graft injury. Results: Data yielded by the application revealed that B cells, Plasma cells, CD8 T cells, CD4 memory T cells, and CD8 memory T cells were greater in PCAR than in non-PCAR biopsies, while total T cells and CD4 T cells were similar in PCAR and non-PCAR biopsies. Conclusions: Since memory T cells are long-lived and cytotoxic, increased memory T cells in PCAR biopsies suggests persistent injury from these infiltrating cells, possibly explaining the worse outcomes observed in PCAR; hence, memory T cells are a novel potential target for treatment of PCAR using agents such as thymoglobulin.</p>		
Justin Spiriti	5	The self-assembly of viral capsids from	Efforts to Dramatically Improve Structural Fidelity in Molecular	Justin Spiriti, PhD; Daniel M. Zuckerman, PhD

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		<p>individual subunits has attracted significant interest because of its applications in medicine and nanotechnology. Computational simulations have provided much important information about the assembly process. However, because of the large size of the capsids, these simulations have typically used coarse-grained models, in which each subunit of the capsid is represented by no more than about 20 beads. By constructing and using tables of the interaction energy between subunits in terms of their relative displacement and orientation, we are able to use a higher resolution, residue-level model (and, at the same time, increase the speed of Monte Carlo simulations by a factor of up to 20,000</p>	<p>Simulations of Virus Capsid Assembly</p>	
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		<p>compared to simulations without tables). We have applied this tabulation method in conjunction with the weighted ensemble method to simulate the final stages of the assembly of the hepatitis B capsid. Using this combined method, we are able to obtain pathways of the final ~25% of the assembly process.</p>		
Danielle Hu	6	<p>The study of optic nerve head (ONH) architecture is central to understanding ocular diseases such as glaucoma. Our goal was to compare the visualization of ONH structures between 3D reconstructions from sagittal and coronal sections. Pig, sheep, and monkey eyes were fixed in 10% formalin at 0 mmHg within 24 hours of death. The ONH was cryosectioned at 30 microns thickness either coronally or sagittally</p>	<p>Comparison of Optic Nerve Head Structure Visualization Between 3D Reconstructions from Sagittal and Coronal Sections</p>	<p>Danielle Hu, Ning-Jiun Jan, Saundria Moed, Alexandra Judisch, Andrew Voorhees, Kate Davoli, Huong Thi Lan Tran, Ian A. Sigal</p>

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		and the sections imaged with polarized light microscopy. Images were processed on Fiji and registered on Avizo to reconstruct the 3D ONHs. We found sagittal reconstructions to be better than coronal for observing the thickness of the lamina cribrosa and the complex architecture of the vasculature in the peripapillary sclera. The coronal reconstructions provided better detail and clarity of laminar pores and beam shapes. Future experiments will explore the use of staining to improve visibility of vessels in coronal reconstructions.		
Lora McClain	7	BACKGROUND: A major hurdle in the discovery of novel drugs directed toward neurotropic viruses is the inability to generate suitable quantities of live human neurons. The advent of human induced pluripotent cell (iPSC)	Large Scale Generation of Functional Neurons Derived from Human Induced Pluripotent Stem Cells for High Throughput Drug Screenings	Lora McClain, Leonardo D’Aiuto, Yun Zhi, Dhanjit Kumar Das, Madeleine R. Wilcox, Jon W. Johnson, Matthew L. MacDonald, Roberto Di Maio, Mark E. Schurdak, Paolo Piazza, Luigi Viggiano, Robert Sweet, Paul R. Kinchington, Ayantika G. Bhattacharjee

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		<p>technologies have revolutionized the methodological approaches in drug discovery, allowing for a limitless supply of neurons at a scale compatible with high throughput (HTP)/high content analysis (HCA) studies. METHODS: We identified the differentiation conditions for a large-scale generation of neuronal stem cells/early neural progenitor cells (NSCs/eNPCs) and their differentiation into vesicular glutamate transporter 1 (VGLUT1)-positive neurons. iPSC-derived neurons differentiated in HTP plates were utilized to model herpes simplex virus, type 1 (HSV-1) infections. RESULTS: iPSC-neuron membrane currents respond to glutamate, NMDA, AMPA, and GABA using whole-cell voltage</p>		
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		<p>clamp; the iPSC-neurons express synaptic proteins using targeted mass spectrometry. A single plate of NSCs/eNPCs can generate 10 HTP plates of iPSC-neurons at a density of 5,000 cells per well in a 384-well cell culture plate.</p> <p>CONCLUSIONS: Our robust and cost effective differentiation protocol generates functional iPSC-neurons suitable for HTP analysis and drug screenings toward neurotropic viruses.</p>		
Leonardo D'Aiuto	8	<p>Induced pluripotent stem cell-based (iPSC) technologies offer an unprecedented possibility to investigate defects occurring during neuronal differentiation in neuropsychiatric and neurodevelopmental disorders. Neuronal differentiation in classical two-dimensional (2D) culture systems suffers</p>	<p>Generation of Hybrid Two-Dimensional/Three-Dimensional (2D/3D) Neuronal (2D/3D) Neuronal Pluripotent Stem Cells (iPSCs)</p>	<p>Leonardo D'Aiuto, Yun Zhi, Peter Dimitrion, Gerard Apodaca, Dennis R Clayton, Lora McClain, Vishwajit Nimgaonkar</p>

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		<p>from several limitations, including atypical cell-to-cell communication, cellular morphology, and neurite outgrowth. Three-dimensional (3D) systems overcome several limitations of the 2D systems. Despite the superiority of the 3D culture systems, characterization of neuronal morphological features is facilitated in low-density 2D cell culture systems.</p> <p>Method: Human iPSC-derived neuronal progenitor cells (NPCs) were seeded at different cell densities on uncoated or matrigel-coated glass coverslips. Afterward, cell suspensions were removed and attached cells were cultured for 6 weeks in neurobasal medium. Differentiating cultures were characterized by immunocytochemistry.</p> <p>Results: Hybrid 2D/3D cultures were</p>		
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		<p>generated by seeding NPCs on uncoated coverslips. These cultures were characterized by the presence of 2D areas with low neuronal density, alternated with areas where neurons were organized in 3D. Morphological characterization of differentiating neurons was highly simplified in low cell-density areas. An elaborate 3D organization of neurons and glial cells in the 3D areas was revealed by high-resolution confocal microscopy. Conclusion: We have identified culture conditions that combine the advantages of both 2D and 3D neuronal cultures systems.</p>		
Jihe Liu	9		Optical Control of Protein Function by Genetically Encoded Photocaged Unnatural Amino Acids	Jihe Liu, Alexander Deiters
Eric Miller	10	This work demonstrates the utility of TiO ₂ - supported LiBH ₄ , which was previously used as	Carbonyl Reductions with Reagents on Solid Support: Titanium Dioxide Supported Borohydride	Eric Miller; Matthew G. LaPorte, PhD; Peter Wipf, PhD

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		<p>a method for hydrogen storage in chemical synthesis. LiBH₄ supported on mesoporous TiO₂ was used to perform facile and stoichiometric reductions of aldehydes and ketones. Reductions of ketones and aldehydes proceeded to completion within 10 min, and work-up consisted of hydrolysis with dilute acid, filtration, and extraction. Reduction of esters was disfavored, allowing for the selective reduction of an aldehyde or ketone in the presence of an ester. Reduction of carboxylic acids, nitriles, and amides was also not favorable. This method was later applied in the synthesis of more complex products in multistep reaction pathways.</p>		
Seyed Reza Mirhassani Moghaddam	11	Slips and falls are a serious safety problem.	Multiscale Computational Modeling of Shoe-Floor Hysteresis	Seyed Reza M. Moghaddam, Kurt E. Beschorner

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		<p>Insufficient friction between shoe and floorings has been identified as a risk factor of slips and falls. Previous research has shown that increasing the available coefficient of friction between (COF) shoes and floors is an effective strategy for preventing slip-and-fall accidents. In this study, a multiscale computational model is introduced for predicting the COF between shoes and floor based on the shoe and floor microscopic surface features (i.e., roughness) and material properties and the macroscopic geometry of the shoe sole. The model has been applied to simulate the available friction between three boots and vinyl flooring and validity of the model predictions has been assessed via comparing model results with slip-</p>	<p>Friction</p>	
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		<p>resistance experiments. The model predicts that when having similar surface features, softer shoe soles will result in higher COF due to a more distributed contact pressure and a higher contact area. Our human subject unexpected slipping studies also showed that people wearing softer shoe soles had fewer rates of slips and falls in a laboratory setting that validates model predictions. The model shows feasibility of predicting COF using computational modeling techniques in a way that predicts slipping risk.</p>		
Amir Mostafaei	12	<p>Additive manufacturing (AM) provides the possibility of direct manufacturing of complicated, high performance components. Powder bed binder jet printing (PB-BJP) is one AM method, in which</p>	<p>Power Bed Binder Jet Printing of Alloy 625: Sintering, Microstructure, and Mechanical Properties</p>	<p>Amir Mostafaei, Erica Stevens, Colleen Hilla, Eamonn Hughes, Markus Chmielus</p>

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		<p>powder is deposited layer-by-layer and selectively joined with a binder in each layer. Since the powder does not get melted during PB-BJP, the density after printing is below 70% and heat treatments are needed to densify as-printed parts. In this study, the influence of different thermal process parameters on density and grain microstructure and mechanical properties of printed Alloy 625 parts were investigated. Density and mechanical measurements were conducted before and after sintering at temperatures ranging from 1220°C to 1,280°C using Archimedes principles, image analysis on the optical microscopy studies, microhardness measurements and tensile tests. The microstructure of the</p>		
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		<p>sintered samples and compositional analysis were investigated with optical microscopy and scanning electron microscopy equipped with electron dispersive spectroscopy. Conclusions were made about the influence of sintering temperature on the density, microstructure and mechanical properties.</p>		
Andrew Voorhees	13	<p>Elevated levels of mechanical stress are associated with glaucomatous damage within the neural tissues of the optic nerve head. The initial site of this damage is the lamina cribrosa (LC). Much research has gone into modeling how the LC deforms under increased intraocular pressure. However, most of these models treat the LC as a homogenous structure, without distinguishing the collagen rich meshwork of trabecular</p>	<p>Microscale Mechanical Modeling of the Optic Nerve Head</p>	<p>Andrew P. Voorhees, PhD; Ning-Jiun Jan; Ian A. Sigal, PhD</p>

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		<p>beams that provide mechanical support from the sensitive retinal ganglion cell axons within. Collagen is a non-linear, anisotropic material with a stiffness as high as 3-4 orders of magnitude greater than that of neural tissue. Using fiber orientation data from high-resolution microscopy, we developed finite element models that capture the natural inhomogeneity and anisotropy of the LC. We have found that the deformation of the neural tissue can exceed the deformation of the collagenous beam by an order of magnitude. The results of our model improve our understanding of how intraocular pressure is transmitted to the retinal ganglion cell axons of the optic nerve head and may help identify structural</p>		
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		predictors of glaucoma susceptibility.		
Jennifer C. Boatz	14	Wild-type gamma-D-crystallin (γ Dc) is extremely stable and soluble (>400 mg/mL), and disruption of the inherent solubility encourages aggregation and subsequently cataract formation. Two predominant mechanisms of aggregation have been advanced, which emphasize the formation of either amyloid-like fibrils or domain swapped aggregates. It is crucial to determine the structure of γ Dc in the aggregated state to determine whether either mechanism is at play. We use Nuclear Magnetic Resonance (NMR) to investigate the atomic structure of P23T γ Dc in the solid-state. Aggregates are obtained by exposing γ Dc to varying pH conditions, thereby	A Tale of Two Conformations: Solid-State NMR Reveals Two Structurally Distinct Aggregates Formed by a Cataract-Forming Gamma-D-Crystallin Mutant	Jennifer C Boatz; Matthew J Whitley, PhD; Cody L Hoop, PhD; Angela M Gronenborn, PhD; Patrick C A van der Wel, PhD

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		<p>revealing how pH influences aggregation. Since the chemical shifts in solution and the solid-state are exquisitely sensitive to structural changes, the solution and solid-state spectral parameters are directly comparable. We are able to probe in a residue and site-specific fashion how the structure of γDc changes between soluble and aggregated states. Multiple aggregated samples of γDc were evaluated by electron microscopy, X-ray powder diffraction, and multidimensional magic-angle-spinning (MAS) NMR. Depending on the aggregation conditions, different conformations of γDc are directly observed. Our data reveal that aggregation conditions affect the macroscopic appearance of the aggregates and their detailed atomic</p>		
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		structure. Therefore, distinct molecular mechanisms for crystallin misfolding and aggregation exist.		
Erica Stevens	15	Laser Engineered Net Shaping (LENS) is a method of additive manufacturing that is used most commonly for the repair of parts. However, with each deposited layer, additional heat treatments are introduced to material below the new layer. The microstructure and properties of LENS-created samples are strongly affected by this thermal history, but have not been extensively examined. This study investigates the microstructures of LENS-fabricated Inconel 718 (IN718) samples and proposes links to processing parameters and resulting properties. IN718 prisms were created using LENS on an IN718	Influence of Processing Parameters on Structure and Properties of LENS-Printed Inconel 718	Erica Stevens; Jakub Toman; Pu Zhang; Colleen Hilla; Eamonn Hughes; Albert To, PhD; Markus Chmielus, PhD;

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		<p>substrate, then select samples were cross-sectioned or sliced to access different layers. Microscopy was used to document structure, energy-dispersive X-ray spectroscopy (EDS) was used to evaluate composition gradients and identify phases, and electron backscatter diffraction (EBSD) was used to distinguish grain size and distribution. Each sample was also tested using Vickers microhardness in order to draw conclusions about mechanical properties.</p>		
Jakub Toman	16	<p>Magnetic shape-memory alloys (MSMAs) with magnetic field-induced reversible plastic deformation of up to 10% in single crystalline form have potentially a wide range of applications as actuators, sensors, power-generation devices, pumps and are also investigated for</p>	<p>Magnetic Shape-Memory Alloy Production by Laser Metal Deposition: Exploring a New Processing Path</p>	<p>Jakub Toman, Yuval Krimer, Peter Müllner, Markus Chmielus</p>

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		<p>their high-temperature shape memory and magneto-caloric properties. We explore laser engineered net shaping (LENS) additive manufacturing (AM) for producing polycrystalline MSMA. In LENS, powder feeding nozzles spray metal powder into a melt pool that was created by a laser positioned in the center of the nozzles. With LENS, MSMA can be produced in different shapes that have not been possible so far. The printed samples have a composition of Ni_{53.2}Mn_{26.9}Ga_{19.9} (2% less gallium than the powder feed stock). We will present first results of the structural and magnetic properties of the printed parts and discuss merits of using AM for MSMA.</p>		
Ning-JiunJan	17	Our goal was to characterize the collagen microstructure	Collagen Microstructure Patterns in the Optic Nerve Head	Ning-Jiun Jan, BS; Saundria Moed, GED; Ryan O'Malley, GED; Huong Tran; Ian A Sigal,

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		<p>throughout the optic nerve head. In particular, we determined if there were discontinuities in the collagen crimp period between the lamina cribrosa (LC) and adjacent peripapillary sclera (PPS). Four sheep eyes were fixed (2 at 0mmHg, 2 at 10mmHg). They were sectioned coronally (30μm) and imaged with polarized light microscopy. Crimp period was measured manually using FIJI. We found that the collagen crimp period in the PPS increased with distance from the canal edge ($P < 0.01$), while the crimp period in the LC was unrelated to distance from the canal edge ($P > 0.01$). For each eye, we found that near the canal edge, the collagen crimp period of the proximal PPS rim matched that of the LC ($P > 0.8$). Pooling data from all eyes together,</p>		PhD
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		<p>we found that the crimp period in the PPS had two distinct regions. The first ~500 microns from the canal edge had rapidly increasing crimp period with distance from the canal edge, and after that, the crimp period increased much slower and became more variable ($P < 0.01$). While the role of these regions is unknown, we hypothesize that it provides a smooth transition of biomechanical properties from LC to PPS.</p>		
Mason Lester	18	<p>The main risk factor for glaucoma is elevated intraocular pressure, however it is still unclear how this pressure affects an eye. A large part of what determines patient-specific reactions to changes in intraocular pressure stems from the underlying collagen microstructure. Our</p>	Collagen Crimp Period Around the Eye	<p>Mason Lester, Ning-Jiun Jan, Yujie Mu, Michael Iasella, Garrett Grube, Andrew Levandoski, Zach Adgate, Ian A. Sigal</p>

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		<p>goal was to characterize the collagen microstructure in the whole eye globe. Specifically, we measured the regional variations in collagen crimp period over the whole globe. Three sheep eyes were fixed at 0 mmHg pressure. The eyes were cryosectioned axially at 30 μm and imaged using polarized light microscopy. Crimp period was then measured manually. Overall 2,568 manual measurements of period were made. In the sclera, the nasal and temporal collagen crimp period were not significantly different ($P>0.1$). However, in the cornea, the nasal and temporal collagen crimp periods were significantly different ($P<0.0001$). The collagen crimp period overall was distributed in a double hump</p>		
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		<p>shape, with small crimp period around the lamina cribrosa and in the cornea and larger around the equator. Understanding the collagen crimp period distributions around the globe bring us a greater understanding on the workings of the eye and sensitivity to intraocular pressure.</p>		
Chuyuan Zheng	19	<p>Tin-oxide nanowires play an important role in PEC solar cells. Our goal is to fabricate tin-oxide nanowires using VLS mechanism and observe samples via SEM. Parameter studies of this experiment includes temperature, oxygen flow, the mass of tin source and mainly focuses on finding out empirically ideal conditions for nanowire growth. In this experiment, SnO₂ nanowires on two substrates, namely FTO glass and stainless steel mesh, are synthesized</p>	<p>Parameter Study of Tin-Oxide Nanowire Growth on FTO and Stainless Steel Mesh Substrates</p>	<p>Chuyuan Zheng; Gill-Sang Han, PhD</p>

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		<p>successfully and SEM observations of nanowires grown shows the ideal temperature reaction matches previous studies to a certain extent. The optimized conditions for NW growth is found to be 700/500°C for FTO glass and 800/600°C for stainless steel mesh. Changes in terms of nanowire characteristics are minimal when we adjust the amount of tin source and oxygen flow within a certain range, and it can be proved that temperature has a major effect on NW growth.</p>		
Abraham Cullom	20	<p>The purpose of this study was to investigate the enveloped virus Phi6 as a research surrogate for Ebolavirus in the hopes of avoiding the high costs inherent in Biological Safety Level 4 procedures, thus expediting environmental studies examining Ebola. The</p>	<p>Φ6 Disinfection with Hypochlorite in Deionized Water</p>	<p>Abraham Cullom, Kyle Bibby</p>

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		<p>research was conducted to test the disinfection kinetics of the bacteriophage exposed to hypochlorite disinfectant in deionized (DI) water (pH 6.3). Hypochlorite was added to the DI water containing suspended virus to a target concentration and then, after a specified length of time, neutralized using sodium thiosulfate at a ratio verified to sufficiently quench any free chlorine by preliminary experiments. Following the creation of serial dilutions, the virus was then grown in host strain <i>P. syringae</i> strain (HB10Y) on LB plates overnight, and then plaques were counted. Initially, a higher concentration of virus was used; however, the suspension media eliminated too much of the free chlorine to maintain a stable dose</p>		
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		<p>concentration and thus obtain a reliable concentration-time curve. The phage appeared to be extremely labile, exhibiting a greater than 99.9% reduction at even a 0.025 mg-min/L dose. Notwithstanding, preliminary quenching experiments and successful control trials suggest that the bacteriophage was not dying for reasons other than disinfectant exposure.</p>		
Ni'a Calvert	21	<p>INTRODUCTION: Hybrid masonry is a structural system that consists of reinforced concrete masonry wall, steel frames, and steel connectors [2]. In this study, we focus on how various hybrid masonry structures of Type 1 react to the 1994 Northridge Earthquake. METHODS: Numerical data were obtained through large-scale experiments of small</p>	<p>Responses of Hybrid Masonry Structures in 1994 Northridge Earthquake Simulated Using Finite Element Analysis Program</p>	Ni'a Calvert

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		<p>hybrid masonry structures conducted at the University of Illinois Urbana-Champaign [1]. These data were then used to configure hybrid masonry models on FEAP. Simulations were run for various structures of Type 1 to further explore which designs would optimize energy dissipation.</p> <p>DATA PROCESSING: After each successful simulation, a final damage picture was produced.</p> <p>RESULTS/DISCUSSION: Since a weaker connector is more ductile than a stronger connector, structures with smaller connectors indicated less damage done to the masonry panel, but more deflection to connectors. Ideally, it is easier and more cost-effective to replace damaged connectors than to replace masonry panels after a seismic</p>		
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		<p>event. REFERENCES 1. Gao, Zhenjia. Computational Framework for the Analysis of Hybrid Masonry Systems Using an Improved Non-local Technique, 1-3, 2014. 2. National Concrete Masonry Association. Hybrid Masonry Construction, 1-8, 2010. ACKNOWLEDGMENTS: Funding was provided by the Swanson School of Engineering and the Office of the Provost.</p>		
Adedoyin Ojo	22	<p>3D printing technology boasts a wide range of applications, including culinary arts, medicine and health care, with many more emerging every day. One such innovation currently being explored is the use of 3D printing technology in the creation of edible food. The main objective of this project was to design a compact powder-based 3D food printer that uses Binder</p>	<p>Let's Print Some Food : Designing a Compact Binder Jetting 3-D Food Printer</p>	Adedoyin Ojo

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		<p>Jetting technology. This particular project focused on the binding process of the powder-based food printing. The two objectives were to identify potential binder combinations and then test the combinations for suitability. In order to test the different binder combinations, it was necessary to construct a platform in the same configuration as the powder-based 3D-printing technique. After several design iterations and modifications, a final model was developed that can be used as an effective binder testing mechanism. As this project is still in its initial stages, more extensive research will be conducted to further develop the proposed product.</p>		
Cody Moore	23	<p>Purpose: Bacterial pneumonia has been shown to be a potential risk factor in the</p>	<p>Effect of Aerosolized Antimicrobials on Pseudomonas Recurrence and Bronchiolitis Obliterans Syndrome After Lung</p>	<p>Cody A. Moore, PharmD; Joseph M. Pilewski, MD; John F. McDyer, MD; Cynthia J. Gries, MD; Christopher R. Ensor,</p>

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		<p>development of acute cellular rejection (ACR) and bronchiolitis obliterans syndrome (BOS) in lung transplant patients. Moreover, loss of lung allograft function is primarily due to BOS, with only 55% of patients surviving five years post-transplantation. The aims of this study were to assess the effects of aerosolized antimicrobials on infection burden, ACR, and BOS progression after lung transplantation.</p> <p>Methods: This was a retrospective single-center cohort study of patients who underwent lung transplantation from January 1, 2009 to December 31, 2014 and were colonized with <i>Pseudomonas</i> spp. Patients were divided into two cohorts based on aerosolized antimicrobial use of 28</p>	Transplantation	PharmD
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		<p>days or greater. The primary outcome was days to positive Pseudomonas reinfection. Secondary outcomes included ACR burden as defined by composite rejection standardized score (CRSS), and time to BOS progression. Results: Time to Pseudomonas culture positivity was similar between the aerosolized antimicrobial and control cohort, with a median of 371 (IQR 138 – 828) days versus 365 (IQR 140 – 685) days, respectively (p=0.342). Conclusion: Results suggest that aerosolized antimicrobials did not affect time to Pseudomonas recurrence after lung transplantation.</p>		
Ling Tian	25	<p>Background: Surgical technique improvements make preserving more liver parenchyma during surgical resection more</p>	<p>Trend of Liver Parenchymal Preservation and Minimal Invasion During Liver Resection at ISMETT – a 26-Year Study</p>	<p>Ling Tian; Duilio Pagano, MD; Salvatore Gruttadauria, MD</p>

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		<p>achievable. Hypothesis: As a major transplantation center in the Mediterranean region, ISMETT has adapted to operate on liver parenchymal preservation and minimally invasive procedures. Methods: Surgical data of patients who underwent liver resection from 1999-2015 at ISMETT were collected and statistically analyzed. Results: Analysis by separating the whole time period into three parts (1999-2005, 2006-2010, 2011-2015) revealed that during 1999-2005, there are 235 cases including 67 major liver resections (28.51%). During 2006-2010, there are 285 cases including 125 major liver resections (43.86%). During 2011-2015, there are 342 cases including 67 major liver resections (19.59%). However,</p>		
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		<p>after excluding living liver donor donation cases, major liver resection numbers changed from 47 (20.00%) to 88 (30.88%) and 48 (14.04%) through the three periods. Cases performed laproscopically went up from 6 during 1999-2005, to 27 during 2006-2010, and to 126 during 2011-2015. Choice of surgical methods has also changed significantly. The most common reasons for liver resection are primary tumor and hepatic cysts; other reasons include liver metastasis, living donor liver donation, or trauma. Conclusions: ISMETT has increased minimally invasive procedures. More data is required to determine whether it adapted to preserve more liver parenchyma.</p>		
Parichat Duangkhae	26	Dengue virus (DENV) is	Defining the Targets of Dengue	Parichat Duangkhae, BSc;

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		<p>the most important arboviral infection, introduced into humans by the bite of infected mosquitoes. Although Langerhans cells (LCs) have been implicated as the main targets of DENV, dynamics of infection remain unclear. To determine the targets of infection, human skin explants were inoculated with DENV-2 16681 strain and analyzed by immunofluorescence (IF) after intervals of incubation using antibodies to cell-specific markers and viral protein NS3. Time course experiments showed the first major targets were basal keratinocytes, within 6-8 h. From 12-48 h abundant virus replication was detected in LCs, dermal macrophages (dMØs), and dermal fibroblasts. Explants infected with DENV-2 primary isolate</p>	<p>Virus Infection in Human Skin</p>	<p>Amanda P. Smith, MS; Ernesto T.A. Marques, Jr., MD, PhD; Kate D. Ryman, PhD; Simon C. Watkins, PhD; Simon M. Barratt-Boyes, BVSc, PhD, Dip ACVIM</p>
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		reaffirmed replication in basal keratinocytes, LCs, and dMØs. Quantitative analysis indicated exposure to DENV resulted in significant infiltration of dMØs into dermis. Real-time qPCR showed significant up-regulation of IL-1 α , IL-1 β , MIP-3 α , IL-8, and IL-10, at 48 h. IF confirmed the copious expression of IL-1 β , IL-8, and MIP-3 α genes, suggesting that DENV initially infects basal keratinocytes which may release factors promoting significant influx of MØs into the dermis; subsequently replicating DENV to high levels. These studies reveal that DENV infection of human skin is a dynamic process involving sequential interactions and recruitment of distinct cellular targets.		
Venkata Sashi Gollapudi	27	Combination-therapy of chemotherapeutics plus the late autophagy	Late, but not Early, Inhibition of Autophagy Induces Apoptosis in Lung Cancer in Combination with	Venkata Sashi Gollapudi, Peng Deng, Eileen Bauer, PhD

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		<p>inhibitor hydroxychloroquine (CQ) is already successfully administered in clinical trials like kidney cancer, and aims to increase apoptosis. CQ's long history as antimalarial prophylactic and its low cost made it a drug of choice to inhibit autophagy. Here we show in human lung cancer cells (HTB56) that autophagy inhibition and its associated shift towards apoptosis is dependent on near completion of the autophagic process. Methods: HTB56 were treated with 5-fluorouracil (5-FU) or Gemcitabine +/- the LATE inhibitor, CQ, or the EARLY inhibitor spautin-1. Drug-induced autophagy and apoptosis was analyzed using Western blotting against Caspase-3, TUNEL staining, DNA fragmentation.</p>	Chemotherapeutics	
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		<p>Cytotoxicity and physiologic relevant endpoints of proliferation and migration were assayed. Results: Increased apoptosis and autophagy was observed in HTB56 treated with chemotherapeutics over time as detected by cleavage of Caspase3, Parp, and markers of autophagic flux. Apoptosis was robustly enhanced in cells treated additionally with CQ but not Spautin1. Conclusion: We found that near-completion of the autophagic process is needed to induce apoptosis. In fact, EARLY inhibition promotes cancer cell survival. We demonstrate the importance of autophagy for homeostasis and that targeting its inhibition therapeutically needs to</p>		
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		be critically timed.		
Joe-Marc	28	<p>T cell Ig and ITIM domain (TIGIT) is an inhibitory receptor which inhibits CD8+ T cells by direct T cell–intrinsic effects and by competition with the stimulatory receptor CD226 for binding with CD155 and CD112 expressed on epithelial cells, APCs and melanoma cells. Most recently, TIGIT expression has been reported on CD8+ tumor infiltrating lymphocytes (TILs) and its blockade in the CT26 mice tumor-bearing model synergized with PD-1 blockade to promote tumor rejection. Here, we have investigated the expression of TIGIT in combination with PD-1 on NY-ESO-1-specific CD8+ T cells from PBMCs and on CD8+ TILs of patients with metastatic melanoma. We have evaluated</p>	<p>Tigit and PD-1 Impair Tumor Antigen-Specific CD8+ T Cells in Melanoma Patients</p>	<p>Joe-Marc Chauvin, PhD; Ornella Pagliano, PhD; Julien Fourcade, PhD; Zhaojun Sun, MD, PhD; Hong Wang, PhD; Cindy Sander, BS, MT, ASCP; John M. Kirkwood, MD; Tseng-hui Timothy Chen, PhD; Mark Maurer, PhD; Alan J. Korman, PhD; Hassane M. Zarour, MD</p>

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		<p>whether the blockade of TIGIT alone or in association with PD-1 blockade could reverse the dysfunction of tumor antigen-specific CD8+ T cells in melanoma patients. Our findings show that TIGIT together with PD-1 regulate the expansion and function of tumor antigen-specific CD8+ T cells and CD8+ TILs in melanoma patients. They suggest the presence of an imbalance between TIGIT and CD226 expression by CD8+ TILs. They support the use of dual TIGIT and PD-1 blockade to stimulate potent antitumor CD8+ T cells responses in patients with advanced melanoma.</p>		
Xubo Wu	29		Saquinavir Inhibits TNF- α Secretion by Macrophage Treated with TLR9 Agonist	Xubo Wu, Zhengzheng Yan, Tunliang Li, Eileen Bauer, Timothy R Billiar, MD
Aditi Nayak	30		Chemokine Receptor Down-Regulation in Mechanical Circulatory Support Patients with	Aditi Nayak, MD; Timothy N Bachman, MS; Karen Hanley-Yanez; Charles McTiernan, PhD;

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			Right Ventricular Failure	Dennis McNamara, MD,MS; Robert L Kormos, MD; Oriana Hunter, PhD; Ana Inashvili, MD; Luigi Lagazzi, MD; Jeffrey Teuteberg, MD; Marc A Simon, MD, MS
Oluwabukola Gbotosho	31	<p>Patients with sickle cell disease (SCD) have elevated levels of placenta growth factor (PlGF), which promotes expression of the pulmonary vasoconstrictor endothelin-1 (ET-1) contributing to pulmonary hypertension, an important life-limiting complication of SCD. In SCD patients, markers of high iron burden are associated with the highest PlGF levels, leading us to hypothesize a mechanistic link between excessive iron and the induction of the PlGF protein. By using cultured human erythroid cells (K-562 cells) treated with heme-bound iron</p>	<p>Pathological Regulation of Angiogenic Factor Expression in Erythroid Cells by Heme-Bound Iron Contributes to Pulmonary Hypertension in Sickle Cell Disease</p>	<p>Olawbukola Gbotosho, Deva Sharma, Maria G. Kapetanaki, Gregory J. Kato.</p>

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		<p>(hemin) as an in vitro experimental system of iron overload, we have documented a dramatic increase of PIGF mRNA levels. Gene expression knockdown and small molecule inhibitor and activator experiments have revealed a central role of the antioxidant Nuclear factor (erythroid-derived 2)-like 2 (NFE2L2 or NRF2) in the transcriptional regulation of several genes suggesting a mechanism where iron overload triggers the cell's antioxidant response, which in turn causes the up-regulation of PIGF. The elucidation of the mechanism by which erythroid cells respond to iron levels would advance not only our understanding of iron-mediated oxidant stress in the pathophysiology of pulmonary hypertension in sickle cell disease (and</p>		
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		potentially in general vasculopathy), but would also reveal the role of PIGF in normal erythroid differentiation.		
Timothy Bachman	32	<p>Introduction: Right Ventricular (RV) failure affects 9-44% of left ventricular assist device (LVAD) recipients. Chemokines play a key role in cardiac self-regulation and the development and progression of heart failure. We sought to determine if chemokine levels were associated with hemodynamic evidence of RV failure. Methods: Pre-LVAD RV pressure waveform morphology was quantified by the square area of a rectangle bounded by recurring landmarks on waveforms. Inflammatory gene expression was examined in patients' blood collected 24 hours prior to implant</p>	<p>Right Ventricular Failure in Patients with Left Ventricular Assist Devices Associates with Downregulated Chemokine Receptors and Altered Right Ventricular Pressure Waveforms</p>	<p>Aditi Nayak, MD; Timothy N. Bachman, MS; Karen Hanley-Yanez; Charles McTiernan, PhD; Dennis McNamara, MD, MS; Robert L. Kormos, MD; Oriana Hunter, PhD; Ana Inashvili, MD; Luigi Lagazzi, MD; Jeffrey Teuteberg, MD; Marc A. Simon, MD, MS</p>

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		<p>and in healthy controls. Results were expressed as PCR cycles to threshold (CT) with more highly expressed genes having a lower CT and normalized to GAPDH. Results: Compared to controls (n=8), many chemokines were downregulated in LVAD patients (n=11): CCR3 through CCR7 had significant decreases (log-fold) (P<0.05). Square area was significantly lower in LVAD patients with RV failure defined as need for Right VAD or inotropes >14 days (n=7; P=0.04). CCR5 was further downregulated in patients below median square area of 7.773 (2.15 fold decrease in transcript levels, p=0.037). Conclusion: Chemokines are downregulated in patients requiring LVAD. RV failure post-LVAD</p>		
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		may be predicted by RV waveform morphology via lower square area, which is associated with further downregulation of CCR5.		
Nadia Mezghani	33	Tuberculosis (TB) is a contagious respiratory disease that causes more than 1.5 million deaths every year. Although antibiotic treatment has previously been an effective way of treating the disease, TB is rapidly becoming drug-resistant. The use of bacteriophages as a complementary treatment could potentially reduce TB infection and resistance. Over 6,000 phages that infect Mycobacterium smegmatis, a strain of bacteria that is not infectious to humans, have been isolated and a subset are known to infect TB. Phages that are known to infect both M. smegmatis and	The Development of a Complementary Treatment for Tuberculosis Using Phage Cocktails	Nadia Mezghani, Megan Ulbrich, Bryony Brown, Patrick Rimple, Zaritza Petrova, Marcie Warner, Deborah Jacobs-Sera, Welkin Pope, Graham Hatfull

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		<p>M. tuberculosis can be used to create a cocktail for TB treatment. Selected phages for each cocktail are known to grow to high titer, are lytic, and are relatively distinct as they belong to different subclusters. Phage cocktail 1 contains TM4, Fionnbharth, Adaphagia with two deletions (ADD), and D29. Initial trials indicate that extensively phage-resistant bacteria (XPRs) emerge after 4 days. Several XPRs and recombinant phages have been isolated and are being further characterized. Once we have a potent phage cocktail that can kill off M. smegmatis for a significant number of days with minimal regrowth of XPRs, it will be tested on M. tuberculosis.</p>		
Apoorva Kandakatla	34	Vision loss after optic nerve injury remains a persistent clinical	Regenerative Ophthalmology: Modulating the Immune Response to Injury in the CNS Using ECM	Apoorva Kandakatla; Anne Faust; Asma Naqvi, MS; Vibha Reddy; Fardeen Mehdi; Stephen

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		<p>problem due, in part, to the failure of injured retinal ganglion cells (RGCs) to regenerate axons, which often leads to RGC cell death and irreversible vision loss. Extracellular matrix (ECM) bioscaffolds are commonly used clinical devices to facilitate the repair of many tissues. ECM bioscaffolds are thought to work by modulating the innate immune response toward a functional healing response due to degradation of the bioscaffold itself. Bioscaffolds have been previously used for organ, skin, bone, and muscle regeneration. However, few studies have examined the efficacy of these scaffolds following injury to the central nervous system, which includes the brain, spinal cord, and optic nerves. Here, we show that different tissue-</p>	Technology	F. Badylak, DVM, PhD, MD; Michael B. Steketee, PhD
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		<p>specific ECMs differentially modulated microglial phenotype. Tissue-specific ECMs, such as CNS-derived scaffolds for CNS injury, and scaffolds derived from younger source tissues showed enhanced efficacy compared to non-tissue-specific ECM. We found that ECM derived from fetal brain promoted the most RGC survival and axon regeneration. This suggests that ECM bioscaffolds derived from younger, homologous tissues may be the best candidates for increasing site-appropriate repair over scarring, with the long-term goal of preserving and restoring visual function.</p>		
Nicholas Lotz	35	<p>Improved disease treatments based on individual patient conditions may be realized through</p>	<p>A Cell-Scale Model of Pulmonary Epithelial Transport Dynamics in Cystic Fibrosis</p>	<p>Nicholas W. Lotz, Matthew R. Markovetz, Robert S. Parker</p>

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		<p>systems medicine, which incorporates systems biology and systems engineering to aid clinicians in treatment implementation. One potential area for improved patient care is in treating cystic fibrosis (CF). A cell-scale model of an epithelial cell was constructed using the MatLab software suite (© 2014, The MathWorks, Natick, MA). Systems of ordinary differential equations described the transport dynamics of chloride, sodium, potassium, water, and DTPA in the apical surface layer (ASL), cell interior, and blood. An APT-MCMC algorithm fit the model parameters to experimental DTPA transport and ASL volume data, and the model was run to assess agreement with experimental conditions. CF cells</p>		
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		<p>exhibit higher ENaC and CaKC permeabilities but lower transcellular and paracellular hydraulic permeability than non-CF cells. A discrepancy between CF-and non-CF paracellular hydraulic permeability raises the possibility of parameter unidentifiability in the optimization procedure, necessitating further constraints to limit optimized parameters to physiologically reasonable values. When run, the model captures DTPA and ASL volume dynamics and simulates CF cell swelling. Further analysis must be performed to determine whether any experimental increases in apical volume during hypotonic challenge are truly physiological.</p>		
Jessica Craig	36	<p>Every year, traumatic brain injury (TBI) affects an estimated 2.5 million people in the United</p>	<p>Longitudinal Leptin Profiles after Severe TBI: Characterization and Associations with Outcomes</p>	<p>Jessica Craig, Raj Kumar, Michelle Failla</p>

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		<p>States and contributes to over 50,000 deaths. An important goal of TBI research is to identify and study novel biomarkers that predict mortality and outcome following injury in order to inform pharmaceutical and rehabilitative therapies. The purpose of this study was to 1) characterize leptin, a hormone implicated in the pathophysiology of various inflammatory diseases, in a TBI cohort and 2) to investigate the validity of leptin as a novel biomarker. We evaluated 122 patients with severe TBI. CSF data was collected via EVD catheter for all 122 patients for five days following injury; serum data was collected for 81 patients for six days following injury. Leptin concentrations in serum, CSF, and control samples were measured using ELISA methods.</p>		
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		<p>Kruskal-Wallis, Mann-Whitney, and regression analyses were used when appropriate to assess the relationship between leptin levels and various demographic factors, cytokines, functional outcome, and mortality. This study found that in both bivariate and multivariate statistical analysis models, leptin was a valid biomarker for mortality and functional outcome in men but not women following severe TBI.</p>		
Jordan Baird	37	<p>Declines in cognitive function and sleep quality are both characteristics of advancing age. A variety of sleep disturbances are commonly reported in older adulthood, including prolonged sleep onset, daytime napping, earlier waking, and increased likelihood of nocturnal awakenings. Poor sleep</p>	<p>The Relationship Between Sleep Quality and White Matter Microstructure in Older Adulthood</p>	<p>Jordan A. Baird, Lauren E. Oberlin, Agnieszka Z. Burzynska, Michelle W. Voss, Edward McAuley, Arthur F. Kramer, Kirk I. Erickson</p>

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		<p>quality in older adulthood is predictive of impaired cognitive function in multiple domains including memory and executive processes, although the neural mechanisms of this relationship are poorly understood. The present study is the first to explore the relationship between sleep quality and brain white matter in healthy older adults. Using diffusion tensor imaging to determine white matter microstructure, we hypothesized that sleep quality would be associated with white matter microstructural integrity, particularly in fiber bundles that subserve higher-order cognitive processes, including cortico-thalamo-cortical circuits and interhemispheric tracts. A population of 128 cognitively healthy older adults completed the Pittsburgh Sleep</p>		
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		<p>Quality Index, a self-report sleep quality evaluation, and participated in MRI imaging. Voxel-based regression analyses indicated no significant relationship between global PSQI score and white matter microstructure in this sample, after adjusting for age and gender. These findings contradict our original prediction, and suggest that the relationship between sleep quality and cognition may not operate through sleep-related variation in white matter microstructure.</p>		
<p>Hannah Radabaugh</p>	<p>38</p>	<p>Environmental enrichment (EE) is a non-invasive paradigm that promotes significant cognitive recovery after experimental traumatic brain injury (TBI) and has the potential to mimic neurorehabilitation.</p>	<p>Abbreviated Environmental Enrichment Confers Robust Neurobehavioral and Cognitive Benefits in Brain-Injured Female Rats</p>	<p>Hannah L. Radabaugh, Jeffrey J. Niles, Lauren J. Carlson, Christina M. Monaco, Jeffrey P. Cheng, Naima Lajud Avila, PhD, Corina O. Bondi, PhD, and Anthony E. Kline, PhD</p>

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		<p>However, the typical EE paradigm consists of continuous exposure, which may be inconsistent with the clinic. Moreover, females make up approximately 40% of the clinical TBI population, yet they are rarely studied in TBI research. The goal of this study was to test the hypothesis that abbreviated EE would confer neurobehavioral and cognitive benefits in TBI female rats. Anesthetized female rats received a cortical impact (2.8 mm tissue deformation at 4 m/s) or sham injury and were randomly assigned to TBI+EE (4 hr), TBI+EE (6 hr), TBI+EE (continuous), or TBI+STD groups, and respective sham controls. Motor function was assessed on post-operative days 1-5 and every other day from 1-19, respectively.</p>		
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		<p>Spatial learning/memory was evaluated on days 14-19. All EE conditions improved motor function compared to STD housing ($p < 0.0001$). However, only continuous and 6-hr EE enhanced cognitive function ($p < 0.0001$). These data demonstrate that abbreviated EE confers robust neurobehavioral and cognitive benefits in TBI female rats, which supports the hypothesis and strengthens the validity of EE as a preclinical model of neurorehabilitation.</p>		
Elizabeth Meyer	39	<p>Introduction: Traumatic brain injury (TBI) affects 1.7 million people in the USA, making it a significant concern. In addition to motor and cognitive dysfunction, TBI also induces agitation, which hampers acute care/rehabilitation. To manage these</p>	<p>Traumatic Brain Injury-Induced Functional Deficits Are not Exacerbated by Daily Administration of Lorazepam</p>	<p>Elizabeth A. Meyer, Darik A. O'Neil, Amber M. Vozar, Jeffrey P. Cheng, Corina O. Bondi, PhD, Anthony E. Kline, PhD</p>

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		<p>behavioral dysfunctions, antipsychotic drugs (APDs) are administered. Studies have shown that APDs impede the acquisition of spatial learning. Despite the negative effects, some form of sedation is necessary so that physicians can treat disruptive patients. Hypothesis: Lorazepam, a benzodiazepine, will not produce deleterious effects on behavioral outcome after TBI. Methods: Twenty-eight anesthetized adult male rats received either a cortical impact or sham injury and then were randomly assigned to 4 groups where a TBI and corresponding sham group received either lorazepam (1.0 mg/kg) or saline vehicle (1.0 mL/kg) once daily for 19 days. Motor function and cognition were assessed on days 1-5 and 14-19, respectively.</p>		
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		<p>Results: No significant motor and cognitive differences were revealed between the TBI+lorazepam and TBI+vehicle groups ($p=0.60$ and $p=0.09$, respectively).</p> <p>Conclusions: These results suggest that daily administration of lorazepam (1.0 mg/kg) does not impair functional outcome after TBI, which is unlike that reported for APDs.</p> <p>Significance: Lorazepam should be considered as an alternative treatment to control clinical TBI-induced agitation and aggression.</p>		
Heather Tennant	40	<p>Traumatic brain injury (TBI) laboratory models have been associated with declines in long-term learning and memory. Previously, behavioral tests did not focus on the impairments related to the frontal lobe, such as executive function and</p>	<p>Combining Environmental Enrichment and the Antidepressant Drug, Citalopram, Improves Attentional Set-Shifting Performance after Brain Trauma</p>	<p>Heather Tennant; Megan LaPorte; Ihuoma Njoku; Jeffrey Cheng; Anthony Kline, PhD; Corina Bondi, PhD</p>

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		<p>cognitive flexibility. We have begun to employ the attentional set-shifting test (AST), a paradigm analogous to the Wisconsin Card Sorting Test. We demonstrated that a controlled cortical impact (CCI) injury produced significant impairments in executive function and cognitive flexibility in the AST. In the current study, we hypothesized that post-injury exposure to clinically relevant therapies, environmental enrichment (EE) and citalopram, will attenuate cognitive performance deficits on AST alone, but especially in combination. Rats from both surgical conditions, CCI and sham, were exposed to the EE alone or in combination with injections of citalopram, an antidepressant</p>		
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		<p>known to improve cognition in humans. The AST involves a series of increasingly difficult discriminative tasks. Exposure to EE along with daily citalopram provided the most cognitive recovery on AST after injury. The combined treatment mimics rehabilitation and pharmacological treatments performed in a clinical setting. Future studies will continue to investigate the ideal cognitive recovery timeline and specific brain pathways and mechanisms involved in restoring higher function after TBI.</p>		
Lauren Carlson	41	<p>Traumatic brain injury (TBI) is a significant health issue with limited treatments. Therefore, evaluating therapeutic strategies that may translate to the clinic is important. Currently most, if not</p>	<p>Albeit Nocturnal, Rats Subjected to Traumatic Brain Injury Do Not Differ in Performance Whether Tested during the Day or Night</p>	<p>Lauren J. Carlson; Jiahu Wei; Peter J. Niesman; Megan J. LaPorte; Jeffrey P. Cheng; Corina O. Bondi, PhD; Anthony E. Kline, PhD</p>

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		<p>all, preclinical studies are conducted during the day, which is not when rats are most active. The possibility exists that the timing of testing is not optimal, which may preclude potential benefits of some treatments. The goal of this study was to determine if differences in recovery exist in TBI rats when assessed during the day vs. night. The hypothesis was that the night group would perform better than the day group in all behavioral tasks. Anesthetized male rats received a cortical impact or sham injury and were randomly assigned to either day or night testing. Motor function was conducted on post-operative days 1-5 and cognition on days 14-18. No significant differences were revealed between the TBI rats tested during the day vs. night</p>		
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		<p>for any task ($p > 0.05$). These data suggest that the time rats are tested does not affect performance, which does not support the hypothesis. The finding is important because it validates the interpretations from numerous studies conducted when rats were tested during the day, vs. their natural nocturnal period.</p>		
Sonya Besagar	42	<p>Optimizing environmental enrichment to model preclinical neurorehabilitation Traumatic brain injury (TBI) affects 1.7 million people in the USA each year. One therapy that has been investigated is environmental enrichment (EE), which confers cognitive and motor recovery when provided early and continuously after TBI vs. standard (STD) housing. However, this paradigm is not</p>	<p>Optimizing Environmental Enrichment To Model Preclinical Neurorehabilitation.</p>	<p>Megan J. LaPorte; Hannah L. Radabaugh; Heather M. Tennant; Sonya Besagar; Jeffrey P. Cheng; Naima Lajud Avila, PhD; Corina O. Bondi, PhD; Anthony E. Kline, PhD</p>

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		<p>clinically ideal as patients will not engage in rehabilitation until after critical care has ended. Once rehabilitation is initiated, the duration of the therapy is limited, often ranging from 3-6 hours/day. To mimic the clinic, this study was designed to test the hypothesis that delayed-and-abbreviated EE would confer similar behavioral benefits as early-and-continuous EE. Anesthetized male rats were subjected to a cortical impact or sham injury and randomly assigned to TBI+EE (continuous), TBI+EE (rehabilitation; i.e., 3-day-delayed, 6-hr-day), and respective sham controls. Motor function was assessed on post-operative days 1-5 and cognitive on days 14-19. EE, regardless of timing, improved function</p>		
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		<p>compared to STD (p<0.0001). There were no differences between TBI+EE (continuous) and TBI+EE (rehabilitation); p>0.05. These data demonstrate that delayed and abbreviated EE produces motor and cognitive benefits similar to continuous EE after TBI, which lends credence to EE as a preclinical model of neurorehabilitation.</p>		
Yu Zhou	43	<p>Plasma cells (B220low/-CD138hiCD44hiBlimp1+; PCs) play an essential role in humoral immunity through secretion of immunoglobulin. Recent studies have revealed that PCs are also able to express high levels of various cytokines, including IL-10. IL-10 contributes to the inhibitory function of regulatory B cells (Bregs). IL-10 expression by PCs suggests that these cells may</p>	<p>The Contribution of IL-10+ Plasma Cells to “Breg” Function in Transplantation</p>	<p>Yu Zhou, David Rothstein</p>

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		<p>contribute to Breg function. We now aim to identify the contribution of PCs to this Breg function. In the absence of in vitro stimulation, splenic PCs had a much higher frequency of IL-10 expression (~47%) than B cells (<1%). While PCs are relatively uncommon in spleen (0.3%~0.7% of B cells), they comprise about 20% to 35% of all IL-10 produced by cells of B lineage. When isolated splenocytes are stimulated in vitro, the frequency of IL-10+ PCs remains similar. However, IL-10 expression by B cells increases markedly reaching 4-7%. Thus, after stimulation in vitro, only 2-6% of B cell lineage IL-10 comes from PCs. Similar findings were obtained examining bone marrow (BM). Thus, the contribution of PCs to</p>		
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		<p>“B cell” IL-10 depends on how the assay is performed. Their role in allograft tolerance is now being studied using hCD20-Tam-Cre X BLIMP-1fl/fl mice.</p>		
Johnathon Schiebel	44	<p>To exert their therapeutic action, probiotic Saccharomyces strains must survive harsh gastrointestinal tract environments. Lipid droplets accumulate in cells which undergo stress-inducing situations, supposedly having a protective role. We sought to investigate if probiotic Saccharomyces strains would contain higher lipid content than their non-probiotic counterparts, either naturally or when submitted to gastrointestinal tract stresses. We observed that lipid droplets’ accumulation rates varied heterogeneously among the tested</p>	<p>Lipid Droplet Levels Vary Heterogeniously in Response to Simulated Gastrointestinal Stresses in Different Probiotic Saccharomyces Cerivisiae Strains</p>	<p>Bruno Douradinha, PhD; F. S. Martins, PhD; Ernesto Marques, MD, PhD; M. Montero-Lomeli; L. Nimrichter, PhD; F. A. Bozza, MD, PhD; P. T. Bozza, MD, PhD; M. Aronovich; C. M. Maya-Monteiro, MD, PhD; J. G. Schiebel; G. S. Matos; M. L. Palma; D. Zamith-Miranda</p>

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		<p>Saccharomyces strains and that their levels increase in response to simulated bile salts or gastric environments. Our results suggest lipid droplets participate in the protective mechanisms against gastrointestinal stresses in probiotic Saccharomyces yeasts.</p>		
Mark Zaki	45	<p>In schizophrenia, alterations within the prefrontal cortical inhibitory system appear to be most prominent in fast-spiking parvalbumin-containing interneurons. Because these neurons are essential for gamma-oscillations, which are necessary for proper cognitive function, alterations in parvalbumin neurons may contribute to cognitive deficits observed in schizophrenia. Gamma-oscillations require the excitation of</p>	<p>Altered Cortical Expression of the Immediate Early Gene NARP in Schizophrenia: Impact on Parvalbumin Neurons.</p>	<p>Mark M. Zaki; Sohei Kimoto, MD, PhD; H. Holly Bazmi, MS; David A. Lewis, MD</p>

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		<p>parvalbumin neurons via AMPA receptors. The clustering of these AMPA receptors at excitatory inputs onto parvalbumin neurons requires the neuronal pentraxin NARP. Consequently, we examined whether NARP expression is altered in the prefrontal cortex of schizophrenia subjects. Mean NARP mRNA levels were significantly lower in postmortem schizophrenia subjects by quantitative PCR (-26%, n=62) and in situ hybridization (-40%, n=20) compared to matched controls. Comorbid factors assessed did not account for lower levels of NARP mRNA in schizophrenia subjects. Also, NARP mRNA expression was not altered in monkeys exposed to antipsychotic medications. Finally,</p>		
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		<p>NARP mRNA levels were positively correlated with the mRNA for the GABA-synthesizing enzyme, GAD67. Thus, lower NARP mRNA expression in the prefrontal cortex might contribute to lower excitatory drive to parvalbumin neurons, resulting in an activity-down regulation of GABA synthesis, which could provide a molecular basis for altered gamma-oscillations and impaired cognition in schizophrenia.</p>		
Megan Link	46	<p>Positive transcription elongation factor b (P-TEFb) is critical for the completion of mRNA synthesis. Dysregulation of this factor is associated with cancer and cardiac hypertrophy. The snRNA 7SK sequesters and inactivates P-TEFb through an intermediary protein, HEXIM, which binds a</p>	<p>HNRNP K Regulates Hexim's Ability To Interact with Stem I on 7SK RNA</p>	<p>Daniel C. Totten; Megan C. Link; Andrea J. Berman, PhD</p>

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		<p>stem-loop (Stem I) of 7SK RNA to form an inhibitory ribonucleoprotein (RNP) complex. When released from HEXIM and P-TEFb, 7SK RNA nucleates another set of RNPs by interacting with heterogeneous nuclear ribonucleoproteins (hnRNPs). We hypothesize that the amount of active P-TEFb in the cell is dependent on the ability of HEXIM to gain access to the RNA, and that Stem I accessibility is hindered by these hnRNPs. We identified two potential binding sites on Stem I for hnRNP K. In vitro binding analysis shows two molecules of hnRNP K bind each Stem I with micro-molar affinity. Structure probing assays revealed that hnRNP K melts Stem I, hindering the double-stranded binding capabilities of</p>		
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		<p>HEXIM, thereby allowing hnRNP K to displace HEXIM in competition assays. These characterizations of the interaction between hnRNP K and Stem I will aid in proposing a mechanism by which the hnRNPs regulate cellular levels of P-TEFb, a critical step in the identification and development of drug targets.</p>		
Amogha Vijayvargiya	47	<p>Contractile vascular smooth muscle cells (VSMC) play a key role in the regulation of arterial blood vessel tone and cardiovascular health. In many vascular diseases, VSMCs undergo a phenotypic switch from a contractile to a synthetic phenotype, where the contractile markers myosin heavy chain (myh11) and smooth muscle alpha actin (smaa) are reduced and proliferation increases.</p>	<p>Cytochrome B5R3 Regulates Vascular Smooth Muscle Phenotypic Switching</p>	<p>Amogha Vijayvargiya; Anh T. Nyguyen, PhD; Megan P. Miller; Scott Hahn; Adam C. Straub, PhD</p>

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		<p>Evidence from our lab demonstrates that cytochrome b5 reductase 3 (Cyb5R3) regulates the redox state of soluble guanylate cyclase to control cyclic guanylate monophosphate (cGMP) levels and maintain contractile phenotype in VSMCs. To test this hypothesis, we used non-targeting (NT) and Cyb5R3 knockdown (KD) rat aortic and brain VSMCs and serum starved them for 24, 48, and 72 hours to induce phenotypic switching. Measurements of myh11 and smaa using RT-qPCR were made. We observed that the RNA levels of both myh11 and smaa increased with time in the non-targeting VSMCs but not in the Cyb5R3 knockdown VSMCs. Additionally, human Alzheimer's disease brain sections with severe angiopathy</p>		
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		<p>were stained for Cyb5R3 and smaa, and showed a significant reduction in expression. Preliminary data suggest that Cyb5R3 is essential for VSMC phenotypic switching, which may unravel a new therapeutic target for treating individuals with cardiovascular disease.</p>		
<p>Sarah Duplaga</p>	<p>48</p>	<p>PURPOSE: Bicuspid aortic valve (BAV) is the most common congenital heart defect. Patients with this defect have an increased risk for aortic aneurysm and dissection. Although the overall cause of BAV and its connection to aneurysm formation remains unknown, several mutations of the gene GATA5 have been identified and linked to bicuspid aortic valve morphology in both human and mouse models. The purpose of this study is to determine if there is a</p>	<p>The Influence of GATA5 Mutations on Bicuspid Aortic Valve-Associated Aortopathy</p>	<p>Sarah Duplaga; Jennifer Hill, MFS; Thomas Gleason, MD; Julie Phillippi, PhD</p>

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		<p>correlation among BAV, aneurysm formation, and a single nucleotide polymorphism (SNP) within the regulatory elements of GATA5.</p> <p>METHODS: Polymerase chain reaction (PCR) was used to amplify and detect the SNP in 219 patient samples.</p> <p>RESULTS: It was determined that the mutated SNP was more commonly found in patients with an aneurysm regardless of valve morphology. It is likely that unregulated overexpression of GATA5 is a factor that influences aneurysm formation.</p> <p>CONCLUSION: Subsequent experiments will investigate the influence of the function of GATA5 as a regulatory protein on the expression of the gene eNOS. If a genetic correlation is determined, it could</p>		
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		lead to genetic testing as a new method of diagnosing BAV, and determining risk stratification for aortic catastrophe, and could also be beneficial in family planning.		
Julianna Buchwald	49	<p>Purpose: Bicuspid aortic valve (BAV) occurs in 1-2% of the population. Although the mechanism of BAV is unknown, it is associated with thoracic aortic aneurysm (TAA) and aortic dissection.</p> <p>Methods: Proximal ascending aortic tissue from patients undergoing aortic valve and/or ascending aortic replacement due to aneurysm was harvested with informed patient consent and IRB approval. Medial smooth muscle cells (SMC) were treated with oxidative stress. Cell viability due to reactive oxygen species (ROS) accumulation in</p>	Smooth Muscle Cells from Bicuspid Aortic Valve Patients Exhibit Increased Cell Viability in the Presence of Antioxidants and Oxidative Stress	Julianna E. Buchwald; Marie Billaud, PhD; Jennifer Hill, MFS; Julie A. Phillippi, PhD; Thomas G. Gleason, MD

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		<p>the proximal ascending aorta was measured in the presence of dimethyl fumarate (DMF), a ROS scavenger, using the MTT assay. Results: BAV cell viability was decreased compared to tricuspid aortic valve (TAV) specimens. DMF increased basal cell viability in BAV specimens (p=0.086, n=3) but had little effect on tBHP-induced cell death when compared with TAV specimens.</p> <p>Conclusions: Accumulation of ROS in ascending aortic SMCs compromises cell viability in BAV patients. Antioxidants like DMF may have the ability to reverse oxidative stress in the ascending aorta and improve cell viability via the Nuclear factor (erythroid-derived 2)-like 2 (Nrf2) pathway. Ongoing studies are focused on defense mechanisms via</p>		
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		the Nrf2 pathway in BAV patients through gene expression analysis of target genes using RT-PCR.		
Eishan Ashwat	50	<p>Introduction: Hypoxia can produce free radicals within cells (e.g. reactive oxygen/nitrogen species), which can be detrimental. Previous research showed nitrosylation of caspase-1 by reactive nitrogen species reduced its activity in macrophages. However, it is unknown whether this effect occurs during oxidative stress in hepatocytes, which possess greater antioxidant capacity and alternative functions for caspase-1. We investigated effects of redox stress on caspase-1 nitrosylation/function in a human hepatocyte cell-line. Methods: HepG2 human hepatoma cells were stimulated with LPS</p>	The Effect of Nitrosylation on Cysteine-Based Caspase-1 Activity	Eishan Ashwat; Qian Sun, MD, PhD; Hong Liao, MD; Meihong Deng, MD, PhD; Detcho Stoyanovsky, PhD; Melanie J. Scott, MD, PhD

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		<p>(100ng/mL) or H₂O₂ (100μM), +/- nitric oxide donor SNAP (455μM) for up to 18h. Additional cells were pretreated with auranofin (3/6mM), a thioredoxin-reductase inhibitor, 1h prior to LPS/H₂O₂ stimulation to determine the relative importance of the thioredoxin antioxidant system on caspase-1 activity. We harvested whole cell lysates to measure caspase-1 activity by fluorescent caspase-1-specific substrate cleavage. Results: Caspase-1 was activated by both H₂O₂ or LPS after 1h. Nitrosylation of caspase-1 (induced by SNAP) decreased caspase-1 activity. Similarly, pretreatment of cells with auranofin also reduced caspase-1 activation in response to H₂O₂ and LPS. Conclusions: Together these findings suggest</p>		
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		<p>caspase-1 is activated by both H₂O₂ and LPS in hepatocytes, and nitrosylation reduces this activity. Thioredoxin-mediated pathways may help maintain caspase-1 activity in hepatocytes.</p>		
Rachel Butch	52	<p>The Epstein-Barr Virus (EBV) is a ubiquitous γ-herpesvirus that infects humans worldwide and causes the inflammatory disease Infectious Mononucleosis. Epithelial cells are transiently infected and are lysed after virion production allowing for transmission; however, EBV-associated cancers, including nasopharyngeal carcinoma (NPC), are associated with latent epithelial cell infection. We hypothesize that EBV Latent Membrane Proteins (LMP) 1 and LMP2A, co-expressed in NPC tumors, contribute to EBV latency in</p>	<p>A New Role for Epstein-Barr Virus LMP1 in Regulating Viral Persistence in Epithelial Cells</p>	<p>Rachel Butch; Sarah Cook; Danielle Seigel; Joseph DeFazio; Laura Wasil, PhD; Kathy Shair, PhD</p>

		<p>infected epithelial cells and that removal of LMP1 or LMP2A would affect EBV persistence in epithelial cells. In this study, epithelial cells are infected with recombinant EBV (EBV-BAC) mutated for LMP1 or LMP2A and compared to wild-type infection. The EBV-BACs also incorporate resistance genes for mammalian selection and the green fluorescence protein (GFP) to monitor for infected cells. Quantitative PCR was used to measure EBV genome loss in serial passage upon removal of drug selection. In wild-type infection, without drug selection, 50% genome loss was reached by experiment day 25. In contrast, deletion of LMP1 maintained stable infection in the absence of drug selection. The wild-type phenotype</p>		
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		can be recovered by re-introduction of LMP1 via trans-complemented expression. Our results support the new hypothesis, LMP1 negatively regulates stable persistence of EBV in epithelial cells.		
Rachel Schusteff	54	Proper gene expression in eukaryotes requires a high level of regulation by various mechanisms. Transcription, the process of converting the information in DNA to RNA by RNA polymerase, is an early stage in gene expression. The five-subunit Paf1 complex associates with RNA Pol II at open reading frames and plays a role in all stages of transcription. Because of its important role in gene expression, it is necessary to understand how the Paf1C travels with Pol II. Rpb1, the largest subunit of Pol II,	The PAF1 Complex Directly Interacts with RNA Pol II In Vivo Through the CDC73 C-Domain	Rachel Schusteff; Ellie Kerr; Margaret Shirra; Karen Arndt

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		<p>contains a heptapeptide consensus sequence (YSPTSPS), known as the Carboxy Terminal Domain (CTD), repeated 26 times in <i>Saccharomyces cerevisiae</i> and 52 times in humans. Previous in vitro approaches have shown that the Cdc73 C-domain (C-terminal residues 201-393) binds to the CTD and indicate that this interaction may be phosphospecific. Using an in vivo BPA crosslinking approach in <i>S. cerevisiae</i>, we show that the Cdc73 C-domain crosslinks to Pol II. Further in vivo crosslinking experiments will determine if having the CTD phosphorylated is necessary to see crosslinking in vivo. Understanding the interactions between the Paf1C and Pol II can help to further the study of gene</p>		
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		expression.		
Rebecca Brown	55	<p>The purpose of this project is to identify the function of a highly conserved palindromic twenty base pair sequence that occurs in the intergenic region of Cluster B mycobacteriophages. It is imperative to understand how mycobacteriophages regulate transcription and translation, because they can be used as tools to manipulate bacteria. Previous work has shown that the majority of these intergenic regions contain promoters, with the sequence occurring between the -10 box and the start codon of the gene. The Cluster B3 mycobacteriophage Akoma was used as a model to study these sequences. The intergenic regions containing this sequence of Akoma</p>	<p>Functional Characterization of Highly Conserved Sequences in Cluster B Mycobacteriophages</p>	<p>Rebecca Brown, Deborah Jacobs-Sera, Rebekah M. Detric, Graham Hatfull</p>

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		<p>were cloned into a promoterless vector containing a ribosome binding site, mCherry gene, and an antibiotic resistance gene. mCherry is a mycobacterial reporter gene that fluoresces red when a functional promoter is upstream to initiate transcription. Promoter strength is determined by the amount of fluorescence measured using a phosphoimager. To determine if this sequence contains a ribosome-binding site, translational fusions were constructed in an mCherry vector without a promoter or a ribosome binding site with the intergenic region upstream of mCherry. Fluorescence was detected, which demonstrates that there is a ribosome-binding site in this region.</p>		
Bryony Brown	56	Isolation of 700+	Immunity Patterns and	Bryony Brown; Cory Hayes;

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		<p>mycobacteriophages on Mycobacterium smegmatis mc2155 and analysis of the genomes shows wide diversity that displays mosaicism allowing for comparative analysis (Hatfull, 2010.) Previous studies on Cluster N phage Charlie illustrated the simple configuration of the immunity cassette required to express the minimal genetic switch, determining whether a phage enters the lytic or lysogenic cycle (Broussard, 2012.) Lysogens (bacteria that contain the phage genomes) of nine Cluster N phages were generated, and a large panel of phages across our collection was tested. These tests showed various exclusion (no infection of the bacteria by the phage) patterns. In particular, Cluster N phages</p>	<p>Characteristics of the Cluster N Mycobacteriophages</p>	<p>Deborah Jacobs-Sera; Welkin H. Pope, PhD; Graham F. Hatfull, PhD</p>
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		MichelleMyBelle, Butters, and Xerxes showed increased resistance to Subcluster A3 phages. To explore these results, genes that could explain this exclusion pattern have been targeted and include genes of unknown function, a Toxin and Antitoxin gene set, and a lipoprotein. Currently, expression vectors are being generated to determine which genes will replicate the immunity patterns of the Cluster N phages in wildtype <i>Mycobacterium smegmatis</i> mc2155.		
Wei Ng	57	Plasmids, bacteria, and some phages encode segregation systems for chromosomal partitioning at cell division. One of several such systems is ParABS, in which ParB binds to conserved parS sites on the chromosome, and ParA ATPase	Characterizing ParB of <i>Mycobacteriophage</i> RedRock	Wei L. Ng, Juan Cervantes, Rebekah M. Dedrick, Valerie M. Villanueva, Travis N. Mavrich, Matthew Olm, Deborah Jacobs-Sera, Graham F. Hatfull

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		<p>translocates ParB-bound DNA. Presumably, ParABS genomes replicate as extrachromosomal prophages and require the ParABS system for prophage maintenance and stability. We constructed a consensus sequence for RedRock parS sites along with those of 27 other bacteriophages with ParABS genomes and predict that there are approximately four distinct specificity groups. This is supported by binding studies demonstrating that RedRock (Subcluster A2) ParB binds Gladiator (A6) parS, but does not recognize Alma (A9) parS, or the parS of KatherineG, a phage that infects Gordonia, a different bacterial host. Moreover, we find that Alma ParB binds specifically to Alma parS, suggesting the</p>		
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		<p>presence of a functional ParABS. We hypothesize that these mycobacteriophages have diversified their partitioning loci to prevent partitioning-based extrachromosomal prophage incompatibility. Further binding assays show differences in RedRock ParB binding affinity to two identical 6-mers separated by a two base-pair spacer, indicating that local genomic context may influence RedRock ParB-DNA interactions. These findings provide insight into the diversity of temperate phages and their prophage maintenance mechanisms.</p>		
Xiaoxi Gao	58	<p>Introduction: Platinum agents are commonly used to treat solid tumors. Platinum-based chemotherapy is toxic and can lead to decreased fertility and</p>	<p>Comparison of Relative Ovarian Toxicities of Two Platinum Agents in a Mouse Model</p>	<p>Xiaoxi Gao; Payal Mital, PhD; Kyle Orwig, PhD</p>

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		<p>early menopause, impacting the post-cancer quality of life in reproductive age women. Carboplatin has largely replaced cisplatin due to its less toxic systemic side-effects. We tested the toxicities of carboplatin and cisplatin on the ovaries in a mouse model by performing differential follicle counts and assessing microvessel density (MVD). Methods: Fifteen C57BL/6 mice were divided into three groups: control, cisplatin (4mg/kg), and carboplatin (30mg/kg). Drugs were administered IP once per week for 4 weeks. Mice were sacrificed 3 weeks post-treatment; ovaries were collected for histology: differential follicle counts (Weigert's hematoxylin staining) and MVD assessments (PECAM-1/CD31</p>		
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		<p>staining) were performed on tissue cross sections. Results: Compared to the control group (779.6 ± 96.9), carboplatin (444.0 ± 123.2) and cisplatin (329.0 ± 75.2) had decreased primordial follicle (PMF) counts. The MVD in the carboplatin (2.10 ± 0.082) and cisplatin (1.70 ± 0.185) treated ovaries was significantly decreased in comparison to the control ovaries (3.60 ± 0.143). Conclusions: Both platinum agents, carboplatin and cisplatin appeared to have similar toxic effects on the ovaries as indicated by comparable reduction in PMF counts and MVD.</p>		
Christopher Divito	59	<p>The striatum is essential for many aspects of mammalian behavior including motivation and movement and is dysfunctional in motor</p>	<p>Loss of VGLUT3 Produces Circadian-Dependent Hyperdopaminergia and Ameliorates Motor Dysfunction and L-Dopa-Mediated Dyskinesias in a Model of Parkinson's Disease.</p>	<p>Christopher B. Divito; Kathy Steece-Collier; Daniel T. Case; Sean-Paul G. Williams; Jennifer A. Stancati; Lianteng Zhi; Maria E. Rubio; Caryl E. Sortwell; Timothy J. Collier; David Sulzer;</p>

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		<p>disorders such as Parkinson's disease. Previous studies have suggested a key role for the vesicular glutamate transporter (VGLUT) 3 in regulating locomotor activity, a canonical measure of basal ganglia output, through its expression by striatal cholinergic interneurons. Here we show that the hyperlocomotor activity observed in mice lacking VGLUT3 occurs during the waking cycle and is accompanied by increased dopamine synthesis, packaging and release in the striatum. We also show that contrary to the prevailing hypothesis, locomotor activity and striatal dopamine levels are surprisingly unaffected by the loss of the transporter from cholinergic neurons. The mice do however show defects in sensorimotor gating and</p>		<p>Robert H. Edwards; Hui Zhang; Rebecca P. Seal</p>
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		<p>habituation. Importantly, we find that loss of VGLUT3 prevents the development of motor deficits and markedly diminishes the appearance of L-dopa mediated dyskinesias in a model of Parkinson’s disease. VGLUT3 thus profoundly regulates striatal function through multiple mechanisms, opening new avenues for understanding the regulation of basal ganglia circuitry and potentially finding new treatment options for Parkinson’s disease and related disorders.</p>		
Ross Carson	60	<p>Hypothesis: Antenatal glucocorticoid hormone treatment has greatly improved clinical outcomes in infants born preterm, but it has serious neurodevelopmental consequences. It has been demonstrated that even one dose of antenatal glucocorticoid</p>	<p>Effect of Dexamethasone on Genome-Wide Expression after Exposure to Statins in Neural Stem/Progenitor Cells</p>	<p>Ross Carson; Anthony Rudine, MD; Donald DeFranco, PhD</p>

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		<p>hormone exposure can predispose an infant to developing depression and anxiety. Recently, our lab has shown that statins influence glucocorticoid signaling pathways and may be able to alter glucocorticoid dependent gene expression. We hypothesize that statins will influence glucocorticoid dependent gene expression in neural progenitor cells.</p> <p>Methods: Mouse neural stem progenitor cells were exposed to clinically relevant concentrations of pravastatin and dexamethasone in vitro. mRNA was isolated for whole transcriptome sequencing analysis. mRNA sequencing was validated by PCR.</p> <p>Results: Our analysis revealed sex-dependent gene expression patterns of mouse</p>		
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		<p>neural progenitor cells exposed to either dexamethasone or pravastatin treatment. In addition, we identified transcripts whose expression was regulated by both dexamethasone and pravastatin.</p> <p>Conclusions: Our results suggest that dexamethasone may have sex-dependent effects on gene expression and, potentially, cortical development. In addition, we have discovered that pravastatin is able to regulate dexamethasone-dependent patterns of gene expression, which may have clinical implications in reducing the negative effects of antenatal glucocorticoid treatment.</p>		
Roni Lahr	61	Cell growth and proliferation rely on the process of ribosome biogenesis to amplify	LARP1 Interacts directly with 5'UTRS Encoding Translation Machinery	Roni M. Lahr, Hiba A. Al-Ashtal, Andrea J. Berman, PhD

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		<p>protein production. Growth signals are funneled through the kinase complex mTORC1 to influence translation of 5'-terminal oligopyrimidine (5'TOP) mRNAs that encode translation machinery. The factor downstream of mTORC1 that recognizes the 5'TOP motif to promote TOP translation has been identified as LARP1. Lar-related protein 1 (LARP1) is an RNA binding protein that is deregulated in several cancers. However, direct recognition by LARP1 to the 5'TOP and its method of mRNA regulation have not been dissected. We hypothesized that the LARP1-specific region called the DM15 contributes to 5'TOP recognition. Since DM15 is unique to LARP1, it represents a target for drug-design</p>		
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		<p>studies. We determined the three-dimensional structures of DM15 alone and bound to a 5'TOP sequence resolved at 1.8 Å and 2.7 Å, respectively. DM15 contains structurally conserved helix-turn-helix repeats, a common protein-interacting fold that has been repurposed to bind a 5' TOP sequence. Interestingly, DM15 does not bind all 5'TOP RNAs. Future studies will focus on the sequence requirements of LARP1. These studies will impart a mechanistic view to the regulation of TOP mRNAs and the role of LARP1 as regulator of ribosome biogenesis.</p>		
Daniel Totten	62	<p>Transcription in metazoans is regulated through pausing and restarting of RNA polymerase II by P-TEFb, a transcription factor. P-TEFb is regulated through the association</p>	<p>Antagonistic Splicing Factors HNRNP A1 and SRSF2 Compete for Binding to SNRNA 7SK</p>	<p>Daniel C. Totten; Andrea J. Berman, PhD</p>

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		<p>with the snRNA 7SK and the 7SK-P-TEFb RNP, which includes SRSF2. Upon P-TEFb dissociation, 7SK RNA binds to several hnRNPs and forms the 7SK-hnRNP RNP. To better understand the maintenance of these mutually exclusive RNPs, we investigated the binding of hnRNP A1 and SRSF2 to Stem III of 7SK RNA. We show for the first time that hnRNP A1 melts Stem III and binds to its 3' half with modest affinity, whereas SRSF2 is unable to open Stem III to access its binding sites and results in a 10-fold lower affinity for Stem III. Further, hnRNP A1 and SRSF2 efficiently compete and occlude binding by the competitor protein upon saturating conditions; both proteins bind the same RNA molecule when lower concentrations of</p>		
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		<p>proteins are used. However, SRSF2 is only efficiently recruited from Stem III to a competing RNA in the presence of UP1, suggesting a model in which hnRNP A1 and SRSF2 help maintain mutually exclusive RNPs through occlusion of the competitor protein, yet work together to aid in the transition between the two 7SK RNPs.</p>		
Brianna Heath	63	<p>Huntington's Disease (HD) is a fatal, autosomal dominant, neurodegenerative disorder caused by a CAG repeat expansion in the huntingtin gene. The disease is characterized by chorea, as well as psychiatric and cognitive symptoms. At present, no treatment able to modify the disease progression is available. HD is characterized by the death of medium striatal spiny neurons</p>	<p>MT1 Receptor-Mediated Neuroprotection in Mouse Model of Huntington's Disease</p>	<p>Brianna Heath; Diane Carlisle, PhD; Robert Friedlander, MD, MA</p>

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		<p>within the brain. One mechanism of cellular damage and neuronal death in HD is mitochondrial dysfunction. Previous research identified melatonin as protective in a mouse model of HD. Neuroprotection was mediated by the MT1 receptor. We examined the effect of MT1 receptor overexpression on the neuroprotective capability of melatonin in the HD mouse model by crossing a transgenic MT1 mouse with the R6/2 mouse. MT1 overexpression protected against activation of caspases, key regulators of neuronal death, but HD behavioral symptomatology was unchanged. This further led to an investigation of the effect of HD on the MT1 receptor expression itself, looking at how</p>		
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		both endogenous and transgenic MT1 are altered in R6/2 mice.		
Maya AlMoussa	64	<p>Extracellular signal-regulated kinase 2 (ERK2) and dual specificity phosphatase 6 (DUSP6) are proteins involved in the mitogen-activated protein kinase (MAPK) pathway, which triggers cell proliferation. DUSP6 dephosphorylates ERK2, which prevents continuous signaling of cell growth. BCI is a DUSP6 inhibitor that prevents the ERK2 mediated activation of DUSP6. BCI reduces cell proliferation in cancer cells, but its binding site and mechanism of action are unknown. Determining how BCI regulates DUSP6 and the MAPK pathway would further our understanding in DUSP6's role in cancer and potentially aid in the development of new cancer drugs. To</p>	Computational Modeling of ERK2, DUSP6, and BCI	Maya AlMoussa, David Koes, PhD

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		<p>create computational models of BCI binding, Amber was utilized to generate ERK2 and DUSP6 simulations and obtain representative conformations. BCI was docked to the selected conformations using SwissDock to identify the best binding sites. The BCI ligands docked closest to the sites implicated in the DUSP6/ERK2 interaction were selected and their binding affinities were calculated using Smina. BCI binding sites were identified near the Tyrosine 185 residue on ERK2, near the KIM domain on the DUSP6 N terminal, and close to the catalytic site on the DUSP6 C terminal. 3 computational models were generated and used to perform a virtual screen for compounds with similar interactions.</p>		
Patricia Donehue	65	A major problem facing the world is the lack of	Analysis of SIX2+ Cells during Mouse Kidney Development and	Patricia Donehue; Maria Giovanna Francipane, MS, PhD;

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		<p>organs available for transplantation. A possible solution is to grow new organs within the body. The Lagasse lab has previously shown that when mouse embryonic kidney fragments are injected into the jejunal lymph nodes of mice, mature and functional nephrons can develop. The transcription factor Six2 marks the nephron progenitor population throughout nephrogenesis. This project investigated whether co-injection of Six2+ kidney cells, together with embryonic kidney fragments can improve the structure and function of the developing nephrons. GFP+ (green fluorescent protein) kidneys were taken from mouse embryos, fragmented, mixed with tdTomato+ Six2+ cells sorted using Fluorescence Activated</p>	<p>Their Contribution to Ectopic Kidney Organogenesis</p>	<p>Eric Lagasse, PharmD, PhD</p>
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		<p>Cell Sorting (FACS), and injected into the lymph nodes of adult nude mice. Five weeks after the injections, some of the injected mice were sacrificed and the lymph nodes were isolated.</p> <p>Immunohistochemistry was also used to identify Six2 expression in the parental embryonic mouse kidneys. It resulted in staining in pretubular aggregates. As expected, the Six2+ stem/progenitor cells were able to incorporate into the grafts, but the engraftment rate was low. The technique needs to be optimized and renal stromal progenitor cells may also be needed to aid in the engraftment.</p>		
Sarah Glatz	66	<p>Exosomes are tiny extracellular vesicles produced by the cell. Recent research has been aimed at</p>	The Ins and Outs of CD63, RAS, and Exosomes	Sarah Glatz; Katrin Reiners, PhD; Christof Kaltenmeier, MD; Olga Shatnyeva, PhD; Michael Lotze, MD; Elke Pogge von Strandmann PhD

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		<p>discovering the influence these protein-containing vesicles have on intercellular communication. CD63 is a protein believed to be highly influential in the formation of exosomes, due to the fact that it is typically found in much higher concentrations in exosomes than in the cell. HEK293 cells were used to perform assays to observe the effects of CD63 on exosome formation. A wildtype line was used as a control, as well as BAG6-KO and CPB/P300-KO. The knockout proteins are known to be important in the exosome formation process. Flow cytometry was used to ensure that the GFP and GFP-CD63 proteins were successfully transfected in all cell lines, and Western Blotting with an anti-GFP antibody confirmed protein expression.</p>		
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		<p>Exosomes were counted using Nanoparticle Tracking Analysis, and similarly transfected HeLa cells were used for microscopy to show the change in CD63 when incubation time was lengthened. CD63 expression was observed with flow antibody in single and co-cultures of Ras mutant and Ras wildtype lines, showing that Ras mutant cells have higher surface expression of CD63 compared to Ras wildtype and expression changes when Ras Mutant and Wildtype are co-cultured.</p>		
<p>Joshua Lorenz-Guertin</p>	<p>67</p>	<p>Neurodevelopment is regulated by signaling through the γ-aminobutyric acid type A receptor (GABA(A)R), a ligand-gated chloride channel. Early in development, intracellular chloride concentration is high; GABA(A)R activation</p>	<p>Depolarizing GABA(A) Receptor Activity Controls Calcium Entry and GABAergic Synaptic Plasticity in a Developmental Dependent Manner</p>	<p>Joshua Lorenz-Guertin; Megan Brady, PhD; Charles Moon; Nicholas Graff; Tija C. Jacob, PhD</p>

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		<p>leads to chloride efflux, depolarization and calcium entry via voltage-gated calcium channels. Later in maturation, extracellular chloride levels increase and GABA(A)R exerts a hyperpolarizing effect. It is not well understood how this switch from depolarizing-to-hyperpolarizing affects calcium-sensitive mediators of GABAergic synaptic composition. We found that following synaptogenesis, GABA(A)R activation in rat cortical neurons leads to a rise in intracellular calcium, suggesting depolarization. We then investigated how development-specific GABA(A)R-mediated calcium increases regulate Ca²⁺/calmodulin-dependent protein kinase II (CaMKII). Biochemical data</p>		
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		<p>indicated that treatment with the GABA(A)R agonist muscimol activates CaMKII early in development, but decreases activation later. Measuring local changes in CaMKII activation using the CaMKIIα FRET sensor, Camuα, found that muscimol does not lead to CaMKII activation following synaptogenesis. Imaging methods probed endogenous and fluorescently labeled GABA(A)R and the scaffold protein gephyrin to follow muscimol-induced alterations in GABAergic synapses. We observed that muscimol increases GABA(A)R subunit diffusion out of synapses and dispersion of gephyrin. Overall, these data suggest that GABA(A)R-mediated increases in intracellular calcium following</p>		
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		synaptogenesis lead to decreased receptor clustering at GABAergic synapses.		
Anne Faust	68	After injury, central nervous system (CNS) neurons fail to regenerate damaged axons. This failure is due, in part, to changes in the extracellular matrix (ECM) due to the primary injury and secondary changes induced by reactive gliosis and a pro-inflammatory innate immune response that lead to permanent scarring. Currently, a clinical treatment is lacking to promote functional ECM repair to prevent scarring and to encourage functional axon regeneration in the CNS. Decellularized ECM bioscaffolds have been used clinically to promote reconstruction in numerous peripheral tissues. However, the use of ECM bioscaffolds in the CNS has been	Tissue-Dependent Effects of Central Nervous System Extracellular Matrix on Hippocampal Cell Regeneration in Culture	Anne Faust; Apoorva Kandakatla; Tanchen Ren, PhD; Asma Naqvi; Vibha Reddy; Alex Comerci; Lydia Lewis; Michael Steketee, PhD

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		<p>minimal. Though the exact mechanisms are unknown, ECM bioscaffolds are thought to work, in large part, by modulating the innate immune response to reduce inflammatory macrophage phenotypes (M1) while increasing anti-inflammatory, pro-repair macrophage phenotypes (M2). Here, we analyzed the tissue-specific effects of CNS ECM bioscaffolds on hippocampal neuron regeneration. We also analyzed the effects microglia treated with the ECM bioscaffolds known to promote an M2 phenotype have on regeneration. We report that CNS tissue-derived and non-CNS-derived bioscaffolds increase hippocampal neuron regeneration and neuronal complexity. Moreover, we show that microglia-</p>		
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		treated ECM bioscaffolds increase regeneration compared to ECM bioscaffolds alone.		
Yuta Naro	69	<p>MicroRNAs (miRNAs) are small, single-stranded non-coding RNAs that have been shown to play a critical role in the regulation of post-transcriptional gene expression. Over 2,500 miRNAs have been discovered in humans and are proposed to play an integral role in regulating more than 60% of protein-coding genes. This provides the basis for regulation of many biological processes, including cell proliferation, cell differentiation, and apoptosis. Consequently, dysfunction of miRNA regulation has been implicated in contributing to many human diseases, most notably cancer.</p>	Development of Small-Molecule Inhibitors of MicroRNA MIR-21 Function	Yuta Naro; Meryl Thomas, PhD; Colleen Connelly, PhD; Alexander Deiters, PhD

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		<p>MicroRNA-21 (miR-21) is arguably the most extensively studied miRNA to date. It was one of the first miRNAs discovered and is the only known miRNA to be overexpressed in nearly all types of human cancers, thus rendering miR-21 an “oncomir” and an attractive target for investigation. Using a luciferase-based reporter assay under the control of miR-21 function, a high-throughput screen of >300,000 compounds led to the identification of several new classes of small-molecule inhibitors of miR-21. Extensive structure-activity relationship investigations delivered several optimized inhibitors, of which their mechanism of action and therapeutic potential were explored. These chemical probes will</p>		
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		provide a better understanding of miR-21 function, as well as provide a basis for the development of new therapeutics.		
Ching-Chung Ko	70	Although a huge number of mycobacteriophage genome sequences are available (at least 870 sequenced), our understanding of the functions of mycobacteriophage genes is very limited. As a gateway to exploring the unknown, mycobacteriophage genes were over-expressed in Mycobacterium smegmatis—a relative of tuberculosis-causing bacteria—to identify those that were detrimental to the host's growth. Using this approach, gene 52 of mycobacteriophage Fruitloop was identified as a toxic mycobacteriophage gene. To understand	The Analysis of Toxicity by Mycobacteriophage Fruitloop Gene 52	Ching-Chung Ko; Graham F. Hatfull, PhD

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		<p>how Fruitloop gp52 kills <i>M. smegmatis</i>, a co-immunoprecipitation assay was performed, followed by mass spectrometry analysis to identify Fruitloop gp52's interacting target(s). As a result, Wag31 of <i>M. smegmatis</i>—an essential protein involved in cell shape and cell wall integrity—was identified as a target. Interestingly, over-expression of Fruitloop gp52 resulted in a change in mycobacterial cell morphology from rod to round, a phenotype similar to that seen when Wag31 was depleted in mycobacteria. Moreover, over-expressing Wag31 allowed mycobacteria to survive in the presence of Fruitloop gp52. Further elucidating the phage-encoded toxic proteins'</p>		
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		mechanisms will advance our knowledge about host-phage interactions. In addition, it also creates opportunities to discover new anti-tuberculosis drug targets at a time when drug-resistant tuberculosis is becoming a severe concern.		
Eva Bach	71	The lateral superior olive (LSO) in the mammalian brain is an auditory nucleus, which encodes the direction of incoming sound by comparing sound level differences between the two ears. During development, inhibitory inputs to the LSO undergo substantial functional and structural refinement to give rise to the precise organization in adults. Activity-dependent long-term potentiation (LTP) is thought to represent a first step in the reorganization of	Activity-Dependent LTP in the Auditory Brainstem	Eva Bach, PhD; Karl Kandler, PhD

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		<p>neuronal circuits, but attempts to demonstrate LTP at inhibitory synapses in the LSO have remained unsuccessful. In this study, we activated inhibitory synapses in brain slices containing the LSO using stimuli that mimic the characteristic, burst-like patterns present in intact animals before hearing onset. Using this stimulus pattern elicited robust and reliable inhibitory LTP. Stimulation protocols deviating from this pattern, but using equal number of stimuli at high frequency or spacing stimuli over the same duration, failed to induce LTP. Thus, the stereo-typical bursts carry important temporal cues to facilitate the strengthening of inhibitory LSO inputs. Current investigations aim to identify the</p>		
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		specific signaling cascades engaged by activity bursts, which will improve our insight into the brain mechanisms of appropriately adjusting inhibitory strength throughout development.		
Jennifer Walker	72	Protein-protein interactions, which are important for most cellular processes, are not as static as we assume. They are actually changing constantly due to random genetic drift. When an incompatibility arises in interacting proteins, compensatory changes must occur for the interaction to continue. Through Orthologous Gene Replacement, we tested orthologous alleles for their compatibility with the yeast Nuclear Pore, specifically the Y-complex. We observed incompatibility through	Coevolution in the Yeast Nuclear Pore	Jennifer L. Walker; David A. Taft; Brandon S. Small; Nathan L. Clark, PhD

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		<p>growth defects when replacing <i>S. cerevisiae</i> Nup84p with the version from its closest relative <i>S. paradoxus</i>. When testing more divergent species orthologs, the degree of incompatibility increased with divergence in a consistent way, indicating that coevolution was continuous during the evolution of the Y-complex. We used structural analysis to identify amino acid substitutions that may cause incompatibilities between the <i>S. cerevisiae</i> and <i>S. paradoxus</i> Nup84p. Using in vitro evolution we can detect not only the initial growth defects of the strains expressing multiple versions of Nup84, but also the compensatory changes made to restore wild-type fitness. Investigating the</p>		
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		genetic mutations underlying these apparent compensatory changes is our next step. The yeast Nuclear Pore Complex provides an effective model to investigate how incompatibilities arise in protein-protein interactions, and how compensatory changes restore disrupted interactions.		
Sarah Najjar	74	Neuroactive substances that influence cutaneous afferent activity (e.g., ATP, calcitonin gene related peptide (CGRP), acetylcholine, PGE2, glutamate) are released by epidermal keratinocytes. To advance understanding of the mechanisms regulating keratinocyte-neuronal communication, we developed an optogenetic mouse model in which the light-activated cation channel	Optogenetic Control of Neuromodulator Release from Keratinocytes	Sarah Najjar; Marsha Ritter Jones, MD, PhD; Jami Saloman, PhD; Junichi Hachisuka, PhD; H. Richard Koerber, PhD; Brian M. Davis, PhD; Kathryn M. Albers, PhD

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		<p>channelrhodopsin (ChR2) is targeted to K14 keratin expressing keratinocytes. Interestingly, blue light stimulation of the skin of K14-ChR2 mice elicits nocifensive behaviors and action potentials (APs) in cutaneous sensory neurons. To determine how activation of keratinocytes stimulates AP firing in sensory afferents, we are using cultures of primary keratinocytes from K14-ChR2 expressing mice to identify neuroactivators released in response to light stimulation.</p>		
Adam Barsouk	75	<p>UV exposure induces DNA damage, called photoproducts, that, if not repaired by the nucleotide excision repair (NER) pathway, can interfere with DNA replication and transcription, and ultimately cause mutations or chromosome breaks.</p>	<p>Role of Nucleotide Excision Repair Protein XPA in Telomere Preservation Following UVC Exposure</p>	<p>Adam Barsouk, Melinda Sager, Elise Fouquerel, Patricia Opresko</p>

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		<p>Telomeres are nucleoprotein structures that cap chromosome ends. They are comprised of DNA repeats enriched with dipyrimidine sites that are highly prone to UV-induced photoproducts. NER functions at telomeres; however, it is unclear whether NER is essential to preserve telomere integrity. Wild type BJ-hTERT skin fibroblasts, and cells knocked down for NER, were exposed to UVC light and allowed to recover for 24 or 48 hours. Cells were arrested in metaphase, and chromosomes were spread on slides to compare, by telomere fluorescent in situ hybridization (TF-FISH), the occurrence of structural telomeric aberrations, indicative of compromised telomere integrity. NER-deficient cells exhibited</p>		
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		<p>a higher percentage of telomere aberrations compared to the WT before treatment. 5 J/m² UVC exposure induced an increase in telomere aberrations in the WT, and less so in the NER-deficient cells. NER may be important for repairing endogenous damage at telomeres, such as oxidative cyclopurine adducts, but may be less essential in protecting against photoproduct blocks to replication due to the presence of translesion polymerase etc.</p>		
A. Elizabeth Hildreth	76	<p>Cellular growth and development rely on the precise regulation of gene expression. In eukaryotes, the chromatin template acts as a barrier to the transcription machinery. Chromatin consists of nucleosomes, which contain approximately 147 basepairs of DNA</p>	<p>Identifying the Regulatory Role of Chromatin in Transcription Termination</p>	<p>A. Elizabeth Hildreth; Karen M. Arndt, PhD</p>

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		<p>surrounding an octamer of histone proteins H2A, H2B, H3, and H4. To faithfully express the genetic material, transcription factors regulate RNA polymerase II activity during transcription initiation, elongation, and termination. The Nrd1-Nab3-Sen1 (NNS) complex regulates termination of many short noncoding and protein coding RNAs in yeast. Very little is known about the role of chromatin in this pathway. I aim to elucidate this relationship using the NNS pathway in <i>Saccharomyces cerevisiae</i> as a model. To screen for histone residues required for termination by the NNS pathway, I have made use of a plasmid library encoding histones with all possible alanine substitutions and a well-characterized</p>		
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		<p>termination reporter. I have identified 10 residues in H3 and H4 with defects in termination, and have begun their functional characterization. Analysis to this point reveals that these residues have widely varying phenotypes, suggesting that they may promote NNS-dependent termination in different ways. Future work will elucidate the mechanisms by which these histone residues regulate proper transcription termination.</p>		
Joshua Sturm	77	<p>Hearing loss leads to a myriad of cellular and synaptic changes in the central auditory system, some of which lead to the perception of phantom sounds (tinnitus). However, the synaptic circuit mechanisms contributing to tinnitus have remained poorly</p>	<p>Neural Circuit Reorganization in the Auditory Midbrain of Mice with Behavioral Evidence of Tinnitus</p>	<p>Joshua Sturm; Hannah Roos; Tuan Nguyen, PhD; Karl Kandler, PhD</p>

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		<p>understood. To identify hearing-loss-induced reorganizations of synaptic circuits that correlate with tinnitus, we applied laser-scanning photostimulation (LSPS) with caged glutamate to map the organization and strength of intrinsic excitatory and inhibitory synaptic inputs onto glutamatergic and GABAergic neurons in the inferior colliculus (IC) of noise-traumatized mice. Tinnitus behavior was quantified using the acoustic startle gap detection method. One week after noise-exposure, about 50% of noise-exposed mice (19/37 animals) showed behavioral evidence of tinnitus, as evidenced by significant reductions in gap-mediated inhibition of the acoustic startle reflex. All noise-traumatized</p>		
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		<p>mice had similar hearing loss and exhibited substantial reorganization in IC circuits. Interestingly, however, only mice with tinnitus showed a profound shift in the balance of synaptic excitation and inhibition in both glutamatergic and GABAergic neurons. Our findings suggest that in the IC, noise trauma leads to a complex yet cell-type specific reorganization of excitatory and inhibitory local circuits, the nature of which correlates with the presence or absence of behavioral evidence of tinnitus.</p>		
Caitlin Czajka	78	<p>Muscle loss exceeding skeletal muscle's inherent regenerative repair capacity results in fibrosis and loss-of-function, phenomena of clinical significance for military and civilian trauma victims. Decellularized</p>	<p>Matristem Decellularized Matrix Upregulates Wound Healing Genes and Promotes Angiogenesis in Ischemic Skeletal Muscle</p>	<p>Caitlin A. Czajka, PhD; Johannes C. Kuttan, MS; Thomas W. Gilbert, PhD; Jeffrey S. Isenberg, MD, MPH</p>

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		<p>extracellular matrix has been used as a wound treatment given its biodegradable nature and ability to modulate growth factor signaling and inflammation. The mechanism of therapeutic efficacy of a commercially-available decellularized porcine bladder matrix product, MatriStem[®] MicroMatrix[®], in skeletal muscle wound healing is unknown. We hypothesized that MatriStem[®] treatment would promote angiogenesis, upregulation of self-renewal gene transcription factors, and suppression of reactive oxygen species formation to improve skeletal muscle healing. Using a murine model of hind limb volumetric muscle injury with and without femoral artery ligation-induced ischemia and MatriStem[®] treatment,</p>		
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		<p>we performed laser Doppler, histologic, and gene expression analyses 3, 7, and 14 days post-injury. We report that treatment with MatriStem® increased total cellular recruitment and mean vascular density in ischemic and non-ischemic wounds, and promoted upregulation of wound healing genes 3 days post-injury in non-ischemic wounds. Ischemic and non-ischemic wounds treated with MatriStem® showed resolution of wound healing gene expression by 14 days post-surgery. We conclude that MatriStem® promotes cellular infiltration and modulation of wound healing gene expression to enhance skeletal muscle wound healing.</p>		
Tunliang Li	79	<p>Introduction: Acetaminophen (APAP) is a commonly used analgesic. Its overdose</p>	<p>Saquinavir Attenuates Acetaminophen-Induced Liver Toxicity</p>	<p>Tunliang Li; Peng Deng; Venkata Sashi Gollapudi ; Eileen M Bauer, PhD; Timothy R.Billiar, MD</p>

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		<p>can lead to fulminant hepatic failure. Our group has previously observed the HIV-Protease Inhibitor Saquinavir (SQV) is a potent inhibitor of excessive HMGB 1-TLR4 driven inflammation in macrophages. Here, we test the hypothesis that SQV attenuates DAMP mediated APAP-induced liver toxicity in mice via a mechanism involving apoptosis. Methods: Murine model of APAP overdose: briefly, mice were injected with an APAP overdose with or without therapeutic administration of SQV at 3 hrs. Blood was analyzed for AST/ALT levels 12 hrs post APAP injection; liver necrosis was quantitated histologically and Western blot analysis of liver tissue was used to determine signaling events. Results: Treatment with SQV robustly attenuated</p>		
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		<p>APAP-induced liver toxicity when given therapeutically, resulting in reduced ALT/AST levels and liver necrosis. Interestingly, SQV increased serum IL-6 levels while lowering HMGB1 levels. In addition, PARP cleavage and caspases 3 cleavage, both markers of apoptosis, were increased in SQV treated mice.</p> <p>Conclusion: Therapeutic administration of SQV attenuates liver damage induced by an APAP overdose in mice. Our findings of a mammalian target for SQV in this setting show great potential for future clinical trials, hopefully leading to repurposing of this drug.</p>		
Jacqueline Starr Welty	80	<p>The Cockayne syndrome B (CSB) protein is an SNF2/SWI2 helicase with a function in transcription-coupled nucleotide excision</p>	<p>Cockayne Syndrome Protein B Recruits Homologous Recombination Machinery at Transcriptionally Active Damage Sites</p>	<p>Leizhen Wei, PhD; Satoshi Nakajima, PhD; Michael Tsang, PhD; Zhiyuan Shen, MD, PhD; Arthur S. Levine, MD; Li Lan, MD, PhD</p>

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		<p>repair. How CSB orchestrates repair of other transcription-blocking lesions is largely unknown. To elucidate CSB function in DNA repair, we introduced genome site-specific oxidative damage and determined the impact of transcription on repair factor assembly, finding that KU and MRN complexes are recruited to damage sites independent of transcription. Recruitment of RPA1, RAD51C, RAD51 and RAD52, however, is strictly governed by active transcription and requires wild type CSB function. We show that the ATPase activity of CSB is indispensable for loading of these recombination factors. Moreover, CSB is important in countering radiation-induced DNA damage both in cellular and animal CSB models.</p>		
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		<p>Taken together, our results have uncovered a novel, recombination-based mechanism by which CSB protects DNA from oxidative damage at transcriptionally active sites, and may provide insight into the neurodegeneration of Cockayne syndrome.</p>		
Isabella Kopits	81	<p>Oncolytic virotherapy is a novel cancer treatment. It acts through direct oncolysis and virus-elicited antitumor immunity. Genetically engineered oncolytic vaccinia viruses (VVs) are used: WT, vJS6, vSC20, vSP, vvDD, and vvDD-A34R. We asked two questions: How potent are these viruses, and do VVs generate ICD? We hypothesize genetic mutations may affect death pathways and ICD. Three key parameters of ICD are cell surface exposure of calreticulin (CRT), extracellular release of</p>	<p>Oncolytic Vaccinia Viruses: Oncolytic Potency and Immunogenic Cell Death</p>	<p>Isabella M. Kopits; Roshni Ravindranathan, MS; David L. Bartlett, MD; Z. Sheng Guo, PhD</p>

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		<p>ATP and HMGB1. Human breast, colorectal, cervical and lung cancer cells were infected with viruses at MOI of 0.1. Cell viability was determined by MTS assays. For analysis of ICD, H1299 cells were treated with viruses at MOI of 10, harvested, and analyzed for ecto-CRT by flow cytometry. The conditioned media were analyzed for extracellular ATP and HMGB1. Although sensitivity to vaccinia varied across cell lines, vvDD and vSP were consistently the most potent. We observed enhanced ecto-CRT and extracellular ATP from cells infected by certain viruses, indicating ICD. It appears some viral genes may affect the degree of ICD, thus the ability to induce antitumor immunity. Our findings indicate some genetically engineered VVs are</p>		
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		highly effective oncolytic viruses and may lead to more potent ICD in cancer cells.		
Brianna Mayfield	82	Fertilization in the African clawed frog, <i>Xenopus laevis</i> , employs two distinct mechanisms to block multiple sperm from fertilizing an egg, called the fast and slow block to polyspermy. The fast block consists of a rapid, fertilization-evoked positive shift in membrane potential that deters additional sperm from entering. This rapid block results from a net efflux of Cl ⁻ , but the channel that mediates this current has not yet been identified. The calcium-activated chloride channel TMEM16a has been recently identified within <i>X. laevis</i> oocytes and we hypothesized that it plays a role in the fast block. To examine the importance of these	TMEM16A Is an Important Mediator of the Fast Block to Polyspermy in <i>Xenopus Laevis</i> Eggs	Brianna L. Mayfield; Anne E. Carlson, PhD

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		<p>channels, we used two selective inhibitors, MONNA and T16Ainh-A01, to block TMEM16a channels in mature <i>X. laevis</i> eggs. Eggs were analyzed by whole-cell recording for variations in fertilization-evoked depolarizations. We found that both TMEM16a inhibitors increased polyspermy and slowed the rate of fertilization-evoked depolarizations. We also found that with 30uM MONNA, fertilization failed to evoke any depolarization. These data suggest that TMEM16a mediates the fast block in <i>X. laevis</i>. This characterizes the first molecular identity of a channel that mediates the fast block to polyspermy in any species.</p>		
Katherine Wozniak	83	Preventing polyspermy is essential for the normal embryonic development of most	Identifying the Calcium Source Needed for the Fast Block to Polyspermy	Katherine Wozniak; Anne E. Carlson, PhD

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		<p>animals. The two most ubiquitous blocks to polyspermy, the slow and fast block, create a physical barrier to prevent additional sperm entry minutes after fertilization and induce an electrical barrier seconds after fertilization, respectively. In <i>Xenopus laevis</i>, the fast block is characterized by an increase in intracellular calcium and efflux of chloride that depolarizes the egg membrane. Although the calcium increase is crucial for the fast block, the source of this calcium remains unknown. We reason that calcium either enters into the egg from the extracellular environment or is released from the endoplasmic reticulum (ER) via an inositol 1,4,5-triphosphate (IP3) mediated pathway. To test these hypotheses,</p>		
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		<p>whole-cell recordings were performed on eggs inseminated in solutions containing: 1) 0 mM Ca²⁺, 2) Gd³⁺ (a calcium channel inhibitor), or 3) Xestospongins C (a cell-permeable ER IP₃ receptor inhibitor). We recorded normal depolarizations from fertilized eggs where extracellular calcium was lacking or blocked, yet we did not observe depolarizations when calcium release from the ER was inhibited. Taken together, these data suggest that the primary source of calcium needed for the fast block to polyspermy is released from the ER.</p>		
Eric Griffin	84	<p>The plant microbiome is a key determinant of plant health and productivity and has recently received considerable attention. Leaves, in particular, comprise one of the</p>	<p>Soil Resources and Tree Hosts Structure Bacterial Endophyte Communities among Woody Seedlings in a Mature Tropical Forest</p>	<p>Eric A. Griffin; Steven W. Kembel, PhD; Alyssa A. Carrell, PhD; S. Joseph Wright, PhD; Walter P. Carson</p>

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		<p>world's largest microbial habitats, though no study has empirically evaluated the degree to which host species and resource availability structure leaf bacterial assemblages. We used high-throughput sequencing to quantify community composition of bacterial endophytes (inside leaves) among woody seedlings in a tropical forest in Panama. We tested the following hypotheses:</p> <p>1) The Host Tree Hypothesis: bacterial endophyte communities sharply contrast among host tree species. 2) The Limiting Nutrient Hypothesis: bacterial endophyte communities sharply contrast among soil nutrients. We used five woody species (<i>Alseis blackiana</i>, <i>Desmopsis panamensis</i>, <i>Heisteria concinna</i>, <i>Sorocea affinis</i>, and <i>Tetragastris</i></p>		
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		panamensis) in the shaded understory in large replicated plots where nitrogen, potassium, and phosphorus were added in a fully factorial design. Overall, our results indicate that bacterial community assemblages sharply contrast among host species and soil resource treatments. In addition, there are significant overlaps of particular bacterial taxa among species, suggesting that a “core microbiome” exists among all species. To our knowledge, this is the first empirical study to demonstrate that soil resources and host species determine bacterial endophyte community structure.		
Eun Kim	85	Ebola hemorrhagic fever is one of the most fatal viral diseases caused by Ebola virus (EBOV). Although infections only occur	Immunogenicity of a Recombinant Subunit Vaccine Based on the Glycoprotein of Ebola Virus in Mice	Eun Kim, PhD; Shaohua Huang, PhD, Tom Kenniston, Geza Erdos, PhD; Andrea Gambotto, MD, PhD

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		<p>frequently in Central Africa, the virus has the potential to spread globally and there is no effective antiviral therapy or licensed vaccines currently available. In this study, we have generated the recombinant subunit vaccine containing the extracellular portion of the Ebola glycoprotein (rEBOV-Gp) fused to the T4 fibrin fold on trimerization domain (F) with or without the fusion of a Toll-like receptor 4 (TLR-4) agonist peptide (RS01 or RS09). C57BL/6 mice immunized with rEBOV-GpF + MPLA subcutaneously and with the patches of rEBOV-GpF-RS01 or -RS09 intradermally were elicited EBOV-Gp specific antibodies significantly. Moreover, we tested the biological functional activity of TLR4 agonist peptide by treating human or</p>		
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		<p>Rhesus macaque PBMC with 2.5 µg of each rEBOV-GpF proteins. While RS01 rarely stimulated, RS09 did PBMC to secrete cytokines resulting in activation the innate immune system and initiation inflammation as an adjuvant. Our data suggested that recombinant subunit vaccine-based EBOV-GpF is sufficient to induce immunogenicity in mice and could be developed as an effective vaccine against Ebola virus infection for further development.</p>		
Shifan Ma	86	<p>Combination therapy has become a popular treatment for various diseases in clinics. By using a combination of several herbs, traditional Chinese medicinal formula can achieve synergistic effects. However, identifying the active constituents, the molecular and</p>	<p>CVD-Specific Chemogenomics Database for System Pharmacology and Synergistic Mechanism Analysis of Traditional Chinese Medicinal Formula, Sini Decoction</p>	<p>Shifan Ma, MS; Hai Zhang, PhD; Zhiwei Feng, PhD; Peng Yang, PhD; Lirong Wang, PhD; Xiang-Qun Xie</p>

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		<p>synergistic mechanisms remain a challenging task. Here, we used Sini Decoction, a complex herbal mixture for treatment of cardiovascular diseases, as a model to explore the synergism mechanism by combined computational and experimental approaches. We first constructed a cardiovascular diseases specific chemogenomics database, including 984 target proteins, 924 drugs, 2,080 chemicals, and 276 associated pathways. With the implemented cheminformatics tools, Sini Decoction ingredient-target interaction network was constructed and visualized. We revealed the representative active ingredients as aconitine, liquiritin and 6-gingerol, and also identified their targets</p>		
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		<p>involving beta-adrenergic receptor and angiotensin-converting enzyme. We predicted and experimentally confirmed that the arrhythmia side effect of aconitine can be alleviated by liquiritin, and the cardiac effects of aconitine can be increased by co-administering 6-gingerol. Our results demonstrate that the constructed disease-specific database was successfully applied for systems pharmacology analysis of complicated herbal formula in predicting underlined molecular mechanisms for synergism, which will provide insight into understanding a combinational therapy.</p>		
Abhishek Mandal	87	<p>Cytochrome c (cyt-c) plays a key role in activating intrinsic apoptosis. Understanding this process has implications for treatment of</p>	<p>To Unfold or not to Unfold? Structural Insights of Cardiolipin-Bound Cytochrome c by Solid-State NMR</p>	<p>Abhishek Mandal; Cody L. Hoop, PhD; Ravindra Kodali, PhD; Marissa Di; Maria DeLucia; Valerian E. Kagan, PhD, DSc; Jinwoo Ahn, PhD; Patrick C.A. van der Wel, PhD</p>

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		<p>Huntington's disease and cancer. A required signaling event in this apoptotic pathway is peroxidation of mitochondrial lipid cardiolipin (CL) by cyt-c. A crucial open question is regarding structural changes in the bound cyt-c that allow its covalently attached heme to catalyze the peroxidation of CL acyl chains. We use Magic-angle-spinning (MAS) and static solid-state NMR (ssNMR) on uniformly ¹³C,¹⁵N-labeled cyt-c bound to CL-containing vesicles to gain site-specific insights into the structure and the dynamics experienced by bound cyt-c. A comparison of MAS chemical shifts of the bound cyt-c to solution NMR shifts on the soluble protein leads us to the startling conclusion that cyt-c does not experience</p>		
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		<p>major unfolding upon binding. Peroxidase assays reveal that binding to CL leads to higher activity rates. We conclude that the increase in peroxidase activity of CL-bound cyt-c is not a result of extensive unfolding in cyt-c upon binding. We instead propose an alternative mechanism, whereby the membrane's dynamics bring the active site of cyt-c in close proximity to CL-acyl chain, allowing localized structural/dynamical change in the protein to be enough to allow this reaction.</p>		
Harman Ghuman	88	<p>Stroke is a severe cerebrovascular trauma that results in localized brain tissue injury, affecting nearly 800,000 Americans each year. In recent studies, extracellular matrix (ECM) derived from urinary bladder lamina propria and basement</p>	<p>ECM Hydrogel Injection for the Treatment of Stroke: Characterization of Acute Host Cell Invasion</p>	<p>Harman Ghuman, Andre R Massensini, PhD; Terry Kim, Christopher J Medberry, PhD; Francesca J Nicholls, Stephen F Badylak, DVM, PhD, MD; Michel Modo, PhD</p>

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		<p>membrane has shown therapeutic potential in reconstructing the urinary tract, demonstrating ECM's remodeling properties. The goal of this study was to fill the stroke cavity with ECM derived hydrogel in the transient middle cerebral artery occlusion rat model of stroke and evaluate its therapeutic potential. ECM at different concentrations (0, 1, 2, 3, 4, 8 mg/ml) was slowly injected into the infarct cavity and the brains were perfused 1-day post-injection to analyze gelation and cell infiltration. Immunohistochemistry analysis revealed a reliable delivery of ECM to the lesion cavity. However, ECM concentrations <3mg/ml did not gel and were not retained in the cavity. A significant host cell</p>		
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		<p>infiltration was observed within 24 hours post-injection; of these, 20-30% were putative microglia/macrophages (Iba1+) across all concentration groups. The number of astrocytes (GFAP+) cells invading the ECM acutely was negligible. This characterization demonstrates that an ECM hydrogel can be readily injected and retained within a lesion cavity while attracting host cells into the damaged region.</p>		
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