THE NATIONAL CONSTITUTION CENTER 12TH NOVEMBER | 2019 1 1 A M - 6 : 3 0 P M



The Pharmacology Graduate Group at the University of Pennsylvania proudly presents its 35th Annual Student

Symposium

## **KEYNOTE SPEAKER**

### LISA SHIPLEY, PHD

Vice President | Global Digital Analytics & Technologies

MERCK & CO.

Smart Trials: Moving from Site-centric to Patient-centric Clinical Trials



#### **SCHEDULE OF EVENTS – 2019 SYMPOSIUM**

#### **KIRBY LOBBY**

11:00 AM ..... Registration and boxed lunches

#### **KIRBY AUDITORIUM**

12:00 - 12:15 PM ...... Opening Remarks - Chair of Pharmacology Graduate Group

12:15 - 1:45 PM ..... Student Talks – Session 1

#### Nathan Kendersky (Maris Lab)

Investigating the Oncogenic Role and Regulation of DLL3 in Neuroblastoma

#### Theresa Patten (De Biasi Lab)

Investigating the role of flavorants in nicotine reward: a mouse model to study vaping

#### Joseph Johnson (Lynch Lab)

*Frataxin deficiency induces Drp1-dependent mitochondrial fragmentation in cellular models of Friedreich ataxia* 

#### **BOGLE CHAIRMAN'S ROOM**

1:45 – 2:45 PM ..... Student Poster Session

#### **KIRBY AUDITORIUM**

*2:50 – 4:10 PM* ..... Student Talks – Session 2

#### Laura Puentes (Mach Lab)

Beyond the nucleus: the role of poly(ADP-ribose) in promoting  $\alpha$ -synuclein aggregation and neurotoxicity

#### Edward Chuang (Shorter Lab)

Small molecule enhancers of the human Hsp70/Hsp40/Hsp110 disaggregase system

#### Jack Jacobs (Sehgal Lab)

Anandamide metabolites protect against seizures through the TRP channel Water witch in Drosophila melanogaster

#### **KIRBY LOBBY**

4:15 - 4:30 PM ..... Coffee Break

#### **KIRBY AUDITORIUM**

4:30 PM ..... The John S. O'Brien Memorial Lecture

Lisa A. Shipley, Ph.D., Vice President, Digital and Analytics Technologies Merck Research Laboratories

Smart Trials: Moving from Site-centric to Patient-centric Clinical Trials

**DELEGATES CAFE** 

5:45 - 6:45 PM ..... Cocktail Reception

#### John S. O'Brien Memorial Lecture



Lisa A. Shipley, Ph.D. Vice President, Digital and Analytics Technologies Merck Research Laboratories

Dr. Shipley is Vice President of Digital and Analytics Technologies in Merck Research Laboratories. She has the overall responsibility to design, operationalize, and direct Discovery, Preclinical and Early Development's (DPED) contribution to Merck's digital vision. In partnership with key technical lines, she is responsible for the leadership, operational and strategic management of initiatives focused on advancing knowledge, experience and capabilities in digital technologies, data management and analysis to transform the use of digital health approaches in all stages of drug discovery and clinical trial management, moving from a site-centric to patient centric model of drug development. Dr. Shipley joined Merck and Company in 2008 as the Vice President of Pharmacokinetics, Pharmacodynamics, and Drug Metabolism before moving into her current role. Prior to joining Merck, Dr. Shipley spent over 20 years at Eli Lilly and Company in roles of increasing responsibility including the positions of executive

director, Lean Six Sigma and vice president Drug Disposition, PK/PD and Trial Simulations. Dr. Shipley obtained her undergraduate degree from McDaniel College and her doctoral degree in Pharmacology and Toxicology from the University of Maryland at Baltimore. Her postdoctoral training was conducted at the Walter Reed Army Institute of Research as a National Research Council Fellow elucidating the metabolism and pharmaco-kinetics of antileishmanial and antimalarial drugs under development by the U.S. Army.

Dr. Shipley has authored or co-authored three book chapters, over 25 journal articles, 40 abstracts on drug metabolism, pharmacokinetics, analytical assay development, drug disposition and digital clinical trials and has been granted five patents. She has chaired sessions at the Gordon Research Conference in Drug Metabolism, the Society of Toxicology, the American Association of Pharmaceutical Sciences, International Conference on Drug Development, PhRMA workshops and the Drug Information Association. She has served as the chair of the Drug Metabolism Technical Group within the Pharmaceutical Research and Manufacturing Association (2007-09), a member of the IQ Consortium and as a member of the International Society of the Study of Xenobiotics Council (2010-12). She has also served as a reviewer for Drug Metabolism and Disposition, Journal of Clinical Pharmacology, the Journal of Chromatography and Toxicology and Applied Pharmacology, and a lecturer for the University of Indiana School of Medicine and Purdue University. She was awarded the 2000-2001 Chairman's Ovation Award for leadership in motivating and developing people, the LRL President's Award for Diversity in 2007, the Chairman's Award in Environmental Health and Safety in 2013 and was awarded the NAFE Women of Excellence Healthcare Champion in 2017.

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Special thanks to the 3<sup>rd</sup> year students for planning and organizing this year's Pharmacology Student Symposium



Front Row (Left to right): Jerrick To, Monica Thapaliya, Lauren Shaw, Kryshawna Beard, Khadija Wilson, Nicole Robles-Matos, Kate Webb, Laura Romano

Back Row: Ziyang Xu, Shivesh Ghura, Michael Hart, Daniel Jacome, Dan Brown, Varun Bahl, Anne Fosnocht, John Maurer, Ross Pirnie

## And many thanks to Sarah Squire for coordinating the PGG symposium!

The Pharmacology Graduate Group's



**35th Annual Student Symposium** 

# Student Speakers

#### Nathan Kendserky

Advisor: John Maris, MD

Neuroblastoma is a pediatric solid tumor that arises from deregulated development of the sympathetic nervous system. The 5-year survival of patients with high-risk neuroblastoma is only 50% and survivors have life-long morbidities from intensive chemotherapy. This underscores the need to identify biologically relevant and clinically actionable targets for children with high-risk disease. A subset of neuroblastoma tumors is driven by a core regulatory circuit (CRC) that includes seven transcription factors (TF) (ASCL1, MYCN, PHOX2B, HAND2, ISL1, GATA3, TBX2) driven by a strong enhancer element. Additionally, each TF regulates expression of itself and the other CRC TFs. Here, we present an integrated epigenomics and RNA-sequencingbased approach to identify neuroblastoma tumor cell-specific surface molecules regulated by the CRC: molecules we hypothesize are amenable to immunotherapy. With CRC ChIP-sequencing data, we used the bedtools and HOMER toolkits to identify genes bound by these TFs. We performed differential expression with limma voom comparing RNA-sequencing data from neuroblastoma patients (TARGET, N=162) and 25 normal tissues (GTEx, N=1641). Our analysis identified several candidate genes that are known immunotherapeutic targets in neuroblastoma (ALK, L1CAM, DLL3). Of those genes, we prioritized Delta-like canonical notch ligand 3 (DLL3), a differentially expressed, tumor-associated protein abundant on the surface of neuroblastoma cells. We observe a strong correlation (RNA-seq) between DLL3 and ASCL1 expression in cell lines (R=0.803, p=4.62e-10) and patient samples (R=0.711, p=1.56e-24). To understand downstream signaling associated with DLL3, we performed shRNA knockdown in cell lines with high DLL3 expression and observed a dramatic reduction in cellular viability and proliferation. These data suggest components of the CRC may regulate DLL3 and cause DLL3 overexpression in neuroblastoma. Our data also support previous studies that have detailed DLL3 as an inhibitory Notch ligand, which show Notch de-repression results in a significant loss of fitness. Together, our results support DLL3 as a candidate immunotherapeutic target in neuroblastoma, which warrants further investigation into its oncogenic function. Ultimately, targeting CRCbound cell-surface proteins represents a novel way to exploit transcriptional dependencies in neuroblastoma and should abrogate classical mechanisms of immune escape, such as selection of subclones with low or absent target expression.

Investigating the role of flavorants in nicotine reward: a mouse model to study vaping

#### **Theresa Patten**

Advisor: Mariella De Biasi, Ph.D.

E-cigarettes (e-cigs) are popular across age groups, with approximately 9 million adults and 3.6 million school-aged students using these products. A hallmark feature of e-cigs is the availability of non-traditional flavorants (e.g. fruit, candy, alcohol). Flavored ecigarettes are commonly used to initiate nicotine use in adolescence or to attempt nicotine cessation in adulthood. We developed a longitudinal animal model that mimics the life of a "vaper", in which mice initiate nicotine use in adolescence and continue into adulthood. Using this model, we can study the effect of a fruit-flavorant on nicotine consumption and preference introduced either in adolescence or in adulthood. Male and female C57BL/6J mice were tested in a 2-bottle choice paradigm that involves three phases: (1) mice initiate nicotine use in adolescence with either unflavored nicotine or flavored-nicotine, (2) throughout young adulthood all mice receive unflavored nicotine in the 2-bottle choice test, (3) flavor is then either introduced for the first time or reintroduced into the nicotine bottle in adulthood. Adolescent mice preferred a fruit-flavored nicotine solution over an unflavored solution during adolescence. In addition, adolescent mice with access to flavored-nicotine consumed higher daily doses of nicotine than those with access to unflavored nicotine. Adult mice exposed to flavored-nicotine for the first time in adulthood maintained their baseline nicotine consumption despite the addition of flavorants to the nicotine bottle, while mice that were re-introduced to flavored-nicotine in adulthood significantly increased their nicotine consumption. Our data in adolescent mice recapitulate clinical data which have shown (1) a higher preference for and (2) increased consumption of flavored nicotine compared to unflavored or tobacco-flavored nicotine. In addition, our data suggest that for adolescents currently using a flavored tobacco product, avoiding previously nicotine-paired flavorants could be a key element to their success in future nicotine cessation attempts.

#### Joseph Johnson

Advisor: David Lynch, MD, Ph.D.

Friedreich ataxia (FRDA) is a neurodegenerative disease leading to ataxia, dysmetria, dysarthria, and cardiomyopathy, for which no treatment is available. The disease is caused by genetically-induced deficiency in frataxin, a mitochondrial matrix protein critical for iron-sulfur cluster biosynthesis and ATP production. However, the role of frataxin in mitochondrial dynamics in FRDA pathophysiology remains largely unknown. Here, we report that frataxin deficiency induces Drp1-dependent mitochondrial fragmentation in cellular models of Friedreich ataxia. FRDA patient fibroblasts exhibit excessively fragmented mitochondrial networks, a phenotype that is reversible by overexpression of wild type frataxin or a metabolically inactive frataxin point mutant. Indeed, siRNA knockdown of frataxin in healthy fibroblasts significantly increases the percentage of cells with fragmented mitochondrial networks and increases mitochondrial network fragmentation in each cell. Furthermore, frataxin knockdown significantly increases the localization of the mitochondrial fission protein phospho-Drp1 (Ser616) to sites of mitochondrial fragmentation, suggesting that frataxin knockdown may cause mitochondrial network fragmentation through a Drp1-dependent pathway. Selective Drp1 inhibition prevents frataxin-knockdown-induced mitochondrial fragmentation, although it does not reverse mitochondrial fragmentation in FRDA patient fibroblasts. Moreover, frataxin knockdown does not alter cellular ATP levels, but inhibiting Drp1 in frataxin knockdown fibroblasts decreases ATP levels, suggesting that frataxinknockdown-induced mitochondrial network fragmentation is critical to maintain ATP Our findings thus demonstrate that frataxin deficiency causes excessive levels. mitochondrial fragmentation through a Drp1-dependent mechanism, and that fragmentation may represent a homeostatic mechanism that initially maintains normal ATP levels in frataxin deficient cells but chronically plays a less defined role in cell viability.

### Beyond the nucleus: the role of poly(ADP-ribose) in promoting $\alpha$ -synuclein aggregation and neurotoxicity

#### Laura Puentes

Advisor: Robert Mach, Ph.D.

The exact cause of Parkinson's disease (PD) remains unknown; however, a recent finding by Kam et al. is shedding new light on poly(ADP-ribose) (PAR) as a key mediator of aberrant a-synuclein neurotoxicity in PD. PAR is a polymer that is primarily biosynthesized in the nucleus by Poly(ADP-ribose) Polymerase-1 (PARP-1). In the last decade, extensive research has been done exploring the role of PAR in modulating cellular functions outside of the nucleus. In this project, our focus lies on studying the interactions between PAR and pathologic a-synuclein. Specifically, we are interested in assessing the role of PAR in promoting a-synuclein aggregation, along with elucidating PAR-binding sites on fibrillar forms of a-synuclein --- in order to better inform our development of PET imaging tracers for PD. To address these research questions, we employed a wide array of in vitro and ex vivo techniques which allowed us to identify the amino acid residues that are involved in PAR-binding and study the molecular effects that arise from this interaction. Our results suggest that increased intracellular levels of PAR promote the formation of oligomeric conformations of a-synuclein and that the interaction between PAR and fibrillar a-synuclein involves positively-charged amino acid residues on the N-terminal region of the protein. Together, these results unveil important information on the availability of sites on a-synuclein for targeting with either imaging or therapeutic modalities and hints at the potential of using PARP-1 inhibitors to decrease intracellular PAR levels and possibly reduce the formation of aberrant forms of asynuclein in PD.

#### Small molecule enhancers of the human Hsp70/Hsp40/Hsp110 disaggregase system

#### **Edward Chuang**

Advisor: James Shorter, Ph.D.

Proteins perform a myriad of essential and non-essential functions within the cell; however, proteins must be properly folded in order to function. During cellular stress, proteins may become misfolded and aggregate through aberrant intermolecular interactions. The 70 and 40 kDa heat shock proteins (Hsp70 and Hsp40) form one of the predominant molecular chaperone systems within the cell that unfolds and refolds misfolded proteins. However, aggregated proteins contain stable intermolecular interactions that are more difficult to break. Hsp110, a member of the Hsp70 superfamily, collaborates with Hsp70 and Hsp40 to enable disassembly of protein aggregates and restoration of native protein function. Our lab has shown that the metazoan disaggregase system (MDS) comprising of Hsp70, Hsp40, and Hsp110 family members refolds disordered aggregates such as urea-denatured luciferase and heat-denatured GFP in vitro. The human genome contains 12 Hsp70 genes, over 50 Hsp40 genes, and 4 Hsp110 genes, giving rise to thousands of three-component combinations of the MDS. Select combinations more effectively disassemble  $\alpha$ -synuclein amyloid than others, suggesting that different combinations of the MDS can have drastically different efficacy against the same substrate. This combinatorial phenomenon may be the key to understanding how a disaggregase system of under a hundred genes could chaperone a proteome of tens of thousands of proteins. We have purified a number of Hsp70, Hsp40, and Hsp110 proteins that are expressed in humans and systematically assessed the disaggregase activity of each combination against aggregated substrates. We have also identified a number of small-molecule modulators of disaggregation activity. These small-molecules are promising candidates for the treatment of neurodegenerative diseases. The results presented here further our understanding of the MDS and provide crucial therapeutic leads for a devastating class of diseases.

Anandamide metabolites protect against seizures through the TRP channel Water witch in Drosophila melanogaster

Jack Jacobs

Advisor: Amita Sehgal, Ph.D.

Endocannabinoids are protective against seizures, but their mechanism of action is still unclear as they can have effects independent of known cannabinoid receptors. Using *Drosophila melanogaster*, which lack cannabinoid receptor 1 and 2, we report here that the endocannabinoids anandamide and 2-arachidonoylglycerol protect against seizures in multiple fly seizure models. Surprisingly, we find that inhibition of anandamide catabolism renders flies insensitive to the anticonvulsant effect of anandamide, indicating that anandamide metabolites are responsible for the observed seizure protection. Consistent with this finding, arachidonic acid, a direct metabolite of anandamide, is protective against seizures. To identify downstream effectors, we tested for a role of TRP channels and find that the TRPV1 antagonist capsazepine blocks the protective effect of anandamide. Also, a targeted genetic screen of TRP channels identifies *water witch* as a mediator of the anti-seizure action of anandamide. Through the use of a *Drosophila* model, this study reveals the unappreciated role of arachidonic acid in seizure protection and identifies a cannabinoid receptor 1/2-independent mechanism of endocannabinoid seizure protection.

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## Poster Abstracts

#### Glycolytic Flux as the Central Mediator of Glucagon Secretion

#### Varun Bahl

Advisor: Klaus Kaestner, Ph.D.

Maintaining glucose homeostasis is central to our health, and its failure results in debilitating diseases such as diabetes. Diabetes mellitus affects over 425 million people worldwide and is a leading cause of death in many countries. The pathophysiology of type 2 diabetes (T2D) is bihormonal, with both insufficient insulin production by beta-cells and elevated glucagon release by alpha-cells. While a great deal of effort has been devoted to understanding the molecular events controlling insulin secretion from beta-cells, the exact mechanisms governing glucagon release by alpha-cells are still not completely understood, though a role for glycolytic flux was recently demonstrated by alpha-cell specific gene ablation of glucokinase (Gck). This is a critical knowledge gap, as the normal suppression of glucagon secretion by elevated glucose levels fails in T2D patients, contributing to hyperglycemia through stimulation of hepatic glucose production. Using single cell RNAseg of islets from T2D organ donors, we have made the striking discovery that G6PC2, encoding the islet-specific glucose-6-phosphatase 2, is dramatically upregulated in alpha-cells in these patients. G6PC2 limits glycolytic flux by creating a futile cycle with GCK that likely hinders glucose-mediated suppression of glucagon secretion. We hypothesize that reduced glycolytic flux is a central driver of alpha-cell dysfunction in T2D. We will address this overarching hypothesis through innovative mouse models developed in the Kaestner Lab, as well as loss- and gain-of-function ex vivo studies in mouse and human pancreatic islets.

#### Exploring the role of the gut microbiome in COX-2 selective and nonselective NSAIDinduced gastroenteropathy

#### Kayla Barekat

Advisor: Garret FitzGerald, M.D., FRS

Nonsteroidal anti-inflammatory drugs (NSAIDs), used to treat pain and inflammation, have been associated with cardiovascular (CV) and gastrointestinal (GI) adverse events, including myocardial infarction, stroke, intestinal bleeding, ulceration, and stenosis. Traditional NSAIDs, like naproxen and indomethacin, exert their effects by inhibiting both cyclooxygenases (COX) -1 and -2 and have long been recognized to cause GI complications in up to 30% of patients. This toxicity was attributed to inhibition of COX-1-dependent synthesis of prostaglandin (PG) E2 and prostacyclin (PGI<sub>2</sub>) in gastroduodenal epithelial cells, which are involved in protection of the GI mucosal barrier. Thus, the COX-2 selective NSAIDs, including celecoxib, were developed in an attempt to avoid the GI complications; however, COX-2 selective NSAIDs are also associated with GI toxicity. Moreover, inhibition or genetic deletion of COX-1 alone does not result in spontaneous GI lesions, and concomitant inactivation of COX-2 is necessary to cause GI damage in mouse models. Thus, further research is necessary to elucidate the mechanisms underlying NSAID-induced gastroenteropathy. Our previous studies have shown that there is a bidirectional interaction between NSAID treatment and the gut microbiome. Gut bacteria with β-glucuronidase activity enable enterohepatic recirculation of NSAIDs, thus prolonging systemic exposure of the parent drug and augmenting its pharmacodynamic effect. Furthermore, removal of bacteria by antibiotic treatment results in faster drug clearance and reduces the GI toxicity associated with indomethacin. Taken together, there is still a missing link between differential inhibition of the COX enzymes and subsequent impact on the gut microbiome in eliciting gastroenteropathy, and variation in gut bacterial composition may help explain the wide range in NSAID tolerance across individuals. Novel genetic and pharmacological approaches are being applied to address the hypothesis that a differential impact on the gut microbiome contributes to a divergent incidence of gastroenteropathy following suppression of COX-1+COX-2 vs COX-2 alone. This translational project paves the way for clinical trials examining the impact of concomitant antibiotics on NSAID efficacy and toxicity in patients.

#### Brain-derived Exosomes as Diagnostic Biomarkers of Traumatic Brain Injury

#### Kryshawna Beard

**P**3

Advisors: David Meaney, Ph.D. and David Issadore, Ph.D.

Traumatic brain injury (TBI) is characterized by diverse primary mechanisms of injury (closed vs open head injury, deceleration injuries, focal, and diffuse injuries) that lead to the development of secondary pathological cascades that drive neurological deficit post-TBI. These secondary injury processes include inflammation, gliosis, axonal shearing, edema, and vascular injury, and each plays distinct, patient-dependent roles in TBI pathology. Inability to separate patients based on the presence of these different endophenotypes represents a major challenge for diagnosis and treatment of TBI. The goal of the present study was to identify blood-based biomarkers that relate to the postconcussive state to improve clinical diagnosis and management of TBI. Extracellular vesicles including exosomes isolated from patient plasma have emerged as promising potential biomarkers for TBI due to their ability to cross the BBB into systemic circulation with molecular cargo (proteins, RNA, and metabolites) intact for analysis. The Issadore lab has developed a novel microfluidic platform for rapid isolation of brain-derived (GluR2-expressing) exosomes providing a tool with which the biochemical state of neurons and glia can be directly assessed post-TBI. We used the ultra-sensitive, single molecule array (SIMOA) assays to quantify concentrations of the 7 protein biomarkers, 4 brain-specific markers (Tau, UCHL-1, NFL, and GFAP) and 3 cytokines (IL6, IL10, TNF) in the plasma and brain-derived exosomes of mild TBI (mTBI) patients (N=30) and controls (N=23). We report that concentrations of plasma and exosome GFAP, NFL, Tau, and UCHL1 were elevated in mTBI patients compared to controls (p=0.019 and p=0.0280 respectively). Discrimination of mTBI patients from controls was most accurate, specific, and sensitive when machine learning algorithms on the panel of biomarkers were used compared to logistic regression models of single biomarkers. Specifically, highest accuracy and specificity was observed when exosome Tau and whole plasma GFAP levels were combined (AUC =0.93, accuracy = 0.88). This data suggests that neuron-derived exosomes contain information that characterizes the injured and recovering brain. It also suggests that analysis of a panel of biomarkers from a combination of both blood and exosomal compartments could lead to more accurate diagnosis of mTBIs.

#### **Tatiana Blanchard**

Advisor: Beatriz Carreno, Ph.D. and Carl June, M.D.

Ewing Sarcoma (ES) is the second most common malignant bone tumor predominantly affecting children and young adults. Standard of care high-dose chemotherapy yields a poor prognosis for patients with high-risk recurrent disease with a 5-year overall survival of < 10%. Recent successes in the field of cellular immunotherapy for the treatment of hematological malignancies have reinvigorated efforts investigating the use of adoptive cell therapies (ACT) for solid tumors including sarcomas. ACT strategies utilizing T cells redirected against tumor-associated antigens (TAA) such as NY-ESO-1 have yielded promising results for the treatment of synovial sarcoma, however highly specific targets for ES remain to be identified. The identification of appropriate antigenic targets poses a key challenge to effective immunotherapeutic strategies. The target antigen should be highly expressed in tumor cells with minimal expression in normal tissue. At the molecular level, ES is driven by t(11:22)(q24;q12) translocations resulting in EWSR1-FLI1 fusion in 85 % of ES cases. We have identified EWSR1-FLI1 fusion to result in aberrant expression of cancer testes antigen Lipoxygenase Homology Domains 1 (LOX¬HD1) which has been determined to be required for ES cell growth and tumorigenesis. We hypothesize that LOXHD1 is a TAA targetable by T cell-based immunotherapies for the treatment of ES, relying on the rationale that LOXHD1 specific epitopes are processed and presented, immunogenic, and can elicit cytotoxicity from LOXHD1 specific CD8+ T cells. Using netMHC4.0 in silico epitope prediction, we identified 17 LOXHD1 epitopes with predicted strong binding affinity (<100 nM) to HLA-A\*02:01. The immunogenicity of LOXHD1 epitopes was confirmed by the generation of LOXHD1-specific CD8+ T cell responses from healthy donors following in vitro stimulation and expansion of autologous CD8+ T cells using peptide-pulsed matured monocyte-derived dendritic cells and artificial antigen presenting cells. Using this methodology, we identified a total of 6 peptides (35%) to be immunogenic as determined by IFN-Î<sup>3</sup> secretion. Ongoing studies include (1) utilization of a novel proteomic strategy using human ES cell lines engineered to express specific HLA alleles to further validate processed and presented epitopes and (2) isolation of TCRs to redirect T cells to LOXHD1. Isolated TCRs will be evaluated for LOXHD1 antigen-specificity as well as T cell medicated cytotoxicity ES tumor cells. This study will serve as a platform to identify and characterize LOXHD1-specific CD8+ TCRs which may have implications for ES patients in need of novel treatment strategies.

P5

#### Nanoparticle-Mediated CRISPR/Cas Delivery for Targeting Driver Oncogenes

#### Dan Brown

Advisor: Saar Gill, MD, Ph.D.

Chronic myeloid leukemia (CML) is a hematological malignancy driven by the BCR-ABL fusion oncogene. BCR-ABL, formed via a chromosomal translocation t(9:22), vields a constitutively active tyrosine kinase that promotes unregulated myeloid cell proliferation. The current standard of care for CML involves administering tyrosine kinase inhibitors (TKIs) such as Imatinib (Gleevec). However, TKI therapy is not curative and prolonged administration may select for point mutations within the kinase active site that confer TKI resistance, necessitating the development of novel therapeutics that provide complete and persistent eradication of this disease. A potential approach toward this goal involves genomic modulation via a BCR-ABL-targeted CRISPR/Cas9 system. This system will consist of spCas9 mRNA and BCR-ABL breakpoint-specific single guide RNA (sgRNA), which will introduce single base pair insertions and deletions (indels) selectively within the fusion oncogene while sparing endogenous BCR and ABL genes. spCas9 mRNA and the sgRNA will be encapsulated in novel lipid nanoparticles (provided through a collaboration with Dr. Michael Mitchell at the Penn School of Bioengineering) to facilitate delivery and reduce degradation of the nucleic acids in vitro and vivo. Additional approaches involve targeting other components of the BCR and ABL genes, such as the N-terminal oligomerization domain in BCR and the kinase domain of ABL.

P6

Mechanical strain activates microglia through the P2X7 receptor in a model of glaucoma

Keith Campagno

#### Advisor: Claire Mitchell, Ph.D.

The interaction between mechanical strain, activation of innate immunity, purinergic receptor signaling, and neuronal loss may provide a mechanism by which elevated intraocular pressure (IOP) may lead to retinal ganglion cell (RGC) loss. We found that RGC distribution was similar in the central and middle areas of the retina, but sparser in the periphery. Elevated IOP correlated with microglia morphology emblematic of activation and an increase of gene expression of TNFa, iNOS, ARG1, YM1, and decrease of TMEM119. Increased ATP concentration in the vitreous humor after IOP elevation, and decreased morphological changes in retinas from P2X7-/- implicate purinergic signaling as a contributing factor. The addition of P2X7R agonist BzATP to ex vivo retinal wholemounts from Cx3CR1-GFPGFP/+ resulted in increased fluorescence. consistent with responses from resident microglial cells. Isolated microglia express P2X7R and respond to BzATP with Ca2+ spikes and rapid process retraction that are abolished with P2X7R inhibitor A 839977. ATP and the P2X7R agonist BzATP increased the expression of some of the same activation genes as observed in vivo with elevated IOP. Finally, RGC loss was correlated with microglia morphological alteration in C57 but not P2X7-/- retinas. In summary, this study links mechanical strain and the P2X7 receptor to microglia activation and inflammation, and implicates purinergic signaling in microglia with neuronal loss.

Nr4a1 activation suppresses cocaine-induced behavior via epigenetic regulation of homeostatic target genes.

#### **Marco Carpenter**

Advisor: Elizabeth Heller, Ph.D.

Endogenous homeostatic mechanisms can restore normal neuronal function following cocaine-induced neurotoxicity. Such mechanisms may be exploited in developing novel therapies for cocaine addiction, but a molecular target has not yet been identified. Here we profiled mouse gene expression during early and late cocaine abstinence to identify putative regulators of neural homeostasis. Cocaine regulated expression of the transcription factor, Nr4a1, and its target gene, Cartpt, a key molecule in mitigating dopamine metabolism. Given that chromatin modifications confer long-lasting changes in gene expression necessary for stable cellular and behavioral phenotypes, histone modifications acquired during abstinence may cause individual genes to "remember" prior drug exposure. We found that the sustained activation of Cartpt at late abstinence was coupled with depletion of the repressive histone modification, H3K27me3, and enrichment of activating marks, H3K27ac and H3K4me3. Using CRISPR-mediated Nr4a1 activation, we demonstrate the direct causal role of Nr4a1 in this epigenetic mechanism of sustained gene expression and in repression of cocaine-evoked behavior. Further we show the preclinical efficacy of Csn-B, a small-molecule agonist of Nr4a1, in activating Nr4a1 expression in NAc, attenuating cocaine behavioral ¬responses, and enhancing homeostatic gene transcription. Our findings provide evidence that targeting endogenous changes in homeostatic gene expression across abstinence is a potential strategy to combat cocaine addiction. Herein, we establish Nr4a1 as a key regulator of persistent gene transcription during cocaine abstinence and as a promising therapeutic target for reversing cocaine-mediated behaviors.

## Disruption of H19/Igf2 imprinting causes lethality in a mouse model with a humanized H19 paternal allele

#### Suhee Chang

Advisor: Marisa Bartolomei, Ph.D.

In mammals, a small number of genes are expressed in a parent-of-origin-specific manner. Aberrant expression of these genes is associated with human imprinting disorders such as Beckwith-Wiedemann syndrome (BWS) and Silver-Russell syndrome (SRS). Cis-regulatory elements, called imprinting control regions (ICRs), mediate this allele-specific gene regulation. The *H19/Insulin-like growth factor 2 (Igf2)* ICR [**IC1**] interacts with the zinc-finger protein CTCF. CTCF binds to unmethylated maternal IC1 and acts as an insulator to block shared enhancers from interacting with the *Igf2* promoter, allowing the enhancers to interact with the *H19* promoter. Paternal IC1 is DNA methylated, preventing binding of CTCF and letting the enhancers interact with the *Igf2* promoter. In human, various mutations of IC1 have been reported to be associated with BWS and SRS cases.

Although the mechanism of *H19/Igf2* imprinting is conserved in mouse and human, mouse IC1 (mIC1) differs from human IC1 (hIC1) in several aspects. This complicates studying human genetic mutations of IC1 using mouse models. To better model human BWS/SRS mutations in mouse, we have generated a mouse model with hIC1 replacing the endogenous mIC1 [**H19hIC1**]. The paternal transmission of hIC1 resulted in loss of DNA methylation which led to increased *H19* expression and ablated *Igf2* expression, and perinatal lethality and decreased embryonic weights. To examine if increased *H19* expression is responsible for this lethality, we have generated*H19*null mice [**H19\DeltaH19**]. Lethality and decreased weight were not rescued in H19 $\Delta$ H19/hIC1 mice. Although the previously increased *H19* expression was mostly reduced, the *Igf2* expression is causing the lethality, we used another mouse model with IC1 deletion [**H19\Delta3.8**]. Surprisingly, H19 $\Delta$ 3.8/hIC1 neonates were rescued from lethality and decreased weight. *Igf2* and *H19* expression was comparable between H19 $\Delta$ 3.8/hIC1 neonates and their wild-type littermates depending on tissues.

#### Ryan Cupo

Advisor: James Shorter, Ph.D.

Skd3 is a HCLR-clade mitochondrial AAA+ protein, consisting of an N-terminal mitochondrial targeting signal, a short unstructured domain of unknown function, four ankyrin repeats, and a nucleotide-binding domain. Mutations in Skd3 result in a subtype of the severe mitochondrial disorder, 3-methyglutaconic aciduria (3MGA). 3MGA mutations in Skd3 cluster in the nucleotide binding domain. Little is known about Skd3, its function, or the effect of 3MGA mutations on its activity. Using cell biology, yeast genetics, and biochemistry we have explored the function of Skd3.

P10

Charting Hydroxymethylcytosine at Single-Base and Single-Cell Resolution

#### **Emily Fabyanic**

Advisor: Hao Wu, Ph.D.

DNA cytosine methylation has a profound impact on genome stability, transcription, and development. The recent discovery that ten-eleven translocation (TET) enzymes iteratively oxidize methylcytosine (mC) has triggered a paradigm shift in our understanding of how changes in DNA methylation are coupled to normal mammalian development and human disease.1 Hydroxymethylcytosine (hmC), otherwise referred to as "the sixth base," is the most prevalent oxidized form of methylcytosine (ox-mC). Genetic and functional studies indicate that TET enzymes and ox-mCs may play important roles in cellular differentiation, organismal development, and carcinogenesis.2 The potential function of hmC in mature mammalian neurons is of particular interest as it accumulates during peak synaptogenesis and critical periods of synaptic pruning in maturing, early postnatal neurons and in adult neurons can comprise as much as 40% of modified cytosine bases.3 As the function of single neurons depends on their unique context (e.g. position, circuitry, state), it is important to study underlying epigenetic regulatory systems at the single-cell level in order to successfully probe the implications of this epigenetic modification, in vivo.4 Here, I report the development of a novel hmCmapping method for application to single cells to study heterogeneous tissues, like the brain. Our technique has the potential to allow for the study of epigenetic heterogeneity among neuronal subtypes and will also be a powerful tool enabling systematic analysis of hmC at non-coding, gene regulatory regions in the brain in a subtype-specific manner, without requiring cellular sorting.

P11

Characterizing the protein tyrosine phosphatase SHP2 as an oncoprotein and therapeutic target in neuroblastoma

#### **Mark Gerelus**

Advisor: Yael Mossé, M.D.

Significant advances have been made over the past several years in understanding the genetic landscape and heterogeneity of neuroblastoma (NB), an extra-cranial solid tumor of neural crest origin. Our lab's discovery that heritable and somatic activating mutations in the receptor tyrosine kinase (RTK)-encoding anaplastic lymphoma kinase (ALK) oncogene in NB has positioned ALK as the major tractable oncogene product for targeted therapy in NB. An ongoing clinical trial being conducted by our lab with the next generation ALK inhibitor lorlatinib reveals potent anti-tumor activity followed by eventual resistance to the compound and rebound of tumor growth for which there is no other option for treatment. This reveals a crucial need to determine combination treatments targeting downstream of ALK to combat relapse. A potential downstream effector, the Src homology region 2-containing protein tyrosine phosphatase (SHP2), has been implicated in RTK-driven cancers. Recently, a novel allosteric small molecule inhibitor targeting SHP2, called SHP099, has been developed and studied in the context of RTKdriven cancers. While SHP2 inhibition alone is not sufficient to result in durable antitumor activity, studies have shown that combining an RTK-targeting inhibitor with SHP099 can resensitize RTK inhibitor-resistant cancer models. Therefore, I hypothesize that combining SHP099 with lorlatinib will resensitize ALK inhibitor-resistant NB models to small molecule inhibition. Studies testing this hypothesis will provide evidence for which patient populations would benefit from this combination for future clinical trial design and translation to the clinic. In addition to defining the therapeutic effect of inhibiting SHP2 activity via SHP099, preliminary studies suggest that there are differences in protein-protein interactions with SHP2 and nuclear localization of proteins when comparing SHP099-treated cells to cells depleted of SHP2 via shRNA. Most of the published studies investigating SHP2 thus far focus on the phosphatase activity of SHP2. However, my preliminary data suggest that SHP2 may contribute to NB independent of its phosphatase activity. Therefore, I hypothesize that there is a phosphatase-independent oncogenic role of SHP2 in ALK-driven high-risk NB. Studies testing this hypothesis will shed light on this overlooked potential role of SHP2 and allow for more rational drug development targeting SHP2 to result in a clinically impactful treatment option.

#### P12

Interactions between HIV, cigarette smoking and antiretrovirals in an in vitro model of HIV-induced neurotoxicity

#### Shivesh Ghura

#### Advisor: Kelly Jordan-Sciutto, PhD

Even though the mortality of HIV has decreased due to antiretrovirals (ARVs), HIVassociated neurocognitive disorders (HAND) remain prevalent, affecting 50% of HIV+ patients. HAND is a spectrum of cognitive, memory, and motor dysfunction that can present with mood and addictive disorders. Specifically, 50-70% of HIV patients abuse nicotine, emphasizing the importance of studying the effects of nicotine on antiretroviralmediated suppression of HIV-replication and its associated toxicity. Previously, in vitro experiments indicate that HIV-replication in macrophages and microglia can be altered in the presence of nicotine or cigarette smoke extract. However, these studies were not conducted in the presence of antiretroviral treatments, which have been shown to cause direct toxicity to neurons. Importantly, indirect toxicity of antiretrovirals on neurons via their effect on macrophages remains unknown. We hypothesize that nicotine and certain ARVs interact to alter HIV replication in macrophages and subsequent cytokine and/or neurotoxin release. Specifically, nicotine increases HIV replication rate and neurotoxicity associated with antiretrovirals while decreasing the efficacy of antiretrovirals. Mock and HIV-infected monocyte-derived macrophages (HIV-MDM) were treated with nicotine and/or lopinavir. Supernatants were sampled to track HIV-replication and HIV-MDMinduced neurotoxicity. Understanding the interaction of nicotine and ARVs will aid in development of therapeutics that alleviate neurotoxicity and reduce the rate of substance abuse in people living with HIV.

Platinum drug-mediated secretion of the danger-associated molecular pattern (DAMP) high mobility group-1 (HMGB1)

#### Kevin Gillespie

Advisor: Ian Blair, Ph.D.

High mobility group-1 (HMGB1) is a chromatin-associated protein that also acts as a critical mediator of inflammation, thrombosis, and the innate immune response. Although post-translational modifications (PTMs) to HMGB1 have been studied in multiple models and cell types, there is no identified consistent pattern of HMGB1 PTMs that regulate HMGB1 transport between the nucleus and cytosol as well as release to the extracellular space. We have discovered that upon treatment with platinum drugs, there is a dosedependent release of HMGB1 from HepG2 human hepatocellular carcinoma cells and A549 human adenocarcinoma lung cancer cells, with cisplatin as the most potent. We have also observed indications of differences in HMGB1 among nuclear, cytosol, and media fractions. Expanding our ultrahigh performance-liquid chromatography-high resolution mass spectrometry (UHPLC-HRMS) methodology, we have sufficiently increased our coverage to characterize PTMs throughout the entire HMGB1 protein in these fractions. Platinum chemotherapeutic agents are often used in combination with other cancer treatments like immunotherapy, especially in non-small cell lung cancer (NSCLC), and multiple studies suggest these drugs may have immune-potentiating effects. We hypothesize that platinum drug damage to nuclear DNA induces structural changes to HMGB1 that mediate its translocation and secretion.

#### Development of pH sensitive probes for in vivo Cerenkov imaging

#### Andrea Guzman

Advisor: Jim Delikatny, Ph.D.

Increased acidity in the tumor microenvironment (TME) plays a role in the invasion and metastasis of cancer cells and contributes to chemotherapeutic resistance. This metabolic hallmark has sparked interest in the exploration of extracellular tumor pH measurement and imaging in vivo. The decrease in tumor microenvironment pH is due to a deregulated metabolism predominantly arising from increased glycolytic flux in cancer cells. Cerenkov radiation emitted by  $\beta$ -particles is a potential tool for pH imaging in vivo. pH-sensitive fluorophores can selectively attenuate Cerenkov radiation's continuous and multispectral emission through selective bandwidth guenching (SBQ) and produce Cerenkov Radiation Energy Transfer (CRET). SBQ and CRET provides a quantitative readout that can be correlated with a pH value, resulting in a non-invasive technique for pH imaging in vivo. We hypothesize that selective absorption of the Cerenkov multispectral emission by pH sensitive fluorophores will provide accurate pH measurements of the TME through Cerenkov imaging. In the current project, 5,6carboxynaphthofluorescein succinimidyl ester was conjugated to 4-aminobutyl DOTA in a 1:1 molar ratio to produce a pH-sensitive probe suitable for chelation with 68Ga. The Cerenkov emission of 68Ga is 10-fold greater than 18F, the radioemitter previously studied in our lab, thus creating a pH sensor with increased signal to noise. The conjugated product (NFbD) was successfully chelated with 69,71Ga and 68Ga and the complex (NFbD-Ga) maintained its pH indicator capability after chelation (pKa= 7.7, λex= 600 nm, λem= 669 nm at pH 9). Cerenkov imaging of NFbD-Ga showed marked pH-dependent differences in attenuation, measured at 600 nm and standardized to 840 nm. Cerenkov radiation energy transfer (CRET) was observed at 680 nm. Cerenkov imaging with NFbD-Ga is sensitive and can detect pH changes as low as 0.2 pH units. To assess whether Cerenkov radiation could be observed in tumors, the radiolabeled complex was injected into athymic nude mice bearing MDA-MB-231 and 4175-Luc+ breast cancer tumors. Average radiance readout corresponding to Cerenkov imaging showed detectable CRET signals for each tumor, which is favorable for in vivo imaging due to decreased tissue scattering and absorption. Reasonable pH values have been obtained by interpolation, fitting average radiance signal of tumors to a Cerenkov pH titration curve. The development and characterization of this novel probe for Cerenkov imaging of the tumor microenvironment pH expands the realm of optical imaging and validates the potential of Cerenkov radiation for critical biomedical applications.

P15

#### Michael C. Hart

Advisor: Jim Delikatny, Ph.D.

Lung cancer is the leading cause of cancer related death. Non-small cell lung carcinoma (NSCLC) is the most commonly diagnosed lung cancer in the United States with a fiveyear survival rate of approximately twenty percent. The primary treatment for NSCLC is tumor resection with adjuvant chemotherapy. Surgery to remove lesions currently relies on preoperative imaging and intraoperative tissue palpation. In order to improve complete tumor resections, our lab has designed a caged fluorophore, DDAOarachidonate (DDAO-AA), that is activated by cytosolic phospholipase A2 (cPLA2). cPLA2 has been reported to be upregulated in a variety of cancer types including NSCLC. When cPLA2 is present, DDAO-AA is activated by the cleavage of arachidonic acid resulting in free DDAO which can be excited at 600 nm and fluorescence measured at 660 nm. This project focuses on the preclinical validation of DDAO-AA for intraoperative imaging of tumor margins. Testing of different liposomal formulations showed the optimal formulation used egg phosphatidylcholine resulting in a consistent size of 106 nm and PDI of approximately 0.1 with a zeta potential of 16.2 mV. In an assay using 0-100 units of isolated secretory phospholipase A2 (sPLA2), DDAO-AA showed a significant increase in activation with the concentration of enzyme. In KLN 205-Luc+ cells treated with DDAO-AA, the probe showed a minor increase in activation compared to when no cells were present. Finally, ex vivo studies incubating DDAO-AA with human lung tumor or normal human lung tissue showed significantly higher fluorescence of the tumor tissue. These data suggest that DDAO-AA could be a promising agent for measuring cPLA2 activity for imaging lung tumor margins.

<u>A cell non-autonomous mechanism of versican proteolysis contributes to cerebral</u> <u>cavernous malformations</u>

#### **Courtney Hong**

Advisor: Mark Kahn, M.D.

Cerebral cavernous malformations (CCMs) are thin-walled, dilated vascular abnormalities that occur predominantly in the CNS and are a major cause of hemorrhagic strokes and seizures. Currently, there are no medical therapies for this progressive disease other than invasive neurosurgery. CCMs are caused by genetic mutations that result in the loss of a heterotrimeric adaptor complex required to negatively regulate MEKK3 signaling and the expression of the KLF2 and KLF4 transcription factors in brain endothelial cells (BECs). Recently, we have identified endothelial Toll-like receptor 4 (TLR4) and the gut microbiome as critical upstream stimulators of MEKK3 signaling. However, the downstream effectors relevant to disease pathogenesis remain unknown. The aim of this study is to evaluate the role of ADAMTS proteases and their substrate, the extracellular matrix proteoglycan versican, as candidate downstream targets of this causal MEKK3 pathway. Using a neonatal model of CCM disease and a combinatorial rescue approach, we have demonstrated that endothelial deletion of ADAMTS5 can significantly reduce lesion volume, while overexpression of ADAMTS5 is sufficient to recapitulate key morphological and molecular features associated with early CCMs. Rather than exacerbating the phenotype, we also found that genetic reduction of versican prevents CCMs, suggesting that cleavage of versican and not the loss of the protein is critical for lesion formation. Taken together, these studies identify a requirement for ADAMTS5 and versican proteolysis and further define the molecular mechanism through which MEKK3-KLF2/4 signaling drives CCM disease.

#### **Daniel Jacome**

Advisor: Mark Sellmyer, M.D., Ph.D.

Cell-cell interactions are integral to the proper function of multi-cellular organisms. In vivo monitoring of cell-cell interactions has been challenging, especially deep within an animal. Current approaches have significant limitations. For example, intravital microscopy requires a predetermined area for imaging, lacks a signal capable penetrating through tissues for detection of deep interactions, and insertion of the window/microscope can perturb the local biology. The need for improved imaging technologies has been highlighted as cell-based therapies have entered the clinic and have demonstrated great efficacy against hematologic cancers. Despite this success, targeting of solid tumors has not yielded the same results and many questions regarding T cell-solid tumor engagement, the tumor microenvironment, and T-cell persistence have arisen. Thus, it is increasingly important to study these phenomena in situ and with quantitative measures. We report the development a cell proximity sensing system with the following orthogonal components: (1) a sterically "caged" trimethoprim (TMP) with significantly reduced binding affinity to its protein target, bacterial dihydrofolate reductase (DHFR); (2) an bacterial "uncaging" enzyme (nfsA), nitroreductase (NTR), that liberates TMP; (3) a destabilized bacterial DHFR (dd-DHFR) that is degraded without the TMP ligand; (4) and an optical reporter fused to the destabilized protein. Dose response studies show a 20-fold shift in EC50 of TMP versus caged TMP with signal induction being rescued upon culture with nitroreductase expressing cells. Additionally, in vivo studies show 49-fold bioluminescent signal induction. In summary, we believe this platform can aid researchers assess cell-cell interactions on a whole animal scale.

#### Investigating ALCAM as an immunotherapeutic target in neuroblastoma

#### **Jarrett Lindsay**

#### Advisor: John Maris, M.D.

Neuroblastoma is a cancer arising from the developing sympathetic nervous system. Only half of children diagnosed with high-risk neuroblastoma will survive five years, and survive face significant therapy-induced morbidity. those that do Because neuroblastomas arise from developing tissues, they maintain expression of cell-surface proteins not found in normal tissues, which underscores the potential of immunotherapy to improve upon current treatment. Furthermore, many of these cell-surface proteins are regulated by lineage-restricted transcription factors, which we hypothesize may hinder antigen downregulation as a mechanism of resistance to immunotherapy. Using our primary tumor RNA-sequencing data, our lab found the cell adhesion molecule ALCAM is highly expressed in high-risk neuroblastoma. To understand the role of ALCAM overexpression in neuroblastoma, we generated Pearson correlations between ALCAM and all expressed genes in two primary tumor RNA-seq datasets. Gene ontology analysis of the 70 genes most correlated with high ALCAM expression returned enrichment in processes associated with neuronal signaling and development. These data are consistent with the role of ALCAM in development of retinal ganglia, which are derived from the same neural crest progenitors as neuroblastoma. Thus, we hypothesized ALCAM expression may be driven by a network of transcription factors termed the neuroblastoma core regulatory circuit (CRC). The CRC is a feed-forward transcriptional regulatory loop in which each member drives the expression of itself and the others, together defining a noradrenergic phenotype. This phenotype is characterized by high expression of genes associated with neuronal function, such as tyrosine hydroxlase and dopamine beta hydroxylase. We investigated the ALCAM locus using ChIP-seq data (from two neuroblastoma cell lines) targeting all seven transcription factors of the CRC. The ALCAM locus showed binding of every CRC transcription factor, as well as the presence of an upstream enhancer (H3K27ac). Finally, an anti-ALCAM antibody-drug conjugate (CX-090) demonstrated low- to sub-nanomolar IC50 concentrations in five neuroblastoma cell lines. Together, these data suggest ALCAM expression may be driven by critical transcription factor networks in neuroblastoma, highlighting ALCAM as an attractive target for immunotherapy development

#### Dania Malik

#### Advisor: Aalim Weljie, Ph.D.

Sleep and circadian disruption independently have been shown to alter metabolism and are associated with adverse health risks. Circadian rhythms impose a form of regulation on various metabolic and biological processes, including sleep-wake cycles, thus understanding the interactions between the two is of high importance. To this end, untargeted liquid chromatography-mass spectrometry was utilized to assess lipidome level differences in a sleep and circadian paradigm. Discriminant analyses indicate overall lipid-level differences between circadian and sleep groups with conserved changes observed in two short sleep mutants, fumin and sleepless, compared to wild type Drosophila. However, assessing metabolite usage and synthesis is difficult to discern from steady state analyses. Here, an in vivo metabolic labelling platform utilizing stable isotope tracers has been adapted to enable rhythmicity of lipid biosynthesis and consumption in sleep and circadian paradigms to be assessed in a comprehensive manner. Wild type Drosophila were challenged with uniformly labelled glucose at 2-hour resolution for 48 hours. The metabolic fate of glucose carbons into lipids was monitored via 2-D Nuclear Magnetic Resonance Spectroscopic experiments. Initial analyses of glucose metabolic fate into lipids in wild type Drosophila indicates robust rhythmicity in lipid biosynthesis with potential overlap with feeding rhythms. Future experiments will incorporate short sleep and clock mutants to enable sleep and circadian driven differences in lipid biosynthesis to be separated.

#### **Dylan Marchione**

#### Advisor: Benjamin A. Garcia

Abstract:

Endometrial stromal sarcoma (ESS) is a rare uterine tumor with frequent alterations in genes encoding subunits of polycomb repressive complex 2 (PRC2), a master epigenetic regulator. Rather than causing loss-of-function, these mutations fuse a poorly characterized zinc-finger protein, JAZF1, to the N-terminus of either SUZ12 or PHF1. While prior studies suggest that JAZF1-SUZ12 fusion renders PRC2 inactive, the function of the JAZF1-PHF1 protein has not been studied mechanistically. We sought to leverage archival pathology samples in order to determine how these mutations affect the epigenome and global protein expression. We also established a cell model for further mechanistic interrogation. Contrary to several prior reports, we observe high levels of H3K27 methylation in both JAZF1-SUZ12 and JAZF1-PHF-expressing ESS, suggesting that the fusion proteins do not cause PRC2 loss-of-function. Moreover, in add-back experiments, JAZF1-SUZ12 can partially compensate for SUZ12 deletion, restoring methylation levels to near wild-type levels. Affinity proteomic characterization suggests that JAZF1-SUZ12 is assembled into a PRC2-like complex. GSEA of whole proteome data from ESS tumors revealed aberrant expression of PRC2 target genes. We hypothesize that JAZF1-SUZ12 and related fusions may hijack the repressive chromatin machinery in overlapping, but distinct, ways in order to drive cell transformation.

P21

<u>Circuit level analysis of the preoptic area and tuberomammillary nucleus in sleep</u> regulation
### John Maurer

Advisor: Shinjae Chung, Ph.D.

Sleep is evolutionarily conserved across all mammals, yet the precise function of sleep remains unknown. In mammals, sleep is characterized by transitions between rapid eye movement (REM) and non-REM (NREM) sleep states, which are regulated through interactions between numerous neuronal populations. Sleep is negatively regulated by wake-promoting nuclei, resulting in the mutually exclusive states of sleep and wakefulness. Numerous sleep-active and wake-active brain regions have been identified, but it remains unclear how these different neuronal populations coordinate their actions to regulate sleep and wakefulness. The preoptic area (POA) of the hypothalamus contains sleep-active GABAergic neurons, and work from our lab has shown that activation of POA GABAergic axons projecting to the tuberomammillary nucleus (TMN) promotes sleep. Conversely, lesions to the TMN, the sole source of the neurotransmitter histamine in the brain, have been known to cause profound somnolence, suggesting this brain region is a prominent wake center. In addition to histamine, the TMN also contains populations of GABAergic and glutamatergic neurons. However, it is unclear which of these neuronal populations are crucial for wakefulness and if their innervation of the POA promotes arousal. The present experiments use transgenic mice to target three neuronal populations (histaminergic, GABAergic, and glutamatergic) to determine neuronal in vivo activity and if activation promotes wakefulness. Parallel studies are investigating if activation of the axon terminals innervating the POA promotes wakefulness. Preliminarily findings suggest that optogenetic activation of glutamatergic cell bodies within the TMN and axon terminals projecting to the POA strongly promotes wakefulness. Furthermore, fiber photometry in the TMN revealed glutamatergic neurons that are wake-active and REM-active and involved in wake- and REM-transitions. While, optogenetic activation of histaminergic cell bodies and axon terminals to the POA had no effect in promoting wakefulness, in vivo activity of histaminergic neurons within the TMN are wake-active and involved with sleep to wake transitions. Taken together, these results provide novel evidence that glutamatergic neurons in the TMN and axons terminals to the POA are a prominent neuronal population that promotes wakefulness. Considering the crucial roles of sleep in physiological function and detrimental effects of sleep deprivation, it is vital to understand circuit-specific mechanisms underlying sleep regulation. P22

Development and validation of a new mouse model to investigate the therapeutic potential of neuron-specific E2F1 knockout for neurodegenerative disease

### **Claire Meurice**

### Advisor: Kelly Jordan-Sciutto

The transcription factor E2F1 modulates the G1-S phase transition of the cell cycle, DNA damage response, and apoptosis. Abrogating E2F1 prevents apoptosis caused by excitotoxic and amyloid-beta treatments of primary neurons, and rescues memory impairment in APP/PS1 double transgenic mice. There is strong evidence for E2F1's involvement in neurodegenerative disease by promoting apoptosis, or de novogenerated neuronal tetraploidy that causes neuronal dysfunction/death. Previous reports of age-dependent memory impairment, anxiety, and systemic pathology in adult E2F1 mutant mice lacking the DNA binding domain (E2F1tm/tm) impede the development of E2F1 targeted therapeutics. Given E2F1's detrimental role in neurons, we hypothesized that neuronal E2F1 deletion was not driving this phenotype. To test this hypothesis, we developed a neuron-specific E2F1 knockout by designing and breeding E2F1 mice with conditional alleles carrying LoxP sites flanking exon 2 and 7 (E2F1fx/fx) with neuronspecific Syn1-cre (Syn+) mice. In parallel, constitutive E2F1 knockout mice (E2F1-/-) were generated from E2F1fx/fx. Middle-aged (12-13mth old) E2F1+/+, E2F1+/- and E2F1-/-, E2F1+/+, Syn+, E2F1fx/fx, E2F1fx/fx;Syn+ mice were tested in novel object recognition, light/dark box, and open field assays to confirm the development of ageassociated phenotypes (previously reported in E2F1tm/tm mice) and to determine if these impairments were absent in neuron-specific E2F1 knockout mice. Context fear conditioning was added to determine if hippocampal memory was impaired by global and neuron-specific E2F1 loss. Results indicate that neuronal E2F1 loss does not produce the impairments observed in E2F1-/-. In fact, E2F1-/- mice do not exhibit hippocampal memory impairment. However, the LoxP insertion site in the E2F1fx/fx mouse may cause an unintended systemic phenotype. Future studies will aim to identify the cell types in which E2F1 loss produces memory-impairment. This research highlights the value of developing a cell-type specific E2F1 therapy for neurodegenerative disease treatment.

### APC Regulation of GSK-3

### **Rebecca Myers**

Advisor: Peter S. Klein

Mutations in Adenomatous Polyposis Coli (APC), a tumor suppressor gene, are implicated in over 80% of human colorectal cancers, and germline mutations in APC cause Familial Adenomatous Polyposis (FAP), an inherited condition that predisposes to colon cancer. APC is a component of a complex that suppresses canonical Wnt signaling by directing the degradation of ß-catenin, an activator of Wnt target genes. In the absence of Wnt ligands, ß-catenin is marked for degradation by phosphorylation by Glycogen Synthase Kinase-3 (GSK-3). This phosphorylation occurs within a complex formed by the scaffolding protein Axin and APC. When APC is mutated ß-catenin is protected from phosphorylation, allowing for accumulation, nuclear translocation, and over-activation of Wnt pathway target genes, leading to colorectal cancer. APC and GSK-3 have been found to play similar, possibly related roles in other signaling pathways such as mTORC1 signaling. Our lab found that APC directly activates GSK-3 and that genetic loss of APC reduces GSK-3 activity, therefore leading to increased Wnt signaling in colon cancer and mTORC1 activation in tumors from FAP patients. We hypothesize that APC regulates GSK-3 through a specific motif within APC, shown previously to be necessary for ß-catenin degradation, and that this regulation applies to other pathways where APC and GSK-3 are both active. The objective of this study is to define the region of APC that regulates GSK-3 activity and test whether APC regulates other signaling pathways downstream of GSK-3 in both in vivo and in vitro model systems. We will also investigate the use of mTORC1 inhibitors in the treatment of recurrent polyps in FAP.

### Sofya Osharovich

Advisor: Jim Delikatny, Ph.D.

Choline kinase  $\alpha$  (ChoK $\alpha$ ) is a lipid kinase that catalyzes the phosphorylation of choline to produce phosphocholine (PC) in the Kennedy pathway of phospholipid biosynthesis. ChoKα is an established cancer biomarker associated with aggressive phenotype, high histological tumor grade, and poor clinical outcome in many human cancers. ChoKa is overexpressed in 60% of human lung tumors. Our lab has constructed a near-infrared (NIR) ChoKα inhibitor, JAS239, that can be employed to assess ChoKα levels in tumor models using fluorescence optical imaging. JAS239 competitively binds to the active site of ChoKa, attenuates PC production, and accumulates in tumors in proportion to enzyme expression. JAS239 is fluorescent in the near- infrared region (lex = 745 nm, lem = 775 nm), which is ideal for optical imaging, as light absorption and scattering is decreased in this range. In this study, we evaluate JAS239 for detection of tumor margins and lung metastases in mice and measure ChoKa expression in spontaneous canine adenocarcinomas. We have identified a highly metastatic murine lung cancer cell line, KLN 205, that over-expresses ChoKa. When administered to mice, JAS239 does not accumulate in normal lung tissue and is able to illuminate lung metastases. KLN 205 cells transformed with a luciferase vector (KLN 205 Luc+) were used to track metastasis from the flank to the lungs by bioluminescence imaging. The JAS239 fluorescent signal colocalized with the bioluminescent signal in the lungs, indicating that JAS239 would be useful for identification of primary tumor margins and metastases intraoperatively in mice. Toxicity studies in mice showed that JAS239 is non-toxic at doses up to 50 fold higher than the imaging dose, which is critical to establish prior to translation. Our longterm goal is to translate JAS239 into the veterinary clinic to be used as an intraoperative guide for resection of spontaneously occurring lung tumors in canine patients. Canines with spontaneous lung tumors are an excellent model of the human disease, as they are genetically diverse, are exposed to the same environmental factors, and express similar levels of ChoKa as humans. Immunohistochemistry and Western blots show elevated ChoKα levels and clear tumor delineation in spontaneous canine lung tumors compared to normal lung tissue. Further ChoKα expression profiling of lung cancer will aid in the translational application of intraoperative molecular imaging with JAS239 for detection and margin delineation of lung tumors in a real-time clinical setting.

P25

The Androgenic Impact of AKR1C3 and 11-Ketoandrogens on Polycystic Ovarian Syndrome (PCOS)

### **Ryan Paulukinas**

Advisor: Trevor Penning, Ph.D.

Polycystic ovarian syndrome (PCOS) is the most common endocrinopathy in women of reproductive age affecting 10% of all women and at least 30% of all infertile women. PCOS is characterized by hyperandrogenism and leads to obesity and type 2 diabetes. Our goal is to identify targets for endocrine disrupting chemicals (EDCs) that could influence this disease. Aldo-keto reductase family 1 member C3 (AKR1C3; type 5 17βhydroxysteroid dehydrogenase (HSD) and prostaglandin F synthase) is the prominent peripheral enzyme involved in androgen biosynthesis and the production of prostaglandins of the F series. AKR1C3 overexpression in adipocytes in response to insulin could lead to increased androgen receptor (AR) signaling, increased de novo lipogenesis, and decreased PPARy signaling leading to reduce adipogenesis. This lipid overflow could exacerbate insulin resistance through a feedforward mechanism and promote the lipotoxic profile seen in PCOS. In adipocytes, the 11-oxygenated androgens of adrenal origin may be a potential source of peripheral androgens leading to the androgen excess. Serum samples from PCOS patients have increased levels of 11βhydroxyandrostenedione (11BOH-A4), 11-ketoandrostene-3,17-dione (11K-A4), and 11ketotestosterone (11K-T). 11K-T and 11-ketodihydrotestosterone (11K-5α-DHT) have the same potency as testosterone and dihydrotestosterone in AR reporter gene assays. To determine whether AKR1C3 can convert 11K-A4 to 11K-T and 11-keto-5αand rost ane-3,17-dione (11K-5 $\alpha$ -dione) to 11K-5 $\alpha$ -DHT, kinetic parameters for these reactions catalyzed by recombinant AKR1C3 were estimated using discontinuous UV RP-HPLC enzymatic assays. Detection of UV transparent compounds was accomplished by dinitrophenylhydrazine derivatization. AKR1C3 was found to have catalytic efficiencies for 11K-A4 and 11K-5α-dione that were 5 times greater than its normal substrate A4. By contrast 11βOH-A4 was found to be a poor substrate indicating that it must be converted to 11K-A4 first by 11β-HSD2. The kinetic analysis helps to elucidate the involvement of AKR1C3 and 11β-HSD2 in the formation of the 11oxygenated androgens. The study identifies AKR1C3, 11β-HSD2, AR and PPARy as targets for EDCs that may affect PCOS onset.

P26

Investigating Protein PTMs As Liver-Injury Specific Biomarkers

**Ross Pirnie** 

Advisor: Ian Blair, Ph.D.

Drug-induced liver injury (DILI) is a common clinical concern as well as a major barrier for the development of new therapeutics. Despite its frequency and severity, there are no specific and predictive diagnostic biomarkers for DILI. Post-translational modifications (PTM) to secreted proteins have potential to meet the increasing need for specific biomarkers. The highly conserved DNA-binding protein and cytokine high mobility group box 1 (HMGB1) is actively secreted from immune cells following PTM. Using HPLC-HRMS/MS and live cell immunostaining, we show that HMGB1 is also passively released from necrotic, drug-injured hepatocytes. Due to the unique presence of concentrated ROS and RNS, the intracellular environment of drug-injured hepatocytes has the potential to uniquely modify HMGB1. We show that in vitro, HMGB1 exposure to RNS peroxynitrite results in a unique pattern of oxidation and nitration detectable by HR LC/MS. These modifications interfere with antibody binding, which may have prevented previous detection in biological samples. The modification state and biological function of hepatocyte-released HMGB1 has not been fully elucidated, warranting further study.

P27

A blood vessel-on-a-chip that models hemostasis in humans after a puncture injury

**Izmarie Poventud-Fuentes** 

### Advisor: Lawrence Brass

Studies in mice have shown that during the hemostatic response to penetrating injuries, a hemostatic plug is characterized by a heterogeneous architecture that has highly activated platelets and fibrin restricted to the injury boundaries and the extravascular space. Bridging these studies with hemostasis in humans has been challenging, as it would require invasive surgical procedures. The goal of our study was to develop a microfluidic system that mimics a blood vessel and can recapitulate the dynamic microenvironments to which blood is exposed after a blood vessel breach to better understand hemostasis in humans. This novel microfluidic platform incorporates essential components of hemostasis in a 3-compartment design through which human blood is perfused: (1) an endothelialized "intravascular" channel, (2) a deformable "vessel wall" made of a collagen 3D matrix that contains tissue factor, and (3) an "extravascular" channel to establish a pressure drop across the vessel wall after a puncture injury. Kinetics of platelet accumulation and fibrin formation in the device can be recorded in real time. Afterwards, we study the structure of the resulting hemostatic plug using confocal and scanning electron microscopy. We find that this system recapitulates key features of hemostatic plug formation in vivo, including platelets as the main cellular component, the spatial distribution of activated P-selectin(+) platelets, sensitivity to the presence of tissue factor embedded in the collagen matrix, inhibition of platelet accumulation and contractile forces by an integrin αllbβ3 antagonist, fibrin as essential scaffold for platelets to achieve a stable hemostatic plug, and a functional endothelium that localizes the response to the injury site. The result is a versatile tool that can be used in studies of human blood and to characterize emerging therapeutic approaches in the field of hemostasis and thrombosis.

### Investigating the Efficacy of GluK1-containing Kainate Receptor Inhibition to Treat Alcohol Addiction

### Natalia A. Quijano-Cardé

Advisor: Mariella De Biasi, Ph.D.

Alcohol use disorder (AUD) is a serious neuropsychiatric condition affecting millions of people worldwide. The heterogeneity of the disease underscores the need to expand the number of pharmacotherapeutics to treat AUD patients. Topiramate (TPM) is an antiepileptic drug that has been shown to modulate ethanol drinking patterns in humans. TPM has many pharmacological targets and affects many cellular processes and, therefore the molecular target for its effects on AUD is not clear. Among several mechanisms, TPM acts as a non-selective antagonist of kainate receptors containing the GluK1 subunit (GluK1\*KARs), which is encoded by GRIK1 in humans. Interestingly, pharmacogenetic studies have shown that a single nucleotide polymorphism (SNP, rs2832407) in GRIK1 exerts an influence on the predisposition to develop alcohol dependence and modulates the efficacy of topiramate treatment to reduce drinking. Thus, our study examined the ability of LY466195-mediated selective inhibition of GluK1\*KAR to modulate responses to alcohol in a mouse model of alcohol dependence. Our results indicate that selective GluK1\*KAR inhibition reduces ethanol intake and preference in mice undergoing short-term (24-h) and protracted (1 week) withdrawal in a dose-dependent manner. In mice undergoing short-term withdrawal, 20 mg/kg LY466195 treatment was sufficient to attenuate the manifestation of physical signs of withdrawal. Interestingly, we observed that chronic ethanol exposure in the intermittent two-bottle choice drinking paradigm affects the rewarding properties of ethanol as measured in the conditioned place preference (CPP) paradigm and with in vivo accumbal microdialysis. While mice chronically treated with ethanol in the I2BC failed to acquire/display ethanol CPP (1.5 g/kg ethanol), an acute administration of LY466195 (20 mg/kg) was sufficient to rescue the response observed in alcohol-naïve mice. We also found that LY466195 injection normalized dopamine responses to acute ethanol injection in mice undergoing short-term withdrawal from the I2BC. In summary, our data suggest that GluK1\*KARs play an important role in modulating the reinforcing properties of ethanol that maintain addiction. Overall, our findings support the hypothesis that GluK1\*KARs represent an attractive pharmacological target for the treatment of AUD.

### Nicole M. Robles-Matos

Advisor: Marisa S. Bartolomei, Ph.D.

Environmental exposure to Endocrine Disrupting Chemicals (EDCs) during fetal development may lead to molecular changes that increase susceptibility to adult diseases. For example, EDCs can alter fetal growth and metabolism in utero and disrupt critical set points that promote adult metabolic disorders. The EDC Di-(2-ethylhexyl)phthalate (DEHP) is strongly associated with metabolic changes. DEHP is a ubiquitous plasticizer, present in food packaging, toys, medical devices, and personal care products. DEHP has anti-androgen functions in fetal/placental endocrine systems, interfering with hormonal action. As a result, DEHP exposure during pregnancy may result in adult metabolic defects. However, the mechanisms driving DEHP-induced changes in fetal metabolism and adult diseases are unknown. Recent evidence suggests that EDC-induced changes in metabolic gene profiles may stem from altered epigenetic landscapes. One epigenetic factor, DNA methylation, is particularly vulnerable to environmental exposures as it changes dynamically during fetal development. Thus, we hypothesize that DEHP exposure in utero disrupts DNA methylation in placenta, leading to abnormal cross-talk between the fetus and placenta, which in turn will predispose offspring to impaired metabolism in adulthood. To test this, dams were exposed to two DEHP doses (Lower: 50 µg/kg\*BW/day, Upper: 10 mg/kg\*BW/day) via their diet from pre-conception until embryonic day 10.5 (E10.5) or weaning. Post-weaning, offspring were placed on a control or Western Diet (WD) until postnatal day 182 (PND182). Global DNA methylation was assessed on E10.5 placentas using a Luminometric Methylation Assay. Maternal exposure to upper-DEHP was associated with significantly increased global DNA methylation of E10.5 male placentas. Our data suggest that DEHP alters E10.5 placental global DNA methylation in a dose- and sex-specific manner. Adult metabolic phenotyping included glucose tolerance tests, body weight and body fat. Phenotyping revealed that male offspring exposed to upper-DEHP and challenged with WD have impaired glucose tolerance at PND140 and increased body fat at PND182 while females were unaffected. These results suggest that in utero DEHP exposure at environmentally relevant doses disrupts glucose homeostasis in a sex-specific manner.

### Laura Romano

Advisor: Park-Cho Park, M.D., Ph.D.

Protein homeostasis (proteostasis) is a critical process for maintaining normal cellular function. It involves balance between two fundamental cellular processes: protein synthesis and protein degradation. These two processes must work together because an imbalance in one can create a toxic intracellular environment, such as formation of protein aggregates that sequester functional proteins. However, it is unknown whether protein synthesis and degradation work in a synchronous fashion. We have found that fused in sarcoma (FUS) and proteasome regulator Rpt3 are interacting partners. FUS is a DNA/RNA binding protein that regulates transcription, translation, splicing, and mRNA transport. Mutations in the FUS gene are implicated in neurodegenerative diseases such as frontotemporal dementia and amyotrophic lateral sclerosis. Rpt3 regulates proteasome activity and has been shown to activate 26S proteasome activity. The proteasome is a large complex that is responsible for degradation of intracellular proteins. With this interaction, we hypothesize that protein synthesis and degradation synchronize via the FUS-Rpt3 interaction. Uncovering the nature of this interaction may provide mechanistic insight towards neurodegenerative diseases and potential therapeutic targets.

### **Christopher Roselle**

Advisor: Carl June, M.D.

Genetically engineered T cells expressing a chimeric antigen receptor (CAR) have generated unparalleled success in treatment of acute lymphoblastic leukemia (ALL) with durable response rates as high as 90%. However, the success of CAR T cell therapy in ALL has not been replicated for other tumors, particularly solid tumors, which account for ~90% of cancer deaths in the United States. A fundamental requirement for a successful antitumor response is that CAR T cells persist in a functional state long enough to complete and maintain tumor clearance. However, the enormous demands of tumor clearance, including prolonged antigen exposure, replication stress, and the suppressive tumor microenvironment (TME), can limit the functional persistence of CAR T cells by inducing dysfunctional states such as apoptosis, senescence and exhaustion. The molecular mechanisms driving T cell dysfunction during an antitumor response are unclear and likely multifactorial, however recent evidence suggests that the p53 signaling network may be an important component.

The p53 isoform  $\Delta$ 133p53 $\alpha$  is an endogenous regulator of senescence in human T cells that declines with age and selectively inhibits transcriptional activity of full-length p53. Primary human T cells co-transduced with  $\Delta$ 133p53 $\alpha$  and a CD19-directed CAR demonstrate unprecedented antitumor activity in vitro compared with CAR controls. Intriguingly,  $\Delta$ 133p53 $\alpha$ -transduced CARs exhibit improved tumor clearance only after multiple days of co-culture with the highest tumor burdens, suggesting that  $\Delta$ 133p53 $\alpha$  may improve tolerance to cellular stress. Our findings warrant further investigation of  $\Delta$ 133p53 $\alpha$  as a target to improve the functional persistence of CAR T cells.

P32

### Mechanisms of white matter loss due to HIV infection

### Lindsay Roth

Advisor: Judith Grinspan, Ph.D. and Kelly Jordan-Sciutto, Ph.D

Despite combined antiretroviral therapy (cART), HIV-associated neurocognitive disorder (HAND) occurs in 30-50% of HIV+ patients. Furthermore, white matter pathologies persist in HIV and HAND patients regardless of effective viral control through cART. The thinning of the corpus callosum and disruption of white matter microstructures seen in HIV-positive patients suggest HIV infection may perturb oligodendrocyte (OL) differentiation and/or myelin production. Thus, we hypothesized that HIV infection alters OL differentiation, function, and/or survival, influencing the persistence of HAND in the post-cART era. To examine the effect of HIV infection in the CNS on OL differentiation, we stimulated primary rat oligodendrocyte precursor cells (OPCs) to differentiate into mature OLs, and treated them with HIV-infected monocyte derived macrophage supernatants (HIVMDMS). This model mimics the neuroinflammatory environment of an HIV-infected CNS. To generate HIVMDMS, primary monocytes were isolated and differentiated into macrophages, then infected with HIV. Using this model, HIVMDMS significantly inhibited the differentiation of OPCs, which may explain initial white matter loss in HIV-infected patients. We examined a pathway that might mediate the effect of HIVMDMS called the integrated stress response (ISR). The ISR is a stress response pathway that is initially cytoprotective, but with chronic stress can ultimately lead to cell death. Previously, we have shown that the ISR is activated in neurons and astrocytes of HAND patients via increased pEIF2a staining in the mid-frontal cortex. Data show increased pEIF2α in maturing OPCs after 2-hour treatment with HIVMDMS. Furthermore, pretreatment with ISR inhibitor, trans-ISRIB, prior to HIVMDMS treatment, rescued OL maturation. Finally, previous literature from our labs and others have shown excess glutamate in HIVMDMS mediates excitotoxicity in primary neuronal cultures. In order to examine the role of glutamate on OL maturation, we pretreated maturing OPCs with NMDA antagonist, MK801, prior to HIVMDMS treatment which did not rescue OL maturation; however, pretreatment with AMPA antagonist, CNQX, did rescue OL maturation. These data suggest HIVMDMS-driven inhibition of OL maturation is mediated through AMPA receptors and subsequent ISR activation. These studies demonstrate that further investigation into the effects of HIV are warranted to provide insights into the observed persistent white matter changes seen in HAND patients with implications for their contribution to cognitive impairment.

P33

### TCRvβ CAR T cell therapy for T cell malignant clones

### Lauren Shaw

Advisor: Daniel J Powell Jr, Ph.D.

Peripheral T cell lymphomas (PTCLs) are a group of heterogeneous cancers associated with poor prognosis due to ineffective treatment options and high rates of relapse. Given the success of chimeric antigen receptor (CAR) T cell therapy with certain hematological malignancies, it is an attractive option for the treatment of PTCLs. However, developing a CAR T cell platform to treat T cell malignancies is challenging because there are no tumor-associated antigens (TAAs) to distinguish cancerous T cells from healthy T cells, which make up the immune repertoire of the patient as well as the CAR T cells themselves. A CAR T cell platform for PTCLs that avoids self-depletion, is effective, and avoids immunosuppression in the patient must therefore target a TAA with ubiquitous expression by malignant cells and limited expression by healthy T cells. PTCLs consist of mature, clonally expanded T cells so the malignant population will be derived from one of 24 T cell receptor beta chain variable region (TCRv $\beta$ ) families. We propose that CAR T cells specific for a TCRv $\beta$  family mediates TCRv $\beta$  family-specific lysis of malignant T cells while preserving the majority of the healthy T cell population. To demonstrate this, CAR constructs specific for individual TCRvß family members were designed and generated. The ability of T cells expressing these CARs to recognize and lyse target cells in vitro was assessed by (a) measuring self-depletion of the target TCRv $\beta$ + cell subpopulation within the bulk CAR T cell population using flow cytometry, (b) measuring specific lysis of target cell lines with known TCRv $\beta$  expression using functional killing assays, and (c) measuring lysis of the dominant malignant TCRv $\beta$  clone in a patient sample. TCRv $\beta$ -targeting CAR T cells were also shown to function against target malignant cells engrafted in immunodeficient mice. The development of TCRvß CAR T cell therapy has the potential to provide a high precision treatment option for patients with PTCL that limits healthy immune cell depletion.

P34

Elucidating the role of G Protein-Coupled Receptor Kinase-2 (GRK2) in mast cell mediated allergy and pseudo allergy

### Monica Thapaliya

### Advisor: Hydar Ali, Ph.D

It is well documented that aggregation of high-affinity IgE receptor (FccRI) by allergen on mast cells (MC) plays a central role in the manifestation of allergic diseases, which is the 6th leading cause of chronic illness in the U.S. affecting over 50 million Americans. Recent evidence suggests that there is also an IgE-independent MC activation route mediated via a novel G Protein-Coupled Receptor (GPCR) known as MAS-related GPCR-X2 (MRGPRX2), which is predominantly expressed in human MC. This route of MC activation is commonly known as a pseudo allergic reaction, which accounts for 15% of all adverse drug reactions that often leads to life threatening anaphylaxis. Studies show that MRGPRX2 and its mouse orthologue Mrgprb2 is activated by many US Food and Drug Administration (FDA)-approved peptidergic drugs, neuropeptides, and antimicrobial host defense peptides (HDPs). GPCRs are extensively studied gene family and these receptors are regulated by a process of desensitization via phosphorylation by GPCR kinases (GRKs). A plethora of studies show that GRK2 plays an important role in the vascular function, immunity, and inflammation, but the role of GRK2 in the regulation of MC function was reported only recently that it acts as a positive regulator of IgE/FccRI mediated MC degranulation. However, its role in MRGPRX2 signaling is largely unknown. This study is focused on identifying and elucidating the role of GRK2 in both IgE dependent (FccRI) and independent (MRGPRX2) MC responses. Data shows that upon GRK2 overexpression in Rat Basophilic Leukemia (RBL-2H3) cells both IgE and MRGPRX2-ligands (48/80, Substance P) induced calcium mobilization is enhanced, whereas upon GRK2 knockdown in Human Mast Cell Line (HMC-1) the response is reduced. Similarly, in primary mast cells isolated from mast cell-specific GRK2 knockout mice, both IgE and MRGPRX2-ligand induced response is reduced. Taken together this data shows that GRK2 acts as a common positive regulator of both IgE/FccRI and MRGPRX2/Mrgprb2 signaling. This is the first study that has introduced GRK2 in MRGPRX2/Mrgprb2 regulation. A comprehensive understanding of the mechanism of action of GRK2 will aid in the development of potential therapeutics in both allergic diseases and pseudo allergic drug reactions.

P35

### Examining dendritic cell heterogeneity in the tumor microenvironment

### **Jerrick To**

Advisor: Malay Haldar MD, Ph.D.

Dendritic cells (DCs) are a heterogenous population of immune cells that survey local tissue environments and instruct T cell function during an immune response. DCs are present in the tumor microenvironment and are reported to have stimulatory properties that are critical for a successful T cell-mediated anti-tumor response but also tolerogenic properties that enable uncontrolled tumor growth. Thus, understanding the division of stimulatory and tolerogenic properties within tumor DCs is important to any considerations of targeting DCs for cancer immunotherapy. However, the study of bona fide DCs in the tumor is obstructed by shared surface markers with other related immune cells such as macrophages and monocytes. We analyzed the heterogeneity of DCs within murine tumors using genetically engineered DC-reporter mice and single cell RNA-sequencing. Consistent with existing literature, we identified CD103+ DCs and CD11b+ DCs in their resting, activated, and migratory states, which we further validated by FACS. Additionally, we uncovered a division within CD11b+ DCs into two subsets demarcated by the presence or absence of CD301b expression. CD11b+301b+ DCs have been described elsewhere to promote a Th2 profile, but their prevalence and role in solid tumors is poorly understood. Our preliminary data suggests that CD11b+CD301b+ tumor DCs may suppress anti-tumor immune responses. The proposed studies aim to characterize the function of CD11b+CD301+ DCs in tumor immunity.

P36

### Premature induction of Lysyl Oxidase drives early arterial stiffening in Hutchinson-Gilford Progeria Syndrome

### Ryan von Kleeck

Advisor: Richard Assoian, Ph.D.

Arterial stiffening is a hallmark of premature aging in Hutchinson-Gilford Progeria Syndrome (HGPS), but the key molecular regulators initiating arterial stiffening in HGPS remain unknown. To identify these early events, we compared arterial mechanics and ECM remodeling in very young HGPS (LMNAG609G/G609G) mice to those of agematched and much older wild-type mice. Biaxial inflation-extension tests of carotid arteries of 2-month mice showed that circumferential stiffness of HGPS arteries was comparable to that of 24-month WT controls whereas axial arterial stiffening, an additional hallmark of normal aging, was mostly spared in HGPS. Transmission electron microscopy could identify increased amounts of collagen within the elastin folds of HGPS carotid arteries, but this change was barely detectable by immunostaining carotid cross sections or aortic qPCR. In contrast, immunostaining and RT-qPCR readily revealed an increased expression of Lysyl oxidase (LOX) and its family members in young HGPS arteries. Moreover, treatment of HGPS mice with the pan-Lox inhibitor betaaminopropionitrile (BAPN) restored near-normal circumferential arterial mechanics to HGPS carotid arteries, causally linking LOX upregulation to premature arterial stiffening in HGPS. This premature increase in arterial LOX expression in HGPS foreshadowed the increased expression of LOX which accompanied circumferential arterial stiffening during normal aging.

P37

#### Investigating drug-induced neuroadaptations to the Medial Habenula circuitry

#### Kate Webb

Advisor: Mariella De Biasi, Ph.D.

Opioid dependence has emerged as one of the leading public health concerns of the 21st century. The opioid crisis been paralleled in time by a rise in the popularity of e-cigarettes and subsequent nicotine use, especially among adolescents . A specific

connection between nicotine and opioid use is clinically apparent, with a reported 73-94% of methadone-maintained patients smoking cigarettes. While a functional link between these drugs has been drawn via work in animal models, the circuits by which they exert their effects during states of co-dependence have yet to be fully described. One region of particular interest, but consistently understudied, is the medial habenula (MHb). The medial habenula is a bilateral epithalamic structure that has been shown to regulate aversive behavioral states associated with dependence on and withdrawal from various drugs, including nicotine and opioids. Utilizing a genetically encoded calcium indicator (GCaMP7b) and fiber photometry, I aim to identify nicotine and morphineinduced neuroadaptations to the medial habenula in live, freely behaving mice. First, pharmacologically and physiologically relevant methods of drug delivery were established with an electronic vapor delivery system (nicotine) and a two-bottle choice paradigm (morphine). Then, ability to specifically target the cholinergic neurons of the MHb was confirmed with stereotaxic injection of a Cre-dependent AAV virus encoding GCaMP7b in adolescent ChAT-Cre mice. Using these models and fiber photometry, I plan to study MHb cholinergic activity during states of initial exposure to, dependence on, and withdrawal from either nicotine or morphine. Following separate drug characterizations, I will study activity in the same circuit during a state of co-dependence to and withdrawal from both drugs. Elucidating the role of the medial habenula in nicotine-opioid co-dependence will provide valuable insight and aid in the identification of new targets to treat polysubstance use disorders and curb current drug epidemics.

#### P38

<u>Understanding epigenome and proteome remodeling caused by novel germline histone</u> H3.3 mutations during neurodevelopment

#### Khadija Wilson

Advisor: Benjamin A. Garcia, Ph.D.

Histone H3.3 (H3.3) is a histone variant that plays a role in cellular inheritance as ablation of H3.3 expression leads to loss of active gene states and dysfunction of heterochromatin telomeric structures. *H3F3A* and *H3F3B*, the two genes known to

encode H3.3, are ubiguitously expressed in all human cells with higher expression in the ovaries, testes, and brain. Somatic mutations in the H3F3A genes have been reported as oncogenic drivers of pediatric glioblastomas. More recently, here at the Center for Applied Genomics at the Children's Hospital of Philadelphia novel germline mutations in both H3F3 genes have been discovered in a small cohort of patients who suffer from a common pattern of neurodevelopmental disorders, seizures and craniofacial abnormalities. Here we hypothesize that mutant H3.3 (mH3.3) change the regulatory capacity of mH3.3 containing chromatin and therefore modulate gene expression and ultimately the cellular proteome. To this end, we developed stable murine astrocyte cell lines expressing either wild type H3.3 or mH3.3 (G90R, T45I) to study by quantitative mass spectrometry the histone post translational modification changes to the mH3.3 containing nucleosomes and subsequent proteome alterations. Our preliminary data has identified downregulation of chromatin remodeler proteins, as well as upregulation of mitochondrial proteins following reprogramming of the mH3.3 encrusted epigenome. Ultimately, our studies aim to identify and validate potential epigenetic and proteomewide factors involved in these novel neurodevelopmental disorders. Understanding the basic mechanisms of how these new histone mutations function in neurodevelopment may allow re-classification of epigenome reprogramming in neurological contexts.

#### P39

# Analysis of how Structural Changes in Mutated ALK Kinase Domain Affect Drug Binding using Molecular Docking and Molecular Dynamics Simulations

#### Gabriela Witek

Advisor: Yaël Mossé, M.D.

Constitutive activation of receptor tyrosine kinases (RTKs) causes dysregulation of their signaling and can drive uncontrolled growth leading to cancer. Anaplastic Lymphoma

Kinase (ALK), an RTK in the insulin family, is the primary oncogenic driver in neuroblastoma (NB), most common cancer in infants. Mutations in the ALK kinase domain are responsible for the hereditary form of NB and are also somatically acquired in 14% of patients with the most aggressive form of the disease, positioning ALK as a promising target for NB therapy. The three most common ALK mutations at position R1275, F1245, and F1174, have transforming in vitro abilities and result in differential kinase activation. Crizotinib, a first-generation small molecule ATP-competitive inhibitor of the ALK tyrosine kinase, showed limited anti-tumor activity in patients with relapsed NB harboring ALK F1174 and F1245 mutations. It was recently demonstrated that lorlatinib, a novel ATP-competitive ALK inhibitor overcomes this de novo resistance. Moreover, studies suggest that these hot-spot mutations cause disruption of the autoinhibitory interactions and result in ALK activation. Our combined computational work involving molecular docking and molecular dynamics simulations and experimental work involving biochemical assays on purified ALK kinase constructs aim to show how mutations within the ALK kinase domain cause structural changes and affect crizotinib and lorlatinib binding to the kinase.

### P40

### Synthetic DNA Delivery by Electroporation Promotes Robust in vivo Post-Translational Modification of Broadly Neutralizing anti-HIV Immunoadhesin

### Ziyang Xu

Advisor: David Weiner, Ph.D.

Despite ongoing efforts, no vaccines have yet succeeded in inducing antibodies that are considered broadly neutralizing (bNabs) against HIV-1 in NHPs and humans. Passive transfer of bNabs is an important alternative preventive or therapeutic strategy for HIV-1. While exciting, this approach has only recently entered clinical evaluation and

warrants further investigation. For these mAbs to be efficacious in preventing HIV-1 infection, neutralization breadth remains a key issue. Accordingly, novel molecules possessing broader neutralization activity have been designed. Among these, the broadest and the most potent are immunoadhesins that contain extracellular domains of CD4 which impart these molecules neutralization breadths, and a peptide that mimics either the N-terminus of CCR5 or crucial binding site of CD4 inducible antibodies to enhance the neutralization potency. The biological production of these complex molecules can be challenging as these immunoahesins frequently require posttranslational sulfation by enzymes to interact with the HIV envelope and achieve their full in vivo potency. Here, we report using synthetic DNA and electroporation (DNA/EP) to promote in vivo expression of an anti-HIV-1 immunoadhesin for at least 6 months. Additionally, we engineered a Tyrosylprotein Sulfotransferase 2 (TPST2) variant enzyme that efficiently trafficked to Trans-Golgi Network (TGN) to colocalize with the immunoadhesin. Binding ELISA assay was used to demonstrate that the engineered TPST2 variant delivered by synthetic DNA/EP optimally sulfated the target molecule in vivo at a low plasmid dose (1:1000 relative to plasmid immunoadhesin dose). Additionally, post-translational sulfation enhanced the potency of the immunoadhesin, decreasing its IC50 in neutralizing global panel HIV isolates (CE1176, 0.57 to 0.05 ug/mL; 25710, 1.09 to 0.16 ug/mL; X2278, 0.77 to 0.16 ug/mL; TRO, 0.38 to 0.18 ug/mL; BJOX, 0.56 to 0.19 ug/mL; X1632, 0.75 to 0.27 ug/mL; CH119, 1.66 to 0.52 ug/mL; CNE55 1.92 to 0.75 ug/mL; 246F3, 2.11 to 1.07 ug/mL). This work provides a proof-ofconcept for delivering anti-HIV immunoadhesins and other engineered complex molecules in vivo by advanced nucleic acid.

# **Recent Graduates**



# **Cheyenne Allenby**

School: Duke University B.S. Neuroscience (2014)

Advisor: Caryn Lerman, Ph.D. The Effects of Abstinence from Smoking on Stress Reactivity



# **Alejandro Arroyo**

School: University of Puerto Rico, Río Piedras B.S. Chemistry (2012)

Advisor: Jim Delikatny, Ph.D. Development of bioactive probes for detection of tissue metabolic state using Cerenkov attenuation imaging

# **Grace Coggins**

School: Vanderbilt University B.A. Molecular and Cellular Biology, History of Art (2014)



Exploiting resistance mechanisms to RAS-MAPK inhibition in relapsed neuroblastoma

# **Taylor Hughes**

School: Franklin & Marshall College B.S. Chemistry (2015)

Advisor: Vera Moiseenkova-Bell, Ph.D. Insights into TRPV5 modulation and gating by cryo-EM







# Isabelle Lee

School: Virginia Tech B.S. Biochemistry (2012)

Advisor: Dr. Trevor Penning Estrogenic activity of polycyclic aromatic hydrocarbon ortho-quinones in the human endometrium

### Jessica Murray

School: College of William and Mary B.S. Biology and Chemistry (2013)

Advisor: Trevor Penning, Ph.D.

The role of human aldo-keto reductases and Nrf2 signaling in the bioactivation of polycyclic aromatic hydrocarbons (PAHs) and their nitrated derivatives (nitro-PAHs).



# **Amber Wang**

School: National Taiwan University B.S. Pharmacy (2014)

Advisor: Klaus Kaestner, Ph.D. *Cell-type-specific expression profiling of repopulating hepatocytes* 



### Madhumita Yennawar

School: Pennsylvania State University B.S. Biochemistry and Molecular Biology (2013)

Advisor: Frances Jensen, M.D. AMPA receptor dysregulation and therapeutic interventions in a mouse model of CDKL5 Deficiency Disorder

# **First Year Students**



# **Brandon Anderson**

School: Brigham Young University



# Kimberly Edwards

School: Mount Holyoke



# **Daniel Park**

School: Rutgers University, Camden



# Ryan Paulukinas

School: University of the Sciences



# Elizabeth Pruzinsky

School: Drexel University



# **Alexander Starr**

School: New York University



# Alexandra Vazquez

School: University of Puerto Rico, Rio Piedras Campus



# **Eric Waite**

School: University of Maryland, College Park



# Alyssa Wiest

School: Muhlenberg College



# Veronica Yakovishina

School: CUNY John Jay College of Criminal Justice

# **Current Students**



# Varun Bahl

School: University of California, Berkeley B.A. Molecular and Cell Biology (2016)

Email: varunb@pennmedicine.upenn.edu

Laboratory Rotations (1) Park Cho-Park, M.D., Ph.D. Functional Characterization of PI31 in the Context of Protein Homeostasis. (2) Klaus Kaestner, Ph.D. Can Genomic Mosaicism Explain Regional Differences in Type I Diabetes? (3) Doris Stoffers, M.D., Ph.D. Elucidating the Role of Chac1, SIc7a1, and Gpt2 in stress-induced beta-cell survival.

**Doctoral Thesis** Advisor: Dr. Klaus Kaestner *Regulation and Function of the MEG3 Locus in Human Beta-cells* 



# Kayla Barekat

School: University of California, Irvine B.S. Biological Sciences (2013)

Email: kbarekat@pennmedicine.upenn.edu

Laboratory Rotations (1) Caryn Lerman, Ph.D. Pilot Study for Transcranial Direct Current Stimulation as a Treatment for Adult ADHD (2) Rebecca Simmons, M.D. Transgenerational Bisphenol Exposure Alters Gene Expression in the Liver (3) Tracy Bale, Ph.D. Examining Signaling Between the Prefrontal Cortex and the Basolateral Amygdala in a Pubertal Stress Model

#### **Doctoral Thesis**

Advisor: Garret FitzGerald, MD, FRS Exploring the role of the gut microbiome in NSAID-induced gastroenteropathy.

#### Presentations

SPATT Seminar, Philadelphia, PA, Jan 2018Title: "Exploring the role of the gut microbiome in NSAID-induced gastroenteropathy"

Annual PGG Student Symposium Poster, Philadelphia, PA, Nov 2017 • Title: "Exploring the role of the gut microbiome in NSAID-induced gastroenteropathy"

Candidacy Exam Presentation, Philadelphia, PA, Oct 2017 • Title: "Exploring the role of the gut microbiome in NSAID-induced gastroenteropathy"

Annual PGG Student Symposium Poster, Philadelphia, PA, Oct 2016
Title: "Early prenatal stress predisposes individuals to stress-induced intestinal inflammation during puberty via dysregulation of bacterial signaling to the host immune system"

#### Fellowships

PGG T32 Training Grant, Jul 2017 - Jul 2018



### **Kryshawna Beard**

School: University of Louisville B.S. Chemistry, B.A. Biology (2017)

Email: krbeard@pennmedicine.upenn.edu

Laboratory Rotations (1) Kelly Jordan-Sciutto, Ph.D. Antioxidant effects of flaxseed lignin SDG in HIV associated neurocognitive disorder (2) Jim Eberwine, Ph.D. Single cell transcriptomics in neurons (3) David Meaney, Ph.D. Exosome-based biomarkers for traumatic brain injury

#### **Doctoral Thesis** Advisor: David Meaney, Ph.D. *Exosomes as Biomarkers for Traumatic Brain Injury*



# **Tatiana Blanchard**

School: University of South Florida B.S. Biomedical Science/Minor: Public Health (2010) University of Connecticut Health Center Certificate in Clinical and Translational Research (2011)

Email: btati@pennmedicine.upenn.edu

### **Laboratory Rotations**

<u>(1) Carl June M.D.</u> CRISPR Genome Engineering of Primary Human T cells (2) Daniel Powell Ph.D. T cell target antigens for the treatment of Ovarian cancer and other gynecologic malignancies with chimeric antigen receptors (CARs) (3) Beatriz Carreno Ph.D., and Gerald Linette M.D. Ph.D.</u> Identification of Novel Neoantigens for the treatment of Ovarian Cancer

#### **Doctoral Thesis** Advisors: <u>Carl June M.D.</u>, Beatriz Carreno Ph.D., Gerald Linette M.D. Ph.D. *Engineering Antigen-Specific T cells for Adoptive Cell Transfer - TET2*

### Abstracts/ Posters/Presentations

Genomics-Driven Immunomics Analysis reveal the vast landscape of tumor protective epitopes. 20th Annual CRI Cancer Immunotherapy Symposium, New York City, NY, October 2012. (Oral Presentation)

Duan F, Duitama Jorge, Al Seesi S, Blanchard T, McMahon D, Sidney J, Sette A, Mandoiu I, Srivastava P. A mutation in Transportin3 (Tnpo3) leads to generation of an individually distinct tumor-specific Kd-restricted epitope in the Meth A fibrosarcoma (TUM2P.899) Abstract. The Journal of Immunology May 1, 2014 vol.192 (1 Supplement) 71.23

Chislock E, Pletcher H, Yu L, Warner B, Blanchard T, Sterner C, Belka G, and Chodosh L. Molecular Analysis of Breast Cancer Disseminated Tumor Cells. Cancer Biology Retreat, Mohonk Mountain House, New Paltz, NY. June 15-17, 2015. (Poster) Chislock E, Yu L, Ji X, Shih N, Smith M, Blanchard T, DeMuth W, Morschauser A, Blaesius R, Feldman M, Pletcher C, Moore J, Judge K, DeMichele, Chodosh L. Development of a Flow Cytometry-Based Assay for Clinical Detection and Molecular Characterization of Disseminated Tumor Cells in Bone Marrow. Cyto2017. (Poster)

#### Publications

-Blanchard T, Srivastava PK, Duan F. Vaccines against advanced melanoma. Clin Dermatol 31, 179-190 (2013).

-Duan F, Duitama J, Al Seesi S, Ayres CM, Corcelli SA, Pawashe AP, Blanchard T, McMahon D, Sidney J, Sette A, Baker BM, Mandoiu II, Srivastava PK. Genomic and bioinformatic profiling of mutational neoepitopes reveals new rules to predict anticancer immunogenicity. J Exp Med 211, 2231-2248 (2014).

-Yee S, Lieberman D, Blanchard T, Rader J, Zhao J, Troxel A, DeSloover D, Fox A. Daber R. Kakrecha B, Sukhadia S, Belka G, DeMichele A, Chodosh L, Morrissette J, Carpenter E. A novel approach for next-generation sequencing of rare circulating tumor cells. Hum Mutation (2015).

#### Awards

Florida Bright Futures: Florida Medallion Scholar Recipient August 2006-May 2010 National Society of Collegiate Scholars December 2006-present University of South Florida Merit Scholarship August 2006-May 2010 Nominated as Conference Assistant at the Keystone Symposium - Emerging Cellular Therapies: T Cells and Beyond. Keystone Resort in Keystone, Colorado on Feb 11 - Feb 15, 2018 (Awarded a \$1200 scholarship)

Awarded a Predoctoral Training Grant in Pharmacology, T32GM008076. July 2018-July 2019



Laboratory Rotations (1) Dan Powell, Ph.D. (2) Saar Gill, M.D., Ph.D. (3) Margaret Chou, Ph.D.

### Dan Brown

School: University of Michigan, Ann Arbor B.S. Cell and Molecular Biology (2014)

Email: dbrow@pennmedicine.upenn.edu



### Keith Campagno

School: Rutgers University, New Brunswick, NJ B.A. Cell Biology and Neuroscience (2015)

Email: campagno@pennmedicine.upenn.edu

Laboratory Rotations (1) R. Christopher Pierce, Ph.D. Paternal Cocaine Exposure and Effects on Social Interaction in Progeny (2) Benjamin Garcia, Ph.D. Kinase Inhibitor Library and Phosphorylation-dependent Histone Posttranslational Modifications (3) Doris Stoffers, M.D. Ph.D. Neonatal Exendin-4 Administration Timing and the Effects on Adolescent Mice

**Doctoral Thesis** Advisor: Claire Mitchell, Ph.D. *Lysosomal Dysregulation in Microglia and Neurodegeneration* 

#### Publications

Patel MV, Swiatkowski P, Kwon M, Rodriguez AR, Campagno K, Firestein BL. A Novel Short Isoform of Cytosolic PSD-95 Interactor (Cypin) Regulates Neuronal Development. Mol Neurobiol. 2018 Aug;55(8):6269-6281. doi: 10.1007/s12035-017-0849-z. Epub 2018 Jan 2.

Lu W, Gómez NM, Lim JC, Guha S, O'Brien-Jenkins A, Coffey EE, Campagno KE, McCaughey SA, Laties AM, Carlsson LG, Mitchell CH. The P2Y12 Receptor Antagonist Ticagrelor Reduces Lysosomal pH and Autofluorescence in Retinal Pigmented Epithelial Cells From the ABCA4-/-Mouse Model of Retinal Degeneration. Front Pharmacol. 2018 Apr 19;9:242. doi: 10.3389/fphar.2018.00242. eCollection 2018

Beckel JM, Gómez NM, Lu W, Campagno KE, Nabet B, Albalawi F, Lim JC, Boesze-Battaglia K, Mitchell CH. Stimulation of TLR3 triggers release of lysosomal ATP in astrocytes and epithelial cells that requires TRPML1 channels. Sci Rep. 2018 Apr 10;8(1):5726. doi: 10.1038/s41598-018-23877-3.

Gómez NM, Lu W, Lim JC, Kiselyov K, Campagno KE, Grishchuk Y, Slaugenhaupt SA, Pfeffer BA, Fliesler SJ, Mitchell CH. Robust lysosomal calcium signaling through channel TRPML1 is impaired

by lysosomal lipid accumulation. FASEB J. 2018 Feb;32(2):782-794. doi: 10.1096/fj.201700220RR. Epub 2018 Jan 4.



### **Marco Carpenter**

School: Clark University, B.A. (2014)

Email: cmarco@pennmedicine.upenn.edu

**Doctoral Thesis** Advisor: Elizabeth Heller, Ph.D. *Isolation of Cocaine-Specific Molecular Targets Using A Mouse Self-Administration Paradigm* 

#### Publications

Sanchez, V., **Carpenter, M. D**., Yohn, N. L., & Blendy, J. A. (2016). Long-lasting effects of adolescent oxycodone exposure on reward-related behavior and gene expression in mice. *Psychopharmacology*, 1-12.



### Laboratory Rotations

### Suhee Chang

School: Seoul National University, Seoul, Korea B.S. Pharmacy (2012) M.S. Pharmacy (2014)

Email: suheech@pennmedicine.upenn.edu

#### <u>(1) Kelly Jordan-Sciutto, Ph.D.</u> ER stress-mediated Neurodegeneration in Antiretroviral Therapy for HIV Positive Patients (2) Klaus Kaestner, Ph.D.

Foxl1<sup>+</sup> cells are the essential source of Wnt signaling in the Intestinal stem cell niche (3) Marisa Bartolomei, Ph.D. Disrupted DNA methylation in human induced pluripotent cells

#### Doctoral Thesis

Advisor: Marisa Bartolomei, Ph.D.



# **Edward Chuang**

School: Colby College B.A. Biochemistry and Mathematics (2014)

Email: edchuang@pennmedicine.upenn.edu

#### Laboratory Rotations

<u>(1) Robert Siman, Ph.D.</u> Neuroinflammation and Innate Immunity in Mouse Model of Early Stage Alzheimer Tauopathy (<u>2) James Shorter, Ph.D</u> Characterizing the mechanism of Hsp104(A503V) potentiation (<u>3) Kelly Jordan-Sciutto, Ph.D.</u> Effects of antiretroviral protease inhibitors in primary neurons

#### **Doctoral Thesis**

Advisor: James Shorter, Ph.D.

Studies the aggregation of RNA-binding proteins (RBPs) with prion-like domains such as FUS and TDP-43 that are hallmarks of many neurodegenerative diseases including amyotrophic lateral sclerosis (ALS) and frontotemporal dementia (FTD). Recent literature suggests that human heat shock proteins Hsp40, Hsp70, and Hsp110 regulate RBP-rich stress granule dynamics and are capable of robust protein disaggregation. I aim to identify human chaperones that can disaggregate FUS and TDP-43 as therapeutic targets for the treatment of ALS and FTD, and to identify small-molecule enhancers of this disaggregase activity as potential drug candidates.

#### Publications

Torrente, M.P., E. Chuang, M.M. Noll, M.E. Jackrel, M.S. Go, and J. Shorter. (2016). Mechanistic insights into Hsp104 potentiation. J. Biol. Chem. DOI:10.1074/jbc.M115.707976.

Gates, S.N\*., A.L. Yokom\*, J. Lin, M.E. Jackrel, A.N. Rizo, N.M. Kendsersky, C.E. Buell, E.A. Sweeny, K.L. Mack, E. Chuang, M.P. Torrente, M. Su, J. Shorter, and D.R. Southworth. (2017). Ratchet-like polypeptide translocation mechanism of the AAA+ disaggregase Hsp104. Science. 357(6348):273-279. (\*Co-first author).

Chuang, E.\*, A.M. Hori\*, C.D. Hesketh\*, and J. Shorter^. (2018). Amyloid assembly and

disassembly. J. Cell. Sci. doi: 10.1242/jcs.189928. (\*Co-first author. ^Corresponding author).

Pharmacology Predoctoral Training Grant - T32GM008076 (2015-2017) Blavatnik Family Fellowship in Biomedical Research (2018-2019)



# Ryan Cupo

School: Alvernia University B.S. Chemistry and Mathematics (2015)

Email: ryancupo@pennmedicine.upenn.edu

### Laboratory Rotations

(1) James Shorter, Ph.D.

Potentiation of mitochondrial chaperones Hsp78 and Skd3 to mediate toxic protein misfolding. (2) Garret FitzGerald, M.D.

Differential effect of celecoxib and rofecoxib on mitochondrial quality control and OXPHOS gene expression in cardiac tissue.

(3) Michael Robinson, Ph.D.

Mitochondrial loss and astrocyte proliferation: Using an organotypic oxygen glucose deprivation model to probe the mechanisms of ischemic neuronal injury.

### **Doctoral Thesis**

Advisor: James Shorter, Ph.D.

Our goal is to (1) understand the function of the mitochondrial ClpB chaperones Hsp78 and Skd3 and (2) engineer their activity against toxic disease proteins associated with neurodegenerative diseases.

### Awards

2018-2021 NIH Ruth L. Kirschstein National Research Service Award (NRSA) Individual Fellowship (F31)

2017-2018 Structural Biology and Molecular Biophysics Training Grant

2017 NSF Graduate Research Fellowship, Honorable Mention

### Publications

1. Cupo, Ryan; Augustine, Emily; Shorter, James, "Exploring and enhancing compartment-specific protein disaggregases to combat neurodegenerative diseases," Biophysical Society 62nd Annual Meeting. San Francisco, CA. February 17-21, 2018.

2. Cupo, Ryan; Augustine, Emily; Shorter, James, "Exploring compartment-specific protein disaggregases to combat neurodegenerative diseases," American Society for Cell Biology Annual Meeting, Philadelphia, PA, December 5, 2017.



# **Emily Fabyanic**

School: West Virginia University B.S. in Chemistry, Minor in Biology (2016)

Email: eblythe@pennmedicine.upenn.edu

### Laboratory Rotations

 (1) Julie Blendy, Ph.D.
 Transgenerational Inheritance of Adolescent Stress Exposure Alters Offspring Response to Cocaine
 (2) Joe Zhou, Ph.D. / Hao Wu, Ph.D.
 Adapting Drop-seq Technology for High-Throughput Transcriptome Analysis of Mature Neurons
 (3) Klaus Kaestner, Ph.D.
 Epigenetic Targeting: Inducing Proliferation Through CDKN1C Silencing

**Doctoral Thesis** Adviser: Hao Wu, Ph.D. *Using single-cell techniques to study neural biology* 

#### Publications

Hu, P\*, Fabyanic, E\*, Kwon, D, Tang, S, Zhou, Z, Wu, H. Dissecting Cell-Type Composition and Activity-Dependent Transcriptional State in Mammalian Brains by Massively Parallel Single-Nucleus RNA-Seq. Molecular Cell. 2017; 68: 1005-1015. Appointee of the Cell and Molecular Biology Training Grant (NIH T32 GM-07229) - July 2017

### Awards

Supported under the Cell and Molecular Biology Training Grant


## **Mark Gerelus**

School: Wake Forest University B.A. Chemistry (2013); B.A. Economics (2013)

Wake Forest University School of Business M.A. Management (2014)

Email: mgerelus@pennmedicine.upenn.edu

### Laboratory rotations

(1) Margaret Chou, Ph.D.
Mechanisms of Sarcomagenesis: Development of CRISPR-Cas9 screen to identify novel key regulators
(2) Yael Mosse, M.D.
The role of FAK in ALK-driven Neuroblastoma
(3) Donita Brady, Ph.D.
Combining copper chelation with pharmacological therapy to treat melanoma

### **Doctoral Thesis**

Advisor: Yael Mosse, M.D. Charactering the protein tyrosine phosphatase SHP2 as an oncoprotein and therapeutic target in neuroblastoma

The overall goal of my project is to determine if SHP2 is a molecular vulnerability in NB. I hypothesize that SHP2 is an integral factor in oncogenic signaling which contributes to the survival of NB cells. To test this hypothesis, I will characterize SHP2's role in a broad panel of NB cell lines. I will analyze phenotypic, transcriptional, and proteomic changes upon SHP2 depletion via CRISPR knockout and shRNA knockdown. Furthermore, I will characterize the effects of novel SHP2 inhibitors in vitro and in vivo in the context of extensively characterized NB cells and patient-derived xenografts (PDXs), as well as determine the anti-tumor activity of a novel SHP2 inhibitor in vivo. The significance of this project is that I will assess SHP2's potentially crucial role in NB, findings which will lead to the translation of pharmacological inhibition of SHP2 into the clinical setting as a novel targeted therapy.

### Publications

Synergistic Modulation of Inflammatory but not Metabolic Effects of High-Fat Feeding by CCR2 and CX3CR1.

Zhang H, Hinkle CC, O'Neill SM, Shi J, Caughey J, Lynch E, Lynch G, Gerelus M, Tsai ASD, Shah R, Ferguson JF, Ahima RS, Reilly MP. Obesity (Silver Spring). 2017 Aug;25(8):1410-1420. doi: 10.1002/oby.21900. PMID: 28650582

Lipid-Free Apolipoprotein A-I Reduces Progression of Atherosclerosis by Mobilizing Microdomain

Cholesterol and Attenuating the Number of CD131 Expressing Cells: Monitoring Cholesterol Homeostasis Using the Cellular Ester to Total Cholesterol Ratio. Kaul S, Xu H, Zabalawi M, Maruko E, Fulp BE, Bluemn T, Brzoza-Lewis KL, Gerelus M, Weerasekera R, Kallinger R, James R, Zhang YS, Thomas MJ, Sorci-Thomas MG. J Am Heart Assoc. 2016 Nov 7;5(11). pii: e004401. PMID: 27821400

Transcriptome-Wide Analysis Reveals Modulation of Human Macrophage Inflammatory Phenotype Through Alternative Splicing.

Lin J, Hu Y, Nunez S, Foulkes AS, Cieply B, Xue C, Gerelus M, Li W, Zhang H, Rader DJ, Musunuru K, Li M, Reilly MP.

Arterioscler Thromb Vasc Biol. 2016 Jul;36(7):1434-47. doi: 10.1161/ATVBAHA.116.307573. PMID: 27230130

Procollagen C-endopeptidase Enhancer Protein 2 (PCPE2) Reduces Atherosclerosis in Mice by Enhancing Scavenger Receptor Class B1 (SR-BI)-mediated High-density Lipoprotein (HDL)-Cholesteryl Ester Uptake.

Pollard RĎ, Blesso ČN, Zabalawi M, Fulp B, Gerelus M, Zhu X, Lyons EW, Nuradin N, Francone OL, Li XA, Sahoo D, Thomas MJ, Sorci-Thomas MG. J Biol Chem. 2015 Jun 19;290(25):15496-511. doi: 10.1074/jbc.M115.646240. PMID: 25947382

Nascent high density lipoproteins formed by ABCA1 resemble lipid rafts and are structurally organized by three apoA-I monomers.

Sorci-Thomas MG, Owen JS, Fulp B, Bhat S, Zhu X, Parks JS, Shah D, Jerome WG, Gerelus M, Zabalawi M, Thomas MJ. J Lipid Res. 2012 Sep;53(9):1890-909. doi: 10.1194/jlr.M026674.



## Shivesh Ghura

School: University of Illinois, Chicago B.S. Bioengineering (2015)

Email: sghura@pennmedicine.upenn.edu

Laboratory Rotations (1) Jordan-Sciutto, Ph.D. Role of APP processing in HIV associated neurocognitive disorder. (2) Dr. Lynch, M.D., Ph.D. Stress induced alterations in MAM proteins IP3R and GRP75 in Friedrich Ataxia models. (3) Benjamin Garcia, Ph.D. Mass Spectrometry and Proteomics.

#### **Doctoral Thesis**

Advisor: Kelly Jordan-Sciutto, Ph.D.



## **Kevin Gillespie**

School: Haverford College B.A. Chemistry (2015) American Chemical Society Certification

Email: kevingi@pennmedicine.upenn.edu

Laboratory Rotations (1) Ian Blair, Ph.D. Impacts of Dimethyl Fumarate on Glutathione and Cellular Oxidation (2) Aalim Weljie, Ph.D. HPLC-coupled NMR analysis of small polar metabolites in Drosophila melanogaster (3) Marilyn Howarth, M.D. Investigation into environmental health concerns with agricultural fertilizer applications

**Doctoral Thesis** Advisor: Ian Blair, Ph.D. Secreted HMGB1 Proteoforms as Biomarkers of DNA Damage

#### **Publications**

1. Xiao Zhao, Kristin Lorent, Benjamin J. Wilkins, Dylan M. Marchione, Kevin Gillespie, Orith Waisbourd-Zinman, Juhoon So, Kyung Ah Koo, Donghun Shin, John R. Porter, Rebecca G. Wells, Ian Blair, Michael Pack. Glutathione antioxidant pathway activity and reserve determine toxicity and specificity of the biliary toxin biliatresone in zebrafish. Hepatology, 2016. PubMed PMID: 27102575 2. Andrew J. Worth, Dylan M. Marchione, Robert C. Parry, Qingqing Wang, Kevin P. Gillespie, Noelle N. Saillant, Carrie Sims, Clementina Mesaros, Nathaniel W. Snyder, Ian A. Blair. LC-MS Analysis of Human Platelets as a Platform for Studying Mitochondrial Metabolism. Journal of Visualized Experiments, 2016. PubMed PMID: 27077278

Andrew J. Worth, Kevin P. Gillespie, Clementina Mesaros, Lili Guo, Sankha S. Basu, Nathaniel W. Snyder, and Ian A. Blair. Rotenone Stereospecifically Increases (S)-2-Hydroxyglutarate in SH-SY5Y Neuronal Cells. Chemical Research in Toxicology 2015. PubMed PMID: 25800467.
Nathaniel W. Snyder, Gregory Tombline, Andrew J. Worth Robert C. Parry Jacob A. Silvers, Kevin P. Gillespie, Sankha S. Basu, Jonathan Millen, David S. Goldfarb, Ian A. Blair. Production of

stable isotope-labeled acyl-coenzyme A thioesters by yeast stable isotope labeling by essential nutrients in cell culture. Analytical Biochemistry 2015. PubMed PMID: 25572876; PubMed Central PMCID: PMC4413507.

#### **Poster Presentations**

Biliary toxin biliatresone depletes hepatic glutathione and forms glutathione adducts in larval zebrafish. **Kevin P. Gillespie** et al. Center for Excellence in Environmental Toxicology Symposium. Perelman School of Medicine, University of Pennsylvania. Philadelphia, PA. June 2016.

Asbestos Induced Oxidative Stress in Lung Cells. Liwei Weng, Clementina Mesaros, Nathaniel W. Snyder, **Kevin P. Gillespie**, Robert Parry, and Ian A. Blair. Society of Toxicology. New Orleans, LA. April 2016.

Effects of Asbestos Exposure on the Cellular Redox State Mitochondrial Metabolism. **Kevin P. Gillespie**, Robert Parry, Clementina Mesaros, Nathaniel W. Snyder, Andrew J. Worth, and Ian A. Blair. Superfund Research Program Annual Meeting. San Juan, PR. November 2015.

Monitoring the effects of asbestos on cellular redox state. **Kevin P. Gillespie** et al. Superfund Research Program Grant Update Site Visit. Perelman School of Medicine, University of Pennsylvania. Philadelphia, PA. August 2015.

Monitoring the effects of chemical insults on mitochondrial activity and acyl-CoA metabolism. **Kevin P. Gillespie** et al. Koshland Integrated Natural Science Center Undergraduate Science Research Symposium. Haverford College. Haverford, PA. October 2014.

#### Awards

CTSA Summer Undergraduate Summer Internship, University of Pennsylvania (2013) Koshland Integrated Natural Science Center Summer Scholar, Haverford College (2014) CEET T32 Training Grant (2016-2019)



## Andrea Guzman

School: University of Puerto Rico, Rio Piedras Campus B.S. in Chemistry (2016)

Email: guzma@pennmedicine.upenn.edu

#### **Laboratory Rotations**

(1) Andrew Tsourkas, Ph.D.
Development of a Novel Targeted Photodynamic Therapy Against Prostate Cancer
(2) Donita Brady, Ph.D.
Elucidating the Role of Copper Chaperones in MAPK Signaling
(3) Jim Delikatny, Ph.D.
Synthesis and Characterization of a pH Sensitive Probe for Tumor Microenvironment Imaging

#### **Doctoral Thesis**

Advisor: Jim Delikatny, Ph.D.

Increased acidity in the tumor microenvironment has been shown to play a role in invasion and metastasis of cancer cells. This metabolic hallmark has sparked interest in the exploration of tumor pH measurement and imaging in vivo. The decrease in tumor microenvironment pH is due to a deregulated metabolism led by an increased glycolytic flux in cancer cells. Cerenkov radiation is a potential technique to image this type of metabolic trademark in vivo. The multispectral photon emission of Cerenkov-active radionuclides (such as 18F and 68Ga) can be absorbed by pH-sensitive molecules and its attenuation at certain wavelengths can be quantified by Selective Bandwidth Quenching. Our lab has previously shown the potential of fluorinated naphthofluorescein for pH measurement using Cerenkov imaging. For this project, we will explore the conjugation of pH sensitive fluorophores with DOTA, with the purpose of chelating 68Ga and Y90. This will allow the measurement of quantifiable Cerenkov radiation that will give differential signal due to Selective Bandwidth Quenching, dependent on tumor pH.

#### Memberships

UPenn Pharm 4 GOOD Co-Founder / Co-Chair World Molecular Imaging Society Member UPenn Biomedical Graduate Student Association- Social Chair

#### Presentations

November 2017 Pharmacology Graduate Group Symposium - Poster Synthesis and Characterization of a pH-Sensitive Probe for Cerenkov Imaging of Tumor Microenvironment Guzmán-Ríos A.E., Arroyo A.D., Delikatny J.

September 2018 World Molecular Imaging Conference - Oral Presentation Development of a Naphthofluorescein based pH-Sensitive Probe for in vivo Cerenkov Imaging Guzmán-Ríos A.E., Arroyo A.D., Delikatny J.

September 2018 World Molecular Imaging Conference - Poster Development of a Naphthofluorescein based pH-Sensitive Probe for in vivo Cerenkov Imaging Guzmán-Ríos A.E., Arroyo A.D., Delikatny J.

#### Awards

Supported under T32 Training Grant



## **Michael Hart**

Centre College B.S. in Biochemistry and Molecular Biology (2017)

Email: mihart@pennmedicine.upenn.edu

#### Laboratory Rotations

(1) Kelly Jordan-Sciutto, Ph.D.

Determining the role of the copper transporter CTR1 in PERK activity in the activated unfolded protein response

(2) Yair Argon, Ph.D.

Examining the effects of glucolipotoxicity on the activation of the activity of IRE1, a key mediator of the unfolded protein response

(3) Jim Delikatny, Ph.D.

Elucidating the pharmacology properties of JAS239, a novel near-infrared fluorescent probe in the imaging of tumors with increased choline kinase alpha activity

## **Doctoral Thesis**

Advisor: Jim Delikatny, Ph.D. Determining the mechanism of action of JAS239 in the cytotoxicity of cancer cells



# **Courtney Hong**

School: University of Illinois, Urbana-Champaign B.S. Molecular and Cellular Biology & Psychology (2014)

Email: cohong@pennmedicine.upenn.edu

#### Laboratory rotations

<u>(1) Mark Kahn, M.D.</u> *The role of endothelial MEKK3 signaling in embryonic hematopoiesis* <u>(2) Margaret Chou, Ph.D.</u> *Sinonasal sarcoma: pathogenic mechanisms of a novel gender dimorphic cancer* <u>(3) Nancy Speck, Ph.D.</u> *The role of endothelial MEKK3 signaling in embryonic hematopoiesis* 

#### **Doctoral Thesis**

Advisor: Mark Kahn, M.D.

#### **Publications**

Zhang, L., Trushin, S., Christensen, T.A., Tripathi, U., **Hong, C.**, Geroux, R.E., Howell, K.G., Poduslo, J.F., Trushina, E. (2018) Differential effect of amyloid beta peptides on mitochondrial axonal trafficking depends on their state of aggregation and binding to the plasma membrane. *Neurobiol Dis*, doi: 10.1016/j.nbd.2018.02.003.

Lu, Z., **Hong, C.C.**, Kong, G., Assumpção, A.L.F.V., Ong, I.M., Bresnick, E.H., Zhang, J., and Pan, X. (2018) Polycomb Group Protein YY1 Is an Essential Regulator of Hematopoietic Stem Cell Quiescence. *Cell Rep*, doi: 10.1016/j.celrep.2018.01.026.

Assumpção, A.L.F.V., Jark, P.C., **Hong, C.C.**, Lu, Z., Ruetten, H.M., Heaton, C.M., Pinkerton, M.E., Pan, X. (2018) STAT3 Expression and Activity are Up-Regulated in Diffuse Large B Cell Lymphoma of Dogs. *J Vet Intern Med*. doi:10.1111/jvim.14860. Lu, Z., **Hong, C.C.**, Jark, P.C., Assumpção, A.L.F.V., Bollig, N., Kong, G. and Pan, X. (2017) JAK1/2 Inhibitors AZD1480 and CYT387 Inhibit Canine B-Cell Lymphoma Growth

Tang AT, Choi JP, Kotzin JJ, Yang Y, **Hong CC**, Hobson N, Girard R, Zeineddine HA, Lightle R, Moore T, Cao Y, Shenkar R, Chen M, Mericko P, Yang J, Li L, Tanes C, Kobuley D, Võsa U, Whitehead KJ, Li DY, Franke L, Hart B, Schwaninger M, Henao-Mejia J, Morrison L, Kim H, Awad IA, Zheng X, Kahn ML. Nature. 2017 May 10. doi: 10.1038/nature22075.

#### Awards

Supported under Pharmacology T32 Training Grant



# Jack Jacobs

School: Chapman University B.A. Biochemistry and Molecular Biology (2015)

Email: jacojack@pennmedicine.upenn.edu

Laboratory Rotations(1) Steve Thomas, M.D. Ph.D.β2-adrenergic Signaling in Short-term Memory Formation(2) Roderick Eckenhoff, M.D.IV Administration of the Inhaled Anesthetic Sevoflurane and its Photoanalog Azisevoflurane(3) Amita Sehgal, Ph.D.Effects of Sleep and Circadian Rhythms on Glial Metabolism

### **Doctoral Thesis**

Advisor: Amita Sehgal, Ph.D. Identifying the molecular mechanisms responsible for endocannabinoid effects on sleep and seizures

### Publications

Kellie A. Woll, Wesley Peng, Qiansheng Liang, Lianteng Zhi, Jack A. Jacobs, Lina Maciunas, Natarajan Bhanu, Benjamin A. Garcia, Manuel Covarrubias, Patrick J. Loll, William P. Dailey, and Roderic G. Eckenhoff. Photoaffinity Ligand for the Inhalational Anesthetic Sevoflurane Allows Mechanistic Insight into Potassium Channel Modulation. ACS Chem. Biol. 12, 1353–1362 (2017)



# Daniel Jacome

School: Stevens Institute Tech B.S. Chemical Biology (2017)

Email: jacome@pennmedicine.upenn.edu

#### Laboratory Rotations

(1) Robert Mach, Ph.D. Development of Dopamine D3R Selective Ligands (2) Saar Gill, M.D., Ph.D. Optimization of CAR-T 33 (3) Mark Sellmyer, M.D., Ph.D. Small Molecule Sensing of Cell-Cell Interactions **Doctoral Thesis** Advisor: Sellmyer, M.D., Ph.D. Small Molecule Sensing of Cell-Cell Interactions

#### Awards

NIH T32 Pharmacology Training Grant



## Joseph Johnson

School: St. Joseph's University B.S. (2016)

Email: joedward@pennmedicine.upenn.edu

Laboratory Rotations (1) Chang-Yu Hahn, Ph.D. (2) Kelly Jordan Sciutto, Ph.D. (3) Costas Koumenis, Ph.D. (4) David Lynch, Ph.D.

**Doctoral Thesis** Advisor: David Lynch, Ph.D. *The Functions and Role of Frataxin in Friedrich's Ataxia* 



# Nathan Kendsersky

School: University of Pittsburgh B.S. Molecular Biology, Minors in Chemistry and Music (2016)

Email: namich@pennmedicine.upenn.edu

Laboratory Rotations(1) James Shorter, Ph.D.Defining the structural and mechanistic basis for Hsp104 function(2) Klaus Kaestner, Ph.D.Stimulating β-cell proliferation through targeted epigenetic editing(3) John Maris, M.D.Characterizing the specificity of an antibody-drug conjugate in neuroblastoma cells

## **Doctoral Thesis**

Advisor: John Maris, M.D. Credentialing Delta-like ligand 3 as an oncoprotein and immunotherapeutic target in neuroblastoma.

## Publications

Kristopher R Bosse, Pichai Raman, Zhongyu Zhu, Maria Lane, Daniel Martinez, Sabine Heitzeneder, Komal S Rathi, <u>Nathan M Kendsersky</u>, Michael Randall, Laura Donovan, Sorana Morrissy, Robyn T Sussman, Doncho V Zhelev, Yang Feng, Yanping Wang, Jennifer Hwang, Gonzalo Lopez, Jo L Harenza, Jun S Wei, Bruce Pawel, Tricia Bhatti, Mariarita Santi, Arupa Ganguly, Javed Khan, Marco A Marra, Michael D Taylor, Dimiter S Dimitrov, Crystal L Mackall, John M Maris. (2017) "Identification of GPC2 as an oncogene and candidate immunotherapeutic target in high-risk neuroblastoma." Cancer Cell. PMID: 28898695.

Stephanie N Gates, Adam L Yokom, JiaBei Lin, Meredith E Jackrel, Alexandrea N Rizo, <u>Nathan M Kendsersky</u>, Courtney E Buell, Elizabeth A Sweeny, Korrie L Mack, Edward Chuang, Mariana P Torrente, Min Su, James Shorter, Daniel R Southworth. (2017) "Ratchet-like polypeptide translocation mechanism of the AAA+ disaggregase Hsp104." Science. PMID: 28619716



# **Jarrett Lindsay**

School: University of Illinois, Springfield B.S. Biochemistry (2017)

Email: jlinds@pennmedicine.upenn.edu

Laboratory Rotations (1) Donita Brady, Ph.D. Assessing the role of Copper Binding in PKM2 Function (2) Margaret Chou, Ph.D. Uncovering the role of USP6 in Ewing Sarcoma: turning "cold" tumors "hot" (3) John Maris, M.D. Investigating ALCAM as an antibody-drug conjugate target in neuroblastoma

**Doctoral Thesis** Advisor: John Maris, M.D. *Investigating ALCAM as an antibody-drug conjugate target in neuroblastoma* 



# Lumena Louis

School: CUNY, Brooklyn College

Email: lumenalo@pennmedicine.upenn.edu

Laboratory Rotations (1) Margaret Chou, Ph.D. Regulation of Ubiquitin-like Modification by Tre17/USP6 (2) Peter Klein, M.D. Ph.D. Kinetics of Lithium Mediated Inhibition of GSK-3 (3) David Weiner, Ph.D. Exploring IL-36 as a Potential Adjuvant in DNA Vaccines

**Doctoral Thesis** Advisor: David Weiner, Ph.D.



# Dania Malik

School: Stony Brook University B.S. Biochemistry and Economics (2015) MBA in Finance (2016)

Email: daniam@pennmedicine.upenn.edu

#### Laboratory Rotations

(1) Margaret Chou, Ph.D.
Identification of Novel Drug Sensitivities to Target Liposarcoma
(2) David Lynch, M.D., Ph.D.
Frataxin and Its Link to Mitochondrial Function in a Friedreich's Ataxia Mouse Model
(3) Aalim Weljie, Ph.D.
Distinguishing Sleep Related Metabolic Rhythms in Drosophila

## **Doctoral Thesis**

Advisor: Aalim Weljie, Ph.D. Impact of Sleep Deprivation and Impaired Sleep on Metabolic Rhythms in Drosophila

#### Publications

Malik, D. M., Rhoades, S. & Weljie, A. Extraction and Analysis of Pan-metabolome Polar Metabolites by Ultra Performance Liquid Chromatography-Tandem Mass Spectrometry (UPLC-MS/MS). *Bio Protoc* **8**, doi:10.21769/BioProtoc.2715 (2018).

### Awards

NIH Pharmacology T32 Training Grant (2017, 2018)



## **Dylan Marchione**

School: University of Alabama B.S. Biology M.S. Molecular & Cellular Biology (2014)

Email: dyma@pennmedicine.upenn.edu

## Laboratory Rotations

(1) Olivier Berton, Ph.D.

Investigating the role of histone deacetylase 6 in a mouse model of levodopa-induced dyskinesia (2) Ian Blair, Ph.D. Using LC-MS/MS to interrogate mitochondrial metabolism and the glutathione redox buffer system in

Using LC-MS/MS to interrogate mitochondrial metabolism and the glutathione redox buffer system in cultured and primary human cells

(3) Benjamin Garcia, Ph.D.

Using a kinase inhibitor library to interrogate crosstalk between cytoplasmic signaling and histone post-translational modifications

## **Doctoral Thesis**

Advisor: Benjamin Garcia, Ph.D. The role of histone H3 lysine 36 dimethylation in diffuse intrinsic pontine glioma

### Publications

Weinberg DN\*, Papillon-Cavanagh S\*, Chen H, Chen X, Rajagopalan K, Horth C, Yue Y, Nikbakht H, Marchione DM, et al. H3K36me2 recruits DNMT3A and shapes the intergenic DNA methylation landscape. Nature, In review (2018).

Krug B\*, De Jay N\*, Harutyunyan AS, Deshmukh S, Marchione DM, et al. Pervasive H3K27 acetylation leads to ERV expression and a therapeutic vulnerability in H3K27M gliomas. Science, In review (2018).

Harutyunyan AS\*, Krug B\*, Chen H, Papillon-Cavanagh S, Zeinieh M, Deshmukh S, Chen CC, Belle J, Mikael LG, Marchione DM, et al. H3K27M is essential for glioma tumorigenesis and affects H3K27me3 spread from PRC2 binding sites. Science, In review (2018).

Bhoj EJ, Li D, Marchione DM, et al. Germline mutations in Histone 3 Family 3A and 3B cause a novel pediatric neurologic disorder. Nature Communications, In review (2018).

Yuan ZF, Sidoli S, Marchione DM, Simithy J, Janssen KA, Szurgot MR, and Garcia BA. EpiProfile 2.0: A platform for processing epi-proteomics mass spectrometry data. The Journal of Proteome Research, doi: 10.1021/acs.jproteome.8b00133 (2018).

Simithy J, Sidoli S, Yuan ZF, Coradin M, Bhanu NV, Marchione DM, Klein BJ, Bazilevsky GA,

McCullough CE, Magin RS, Kutateladze TG, Snyder NW, Marmorstein R, and Garcia BA. Characterization of scarcely explored histone acylations links chromatin modifications with metabolism. Nature Communications, doi: 10.1038/s41467-017-01384-9 (2017).

Papillon-Cavanagh S\*, Lu C\*, Gayden T, Mikael LG, Bechet D, Karamboulas C, Ailles L, Karamchandani J, Marchione DM, Garcia BA, Weinreb I, Goldstein D, Lewis PW, Dancu OM, Dhaliwal S, Stecho W, Howlett CJ, Mymryk JS, Barrett JW, Nichols AC, Allis CD, Majewski J, and Jabado N. Impaired H3K36 methylation defines a subset of head and neck squamous cell carcinomas. Nature Genetics, doi:10.1038/ng.3757 (2017).

Lin S, Yuan ZF, Han Y, Marchione DM, and Garcia BA. Preferential phosphorylation on old histones during early mitosis in human cells. Journal of Biological Chemistry, doi: 10.1074/jbc.M116.726067 (2016).

Zhao X, Lorent K, Wilkins B, Marchione DM, Gillespie K, Waisbound-Zinman O, So J, Koo KA, Shin D, Porter J, Wells RG, Blair IA, and Pack M. Glutathione antioxidant pathway activity and reserve determine toxicity and cell-type specificity of the biliary toxin biliatresone. Hepatology, doi:10.1002/hep.28603 (2016).

Worth AJ\*, Marchione DM\*, Parry RC, Wang Q, Gillespie KP, Sallant N, Simms C, Mesaros CA, Snyder NW, and Blair IA. LC-MS analysis of human platelets as a platform for studying mitochondrial metabolism. Journal of Visualized Experiments, e53941, doi:10.3791/53941 (2016).

#### Awards

Clinical & Translational Science Award - NIH TL1TR001880 (Fall 2017) US Human Proteome Organization Travel Stipend (Fall 2017)

#### Presentations

"Altered chromatin-reader interactions in histone-mutant pediatric gliomas." The 65th Annual Conference of the American Society for Mass Spectrometry, Indianapolis IN. (06/07/2017) [Poster]

"Histone H3 mutations drive aberrant chromatin-reader interactions in diffuse intrinsic pontine glioma." The 13th Annual Conference of the United States Human Proteome Organization, San Diego CA. (3/20/2017) [Oral]

"Epigenetic dysregulation in histone H3 K27M mutant pediatric glioblastoma." Mahoney Institute for Neurosciences 33rd Annual Symposium, The University of Pennsylvania, Philadelphia PA. (1/10/2017) [Oral]

"The role of histone H3 lysine 36 dimethylation in diffuse intrinsic pontine glioma." The 32nd Annual University of Pennsylvania Pharmacology Graduate Group Student Symposium, The College of Physicians of Philadelphia, Philadelphia PA. (10/13/2016) [Poster]

"LC-MS/MS of human platelets as a platform for studying mitochondrial metabolism." Metabolism: Fueling Translational Research Symposium, Harvard Medical School, Boston MA. (10/10/2015) [Oral]

"LC/MS reveals distinct effects of menadione and 1,4-dimethoxy-2,3-napthoquinone." The 63rd

Annual Conference of the American Society for Mass Spectrometry, St Louis MO. (06/02/2015) [Poster]



## John Maurer

School: St. Louis University B.S. Psychology (2014)

Email: jmau@pennmedicine.upenn.edu

#### Laboratory Rotations

(1) Mariella De Biasi, Ph.D. Effects of e-cigarette flavorings on oral nicotine self-administration (2) Elizabeth Heller, Ph.D. Neuroepigenetic remodeling in cocaine addiction (3) Shinjae Chung, Ph.D. Activity of preoptic area GABAergic neurons during sleep

#### **Doctoral Thesis**

Advisor: Dr. Shinjae Chung Neuronal and homeostatic regulation of sleep by the preoptic area and tuberomammillary nucleus

#### **Publications**

J. J. Maurer and H.D. Schmidt (2019). "Nicotine addiction and alpha4beta2\* nicotinic acetylcholine receptors". Book chapter in "The Neuroscience Of Nicotine: Mechanisms and Treatment". Elsevier.



# **Claire Meurice**

School: University of Michigan B.S. Neuroscience Honors (2013)

Email: meclaire@pennmedicine.upenn.edu

#### **Laboratory Rotations**

(1) Steven Thomas, M.D. Ph.D. Investigating the role of norepinephrine and histamine in aversive memory retrieval (2) Kelly Jordan-Sciutto, Ph.D. Contributions of HIV Antiretroviral Therapy to the Neurotoxicity in HAND and Identifying Potential Targets for Adjunct Therapies (3) Paul Axelsen, M.D. Thioflavin T: Does it bind to fibrils or defects in fibrils?

#### **Doctoral Thesis**

Advisor: Kelly Jordan Sciutto, Ph.D. *Mechanisms of E2F1-mediated synaptic damage and maintenance in HIV-associated neurocognitive disorders* 

We are interested in the role that the transcription factor E2F1 plays in the development of HIVassociated neurocognitive disorders (HAND). In a variety of neurodegenerative diseases, E2F1 levels are increased, and in an in vitro model of HIV-induced neurotoxicity, calpain-mediated truncation of E2F1 precedes neuronal death. Therefore we aim to identify the protein domain and/or necessary binding partners behind E2F1-mediated maintenance of synaptodendritic health using primary neuronal/neuroglial cultures and a variety of molecular biology techniques.

#### Publications

Kumar, V., Ridzwan, I. E., Grivas, K., Lewis, J. W., Clark, M. J., Meurice, C., Jimenez-Gomez, C., Pogozheva, I., Mosberg, H., Traynor, J.R., & Husbands, S. M. (2014). Selectively promiscuous opioid ligands: discovery of high affinity/low efficacy opioid ligands with substantial nociceptin opioid peptide receptor affinity. Journal of medicinal chemistry,57(10), 4049-4057.

Jackson D.P., Ting J.H., Pozniak P.D., Meurice C, Schleidt S.S., Dao A., Lee A.H., Klinman E., & Jordan-Sciutto K.L. (2018). Identification and characterization of two novel alternatively spliced E2F1 transcripts in the rat CNS. Molecular and Cellular Neuroscience, [Epub ahead of print].

McPherson, K., Leff, E., Li M., Meurice C., Tai S., Traynor J., and Ingram S. (2018). Regulators of G protein Signaling (RGS) proteins promote receptor coupling to G protein-coupled inwardly-rectifying potassium (GIRK) channels. Journal of Neuroscience, [Epub ahead of print].

#### Awards

Pharmacology T32 Training Grant



# **Nick Minutolo**

School: University of Conneticut B.S. Molecular and Cell Biology (2012) M.S. Molecular and Cell Biology (2012)

Email: minutolo@pennmedicine.upenn.edu

#### Laboratory Rotations

(1) Andrew Tsourkas, Ph.D.
Site specific attachment of a chemical cross-linkers to the antibody Fc region
(2) Robert Levy, M.D.
Determining the Optimal Coating Method for Gene Eluting Stents
(3) Daniel Powell, Jr., Ph.D.
Redirecting gene-engineered T cells through covalent attachment of targeting ligands to a universal immune receptor

#### **Doctoral Thesis**

Advisor: Daniel Powell, Jr., Ph.D. Redirecting gene-engineered T cells through covalent attachment of targeting ligands to a universal immune receptor

**Presentations** Poster and Oral Presentation, Translational Research Cancer Centers Consortium 2016

#### Awards

2016 Society for Immunotherapy of Cancer Young Investigators Travel Award



## Jessica Murray

School: College of William and Mary B.S. Biology and Chemistry (2013)

Email: murrayj@pennmedicine.upenn.edu

#### **Laboratory Rotations**

(1) Trevor Penning, Ph.D. Metabolic Activation of Nitroarenes Catalyzed by Aldo-keto Reductases (2) Rebecca Simmons, M.D. Epigenetic Regulation of BDNF following Prenatal Lead Exposure (3) Marilyn Howarth, M.D. Carcinogenic Risk Assessment for Eastwick, PA: Analysis of Air Toxics and the Clearview Landfill

#### **Doctoral Thesis**

Advisor: Trevor Penning, Ph.D.

The role of human aldo-keto reductases and Nrf2 signaling in the bioactivation of polycyclic aromatic hydrocarbons (PAHs) and their nitrated derivatives (nitro-PAHs).

#### Awards/Honors

Solomon Erulkar Traveling Fellowship Celebrating Women in Toxicology, Society of Toxicology Graduate Student Travel Award, Society of Toxicology ACS TOXI Graduate Student Poster Award, 1st Place PhRMA Pre-Doctoral Fellowship in Pharmacology/Toxicology NIEHS T32 Training Grant in Environmental Health Sciences ACS TOXI Travel Award

### Publications

Murray JR, Penning TM. "Carcinogenic polycyclic aromatic hydrocarbons." Comprehensive Toxicology, 3e. Charlene McQueen (Ed.). Elsevier, 2017, 3e. DOI: 10.1016/b978-0-12-801238-3.95691-5.

Murray JR, Mesaros C, Arlt VM, Seidel A, Blair IA, Penning TM. "Role of Human Aldo-Keto Reductases in the Metabolic Activation of the Carcinogenic Air Pollutant 3-Nitrobenzanthrone." Submitted to Chemical Research in Toxicology., Aug 2018.

### Selected Abstracts

Murray JR, Huang M, Mesaros C, Blair IA, and Penning TM. Competing Roles of Human Aldo-keto Reductases and NADPH:Quinone Oxidoreductase in the Bioactivation of 3-Nitrobenzanthrone – Kinetic and Expression Analyses. Society of Toxicology Annual Meeting, San Antonio, TX; March 2018. (Poster Presentation)

Murray JR, Huang M, Mesaros C, Arlt VM, El-Bayoumy K, Blair IA, and Penning TM. Nrf2-Keap1 Signaling and Implications for the Metabolic Activation of Nitroarenes. American Chemical Society, Washington, DC; August 2017. (Poster Presentation)

- Also presented at Cellular and Molecular Mechanisms of Toxicity: Gordon Research Conference, Andover, NH; August 2017.

Murray JR, Huang M, Mesaros C, Arlt VM, El-Bayoumy K, Seidel A, Blair IA, and Penning TM. Nrf2-Keap1 Signaling and Implications for the Metabolic Activation of Nitroarenes. Society of Toxicology Annual Meeting, Baltimore, MD; March 2017. (Poster Presentation)

Murray JR, Howarth MV. Evaluating Cancer Risks for Eastwick, PA: Analysis of Air Toxics and the Clearview Landfill. Community Outreach and Engagement Core (COEC) Stakeholder Advisory Board Meeting. Philadelphia, PA; January, 2016. (Oral Presentation)

Murray JR, Huang M, Mesaros C, Arlt VM, El-Bayoumy K, Blair IA, and Penning TM. Metabolic Activation of Nitroarenes by Human Aldo-Keto Reductases (AKR1C1-AKR1C3). 11th Annual Symposium for the Center of Excellence in Environmental Toxicology. Philadelphia, PA; June, 2016. (Poster Presentation)

Murray JR, Zang T, Arlt VM, Schmeiser HH, Mesaros C, Blair IA, and Penning TM. Metabolic activation of 3–nitrobenzanthrone by aldo–keto reductases (AKR1C1—AKR1C4): evidence for 6-electron reduction. 250th American Chemical Society National Meeting. Boston, MA; August, 2015. (Oral Presentation)

Murray JR, Huang M, Zang T, Arlt VM, Schmeiser HH, and Penning TM. Metabolic activation of 3nitrobenzanthrone by human aldo-keto reductases (AKR1C1-AKR1C4). American Association for Cancer Research Annual Meeting. Philadelphia, PA; April, 2015. (Poster Presentation)



## **Rebecca Myers**

School: Rutgers University B.S. Biological Sciences, Minor in Psychology (2014)

Email: rmy@pennmedicine.upenn.edu

#### **Laboratory Rotations**

(1) Patrick Viatour, Pharm.D. Ph.D.
The cell of origin for hepatocellular carcinoma
(2) Peter Klein, M.D. Ph.D.
APC regulation of GSK-3 in colon cancer and FAP
(3) XianXin Hua, M.D. Ph.D.
Possible interactions between menin and the AMPK pathway

#### **Doctoral Thesis**

Advisor: Peter Klein, M.D. Ph.D. APC Regulation of GSK-3: A Novel Role for APC

#### Publications

Jensen HA, Bunaciu RP, Ibabao CN, **Myers R**, Varner JD, Yen A. Retinoic Acid Therapy Resistance Progresses from Unilineage to Bilineage in HL-60 Leukemia Blasts. *PloS One*. 9(6):e98929.doi:10.1371/journal.pone. 0098929. 2014 June 12.

#### Presentations

Presented a poster "APC Regulation of GSK-3" at the 17<sup>th</sup> Annual Center for Digestive, Liver & Pancreatic Medicine Retreat- September 2016



# Sofya Osharovich

School: West Chester University of Pennsylvania B.S. Biology (2013)

Email: sofyaosh@pennmedicine.upenn.edu

### Laboratory Rotations

(1) James Shorter, Ph.D.
Buffering aberrant oncogene activity with potentiated Hsp104 variants
(2) Ian Blair, Ph.D.
Dimethyl fumarate forms adducts with GSH, depleting intracellular GSH stores in SH-SY5Y cells
(3) Edward J. Delikatny, Ph.D.
Near-Infrared Fluorescent Choline Kinase α Inhibitors for Lung Cancer Imaging and Therapy

## **Doctoral Thesis**

Advisor: Edward J. Delikatny, Ph.D.

#### Publications

Liebov B, Arroyo A, Rubtsova N, Osharovich S, Delikatny J, Popov A. "Non-Protecting Group Synthesis of a Phospholipase C Activatable Probe with an Azo-Free Quencher." ACS Omega. 3:6 (2018): 6867–6873.

#### Awards

Magna Cum Laude Scientific Abstract Award, Pendergrass Symposium, University of Pennsylvania Student Travel Stipend, World Molecular Imaging Congress



## **Theresa Patten**

School: Wake Forest University B.S. Chemistry (2014)

Email: tpatten@pennmedicine.upenn.edu

#### Laboratory Rotations

(1) Julie Blendy, Ph.D.
OPRM1 A118G SNP: Effects on the rewarding value of food and weight gain during nicotine withdrawal
(2) Mariella De Biasi, Ph.D.
Role of α5-containing nicotinic receptors in nicotine/cocaine co-dependence
(3) Tracy Bale, Ph.D.
Effects of early prenatal stress on placental permeability and programming of offspring exosomes

### **Doctoral Thesis**

Advisor: Mariella De Biasi, Ph.D. The short and long-term effects of e-cigarette flavorants on nicotine reward

### Publications

Blume, L. C., Patten, T., Eldeeb, K., Leone-Kabler, S., Ilyasov, A. A., Keegan, B. M., ... Howlett, A. C. (2016). Cannabinoid Receptor Interacting Protein (CRIP) 1a competition with  $\beta$ -arrestin for CB1 receptor binding sites. Mol Pharmacol. 2017 Feb;91(2):75-86. PMID: 27895162

#### **Poster Presentations**

De Biasi, M., Patten T., Perez, E. Influence of flavor additives on e-cigarette consumption during adolescence: development and validation of a mouse model. Society for Research on Nicotine and Tobacco Annual Meeting (2016).

Patten, T.; Perez, E.; Fleites, V.; Johnston S.H.; McLaughlin, I.; De Biasi, M. Sweet flavorants enhance adolescent nicotine reward: a mouse model to study e-cigarettes. Psychiatry Research Day. Philadelphia, PA (2016)

Patten, T.; Perez, E.; Fleites, V.; Johnston S.H.; McLaughlin, I.; De Biasi, M. Sweet flavorants enhance adolescent nicotine reward: a mouse model to study e-cigarettes. Annual PGG Student Symposium. Philadelphia, PA (2016)

Patten T.; Perez, E.; De Biasi, M. Influence of flavor additives on adolescent nicotine reward: development of a mouse model using commercial e-cigarettes. Annual PGG Student Symposium. Philadelphia, PA (2017)

Patten T.; Perez, E.; De Biasi, M. Influence of flavor additives on adolescent nicotine reward: development of a mouse model using commercial e-cigarettes. American College of Neuropsychopharmacology Annual Meeting (2017)

#### Awards

2017 - Chapter Recognition Award for Student Travel - Association for Women in Science Philadelphia

#### **Oral Presentations/Lectures**

April 2017 - Guest Lecturer; Rutgers University-Camden; "A History and Review of Tobacco, Ecigarettes, and Flavored Products"

June 2018 - Guest Lecturer; Bryn Mawr College – STEM Posse Mini Symposium; "My journey through science and the study of flavored e-cigarettes using a mouse model"



## **Ross Pirnie**

School: Bucknell University B.S. Biochemistry/Cell Biology (2017)

Email: rpirnie@pennmedicine.upenn.edu

#### **Laboratory Rotations**

<u>(1) Aalim Weljie, Ph.D.</u> Detecting the Metabolic Effects of Sleep Restriction (2) Ian Blair, Ph.D. Proteomics Investigation of HSA Cysteine-Drug Adduct Formation (3) Robert Levy, M.D. Optimization of Gene Therapy Vector Delivery from Metal Stents

#### **Doctoral Thesis**

Advisor: Dr. Ian Blair Understanding the Mechanisms of Drug Induce Liver Injury



## **Izmarie Poventud-Fuentes**

School: University of Puerto Rico, Mayagüez B.S. Industrial Biotechnology (2013)

Email: ipov@pennmedicine.upenn.edu

#### Laboratory Rotations

(1) Richard Assoian, Ph.D
Role of extracellular matrix stiffness on the regulation of NF-κB
(2) Lawrence Brass, M.D. Ph.D.
Characterization of Tissue Factor localization in blood vessels
(3) Paul Janmey, Ph.D.
Platelet adhesion and spreading in response to different ligands and stiffness

#### **Doctoral Thesis**

Advisor: Lawrence Brass, M.D. Ph.D.

Project description:

Development of a microfluidic system to model and study hemostasis using human blood Studies in our laboratory and others have shown that upon vessel injury in mice, a gradient of the agonists is generated within the vessel wall that result in a heterogeneous architecture of the hemostatic plug. Although the studies in mice give us valuable information, the platelet biology of mice and humans is similar but not the same. There is a need to understand how much of the observations in in vivo systems apply to human blood.

The goal of my project is to develop a microfluidic system with the essential components to recapitulate key features of hemostasis using human blood to investigate clot consolidation, and the distribution of mechanical forces during hemostatic response.

#### Awards

T32 Predoctoral Training Grant in Pharmacology (2015-2017) T32 Hematology Clinical Research Training Grant (2017-present)

#### Publications

Welsh JD, Poventud-Fuentes I, Sampietro S, Diamond SL, Stalker TJ, and Brass LF. (2017), Hierarchical organization of the hemostatic response to penetrating injuries in the mouse microvasculature. J Thromb Haemost, doi: 10.1111/jth.13600

Matsuyama S, Palmer J, Bates A, **Poventud-Fuentes I**, Wong K, Ngo J, and Matsuyama M. (2016) Bax-induced apoptosis shortens the life span of DNA repair defect Ku70-knockout mice by inducing

emphysema. Exp Biol Med, 241(12): 1265-71.

Ngo J, Matsuyama M, Kim C, **Poventud-Fuentes I**, Bates A, Siedlak SL, Lee H-g, Doughman YQ, Watanabe M, Liner A, Hoit B, Voelkel N, Gerson S, Hasty P, and Matsuyama S. (2015) Bax deficiency extends the survival of Ku70 knockout mice that develop lung and heart diseases. *Cell Death and Disease*, 6: e1706.

Rao W, Zhang W, **Poventud-Fuentes I**, Wang Y, Lei Y, Weekes B, Li C, Lu X, Yu J, and He X. (2014) Thermally responsive nanocapsule-encapsulated curcumin and its combination with mild hyperthermia for enhanced cancer cell destruction. *Acta Biomater*, 10 (2): 831-842.

Cui M, Naczynski DJ, Zevon M, Griffith CK, Sheihet L, **Poventud-Fuentes I**, Chen S, Roth CM, and Moghe PV. (2013) Multifunctional albumin nanoparticles as combination drug carriers for intratumoral chemotherapy. *Adv Healthc Mater*, 2: 1236–1245.

#### **Recent Presentations**

Poster: "Development of a microfluidic platform to assess thrombin generation in FVIII deficient whole blood under flow conditions". Hemostasis Gordon Research Seminar and Conference, Waterville Valley, NH. July 2018.

Talk: "Development of a microfluidic system to understand the interplay of platelets and coagulation factors in the process of hemostasis". Platelet Club, University of Pennsylvania, Philadelphia, PA. March 2018.

Talk: "Development of an in vitro system to model human hemostatic response". Systems of Pharmacology and Translational Therapeutics (SPATT) Seminar, University of Pennsylvania, Philadelphia, PA. January 2018.

Poster: "Synthetic blood vessels as tools to understand hemostasis in humans". 33rd Annual Student Symposium, Pharmacology Graduate Group, College of Physicians of Philadelphia, Philadelphia, PA. November 2017



## Laura Puentes

School: University of Central Florida B.Sc Biotechnology

School: University of Oxford M.Sc Pharmacology

Email: lpuentes@pennmedicine.upenn.edu

Laboratory rotations (1) Robert H. Mach, Ph.D. Targeting PARP-1 to deliver Alpha-Particles to Cancer Chromatin (2) Vladimir Muzykantov, M.D. Ph.D. Red Blood Cell Hitchhiking with Affinity Ligands (3) Eric Brown, Ph.D. Identifying ATRi Dependence on PARP-1 Expression

### **Doctoral Thesis**

Advisor: Robert H. Mach, Ph.D.

The goal of my project is to evaluate PARP-1-specific PET tracers to image and quantify PARP-1 expression levels in glioblastoma and measure target engagement of small molecule PARP inhibitors in real time.

#### Publications

Reilly, S., Puentes, L., Hsieh, C., Makvandi, M. and Mach, R. (2018). Altering Nitrogen Heterocycles of AZD2461 Affords High Affinity PARP Inhibitors with Improved P-glycoprotein Properties. ACS Omega, 3(8), pp.9997-10001.

Reilly, S., Puentes, L., Wilson, K., Hsieh, C., Weng, C., Makvandi, M. and Mach, R. (2018). Examination of Diazaspiro Cores as Piperazine Bioisosteres in the Olaparib Framework Shows Reduced DNA Damage and Cytotoxicity. Journal of Medicinal Chemistry, 61(12), pp.5367-5379.

Goldblatt, Greg et al. (2015). Site-Specific Structural Changes in Unmodified and Pyroglutamylated Amyloid Beta Peptide by Isotope-Edited FTIR. Biophysical Journal, 108 (2), pp. 524a.

Presentations (Poster):

Puentes L. Evidence of PARP-1 dependent cytotoxic agents with low target affinity. Poster presented at American Association for Cancer Research Annual Meeting; 2018; Chicago, IL.

Puentes L. Targeting PARP-1 to deliver alpha-particles to cancer chromatin.. Poster presented at American Association for Cancer Research Annual Meeting; 2017; Washington D.C.

### Awards



# Natalia Quijano Cardé

School: University of Puerto Rico, Mayagüez B.S. Industrial Biotechnology (2015)

Email: qnatalia@pennmedicine.upenn.edu

#### **Laboratory Rotations**

(<u>1</u>) <u>Mariella De Biasi, Ph.D</u> Role of kainate receptor antagonism in the treatment of alcohol dependence (<u>2</u>) <u>R. Christopher Pierce, Ph.D.</u> Validation of a mouse model to study cocaine-related epigenetic marks in the nucleus accumbens (<u>3</u>) <u>Elizabeth Heller, Ph.D.</u> Cocaine self-administration paradigm to study neuroepigenetics of cocaine addiction in mice

### **Doctoral Thesis**

Advisor: Mariella De Biasi, Ph.D. Effect of CHRNA5 Genetic Variation on Responses to Ethanol and Nicotine

#### Publications

Perez E, **Quijano Cardé N**, De Biasi M (2015). Nicotinic mechanisms modulate ethanol withdrawal and modify time course and symptoms severity of simultaneous withdrawal from alcohol and nicotine. *Neuropsychopharmacology* **40**: 2327-2336.



## **Nicole Robles-Matos**

School: University of Puerto Rico, Rio Piedras B.S. Chemistry (2017)

Email: nroble@pennmedicine.upenn.edu

## Laboratory Rotations

<u>(1) Trevor Penning, Ph.D.</u> Expression of Estrogen Receptors and the Effect of Estradiol in Mesothelioma Cell Growth (2) Rebecca Simmons, M.D. Effects of Maternal Bisphenol A Exposure on Mouse Pancreatic Immune System (3) Marisa Bartolomei, Ph.D. Investigating the Mechanisms Involved in Adverse Health Effects Following In Utero EDC Exposure

## **Doctoral Thesis**

Advisor: Marisa Bartolomei

Our lab wants to explore in more depth gene-environment interactions in the development of diseases. Specifically, our aim is to investigate how an adverse early life event, like environmental exposure to Endocrine Disrupting Chemicals (EDCs), can lead to an increase risk to develop diseases later in life. Since the exact molecular mechanisms linking an adverse early life event to adult diseases remain unclear, we are considering epigenetic mechanisms as potential mechanisms driving the adult phenotypes since epigenetics can be altered by the exposure to EDCs like BPA and DEHP. Currently, project focuses on the effects of maternal exposure to BPA and DEHP in metabolic, reproductive, neurological and skeletal outcomes in the offspring during adulthood. The ultimate goal of this project is to better understand the effects of prenatal EDCs exposure and the mechanisms through which they work to improve our knowledge of the risks to human health.

### Awards

CEET T32 Training Grant in Environmental Health Sciences



## Laura Romano

School: Rutgers University B.S. Biochemistry (2015)

Email: lromano@pennmedicine.upenn.edu

#### **Laboratory Rotations**

(1) Jeffrey Field, Ph.D.
Potential Role Of The Pak Inhibitor, IPA-3, To Induce Oxidative Stress
(2) Benjamin Garcia, Ph.D.
Potential Epigenetic Role Of Oral Contraceptive-Mediated Protection Against High Grade Serous
Ovarian Carcinoma
(3) Park Cho-Park, M.D., Ph.D.
Mapping the Binding Interaction Between PI31 and TDP-43

#### **Doctoral Thesis**

Dr. Park Cho-Park



# **Chris Roselle**

School: Ithaca College BS Biochemistry (2008)

School: Lehigh University MS Chemistry (2015)

E-mail: croselle@pennmedicine.upenn.edu

#### **Laboratory Rotations**

(1) Mitchell Lazar, M.D. Ph.D.
Effects of a non-circadian light schedule on hepatic lipid metabolism
(2) Carl June, M.D. Ph.D.
Effect of Δ133p53 on CAR T cell proliferation and senescence
(3) Roger Greenberg, M.D. Ph.D.
Identifying New Genetic Vulnerabilities in BRCA-mutant Cancers

#### **Doctoral Thesis**

Advisor: Carl June, M.D. Ph.D "Investigating the role of  $\Delta$ 133p53 $\alpha$  in improving the cytotoxicity and functional persistence of chimeric antigen receptor T cells"

#### Publications

Roselle C, Verch T, Shank-Retzlaff M. "Mitigation of Microtiter Plate Positioning Effects Using a Block Randomization Scheme." Analytical and Bioanalytical Chemistry (2016)

Verch T, Roselle C, Shank-Retzlaff M. "Reduction of Dilution Error in ELISAs Using an Internal Standard." Bioanalysis (2016)

Roselle, C., et al., "Evaluation of a digital dispenser for direct curve dilutions in a vaccine potency assay." J. Immunol. Methods (2017)



# Lindsay Roth

School: Smith College B.A. Biochemistry (2015)

E-mail: rothlind@pennmedicine.upenn.edu

## Laboratory Rotations

(1) Julie Blendy, Ph.D. Multigenerational Effects of Parental Morphine Exposure (2) Kelly Jordan-Sciutto, Ph.D. and Judith Grinspan, Ph.D. The Effect of Antiretroviral Therapies on Oligodendrocyte Growth and Maturation (3) Roderich Eckenhoff, M.D. Structure-Activity Relationship of Dexmedetomidine and Characterization of Photoaffinity Ligands

#### **Doctoral Thesis**

Kelly Jordan-Sciutto & Judith Grinspan. Multiple projects examining the effects of HIV and ART drugs on Oligodendrocyte Maturation. Projects focus on the role of the integrated stress response, stress granule formation and dynamics and the role of RNA-binding protein, TDP-43, in these processes.



## Lauren Shaw

School: University of Pennsylvania B.S. Biochemistry (2017)

Email: lashaw@pennmedicine.upenn.edu

Laboratory Rotations (1) Julie Blendy, Ph.D. Neurobiological mechanisms of early opioid exposure (2) Karin Eisinger, Ph.D. Mechanistic studies of soft tissue sarcoma metastasis (3) Daniel Powell, Ph.D. R Redirecting gene-engineered T-cells through attachment of targeting ligands to universal immune receptors

#### **Doctoral Thesis**

Dr. Daniel Powell, Development of universal immune receptors



# Monica Thapaliya

School: Claflin University B.S. Biochemistry/Mathematics (2016)

Email: thmonica@pennmedicine.upenn.edu

Laboratory Rotations (1) Margaret Chou, Ph.D. (2) Park Cho-Park, M.D., Ph.D. (3) Hydar Ali, Ph.D. and Rebecca Simmons, M.D.

**Doctoral Thesis** Advisor: Dr. Hydar Ali, Ph.D.



## **Jerrick To**

College of Wooster B.A. Biochemistry and Molecular Biology (2017)

Email: totsun@pennmedicine.upenn.edu

## Laboratory Rotations

<u>(1) Saar Gill, M.D., Ph.D.</u> Development of anti-IL1RAP CAR T Cells (2) Dmitry Gabrilovich, M.D., Ph.D. Lipid Regulation of Suppressive Function in PMN-MDSCs (3) Malay Haldar, M.D., Ph.D. Effect of Retinoic Acid on Antigen-Presenting Cells in Solid Tumors

## **Doctoral Thesis**

Advisor: Malay Haldar, M.D., Ph.D.



# Ryan von Kleeck

School: Franklin and Marshall College B.S. Biochemistry and Molecular Biology (2015)

Email: ryanvon@pennmedicine.upenn.edu

Laboratory Rotations (1) Richard Assoian, Ph.D. NFKB's role in the stiffness dependent expression of COX2 (2) Costas Koumenis, Ph.D. MTHFD2 and SHMT2: proteins critical for survival in Myc driven tumors (3) Patrick Seale, Ph.D. Regulation of UCP1 by Early B-Cell Factor 2

**Doctoral Thesis** Advisor: Richard Assoian, Ph.D. Arterial mechanics in Hutchinson-Gilford Progeria Syndrome

#### Publications

The two SAMP repeats and their phosphorylation state in Drosophila Adenomatous polyposis coli-2 play mechanistically distinct roles in negatively regulating Wnt signaling. *Mol Biol Cell* (2015). Kunttas-Tatli E, **Von Kleeck RA**, Greaves BD, Vinson D, Roberts DM, McCartney BM.

The Poly(ADP-ribose) Polymerase Enzyme Tankyrase Antagonizes Activity of the β-Catenin Destruction Complex through ADP-ribosylation of Axin and APC2. *J. Biol Chem* (2016). Croy HE, Fuller CN, Giannotti J, Robinson P, Foley AV, Yamulla RJ, Cosgriff S, Greaves BD, **von Kleeck RA**, An HH, Powers CM, Tran JK, Tocker AM, Jacob KD, Davis BK, Roberts DM.

#### Awards

Pharmacology T32 Training Grant



# Amber Wang

School: National Taiwan University B.S. Pharmacy (2014)

Email: wamber@pennmedicine.upenn.edu

#### **Laboratory Rotations**

(1) Kelly Jordan-Sciutto, Ph.D. Assessing potential neurotoxicity of antiretroviral therapy (2) Klaus Kaestner, Ph.D. Identifying key regulators of liver regeneration (3) Mitchell Lazar, M.D. Ph.D. Developing assay of transposase-accessible chromatin with high-throughput sequencing (ATACseq) in the liver

#### **Doctoral Thesis**

Advisor: Klaus Kaestner, Ph.D. Cell-type-specific expression profiling of repopulating hepatocytes

#### Publications

1. Postnatal DNA demethylation and its role in tissue maturation. Reizel Y, Sabag O, Skversky Y, Spiro A, Steinberg B, Bernstein D, Wang A, Kieckhaefer J, Li C, Pikarsky E, Levin-Klein R, Goren A, Rajewsky K, Kaestner KH, Cedar H. Nat Commun. 2018 May 23;9(1):2040.

2. TRAP-seq identifies cystine/glutamate antiporter as a driver of recovery from liver injury. Wang AW, Wangensteen KJ, Wang YJ, Zahm AM, Moss NG, Erez N, Kaestner KH. J Clin Invest. 2018 Jun 1;128(6):2297-2309.

3. Combinatorial genetics in liver repopulation and carcinogenesis with a novel in vivo CRISPR activation platform. Wangensteen KJ, Wang YJ, Dou Z, Wang AW, Mosleh-Shirazi E, Horlbeck MA, Gilbert LA, Weissman JS, Berger SL, Kaestner KH. Hepatology. 2017 Nov 1. doi: 10.1002/hep.29626. [Epub ahead of print]

#### Awards

1. Travel Award. FASEB Science Research Conference on Fundamental Biology and Pathophysiology of the Liver. 2018

2. Ruth L. Kirschstein National Research Service Award (NRSA) Individual Predoctoral Fellowship (F31DK113666), National Institute of Diabetes and Digestive and Kidney Diseases. 2017-present

- 3. Biomedical Graduate Studies Travel Grant, University of Pennsylvania. 2015, 2016, 2017
- 4. Presidential Poster of Distinction Award, AASLD The Liver Meeting. 2016

5. Predoctoral Training Grant in Pharmacology (T32GM008076), University of Pennsylvania. 2016-2017

#### **Oral Presentations**

TRAP-seq identifies cystine/glutamate antiporter as a driver of recovery from liver injury. Wang AW, Wangensteen KJ, Wang YJ, Zahm AM, Moss NG, Erez N, Kaestner KH. FASEB Science Research Conference on Fundamental Biology and Pathophysiology of the Liver. 2018



# **Katherine Webb**

School: University of Pittsburgh B.S. Neuroscience (2017)

Email: katwebb@pennmedicine.upenn.edu

## Laboratory Rotations

(1) Wade Berrentini, M.D., Ph.D.
L1 Retrotransposition and Cocaine Addiction
(2) Mariella De Biasi, Ph.D.
Inflammation in the Medial habenula- Interpeduncular Nucleus Axis and Alcohol Use Disorder
(3) Elizabeth Heller, Ph.D.
The Epigenetics of Cocaine Addiction - Elucidating a Role for Splice Factors

### **Doctoral Thesis**

Advisor: Mariella De Biasi, Ph.D.

Using a novel micro drive system for in-vivo tetrode recording to characterize neuronal activity in the Medial Habenula and use this tool to understand the neuroadaptations induced in this circuitry owing to nicotine exposure and nicotine withdrawal.

### Awards

T32 Pharmacology Training Grant


### Khadija Wilson

School: Brooklyn College B.S. Biology (2017)

Email: wilsonkh@pennmedicine.upenn.edu

### Laboratory Rotations

(1) Benjamin Garcia, Ph.D.
 Characterization of A549 multicellular tumor spheroid's proteome and histone post translational modifications using MS
 (2) Robert Mach, Ph.D.
 In silico docking analysis of non-selective and selective dopamine D2/D3 receptor radioligands
 (3) Frances E. Jensen, M.D., FACP
 Characterization of mouse hippocampal proteome post-seizure using MS

### **Doctoral Thesis**

Advisory: Benjamin A. Garcia, Ph.D.

My project aims to determine how mutations of the histone variant, H3.3, affects neurodevelopment.



### Gabriela Witek

School: Stony Brook University B.S. Pharmacology (2016)

E-mail: gwitek@pennmedicine.upenn.edu

### Laboratory Rotations

<u>(1) Yaël Mossé, M.D.</u> Optimization of Organoid Primary Cultures from Neuroblastoma Patient-derived Xenografts <u>(2) Jeffrey Michael Field, Ph.D.</u> Role of Polo-like Kinase 1 inhibitors effect on NF1 and NF2 Malignant Peripheral Nerve Sheath Tumor Cell Lines <u>(3) Ravi Radhakrishnan, Ph.D.</u> Understanding Drug Resistance through Docking and Molecular Dynamics Simulations

### **Doctoral Thesis**

Advisor: Yaël Mossé, M.D. Elucidating the role of Anaplastic Lymphoma Kinase signaling in Neuroblastoma

### Publications

Guo, J., Grovola, M. R., Xie, H., Coggins, G. E., Duggan, P., Hasan, R., Juang, J., Lin, D. W., Song, C., **Witek, G. M.**, Berritt, S., Schultz, D. C., Field, J. (2017). Comprehensive pharmacological profiling of neurofibromatosis cell lines. American Journal of Cancer Research, 7(4), 923–934.



**Doctoral Thesis** Advisor: David Weiner, Ph.D.

### **Ziyang Xu**

School: Northwestern University B.A. (2015)

Email: zxu@wistar.org

### DNA encoded HIV vaccine

### Presentations

Oral presentation at 2018 ISV (pending, Atlanta Georgia)

### Publications

"Synthetic DNA Delivery by Electroporation Promotes Robust in vivo Sulfation of Broadly Neutralizing anti-HIV Immunoadhesin eCD4-Ig"; EBioMedicine, 2018 (in revision)

The Pharmacology Graduate Group's



**35th Annual Student Symposium** 

# Faculty Biographies

ien/WWall.com

### Hydar Ali, Ph.D. Associate Professor, Department of Pathology



#### Levy Building, Room 346 Phone: 215-573-1993 Fax: 215-573-2050 Email: <u>alih@upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p4378807

### Research Overview

Mast cells are granulated cells of hematopoietic lineage that reside close to blood vessels primarily at sites exposed to the external environment, such as the skin, oral/gastrointestinal mucosa and respiratory tract. They contribute to vascular homeostasis, innate/adaptive immunity and wound healing. Mast cells are, however, best known for their roles in allergic and inflammatory diseases such as anaphylaxis, food allergy, rhinitis, itch, urticaria, periodontitis, atopic dermatitis and asthma. Mast cells express a newly discovered G protein coupled receptor (GPCR) known as Mas-related G protein coupled receptor X2 (MRGPRX2) and the high affinity IgE receptor (FceRI). As the only mast cell lab at Penn, we are interested in delineating how MRGPRX2 and FceRI contribute to host defense and allergic/inflammatory diseases.

MRGPRX2: Activation of surface epithelial cells by pathogen-associated molecular patterns (PAMPs) results in the generation of host defense antimicrobial peptides (HDPs). These HDPs display potent antimicrobial activity and modulate immune responses via the activation of mast cells through MRGPRX2. In addition to its immunomodulatory function, MRGPRX2 likely participates in pseudo-allergic drug reactions and chronic inflammatory diseases such as urticaria, periodontitis and asthma exacerbation. A unique feature of MRGPRX2 that distinguishes it from other GPCRs is that it is activated by multiple cationic ligands including HDPs, neuropeptides (substance P and hemokinin-1), eosinophil major basic protein (MBP), eosinophil peroxidase (EPO), the neutrophil-derived cathelicidin LL-37 and many FDA approved peptidergic drugs. We are currently using cellular, molecular and imaging approaches to delineate the mechanisms involved in the regulation of MRGPRX2 vitro and humanized mice function in to study its in vivo.

FceRI: Aggregation of FceRI on mast cells by antigen and the release of proinflammatory mediators contribute to the pathogenesis of anaphylaxis and allergic asthma. It is well documented that GPCR kinases (GRKs) and the adapter protein  $\beta$ -arrestin contribute to the desensitization of most GPCRs. We recently made the unexpected observation that GRK2 and  $\beta$ -arrestin2 regulate FceRI-mediated mast cell chemotaxis, degranulation and cytokine gene expression. We are currently utilizing both in vitro and in vivo approaches to delineate how GRK2 and  $\beta$ -arrestin2 regulate FceRI signaling in mast cells to modulate anaphylaxis and allergic asthma.

- Wichayapha Manorak, Chizobam Idahosa, Kshitij Gupta, Saptarshi Roy, Reynold Panettieri Jr and Hydar Ali: Upregulation of Mas-related G Protein coupled receptor X2 in asthmatic lung mast cells and its activation by the novel neuropeptide hemokinin-1 Respiratory Research 19(1): doi: 10.1186/s12931-017-0698-3. January 2018.
- Ali, H: Emerging Roles for MAS-Related G Protein-Coupled Receptor-X2 in Host Defense Peptide, Opioid, and Neuropeptide-Mediated Inflammatory Reactions. Advances in Immunology. Arun Shukla (eds.). Elsevier, 136: 123-162, September 2017.
- Gupta, K, Idahosa, C., Roy, S, Lee, D., Subramanian, H., Dhingra, A.,Boesze-Battaglia, K, Korostoff, J., Ali, H.: Differential Regulation of Mas-Related G Protein-Coupled Receptor X2-Mediated Mast Cell Degranulation by Antimicrobial Host Defense Peptides and Porphyromonas gingivalis Lipopolysaccharide. Infection and

Immunity 85(10): 10 e00246-17 September 2017.

- Subramanian, H., Gupta, K., Ali, H.: Roles of Mas-related G protein-coupled receptor X2 on mast cell-mediated host defense, pseudoallergic drug reactions, and chronic inflammatory diseases. J Allergy Clin Immunol 2016.
- Gupta, K., Kotian, A., Subramanian, H., Daniell, H., Ali, H.: Activation of human mast cells by retrocyclin and protegrin highlight their immunomodulatory and antimicrobial properties. Oncotarget 2015.

Subramanian, H., Gupta, K., Parameswaran, N., Ali, H.: *Regulation of FcRI Signaling in Mast Cells by G Proteincoupled Receptor Kinase 2 and Its RH Domain*. J Biol Chem 289(30): 20917-20927, 2014.\_



### Yair Argon, Ph.D.

### Professor of Pathology And Laboratory Medicine

816B Abramson Research Center Office: (267) 426-5131 Fax: (267) 426-5165 Lab: (267) 426-5130 Email: yargon@pennmedicine.upenn.edu

### **Description of Research**

Communication among cells through secreted ligands and their receptors underlies the organization of tissues. The proper expression of receptors and secretion of protein ligands are dependent on accessory proteins, molecular chaperones, which regulate their biosynthesis and minimize their misfolding. Our work focuses on the molecular chaperones in the endoplasmic reticulum, where membrane and secreted proteins are synthesized.

BiP is a peptide binding protein that controls folding of antigen receptors by binding selectively to some peptides in the newly synthesized proteins. Because of this ability, BiP provides an important quality control function in screening somatically mutated molecules. One project in the lab concerns how BiP recognizes normal Ig sequences and distinguishes them from aggregation-prone somatic mutants. A second project examines the use of BiP as an inhibitor of the pathologic polymerization of antibodies into amyloid fibers.

GRP94 has a different mode of action and therefore biological activity. Although it binds peptides, its specificity is different from BiP. We use combinatorial genetic and biochemical techniques to characterize its preferred binder peptides and identify the features that it recognizes in client proteins. We developed the first cell-based assay for the chaperone function of GRP94, relying on the discovery that GRP94 is needed for production of Insulin-like growth factors, which are needed for cultured cells to cope with stress. We assay variants of GRP94 by expressing them in stressed chaperone-deficient cells. The more functional the variant chaperone, the higher the level of growth factor that is produced and the higher the survival of the cells under stress. This assay enables us to dissect the biochemical mode of action of GRP94.

Another project explores the GRP94-IGF axis in muscle physiology, using mice with targeted deletion of GRP94 in skeletal muscle. We use this model to understand what are the major client proteins of the chaperone in myocytes and to ask how modulation of GRP94 expression affect the recovery of muscle from injury.

A third project utilizes proteomic approaches to identify the interactions among ER chaperones as well as their co-factors, to understand the dynamic nature of the chaperone network and the changes in it during physiological ER stress.

### Selected Publications

- Ostrovsky O, Makarewich CA, Snapp EL, Argon Y.: An essential role for ATP binding and hydrolysis in the chaperone activity of GRP94 in cells. Proc. Nat. Acad. Sci 106(28): 11600-5, 2009 PMCID: PMC2710619.
- Ostrovsky O, Ahmed NT, Argon Y: The chaperone activity of GRP94 toward insulin-like growth factor II is necessary for the stress response to serum deprivation. Mol. Biol. Cell 20(6): 1855-64, 2009 PMCID: PMC2655248.
- Biswas C, Ostrovsky O, Makarewich CA, Wanderling S, Gidalevitz T, Argon Y.: The peptide binding activity of GRP94 is regulated by calcium Biochem. J 405(2): 233-41, 2007.
- Wanderling S, Simen BB, Ostrovsky O, Ahmed NT, Vogen SM, Gidalevitz T, Argon Y.: GRP94 is essential for mesoderm induction and muscle development because it regulates IGF-II. Mol. Biol. Cell 18(10): 3764-75, 2007.

Elkabetz Y, Argon Y, Bar-Nun S.: Cysteines in the CH1 domain underlie retention of unassembled Ig heavy

chains. J. Biol. Chem 280(15): 14402-12, 2005.

- Davis PD, Raffen R, Dul LJ, Vogen MS, Williamson KE, Stevens JF, Argon Y.: Inhibition of amyloid fiber assembly by both BiP and its target peptide. Immunity 13(4): 433-442, 2000.
- Dul JL1, Davis DP, Williamson EK, Stevens FJ, Argon Y.: Hsp70 and antifibrillogenic peptides promote degradation and inhibit intracellular aggregation of amyloidogenic light chains. J. Cell. Biol 152(4): 705-16, 2001.
- Davis DP1, Gallo G, Vogen SM, Dul JL, Sciarretta KL, Kumar A, Raffen R, Stevens FJ, Argon Y.: Both the environment and somatic mutations govern the aggregation pathway of pathogenic immunoglobulin light chain. J. Mol. Biol 313(5): 1023-1036, 2001.
- Vogen S, Gidalevitz T, Biswas C, Simen BB, Stein E, Gulmen F, Argon Y.: Radicicol-sensitive peptide binding to the N-terminal portion of GRP94. J. Biol. Chem 277(43): 40742-50, 2002.
- Gidalevitz T, Biswas C, Ding H, Schneidman-Duhovny D, Wolfson HJ, Stevens F, Radford S, Argon Y.: Identification of the N-terminal peptide binding site of glucose-regulated protein 94. J. Biol. Chem. 279(16): 16543-52, 2004.

### William M. Armstead, Ph.D.



### Research Professor, Department of Anesthesia and Critical Care

3 John Morgan Building Phone: 215-573-3674 Fax: 215-349-5078 Email: <u>armsteaw@uphs.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p10266

### **Research Interests**

Control of cerebral hemodynamics during physiologic and pathologic conditions such as traumatic brain injury, stroke, and cerebral ischemia/reperfusion.

#### **Research Techniques**

Closed cranial window for measurement of pial artery diameter and collection of cortical periarachnoid CSF for vasoactive metabolite concentration determination by RIA, fluid percussion brain injury, global cerebral ischemia, photothrombotic cerebral injury, radiolabelled microsphere regional cerebral blood flow determination.

#### **Research Summary**

Dr. Armstead's research focuses on characterizing mechanisms important in the control of cerebral hemodynamics under physiologic and pathologic conditions such as traumatic brain injury (TBI), stroke, and cerebral hypoxia/ischemia, particularly in the newborn. Current projects focus on interactions between the NMDA receptor and plasminogen activators after TBI, optimizing the efficacy/toxicity ratio of tPA, the only FDA approved treatment for stroke and translational research concerning the roles of sex and age in outcome after pediatric TBI.

- Armstead WM, Hekierski H, Pastor, Yarovoi S, Higazai AAR, Cines DB.: *Release of IL-6 after stroke contributes* to impaired cerebral autoregulation and hippocampal neuronal necrosis through NMDA receptor activation and upregulation of *ET-1* and JNK. *Transl Stroke Research, in press.* Translational Stroke Research 2018 Notes: In press.
- Curvello V, Hekierski H, Pastor P, Vavilala M, Armstead WM. : *Dopamine protects cerebral autoregulation and prevents hippocampal necrosis after traumatic brain injury via block of ERK MAPK in juvenile pigs.* Brain Research 1670: 118-124, 2017.
- Curvello V, Hekierski H, Riley J, Vavilala M, Armstead WM.: Sex and age differences in phenylephrine mechanisms and outcomes after piglet brain injury. Ped Res 82: 108-113, 2017.
- Armstead WM, Riley J, Vavilala MS.: *K channel impairment determines sex and age differences in epinephrine-mediated outcomes after brain injury.* J of Neuroscience Research 95: 1917-1926, 2017.
- Armstead WM, Riley J, Vavilala M: Sex and age differences in epinephrine mechanisms and outcomes after brain injury. J Neurotrauma 34: 1666-1675, 2017.
- Armstead WM, Hekierski H, Yarovoi S, Higazi AAR, Cines DB. : *tPA-A296-299 prevents impairment of cerebral autoregulation and necrosis of hippocampal neurons after stroke by inhibiting upregulation of ET-1*. J of Neuroscience Research 96: 128-137, 2017.

- Armstead WM, Riley J, Vavilala MS. : Preferential protection of cerebral auto regulation and reduction of hippocampal necrosis with norepinephrine after traumatic brain injury in female piglets. Pediatr Crit Care Med 17: e130-e137, 2016.
- Bohman LE, Riley J, Milovanova TN, Sanborn MR, Thom SR, Armstead, WM: *Microparticles Impair Hypotensive Cerebrovasodilation and Cause Hippocampal Neuronal Cell Injury after Traumatic Brain Injury.* J Neurotrauma 33: 168-174, 2016.
- Armstead WM, Riley J, Vavilala MS: Norepinephrine protects autoregulation and reduces hippocampal necrosis after traumatic brain injury via block of ERK MAPK and IL-6 in juvenile pigs. J Neurotrauma 33: 1761-1767, 2016.

Armstead WM, Riley J, Yarovoi S, Higazi AAR, Cines DB: A296-299 prevents impairment of cerebral autoregulation after Stroke through LRP dependent increase in cAMP and p38. Stroke 47: 2096-2102, 2016.



### Rebecca L. Ashare, Ph.D.

Assistant Professor of Psychology in Psychiatry at the Hospital of the University of Pennsylvania

Center for Interdisciplinary Research on Nicotine Addiction 3535 Market St, Suite 4100 Office: (215) 746-5789 Email: <u>rlashare@pennmedicine.upenn.edu</u>

### **Description of Research Expertise**

I am a clinical psychologist and conduct research in translational science, medication development, and neurocognition applied to nicotine dependence. My primary area of research has focused on identifying risk factors for smoking relapse, with a focus on cognitive control, decision-making, and stress, and evaluating novel treatments to improve abstinence rates. My work leverages tools from the fields of psychology, neuropharmacology, and cognitive neuroscience to understand the mechanisms that underlie smoking relapse and mechanisms of efficacy of novel interventions.

### **Research Projects**

Several of my current research projects are focused on the intersection of smoking, HIV, and cognitive function:

One project is investigating whether HIV-infected smokers experience greater withdrawal-related cognitive deficits and whether these deficits explain the high smoking rate in this population.

In collaboration with Center for AIDS Research, we are also evaluating whether targeting the cholinergic pathway among HIV-infected individuals suppresses inflammation and reverses neurocognitive deficits and whether this effect is stronger in chronic tobacco users.

### Selected Publications

Hawk, L.W., Jr., Ashare, R.L., Lohnes, S.F., Schlienz, N.J., Rhodes, J.D., Tiffany, S.T., Gass, J.C., Cummings, K.M. &

Mahoney, M.C.: The effects of extended pre-quit varenicline on smoking behavior and short-term abstinence. Clinical Pharmacology & Therapeutics, 91(2):172-180, 2012.

- Ashare, R.L., Kimmey, B. A., Rupprecht, L. E., Bowers, M.E., Hayes, M. R. & Schmidt, H. D. Repeated administration of an acetylcholinesterase inhibitor attenuates nicotine taking in rats and smoking behavior in human smokers Translational Psychiatry, Jan 19;6: e713, 2016.
- Ashare R.L., Lerman C., Tyndale R.F., Hawk L.W., Jr., George T.P., Cinciripini P. & Schnoll, R.A. Sleep disturbance during smoking cessation: Nicotine withdrawal or side effect of treatment? Journal of Smoking Cessation, Epub 2016/4/12.
- Harrison J, Dochney J, Blazekovic S, Leone F, Metzger D, Frank I, Gross R, Hole A, Mounzer K, Siegel S, Schnoll RA, Ashare RL. The Nature and Consequences of Cognitive Deficits among Tobacco Smokers with HIV: A Comparison to Tobacco Smokers without HIV. J Neurovirol, in press.



### Richard K. Assoian, Ph.D.

Professor of Pharmacology

805 Biomedical Research Building II/III Office: (215) 898-7157 Email: <u>assoian@mail.med.upenn.edu</u>

#### Overview of laboratory research:

We are an interactive group of cell/molecular biologists and bioengineers interested in understanding how cells sense changes in the physical properties of their microenvironment and how they convert this information into chemical signals, behavior and function. Within this broad area, we try to understand how physiological and pathological changes in the stiffness of the extracellular matrix (ECM) affects adhesion receptor signaling, the actin cytoskeleton, and fate decisions such as proliferation, migration and differentiation. We perform mechanistic analyses in cell culture, use genome- and proteome-wide approaches, assess mechanical properties of tissues and cells, and ultimately test physiological and pathological relevance in mouse models of vascular aging, injury, and atherosclerosis.

We are currently working in the following areas.

#### i) Cell Mechanobiology.

The ECM is a dynamic structure that provides both chemical and mechanical cues to cells. Remodeling of the ECM occurs in several diseases and generally tends to increase the stiffness of a cell's microenvironment. The effects of extracellular stiffness on cellular function are difficult to study when cells are cultured on traditional rigid plastic or glass substrata that are irrelevant to in vivo microenvironments. We therefore use deformable substrata (ECM-coated hydrogels) to model the stiffness of tissues that cells inhabit in vivo. With this approach, we can determine how changes in ECM stiffness affect adhesion receptor (integrin and cadherin) expression and signaling as well as downstream gene expression, proliferation, motility and differentiation. High throughput approaches are used to identify transcriptional and post-transcriptional responses to ECM stiffening. We have also used micropatterned substrata to examine the effect of cell-cell adhesion on the spreading and shape requirements for cell proliferation. Recent work with these approaches has led to the identification of stiffness-dependent signaling pathways, specific focal adhesion components controlling cyclin D1 expression, and novel mechanisms of crosstalk between cell-ECM and N-cadherin mediated cell-cell adhesion.

#### ii) Tissue Mechanobiology.

We are using atomic fore microscopy (AFM) and pressure myography ex vivo to interrogate how changes in ECM composition and mechanosensory proteins--often through genetic manipulation of mice--affects vessel mechanics. AFM allows us to detect microheterogeneity in the stiffness of isolated arteries. Pressure myography allows us to probe stress-strain relationships in the pressurized artery and can help to distinguish effects mediated by elastin vs. collagens. Much of our current interest in this area is related to the effects of age on vessel mechanics and mechanosensing.

#### iii) In vivo Mechanobiology

We place significant effort on in vivo mouse models to document the relevance of adhesion receptor signaling and stiffness-sensing to mammalian biology. For example, we use mice to study adhesion receptor signaling and vascular smooth muscle cell (SMC) proliferation during the in vivo response to vascular injury, a model of acute arterial stiffening. By comparing the degree of SMC proliferation in wild-type mice and mice with knock-outs/knock-ins of integrin-regulated, mechanosensing, and cell cycle genes, we can test the importance of the

adhesion- and stiffness-regulated events we detect in primary SMCs cultured on hydrogels as described above. Similar studies are exploring the proliferative effects of N-cadherin and the role of arterial stiffening in SMC dedifferentiation/re-differentiation.

We are also identifying regulators of mechanosensitive signaling, ECM remodeling, and arterial stiffening in vascular disease. One set of studies has focused on apolipoprotein E (apoE). Although best known for its role in reverse cholesterol transport, we found that apoE suppresses the expression of several ECM genes including those for collagen-I, collagen-VIII, fibronectin and lysyl oxidase. These effects protect against arterial stiffening, reduce monocyte adhesion to subendothelial ECM, and provide cholesterol-independent protection against atherosclerosis in mice. Ongoing work focuses on MMP12 as a global inducer of arterial stiffening with age, vascular injury and atherosclerosis. Finally, our newest interest is in mechano-signaling and ECM remodeling in Hutchinson-Guilford Progeria Syndrome, a genetic disease of premature aging and death that is associated with arterial stiffening, atherosclerosis and stroke.

- Cosgrove BD, Mui KL, Driscoll TP, Caliari SR, Mehta KD, Assoian RK, Burdick JA, Mauck RL. : N-cadherin adhesive interactions modulate matrix mechanosensing and fate commitment of mesenchymal stem cells. Nature Materials 15: 1297-1306, 2016.
- Liu SL, Bae YH, Yu C, Monslow J, Hawthorne EA, Castagnino P, Branchetti E, Ferrari G, Damrauer SM, Puré E, Assoian RK: Matrix metalloproteinase-12 is an essential mediator of acute and chronic arterial stiffening. Scientific Reports 5: 17189, 2015.
- Mui, KM., Bae, YH, Gao, L., Liu, S-L. Xu, T., Radice, GL., Chen, CS, and Assoian, RK: N-cadherin induction by ECM stiffness and FAK overrides the spreading requirement for proliferation of vascular smooth muscle cells. Cell Reports 10: 1477-1486, 2015.
- Bae YH, Mui KL, Hsu BY, Liu SL, Cretu A, Razinia Z, Xu T, Puré E, Assoian RK. : A FAK-Cas-Rac-Lamellipodin Signaling Module Transduces Extracellular Matrix Stiffness into Mechanosensitive Cell Cycling. Science Signaling 7: ra57, 2014.
- Kothapalli, D.\*, Liu, S.L.\*, Bae, Y.H., Monslow, J., Xu, T., Hawthorne, E.A., Castagnino, P., Byfield, F.J., Rao, S., Rader, D.J., Pure, E., Phillips, M.C., Lund-Katz, S., Janmey, P.A., Assoian, R.K.: Cardiovascular protection by apoE and apoE-HDL linked to suppression of ECM gene expression and arterial stiffening. Cell Reports 2: 1259-1271, 2012.
- Klein, E.A., Yin, L., Kothapalli, D., Castagnino, P., Byfield, F.J., Xu, T., Levantal, I., Hawthorne, E., Janmey, P.A., and Assoian, R.K.: Cell cycle control by physiological matrix elasticity and in vivo tissue stiffening. Current Biology 19: 1511-8, 2009.



## Narayan Avadhani, Ph.D.

Harriet Ellison Woodward Professor of Biochemistry Chair, Department of Animal Biology

189E Old Vet Phone: 215-898-8819 Fax: 215-573-6651 Email: <u>narayan@vet.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p5359138

### Research Overview

The research in Dr. Avadhani's laboratory is focused on the following aspects of mitochondrial genetics and regulation of mitochondrial membrane biogenesis in mammalian cells:

- 1. Mechanisms of dual targeting of cytochrome P450 and related proteins to ER and mitochondria and mechanisms of activation of the chimeric N-terminal signal by cAMP and other physiological factors.
- 2. Characterization of a novel mitochondria-to-nucleus stress signaling in cells subjected to mitochondrial specific genetic, and or, metabolic stress, which operates through altered [Ca2+]c, and the role of mitochondrial stress signaling in tumor progression and metastasis.
- 3. Regulation of cytochrome oxidase gene expression, and modulation of enzyme assembly/activity under chemical and oxidative stress conditions.
- 4. Role of mitochondrial stress signaling in Embryonic Stem Cell function/differentiation, and mammalian mitochondrial transcription under chemical and oxidative stress in ES cells.

- Iqbal Jameel, Sun Li, Cao Jay, Yuen Tony, Lu Ping, Bab Itai, Leu N Adrian, Srinivasan Satish, Wagage Sagie, Hunter Christopher A, Nebert Daniel W, Zaidi Mone, Avadhani Narayan G: Smoke carcinogens cause bone loss through the aryl hydrocarbon receptor and induction of Cyp1 enzymes. Proceedings of the National Academy of Sciences of the United States of America 110(27): 11115-20, Jul 2013.
- Bajpai Prachi, Sangar Michelle C, Singh Shilpee, Tang Weigang, Bansal Seema, Chowdhury Goutam, Cheng Qian, Fang Ji-Kang, Martin Martha V, Guengerich F Peter, Avadhani Narayan G: Metabolism of 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine by mitochondrion-targeted cytochrome P450 2D6: implications in Parkinson disease. The Journal of biological chemistry 288(6): 4436-51, Feb 2013.
- Bansal Seema, Anandatheerthavarada Hindupur K, Prabu Govindaswamy K, Milne Ginger L, Martin Martha V, Guengerich F Peter, Avadhani Narayan G: Human cytochrome P450 2E1 mutations that alter mitochondrial targeting efficiency and susceptibility to ethanol-induced toxicity in cellular models. The Journal of biological chemistry 288(18): 12627-44, May 2013.
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### Paul H. Axelsen, M.D.

Professor of Pharmacology, Biochemistry, Biophysics, and Medicine

1009C Stellar Chance Laboratories Phone: 215-898-9238 Email: <u>axe@upenn.edu</u> Web: http://www.med.upenn.edu/axelab/

### **Description of Research Expertise**

The Axelsen laboratory is focused on the pathogenesis of Alzheimer's disease, particularly in the roles of oxidative stress and protein lipid interactions. A variety of whole-animal models and in vitro systems are used, as well as a large repository of human brain samples. The laboratory has developed novel isotope-based techniques for characterizing oxidative stress in brain using mass spectrometry and various forms of optical spectroscopy, including infrared, fluorescence, and internal reflection spectroscopy.

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### Gordon Barr, Ph.D.

Associate Professor of Psychology in Anesthesiology and Critical Care

Abramson Research Building, Room 907A Phone: 267-426-9722 Fax: 267-426-8128 Email: <u>barrg@email.chop.edu</u> <u>http://www.med.upenn.edu/apps/faculty/index.php/g275/p8320366</u>

### **Description of Research Expertise**

I study transitions during early development. Transitions are important developmental epochs during which time there are substantial changes in how infants/children/adolescents process information. I am particularly interested in mechanisms of of stress, pain and recovery from damage to the nervous system from that developmental perspective. I study models of acute and chronic pain, infant-mother attachment, the therapeutic and adverse effects of analgesics, especially opiates, and spinal cord injury and recovery from injury. Our lab develops and uses sophisticated behavioral assays in young animals in conjunction with a number of anatomical and neurochemical assays to understand mechanisms by which these transitions occur.

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### Marisa S. Bartolomei, Ph.D.

Professor of Cell and Developmental Biology and Genetics

9-123 Smilow Center for Translational Research Office: 215-898-9063 Lab: 215-898-9063 Email: <u>bartolom@mail.med.upenn.edu</u> http://cdb.med.upenn.edu/people/marisa-s-bartolomei-ph-d/

### **Description of Research Expertise**

One aspect of the research in my laboratory focuses on the study of genomic imprinting in mice. While affecting only a subset of genes in mammals, genomic imprinting results in the unequal expression of the maternal and paternal alleles of a gene. As a consequence, the maternal and paternal genomes are functionally non-equivalent and both are required for normal mammalian development. One imprinted gene, H19, is exclusively expressed from the maternally-derived allele in mice and humans. There are a number of important questions concerning the control of imprinting that are being addressed using the mouse H19 gene. These questions include how and when the inactive and active alleles are differentiated, what sequences designate that a gene is to be imprinted, and what factors function to imprint the gene. Moreover, we are also determining how the environment, including procedures used in Assisted Reproductive Technologies (ART) and endocrine disruptors, affect imprinting and epigenetic gene regulation.

My laboratory also studies the process of X inactivation in mice. X inactivation is the dosage compensation mechanism that female mammals use to silence one X chromosome and to achieve equivalent X-linked expression to males. Certain aspects of this complex multi-step process have been well established, but the molecular and genetic mechanisms controlling this process remain poorly characterized. To isolate factors involved in X inactivation we have employed the following strategies: we have collaborated with Huntington Willard (Duke University) in conducting ENU mutagenesis in the mouse to select for mutations that affect X inactivation; we have participated in studies that assay reactivation of X-linked genes; and we have examined the effects of various mutations and environmental perturbations on X inactivation.

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# Wade Berrettini, M.D., Ph.D.



Karl E. Rickels Professor, Department of Psychiatry

2206 Translational Research Laboratory Building Phone: 215-898-0092 Fax: 215-573-2041 Email: wadeb@mail.med.upenn.edu

### **Research Overview**

An area of interest is the function of a delta opioid receptor SNP, rs678849, in cocaine addiction and in therapeutic response of opioid addicted persons to buprenorphine and methadone.

Another area of interest is somatic DNA variation in CNS disorders, as a source of risk for those illnesses. We have projects in temporal lobe epilepsy, schizophrenia and cocaine addiction, using DNA from human brains of persons with these illnesses to map one type of somatic variation, long interspersed elements (LINE-1s).

A third area of interest is a double-blind, placebo-controlled phase II randomized clinical trial of a novel triple monoamine reuptake inhibitor in cocaine addiction.

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## Seema Bhatnagar, Ph.D.



### Associate Professor of Anesthesiology and Critical Care

Abramson Research Center, Suite 402B Children's Hospital of Philadelphia Office: 267-426-0951 Fax: 215-590-3364 Email: bhatnagars@email.chop.edu

### **Description of Research Expertise**

Our long term goal is to understand why some individuals are vulnerable or resilient to the potentially adverse effects of chronic stress. Chronic stress is a critical factor contributing to the development of affective and anxiety disorders and can precipitate relapse of depression and post-traumatic stress disorder. This intimate association between repeated/chronic stress and affective and anxiety disorders underscores the need to understand fully the neural circuitry that regulates the physiological and behavioral consequences of repeated stress.

We approach this need in two ways, using rat models. First, we are examining the neural circuits that are impacted by stress exposure and how these circuits, in turn, produce dysfunction in physiology and behavior. In these studies, we use state-of-the-art neuroscience techniques, including multiplex PCR and protein arrays,optogenetic stimulation of peptide release, in situ hybridization, tract tracing, immunocytochemistry and western blots, as well as behavioral and pharmacological approaches that allow us to pinpoint the brain regions of interest and to identify specific neural mechanisms. We have used these technical approaches to examine specific cortico-limbic circuits important for regulating stress reactivity. We have found that neural adaptations to chronic stress develop over time and, once developed, are stable.

Second, we examine individual differences in reactivity to stress to understand how some are vulnerable and others resistant to the effects of stress. We have observed that individual differences in how adult animals cope with defeat by a dominant animal have neural and behavioral repercussions. In addition, we have observed that prenatal and early postnatal environmental factors produce enduring effects on neural circuitry regulating stress reactivity. Recently, we have observed the stress of isolation during adolescence produces enduring effects on behavioral, neuroendocrine and neural reactivity to stress and these effects are more pronounced in females. In these developmental studies, we are collaborating to use emerging neuroimaging techniques to examine development of fiber tracts and gray matter in addition to the techniques mentioned above.

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### lan A. Blair, Ph.D.

A.N. Richards Professor of Pharmacology, Department of Pharmacology; Director, Center for Cancer Pharmacology; Scientific Director, Abramson Cancer Center Proteomics Facility; Penn Genomics Frontiers Institute Proteomics Facility Director, Systems Biology, Institute for Translational Medicine and Therapeutics; Director, Molecular Profiling Core, Center of Excellence in Environmental Toxicology

854 Biomedical Research Building II/III Phone: 215-573-9880 Fax: 215-573-9889 Email: <u>ianblair@mail.med.upenn.edu</u> http://www.med.upenn.edu/blairlab/index.shtml

### **Description of Research Expertise**

Establish the use of high-resolution mass spectrometry and molecular biology as tools for conducting sophisticated proteomics, DNA-adductomics, metabolomics, and lipidomics research with a particular emphasis on discovering biomarkers for the early detection of cancer and biomarkers of response in rare diseases

1. Early detection biomarkers of asbestos exposure, mesothelioma, and non-small lung cancer,

Amyloid  $\beta$ -peptides and high-mobility group box 1 (HMGB1) a non-histone chromosomal protein are the two most intensively studied endogenous cellular danger signals known as danger-associated molecular pattern (DAMP) molecules. DAMPs together with pathogen-associated molecular patterns alert the innate immune system by activating signal transduction pathways through binding to pattern recognition receptors (PRRs). PRRs include the receptor for advanced glycation end products (RAGE), toll-like receptors (TLRs), chemokine (C-X-C motif) receptor (CXCR), and T cell immunoglobulin mucin (TIM). Binding to PRRs induces proinflammatory cascades, which trigger the release of cytokines. PRRs are expressed by cells of the innate immune system such as macrophages, leukocytes and dendritic cells. They are also expressed on the surface of vascular cells, fibroblasts and epithelial cells. We have recently demonstrated that HMGB1 is secreted when blood is allowed to clot. Numerous studies have reported that HMGB1 is secreted in o the circulation by cancer patients. However, many of these studies are flawed because they used serum instead of plasma. Furthermore there are 29 reported sites of acetylation on HMGB1 so it is essential that the methodology is available to quantify each of the individual proteoforms. We are currently developing an approach for the analysis of HMGB1 proteoforms in plasma samples from patients with mesothelioma and non-small cell lung cancer as well as subjects who had a heavy exposure to asbestos. We are also guantifying lipid hydroperoxide-mediated DNA damage in lymphocytes from the same population in order to further understand the etiology of the disease. Finally, metabolomics and lipidomics studies are being conducted in order to discover additional biomarkers.

2. Biomarkers of therapeutic response in rare diseases.

There are > 40 rare genetic diseases that result from aberrant protein expression including, Duchene's muscular dystrophy (DMD), spinocerebellar ataxia 1 (SCA-1), and Friedreich's ataxia (FA). Current approaches to developing therapies for these rare diseases primarily involve increasing expression of the normal protein. The necessity for monitoring protein levels was highlighted recently during the US Food and

Drug Administration (FDA) fast-track approval process for the drug eteplirsen (Exondys 51) to treat DMD. The lack of a rigorously validated method to assess up-regulation of dystrophin levels in DMD patients made it difficult to show a therapeutic response. FA is characterized by slowly progressive ataxia and hypertrophic cardiomyopathy. Lifespan is significantly reduced in FA with an average of death of 37-years, most commonly from cardiac-related pathologies. There are no approved treatments for FA, although numerous experimental approaches are being tested, which primarily involve up-regulation of frataxin protein. We have developed a strategy to monitor improvements in mitochondrial metabolism using FA platelets. We are now developing more direct measure of frataxin expression. This will also provide an approach to monitor new therapies that are being developed for rare genetic diseases of aberrant protein expression such as DMD24 and SCA-1.

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#### **Research Overview**

### Julie A. Blendy, Ph.D.

Professor, Department of Pharmacology

2211 Translational Research Laboratory Building Phone: 215-898-0730 Fax: 215-573-2236 Email: <u>blendy@mail.med.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p11852

My research is aimed at understanding the molecular basis for the biochemical and behavioral changes associated with chronic drug use. How drugs exert effects that lead to long-term adaptations within the central nervous system is not well understood. However, alterations in gene expression are a likely mechanism. A group of transcription factors, CREB (cAMP response element binding protein) and CREM (cAMP response element modulatory protein), have been identified as key proteins mediating a transcriptional response to elevated levels of cAMP and/or Ca++. We have shown that mice deficient in CREB show paradoxical responses in behavioral conditioning paradigms to morphine and cocaine. Current projects are aimed at investigating the molecular basis for this differential response with techniques ranging from EMSA's (electromobility shift assays), Western analyses, real time PCR, RNAse protection assays and immunohistochemistry. In addition, recent studies in our lab have identified alterations in depression-like phenotypes in CREB deficient mice. The clinical co-morbidity between addiction and depression is striking. While little is known regarding the cause-effect relationship between these disease states, there are striking similarities at a molecular level, and, as in the case of drugs of abuse, cAMP mediated gene transcription has been implicated in the mechanism(s) of action of antidepressant drugs. Future studies involve the development and use of tissue specific gene-targeting (Cre/loxP system) to inactivate known and/or novel CREB targets to further characterize the molecules and neural circuitry involved in the mechanism of action of drugs of abuse as well as antidepressant drugs. The combined use of pharmacological, behavioral and molecular studies should lead to a better understanding of the biological basis of addiction and depression.

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### Gerd Blobel, M.D., Ph.D.

### Professor, Department of Pediatrics, Division of Hematology

316H Abramson Research Center Phone: 215-590-3988 Fax: 215-590-4834 Email: <u>blobel@email.chop.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p1105

### **Description of Research**

Our lab focuses on the genetic and epigenetic control of hematopoiesis and its disorders. Specifically, we study how tissue-specific transcription factors govern the specification and maintenance of hematopoietic cell lineages. We examine how transcription programs are epigenetically transmitted through mitosis to maintain lineage identity. Our work is leading us deeply into the analysis of chromatin structure, its modifications and organization. For example, we investigate how regulatory elements are spatially organized in the nucleus. We are developing approaches to manipulate higher order chromatin organization as a therapeutic tool for the treatment of diseases affecting the globin genes. For our studies we combine molecular, genomic, biochemical, and imaging approaches with studies in normal and gene targeted mice.

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## Donita Brady, Ph.D.



Presidential Assistant Professor Assistant Investigator, Abramson Family Cancer Research Institute

612 BRB II/III Fax: 215-573-6725 Email: <u>bradyd@mail.med.upenn.edu</u> <u>http://www.cbio.med.upenn.edu/bioTemplate.asp?pageID=13</u>

### **Research Details:**

Transition metals are tightly regulated metabolites that function as structural or catalytic cofactors for specific proteins critical to normal physiology and development. Copper (Cu) is an essential transition metal for a diverse array of biological processes. Aberrant Cu excretion and absorption are manifested in the extremely rare genetic diseases Menkes and Wilson, respectively. The study of these diseases helped elucidate the cellular machinery responsible for the proper acquisition, distribution, and utilization of Cu. Recently Cu has been found to modulate signaling cascades and gene expression signatures in the context of normal physiology as well as the pathophysiology of diseases such as cancer.

For example, while investigating pharmacologically accessible signaling pathways downstream of oncogenic RAS, we recently demonstrated that genetic ablation of the high affinity Cu transporter CTR1 responsible for Cu uptake resulted in decreased RAF-MEK-ERK signaling through loss of the interaction between Cu and the kinases MEK1/2. This is the first example demonstrating Cu directly regulates the activity of a mammalian kinase, and hence has opened up a new way to explore how metals interact with signaling pathways. Capitalizing on the dependence of oncogenic mutations in the RAS effector protein BRAF for MEK1/2 activity, a multifaceted approach was used to examine this new signaling mechanism in the context of BRAF mutation-positive cancer. Specifically, we reported that decreasing the levels of CTR1, or introducing mutations in MEK1 that disrupt Cu binding, decreased BRAFV600E-driven signaling and tumorigenesis. Furthermore, Cu chelators used in the treatment of Wilson disease decreased the tumor growth of cells either transformed by BRAFV600E or engineered to be resistant to BRAF inhibition. This novel signaling paradigm provides a concrete intersection between Cu availability and MAPK signaling and led to the initiation of a phase I clinical trial (NCT02068079) to combine a Cu chelator with a BRAF inhibitor for the treatment of BRAF mutation-positive melanoma.

However, the molecular mechanisms by which Cu directly cooperates with specific signaling molecules to govern diverse cellular functions remain largely undefined. As such, there is a great need for a better understanding of precisely how Cu and other metals are integrated into kinase signaling networks during normal homeostasis and cancer. Moreover, these findings highlight the prospect of manipulating Cu regulation as a novel means to target essential kinase signal transduction pathways in cancer via a novel mechanism of regulation. As such, our laboratory will pioneer this new area of research by utilizing a multidisciplinary approach, from in vivo mouse models of cancer, biochemistry, molecular biology, and pharmacologic interventions.

In this regard, we are focusing on three interconnected research areas. Specifically, i) elucidating the molecular mechanisms and cellular contexts that underlie Cu integration into the MAPK pathway, ii) systematically mapping the landscape of sensitivity and resistance to perturbations in Cu availability as a new strategy to target kinase signal transduction in cancer, and iii) applying these findings to other transition metals and signaling networks in cancer.

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### Lawrence Brass, M.D., Ph.D.

Professor of Medicine, Division of Hematology & Oncology Professor of Systems Pharmacology and Translational Therapeutics Associate Dean, Combined Degree and Physician Scholars Programs, University of Pennsylvania, School of Medicine Director, Penn MSTP

815 Biomedical Research Building II/III Phone: 215-573-3540 Email: <u>brass@mail.med.upenn.edu</u> Lab web site : <u>http://www.med.upenn.edu/brasslab/</u> Faculty listing : <u>http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p15732</u>

### **Research Overview**

My longstanding research and clinical interest is in platelet biology and the mechanisms of platelet activation in response to vascular injury and disease. Platelets are blood cells best known for their role in halting bleeding after vascular injury, but they do many other things as well, not all of which are healthy for humans. People that lack platelets are at risk for life-threatening bleeding. People that have platelets are at risk for the kinds of acute arterial thrombosis that leads to heart attacks and strokes, especially in the setting of atherosclerotic cardiovascular disease. Our goal is to understand the former and prevent the latter. The work we are doing focuses on human biology and pathology, but makes extensive use of genetically engineered mouse models and systems biology approaches as well. Studies currently funded by the NIH Heart, Lung and Blood Institute (NHLBI) and the American Heart Association include efforts to understand how platelet activation is initiated and regulated, how contacts between activated platelets foster thrombus growth and stability, in part by establishing a protected local environment, and how differences among platelets affect responses to injury. Methods that we employ range from the manipulation of gene expression in megakaryocytes to intravital high resolution confocal microscopy and computerized modeling. Campus collaborations include strong links to the School of Engineering and to investigators in the Departments of Medicine, Pediatrics and Pharmacology. Potential rotation and thesis projects can be identified in any of these areas.

#### **Recent publications**

- Welsh John D, Stalker Timothy J, Voronov Roman, Muthard Ryan W, Tomaiuolo Maurizio, Diamond Scott L, Brass Lawrence F: A systems approach to hemostasis: 1. The interdependence of thrombus architecture and agonist movements in the gaps between platelets. Blood 124(11): 1808-15, Sep 2014 Notes: Epub 2014 June 20.
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### Rodney M. Camire, Ph.D.

Associate Professor, Department of Pediatrics

5018 Colket Translational Research Building Phone: 215-590-9968 Fax: 215-590-3660 Email: <u>rcamire@mail.med.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g5165284/p32208

### **Research Overview**

My laboratory is interested in understanding the components of the blood coagulation system, how they interface with activated cells, and how disturbances in their function lead to bleeding and thrombosis. We are also interested in developing therapeutic approaches (protein and gene-based) to mitigate these events which are major causes of morbidity and mortality worldwide. We are interested in questions related to the enzymology, biochemistry, and molecular genetics of enzyme complexes involved in blood coagulation. Numerous systems are employed to answer these questions including kinetic, biophysical, and structural approaches in addition to using in vivo models to make meaningful contributions to the field. The current areas of investigation in the laboratory include:

1. Molecular basis of procofactor activation: We are interested in understanding how FV and FVIII are preserved as inactive procofactors and defining their mechanism of activation. Our work has uncovered surprising and unexpected observations that have fundamentally shifted current thinking about FV activation and its regulation by TFPI.

2. Structural correlates of protease function-basic and translational research: We seek to better understand how processing of inactive serine protease zymogens such as FX and FIX, to their active forms contributes to the expression of binding sites critical to their function. Knowledge from these biochemical studies has been applied to translational studies, some in collaboration with companies, to develop novel protein therapeutics to treat bleeding in hemophilia, trauma, or other conditions.

3. Imaging coagulation reactions in vivo. We have taken advantage of fluorescence approaches developed for physical studies of coagulation enzyme function to develop enabling technologies that permit quantitative measurements of enzyme complex assembly and function in vivo.

4. Employ gene therapy strategies for hemophilia A/B by employing novel modifications to the protein cofactor, factor VIII or zymogen FIX. Using different bioengineering strategies we are interested in modifying FVIII or FIX with unique properties that could be useful in a gene-based approach.

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- Polderdijk, S.G.I., Adams, T.E., Ivanciu, L., Camire, R.M., Baglin, T.P., and Huntington, J.A: Design and characterization of an APC-specific serpin for the treatment of hemophilia. Blood 129(1): 105-113, 2017.
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# Beatriz M. Carreno, Ph.D.



**Research Associate Professor of Pathology and Laboratory Medicine** 

PCAM South Tower, 8th Floor Email: <u>bcarreno@exchange.upenn.edu</u>

#### Selected Publications

Carreno, B.M., Mardis, E.R. : A Shot against Cancer. Scientific American April 2016.

- Hundal, J., Carreno, B. M., Petti, A. A., Linette, G. P., Griffith, O. L., Mardis, E. R., Griffith, M.: pVAC-Seq: A genome-guided in silico approach to identifying tumor neoantigens. Genome Med 8(1): 11, Jan 2016.
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- Carreno, B.M., Becker-Hapak, M, Cornelius, L., Linette, G.P. : High level IL-12p70 producing DC vaccine elicits Tc1-polarized immunity in patients with metastatic melanom. 13th International Symposium on Dendritic Cells, Tours, France Sep 2014 Notes: Poster presentation.
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# Lewis A. Chodosh, M.D., Ph.D.

Professor, Departments of Cancer Biology and Medicine Chair, Department of Cancer Biology Associate Director for Basic Science, Abramson Cancer Center Co-Director, 2-PREVENT Breast Cancer Translational Center of Excellence

614 Biomedical Research Building II/III Phone: 215-898-1321 Fax: 215-573-6725 Email: <u>chodosh@mail.med.upenn.edu</u> <u>http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p20564</u>

#### **Description of Research**

Breast cancer is the most common cancer as well as the leading cause of death from cancer among women worldwide. The Chodosh laboratory uses genetically engineered mouse models, patient samples and computational biology to study the mechanisms by which breast cancers develop, become resistant to therapy, and ultimately contribute to cancer mortality. A broad array of basic and translational research approaches are used to address problems of fundamental clinical importance to cancer patients by elucidating pathways and principles common to human cancers. Particular areas of interest include: pathways regulating cancer development, metastasis, tumor dormancy and recurrence; the use of genomics and computational approaches to understand genetic programs in cancer; and the use of non-invasive imaging approaches to study tumor biology. These approaches employ molecular, cellular, animal, human, and in silico model systems to study the function of key regulatory molecules in tumor biology using genetics, genomics, molecular biology, biochemistry, cell biology, computational biology, functional imaging, animal studies, preclinical trials and clinical investigation.

#### **Recent Publications**

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### Margaret M. Chou, Ph.D.

Associate Professor of Pathology and Laboratory Medicine

816E Abramson Research Center Phone: 267-426-9228 Fax: 267-426-5165 E-mail: <u>mmc@mail.med.upenn.edu</u> http://www.med.upenn.edu/camb/faculty/cgc/chou.html

### Description of Research

My career interest is to understand the mechanisms underlying malignant transformation. The progression of a normal cell into a cancerous one entails profound changes in numerous cellular functions, including its proliferation, survival, and motility/invasiveness, all of which contribute to metastatic behavior. These cell autonomous changes are coupled with alterations in the tumor cells' microenvironment, which exhibits a mutual regulation with the tumor cells and impacts upon the above properties. My work has been aimed at identifying the signaling pathways that play pivotal roles in these processes.

Most recently, we have focused our efforts on elucidating critical pathogenic factors in the development of bone and soft tissue tumors (BSTTs). In comparison to carcinomas and hematological malignancies, much less is known about the etiology of BSTTs, some of which preferentially affect children. A subset of pediatric BSTTs are driven by pathognomonic chromosomal translocations, including Ewing sarcoma, alveolar rhabdomyosarcoma, and aneurysmal bone cyst. Studies in my laboratory are aimed at identifying the mechanisms by which they contribute in disease pathogenesis. We have recently determined that the TRE17/USP6 oncogene acts as a critical pathogenic agent across a number of BSTTs. TRE17 affects multiple aspects of tumor cell biology and simultaneously modulates the tumor microenvironment. The goals of my laboratory are to determine the molecular mechanisms by which TRE17 functions, to identify additional cellular pathways critical for BSTT pathogenesis, and to develop murine models of BSTTs to ultimately allow development of novel therapeutic strategies.

My laboratory also focuses on pathogenic mechanisms of Ewing sarcoma, alveolar rhabdomyosarcoma, and a newly described cancer, sinonasal sarcoma. Efforts are underway to identify the mechanism by which their respective pathognomonic translocations function in these cancers, and identifying novel sensitivities to cytotoxic agents.

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- Lau, AW and Chou, MM.: The adaptor complex AP-2 regulates post-endocytic trafficking through the non-clathrin Arf6-dependent endocytic pathway. Journal of Cell Science 121(24): 4008-4017, Nov 2008.



# Shinjae Chung, Ph.D.

#### Assistant Professor of Neuroscience

Smilow Center for Translational Research, Room 10-133 Philadelphia, PA 19151 Office: 215-746-1122 Email: <u>shinjaec@pennmedicine.upenn.edu</u> <u>https://chunglab.med.upenn.edu/</u>

#### **Research summary**

The goal of our lab is to identify the molecular and neural mechanisms controlling sleep, and to understand how these are interconnected with the neural circuits regulating emotional states in health and disease. To accomplish this, we employ a multi-disciplinary approach including optogenetics, in vivo electrophysiology, imaging, virus-mediated circuit mapping and gene profiling.

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# Akiva S. Cohen, Ph.D.

**Research Associate Professor of Pediatrics** 

816H Abramson Research Center Phone: 215-590-1472 Fax: 267-426-5165 Email: <u>cohena@email.chop.edu</u> <u>http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p17558</u>

#### **Research Summary**

Our principal research interest is focused on the fundamental cellular and molecular mechanisms that underlie cognitive impairments associated with traumatic brain injury. We are primarily concerned with alterations in neuronal excitability in the limbic system of the brain. This system has been shown to play a primary role in higher cognitive function e.g. learning and memory and is damaged in traumatic brain injury. We incorporate a variety of techniques to understand the nature and functional consequences of injury-induced alterations.

Our studies begin with conditioned fear response behavior to assess cognitive impairments and extracellular recording to evaluate injured hippocampal function. Unbiased stereology is then used to quantify the degree of cell death. Excitatory and inhibitory synaptic recording is utilized to further determine the function of surviving neurons. Immunocytochemical and biochemical techniques are used to examine specific proteins that have been altered by injury and may be underlying synaptic and/or circuit dysfunction. The combination of these methodologies should help elucidate putative mechanisms causing injury-induced cognitive deficits. A better understanding of these injury-induced alterations will provide insight for directing the development of potential therapies that would ameliorate cognitive dysfunction in traumatic brain injured patients.

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### D. Kacy Cullen, Ph.D.

**Research Associate Professor Of Neurosurgery** 

105 Hayden Hall / 3320 Smith Walk Philadelphia, PA 19104 Office: 215-746-8176 Fax: 215-573-3808 Email: <u>dkacy@mail.med.upenn.edu</u>

#### **Description Of Research Expertise**

The focus of the Cullen Lab's research in Neurotrauma is the application of engineering principles to better understand the causative mechanisms and pathophysiological responses following traumatic injury to the nervous system. Specific attention is given to neural injury biomechanics and mechanisms of acute biophysical cellular/tissue damage. In the arena of Neural Engineering, the objective is to develop neurotechnology to mitigate trauma-induced deficits or augment the body's capacity for regeneration. Here, focus is given to neural tissue engineering strategies and the development of biohybridized technologies for long-term neurobiological-electrical interfaces.

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### Mariella De Biasi, Ph.D.

Associate Professor of Neuroscience in Psychiatry

Email: <u>marielde@mail.med.upenn.edu</u> https://www.med.upenn.edu/apps/faculty/index.php/g275/p8658175

#### **Description of Research Expertise**

Mariella De Biasi has made significant contributions to the nicotinic field by characterizing a number of nicotinic receptor mutant mice. Her laboratory unveiled the role of various nicotinic acetylcholine receptor (nAChR) subtypes in autonomic function, the mechanisms of anxiety, and the brain circuits underlying nicotine withdrawal. The main focus has been the analysis of mice null for the  $\alpha$ 3,  $\alpha$ 5, and  $\beta$ 4 nAChR subunits. Studies have indicated a prominent role for those subunits in the behavioral effects of both low and high nicotine doses as well as their specific influence on the physical manifestations of nicotine withdrawal. Dr. De Biasi's lab has either generated or acquired a number of viral vectors that we are using to change nAChR expression levels in the whole brain as well as in specific neuronal subtypes.

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### Jim Delikatny, Ph.D. Research Professor, Department of Radiology

317 Anatomy-Chemistry Building Phone: 215-898-3105 Email: <u>delikatn@mail.med.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g275/p15538

#### **Research Overview**

The main interest of this group is the non-invasive detection of metabolic changes that occur during tumor development and in response to anticancer drugs in models of human breast cancer. We employ a number of imaging modalities that include near infrared fluorescence optical imaging, MRI and MRS, PET and Cerenkov imaging. We have an active program in the design, synthesis and characterization of NIR optical contrast agents for the detection of phospholipase and choline kinase expression and activity in tumors and for the detection of pH and redox changes in the tumor microenvironment. Changes in lipid metabolite levels are monitored using MRS to determine potential biochemical markers for the detection of tumors and their early response to therapy and correlated with near-infrared optical imaging using enzyme-activated fluorescent contrast agents to detect enzyme activity in situ. We are pioneering the development of Cerenkov imaging by creating novel radiolabeled probes suitable for determining both location and function using dual PET and optical imaging.

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# Dennis E. Discher, Ph.D.

Robert D. Bent Professor of Chemical & Biomolecular Engineering Director of National Cancer Institute-funded Physical Sciences in Oncology Center @ Penn

129 Towne Building Phone: 215-898-4809 Email: discher@seas.upenn.edu http://www.seas.upenn.edu/~discher/

#### **Research Interests**

- Drug delivery via polymer engineering.
- Cell eng'g and therapy
- Macrophages & phagocytosis: Foreign vs Self
- Molecular & cell biophysics: from extracellular matrix and stem cells to nucleus.
- Diseases ranging from cancer to muscular dystrophy and anemias.

#### **Research Description**

Dr. Discher's research focuses on novel drug delivery systems and cell therapy fundamentals. His lab develops polymer matrices that are optimized for cell growth and differentiation. Among their latest studies are macrophages recognition and phagocytosis, controlling stem cell differentiation with materials, shrinking tumors, developing new polymer forms.

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# Joshua L. Dunaief, MD, PhD

Adele Niessen Professor of Ophthalmology

305B Stellar Chance Philadelphia, PA 19104-6100 Office: 215-898-5235

**Description of Research** 

Age related macular degeneration (AMD) is the most common cause of irreversible blindness, yet its pathogenesis is poorly understood. Evidence suggests that cumulative oxidative damage contributes to AMD and aging in general. The Dunaief lab has found that AMD retinas have iron overload, which can cause oxidative stress. Increased understanding of retinal iron homeostasis may lead to treatments for AMD. To investigate the mechanisms of retinal iron regulation, the lab uses conditional knockout mouse models, human retinal tissue, and retinal cell tissue culture. A mouse line deficient in the iron transporting ferroxidases ceruloplasmin and hephaestin develops age-dependent retinal iron overload and retinal degeneration with features of AMD (Hahn et al., PNAS, 2004). Recent research in the lab indicates that inflammation promotes cellular iron overload in a vicious cycle leading to cell death. Our current focus is on the mechanisms of retinal iron homeostasis and development of therapeutics to protect the retina.

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### James H. Eberwine, Ph.D.

Elmer Holmes Bobst Professor of Pharmacology

38 John Morgan Building Office: (215) 898-0420 Fax: (215) 573-7188 Email: <u>eberwine@upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g275/p5441

#### Research summary

The research efforts of my laboratory are directed towards understanding the molecular basis of neuronal functioning. Our experimental approach is reductionist in nature and involves analysis of gene expression in individual cells dispersed in culture, in the live slice preparation or from fixed pathological tissue specimens. We have developed various procedures that have enabled the analysis of cellular functioning using single cells as the experimental model. These procedures include those that permit an analysis of the mRNA complement, the protein complement and an assessment of mRNA movement and translation within single cells. This level of analysis is important since an individual cells biochemical compostion may be diluted by that of surrounding cells. We are currently generating molecular and bioprocess fingerprints of various cell types and disease states. When this is complete, we hope that it will be possible to alter the cellular response to various challenges by altering the levels of these biological processes in a predictable manner. As part of these studies, we are examining the role of subcellular localization of mRNAs in regulating cellular function. We have shown that multiple mRNAs are localized in neuronal dendrites and have provided a formal proof of local mRNA translation in dendrites. Further, we have recently shown that the intracellular sites of localization and translation of these mRNAs can be altered by synaptic stimulation highlighting for the first time that in vivo translation of a mRNA can occur at different rates in distinct regions of a single cell (translation is primarily exponential in dendrites and linear in the cell soma). These insights into the cell biology of neuronal function highlight the complexities that remain to be understood.

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## Roderic G. Eckenhoff, M.D.



Austin Lamont Professor of Anesthesiology and Critical Care

311A John Morgan Building Office: 215-662-3705 Fax: 215-349-5078 Email: <u>roderic.eckenhoff@uphs.upenn.edu</u> <u>http://www.med.upenn.edu/apps/faculty/index.php/g319/p8434</u>

#### **Research Overview**

#### MOLECULAR PHARMACOLOGY OF INHALED ANESTHETICS

The inhaled anesthetics are considered one of the most important medical advances of all time, are used in over 100 million patients every year, and yet remain the most toxic and poorly understood of all drugs. The goal of my laboratory is a translational understanding of inhaled anesthetic pharmacology. Most of the current work uses biophysical and chemical biological characterization of anesthetic/macromolecular interactions because of the importance of establishing a foundation of knowledge at this most basic level, on which the subsequent superstructure of molecular, cellular and organism understanding will be built. We have developed a wide variety of experimental approaches to study inhaled anesthetics binding to proteins, and the structural and dynamic consequences. Thus, photoaffinity labeling, fluorescence spectroscopy, amide hydrogen exchange, low-affinity elution chromatography and differential/isothermal calorimetry have all been introduced and validated for this purpose. Many protein and peptide models are used, including serum albumin and its domains, odorant binding protein, rhodopsin and other G-protein-coupled receptors, ferritin, and de novo designed helical bundles. Our group also uses NMR spectroscopy, x-ray crystallography and molecular dynamic simulations via close collaborations to gain a detailed atomic-level appreciation for the interactions and consequences in both time and space. In collaboration with Pat Loll of Drexel University, we have characterized halothane, isoflurane and propofol complexes with various proteins. In collaboration with the Dailey and Dmochowski labs (Chemistry), we synthesize novel reagents to allow photolabeling, click chemistry and fluorescence imaging to further identify cellular and molecular substrates of anesthetic action. Proteomic and genomic approaches have permitted initial forave into cell and organism implications of our binding results. Wide collaborations with many other departments and institutions have facilitated a rapid, multidisciplinary attack on some of the most fundamental questions in anesthetic pharmacology.

#### NEURODEGENERATIVE DISORDERS

Our studies of inhaled anesthetics led to the observation that they can potently promote aggregation of selected peptides and proteins. Since a common feature of most neurodegenerative disorders is aggregation of endogenous peptide, inhaled anesthetics may enhance this process, and accelerate the onset of the disorder. Examination of this possibility in a fully translational manner is a growing focus of my laboratory. Current efforts include cell culture, transgenic animals, clinical biomarker studies and associative database studies.

#### **Selected Publications**

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### Amelia J. Eisch, Ph.D. Professor of Anesthesiology and Critical Care

Abramson Research Center, Room 402F

Email: <u>eischa@email.chop.edu</u>

#### **Description of Research Expertise**

I am neuroscientist with a broad interest in how molecular and cellular changes – such as the changes in the number of neurons generated in the hippocampus, a brain region important for learning/memory and regulation of anxiety and the stress response – influence both normal behavior and cognitive functioning. I am interested in how developmental and adult neurogenesis in particular and dentate gyrus plasticity in general contribute to abnormal functioning with relevance to developmental, psychiatric, and neurological disorders. Current Eisch Lab projects span genetic, molecular, cellular, circuit, and functional/behavioral levels, and are funded by NASA and NIH (both the National Institute on Drug Abuse and National Institute on Mental Health).

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### Karin Eisinger, Ph.D. Assistant Professor of Pathology and Laboratory Medicine

Room 414, BRB II/III Office: 215-898-9086 Fax: 215-746-5511 Email: <u>karineis@mail.med.upenn.edu</u> http://pathology.med.upenn.edu/department/people/689/tzipora-sarah-karin-eisinger

#### **Research Expertise**

The role of the Hippo pathway in soft tissue sarcomas

Nearly 15,000 Americans are diagnosed with a form of soft-tissue sarcoma every year and roughly 30% of these tumors will result in potentially lethal lung metastases. The roughly 65 sarcoma subtypes, derived from a variety of mesenchymal tissues including, bone, muscle, cartilage, and fat, present a complex research problem. This complexity has resulted in a distressing lack of funding and no targeted therapies. In fact, sarcoma treatment has not changed significantly in 25 years. Patients are limited to radiation, toxic chemotherapy, and surgery. The discovery of novel targets and mechanisms is therefore critical. Several studies, including my own, have shown that deregulation of the Hippo pathway, and its main downstream effector YAP1, is required for proliferation in several common sarcoma subtypes, including fibrosarcoma, liposarcoma and undifferentiated pleomorphic sarcoma (UPS).

The Hippo pathway is required for proliferation control in sarcoma cells. This signaling hub consists of a kinase cascade whose purpose is to phosphorylate YAP1 leading to its proteasomal degradation. Inactivation of the pathway in response to upstream growth signals leaves YAP1 uphosphorylated allowing its nuclear localization. Nuclear YAP1 co-activates transcription of pro-survival and proliferation targets (i.e. BIRC5, FOXM1), though it can also repress transcription of certain genes. Though it is implicated in sarcomagenesis, regulation of YAP1 and its critical downstream transcriptional targets are virtually unknown in this context. Investigation of these mechanisms will reveal novel therapeutic opportunities for sarcoma patients and potentially in epithelial tumors as well. The "epithelial-to-mesenchymal transition" (EMT) is critical for metastasis of epithelial cancers (i.e. breast, pancreas). Characterization of YAP1 and its targets in mesenchymal cells may help elucidate the role of YAP1 during EMT and metastasis. Interestingly, no common mutations in Hippo pathway components have been reported in sarcomas and copy number loss of the key proteins occurs in only 25% of reported cases. Our recent work highlighted the role of epigenetic silencing in sarcoma; therefore we are investigating the possibility that YAP1 modulators are epigenetically regulated.

#### Mechanisms of sarcoma metastasis

Metastasis is the most lethal aspect of cancer. 30%-50% of all malignancies will metastasize resulting in more than 90% of cancer-related fatalities. There is a critical need for a thorough understanding of metastatic processes and the development of new approaches targeting metastatic cells. For many types of cancer including breast, prostate, kidney and soft tissue tumors the lung is the most common site of metastasis. In fact, soft tissue sarcomas disseminate almost exclusively to the lungs in both humans and preclinical mouse models, highlighting the usefulness of sarcoma models in the study of pulmonary metastasis. The lack of novel therapies against pulmonary metastases can be attributed in part to the technical difficulties associated with studying metastatic cells. Vascular adherence and extravasation have been particularly challenging to investigate due to the difficulty in modeling these processes. One recent hypothesis is that platelets promote metastasis by enhancing extravasation. The role of collagen in activating platelets, through the surface receptor GPVI, during wound healing is well understood; however the contribution of collagen-activated platelets to tumor cell

extravasation and metastasis is unknown. Upon activation, platelets secrete the contents of their alpha and dense granules, which contain signaling molecules that open the endothelial wall of blood vessels during wound healing in order to recruit additional platelets and other cells necessary for repair. During metastasis, this process could be repurposed to allow tumor cells to exit the vasculature and enter the lung.

The tools to evaluate this question mechanistically have not been widely available. However, we have now identified the technology, assays, and models to evaluate tumor cell adherence and platelet-mediated extravasation in the physiologically relevant setting of spontaneous in vivo undifferentiated pleomorphic sarcoma (UPS) metastasis to the lung. These tumors are highly metastatic and we can model pulmonary metastasis using multiple tools already available in my lab including human UPS cells for xenograft, as well as two independent autochthonous genetic models (KrasG12D/+; Ink4a/Arffl/fl and KrasG12D/+; Trp53fl/fl (5)), and allografts of murine tumor cells derived from these genetic models. Our published work using these systems has reported that lung metastases in sarcoma are associated with increased primary tumor expression of the intracellular collagen-modifying enzyme PLOD2/lysyl hydroxylase 2. Excessive lysyl hydroxylation, due to PLOD2, results in secretion of immature collagen molecule aggregates able to physically associate with tumor cells. Other groups have reproduced this observation in breast and liver cancers, suggesting broad implications for our work. We have also shown that PLOD2 is required for the vascular adhesion and extravasation stages of metastasis. However, we do not yet understand how PLOD2 regulates this process. We have found metastatic sarcoma cells residing in pulmonary vessels where they deposit significant amounts of collagen but the importance of this ECM deposition and modification in sarcoma cell extravasation and lung colonization is essentially unknown. These questions are critical as the answers may explain why lung metastases can be succesfully ablated only to reappear within several months. Intravascular tumor cells may be protected from exposure to chemo and radiotherapy due to their vascular adherence and surrounding collagen. Thus, when lung resident tumor cells are killed by chemo/radiation therapy, they can be replaced by surviving cells from the "source blood vessel". The role of deposited collagen in the vessel may be two-fold: 1) to physically allow tumor cell adherence to vascular endothelial cells and 2) GPVI receptor-mediated platelet activation. Our work will evaluate these hypotheses and determine the role of collagen in vascular adherence and extravasation for the purpose of identifying novel therapeutics that could target the molecular processes underlying pulmonary metastases in sarcoma and other cancers..

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### Michael Farwell, M.D.

Assistant Professor of Radiology at the Hospital of the University of Pennsylvania

Hospital of the University of Pennsylvania Department of Radiology Division of Nuclear Medicine and Clinical Molecular Imaging Office: 215-662-7750 Fax: 215-349-5843 Email: michael.farwell@uphs.upenn.edu

#### **Selected Publications**

Chen X, Yang Y, Berger I, Khalid U, Patel A, Cai J, Farwell MD, Langer C, Aggarwal C, Albelda SM, Katz SI: Early detection of pemetrexed-induced inhibition of thymidylate synthase in non-small cell lung cancer with FLT-PET imaging. Oncotarget 8(15): 24213-24223, 2017.

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# Jeffrey Field, Ph.D.

Professor, Department of Pharmacology

1313 BRB 2-3 Phone: 215-898-1912 Fax: 215-573-0200 Email: jfield@upenn.edu http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p16384

#### Research Overview

Systems Pharmacology of Ras signaling in cancer:

Mutations in genes called oncogenes lead to the uncontrolled growth that is the hallmark of cancer. Oncogenes express proteins that regulate signaling pathways essential to the tumor cell. We study the Ras oncogene, one of the most commonly mutated oncogenes. Mutational activation of Ras causes changes in three basic properties of cells. These are: (1) increases in cell proliferation to stimulate growth, (2) reorganization of the actin cytoskeleton to promote invasion and metastases and (3) inhibition of apoptosis to prevent tumor cells from undergoing programmed cell death. Previously, we studied Ras signaling in tumors focusing on the role of Pak kinases, providing the first proof-of-principle that Pak kinases are targets for new targeted therapies. Indeed, numerous companies and academic groups are developing small molecule inhibitors of Pak. More recently we developed a systems approach to study Ras tumors using genomics, high throughput screening and siRNA screening. Ongoing studies are validating lead compounds and genes identified in screens as well as developing new screening platforms. Despite some successes in targeting other oncogenes, Ras presently un-druggable and our screens promise to identify targets and validate drugs against Ras in several cancer models.

#### Cytoskeletal signaling pathways:

We discovered a family of proteins in yeast known as cyclase associated proteins (CAP). In yeast, they are required for Ras signaling, but in mammalian cells, they participate in cytoskeletal signaling. Current studies with CAP use in vivo models to study CAP2 function in cardiac physiology and signaling.

#### Mechanisms of environmental toxicology:

We also use a systems approach to study environmental toxicology. Past work linked one of the most potent carcinogens in tobacco with the most widely reported stress in smokers—oxidative stress.

I direct two graduate courses (Pharm 623 and Pharm 495). Pharm 495 teaches high throughput screening using a hands-on approach to systems cancer biology. I also direct the TREES summer program for High School students and the STEER summer program for college students, two community outreach programs that provide mentoring opportunities for graduate students.

#### **Selected Publications**

Guo Jianman, Grovola Michael R, Xie Hong, Coggins Grace E, Duggan Patrick, Hasan Rukhsana, Huang Jiale, Lin Danny W, Song Claire, Witek Gabriela M, Berritt Simon, Schultz David C, Field Jeffrey: Comprehensive pharmacological profiling of neurofibromatosis cell lines. American journal of cancer research 7(4): 923-934, 2017.

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# Garret A. FitzGerald, M.D.

Chair, Department of Systems Pharmacology and Translational Therapeutics Professor, Departments of Medicine and Systems Pharmacology Robert L. McNeil, Jr., Professor in Translational Medicine and Therapeutics Director, Institute for Translational Medicine and Therapeutics Associate Dean of Translational Research

Smilow Center for Translational Research (SCTR), Room 10-122. Phone: 215 898-1185 Fax: 215 573-9135 Email: <u>garret@upenn.edu</u> <u>http://www.med.upenn.edu/fitzgeraldlab/</u>

#### **Research Overview**

Our laboratory has two areas of interest – prostanoid biology and the role of peripheral molecular clocks in cardiovascular biology, metabolism and aging. Perhaps the distinguishing feature of our groups is that we pursue interdisciplinary translational science with a focus on therapeutics. Thus, we work in different model systems – mammalian cells, worms, fish and mice – but also in humans. Ideally we develop quantitative approaches that can be projected from our experiments in the model systems to guide elucidation of drug action in humans. To this end, we have long utilized mass spectrometry, initially to target the arachidonate derived lipidome, but also the proteome.

Currently, we are interested in several aspects of prostanoid research. We utilize a remarkably broad array of mutant mice to elucidate the biology of the two COX enzymes and the prostanoid receptors. We are particularly interested in the genomic and environmental factors that contribute to variability in response to nonsteroidal antiinflammatory drugs and integrate data from model systems and humans to predict analgesic efficacy and cardiovascular risk.

We are interested in the comparative efficacy and safety of pharmacological inhibition of COXs versus the microsomal PGE synthase–1 and have interest in targeting the macrophage mPGES-1 and the F prostanoid receptor.

In the area of clock biology, we are using cell specific deletions of core clock components to look at how between discrete peripheral clocks influence cardiovascular biology and metabolism. We have a major initiative integrating remote sensing and multi-omics approaches to characterize the human physiological chronobiome as a prelude to seeking discordance in diseases with time dependent phenotypes, such as myocardial infarction, stroke, asthma and depression.

#### **Recent Publications:**

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- Skarke C., Almuddin N., Lawson J.A., Ferguson J., Reilly M. and FitzGerald G.A. Bioactive Products formed in Humans from Marine Lipids. J. Lipid Res. 56: 1808-20 2015.
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## Dmitry I. Gabrilovich, M.D., Ph.D.

Wistar Institute Professor of Pathology and Laboratory Medicine

Phone: 215-495-6955 Email: <u>dgabrilovich@wistar.org</u> https://www.wistar.org/our-science/scientists/dmitry-gabrilovich-md-phd

#### **Research Interests**

The laboratory of Dmitry Gabrilovich focuses on understanding of the role of tumor microenvironment in regulation of immune responses in cancer and tumor progression with specific emphasis on meyloid cells. Based on advances in basic research in the lab they develop new methods of cancer therapy.

Myeloid cells play a major role in regulation of immune responses. They include professional antigen-presenting cells, dendritic cells (DC), macrophages and myeloid-derived suppressor cells. Data generated in his laboratory have demonstrated that differentiation and function of various myeloid cells in cancer is severely affected. Gabrilovich and his team was one of the first who identified the phenomenon of abnormal regulation of DC differentiation and cancer and described the mechanisms regulating this phenomenon. They proposed several therapeutic strategies to overcome those defects. Some of them are currently being tested in clinical trials.

Gabrilovich and his group have found that defects in differentiation of DC are associated with accumulation of immature myeloid cells in tumor-bearing animals and patients with cancer. Under normal conditions, these cells represent an intermediate stage of myeloid cell differentiation. In cancer, however, they lose the ability to differentiate into mature myeloid cells, including granulocytes, DC, and macrophages. They become functionally defective and acquire the ability to suppress immune responses. Gabrilovich together with investigators from other institutions coined the term "myeloid-derived suppressor cells (MDSC)" which is now widely used to characterize these cells. Since 2007, when the term was introduced by Gabrilovich and colleagues, more than 2200 papers studying these cells were published.

His lab looks at different aspects of immature myeloid cell biology in cancer. First, they are trying to understand the signaling pathways that are responsible for accumulation and functional defects of immature myeloid cells in cancer. These pathways include NF-kB, Jak-STAT, Notch, Wnt, Rb, and others. Second, they are investigating cellular and molecular mechanisms of T-cell suppression and tolerance induced as a result of abnormal differentiation of myeloid cells and abnormal DC function. The main focus of this group is on the role of reactive oxygen species and peroxynitrite in regulation of T-cell function. His work demonstrates that reactive oxygen species produced by immature myeloid cells in vitro and in tumor-bearing animals in the presence of tumor-derived soluble factors are substantial contributors to the immunosuppression mediated by these cells in cancer. In recent years Dr. Gabrilovich is focused on the role of lipid accumulation in the defective function of DCs and MDSC in cancer as well as on the mechanisms regulating MDSC migration to form pre-metastatic niche and activate dormant tumor cells.

Gabrilovich and his groups also investigate new immune therapy strategies in cancer. They are exploring several different approaches, including genetically modified DCs, T-cell transfers, checkpoint blockade, and others. In recent years the focus of the lab on the emerging new paradigm of combining conventional chemotherapy, radiation therapy, and immunotherapy.

#### **Recent Publications**

- Cheng P, Kumar V, Liu H, Youn JI, Fishman M, Sherman S, Gabrilovich D. Effects of Notch signaling on regulation of myeloid cell differentiation in cancer. *Cancer Res.* 2014 74(1):141-152.
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#### **Research Interests**

# Benjamin Garcia, Ph.D.

Presidential Associate Professor Departments of Biochemistry and Biophysics Epigenetics Program

Phone: 215-573-9423 (office) Emai I: <u>bgarci@mail.med.upenn.edu</u> <u>http://hosting.med.upenn.edu/garcialab/research/</u>

Quantitative Mass Spectrometry Based Proteomics for Characterizing Modified Proteins and Proteomes

The sequences of the human genome and genomes of many other organisms are now readily available and have revolutionized modern biological research. Nevertheless, the next challenge presently on the horizon (after the post-genome era) is the comprehensive characterization of cellular proteins (i.e. the "proteome"), the 'active/expressed' part of the genome. DNA sequence or mRNA levels alone cannot predict the dynamic aspects of cellular function. Proteins, their post-translational modifications (PTMs) and the multi-protein complexes they form are the driving forces of cellular machinery that control a diverse number of physiological events. These observations have led to the emergence of a new sub-field of contemporary biology called Proteomics: the characterization of the protein complement expressed by a genome of a particular organism, tissue or cell. At the heart of proteomic experiments is the use of nanoflow liquid chromatography-tandem mass spectrometry for the analysis of complex protein mixtures, which is arguably the most rapid, sensitive and accurate technique available for sequence characterization of proteins.

The Garcia laboratory is focused on developing novel mass spectrometry based proteomic methodologies for quantitatively characterizing changes in protein and proteome expression and post-translational modification state during significant biological events, or in response to external perturbation. Our goal is to utilize large-scale proteomic data to improve our understanding of biological processes at the molecular level. Application of our proteomic technology spans several areas of cellular biology, but a couple of main interests are described below.

Towards deciphering the epigenetic Histone Code

Epigenetics refers to stable heritable changes in gene expression that are not due to changes in DNA sequence, such as DNA methylation, RNA interference and histone PTMs. These epigenetic changes are responsible for generating different cell types originating from the exact same genome. Emerging as one key regulator of cellular memory are histones. Histones are small basic proteins that function to package genomic DNA into repeating nucleosomal units (containing ~146 bp of DNA wrapped around two copies each of histones H3, H4, H2A and H2B) forming the chromatin fiber and hence our chromosomes. In general, the packaging of DNA into chromatin is recognized to be a major mechanism by which the access of genomic DNA is restricted. This physical barrier to the underlying DNA is precisely regulated, at least in part, by the PTMs on histones. A wide number of studies show that several single covalent histone modifications such as methylation, acetylation, phosphorylation and ubiguitination located in the N-terminal tails correlate with both the regulation of chromatin structure during active gene expression, or heterochromatin formation during gene silencing (i.e. the "Histone Code"). Nevertheless, it is currently unknown what effects, if any, multiple combinations of histone modifications might exert, and translating the combinatorial modification patterns of histones into biological significance remains a significant challenge. Additionally, these histone PTMs occur on multiple but specific sites, suggesting that histones can act as signaling platforms for proteins that bind or "read" these marks. In support, several proteins that contain special domains that bind various PTM sites on histories have been discovered. The Garcia lab has developed proteomics techniques that are considered state of the art for histone PTM analyses and are used world-wide by many research groups. Therefore, we feel that the utilization of advanced proteomic technology in the chromatin biology field will enhance investigations of histone modifications to a much higher scale. In combination with cell and biochemical experimentation, bioinformatics analysis and other "omics" technologies;

we feel that our large-scale proteomic data will help provide a systems biology outlook on epigenetic processes that will lay the foundation for development of drug treatments for human diseases that are believed to involve epigenetic mechanisms.

Dynamics of proteome-wide PTM mediated signaling pathways

Another goal of the Garcia lab is to develop and apply novel proteomics based methodology to understand how signaling pathways affect cellular functions and ultimately cell phenotypes. We use quantitative mass spectrometry to measure dynamic changes in protein abundances, protein PTM states, and to characterize protein:protein interactions. For example, we are specifically developing large-scale approaches to isolate and characterize a variety of different types of PTM modified proteomes (e.g. protein phosphorylation, methylation, acetylation, glycosylation, ADP-ribosylation, etc.). These types of approaches allow for example, the detection of thousands of modified proteins from cells or tissues. When combined with quantitative proteomics techniques such as stable isotope labeling of amino acids in cell culture (SILAC), these cutting-edge tools allow us to examine with unprecedented detail, the molecular level events involved in various biological processes such as during stem cell differentiation, viral infection, metabolic disorder or cancer progression. We are also very interested in the dynamics of protein modification, and have developed in vivo cellular metabolic labeling strategies to specifically label newly modified proteins. This methodology allows us to determine protein modification turnover rates or kinetics in response to external stimuli. These experiments have allowed us to define for the first time the dynamics of particular classes of modified proteins on a proteome scale. Lastly, we are extremely interested in how these different protein PTM signaling pathways crosstalk with one another, and we are developing the platforms to determine which modifications are found simultaneously on the same proteins, and how this biological code is then transformed to direct a myriad of cellular functions.

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### Saar I Gill, MD, PhD

Assistant Professor Of Medicine At The Hospital Of The University Of Pennsylvania

Smilow Translational Research Center 8-101 Philadelphia, PA 19104 Office: (215) 573-4015 Lab: (215) 573-4015 Email: <u>saar.gill@uphs.upenn.edu</u>

#### **Description of Research Expertise**

Tumor Immunology Chimeric Antigen Receptor T cells Mouse Models of Human Leukemia Murine Xenografts Adoptive Cellular Therapy Genetic Engineering of T cells Flow Cytometry

Investigators in the Gill laboratory work on aspects of cellular immunotherapy for hematologic malignancies, in particular leukemia and lymphoma. We follow an iterative process of target discovery, production of novel chimeric antigen receptors, and their validation in both in vitro and in vivo models. Our goal is to translate new, potent and safe antigen-specific immunotherapy from brainchild to therapeutic agent as quickly as possible.

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# Jerry D. Glickson, Ph.D.

Research Professor, Department of Radiology Director of Molecular Imaging

B-6 Blockley Hall Phone: 215-898-1805 Fax: 215-573-2113 Email: <u>glickson@mail.med.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p6579

#### **Research Interests**

Prediction and Early Detection of Response of non-Hodgkin's Lymphoma

My laboratory initiated the field of NMR spectroscopy of tumors in mice in about 1980 by demonstrating that tumors exhibited detectable changes in bioenergetics, pH and phospholipid metabolism that could be utilized for detection and prediction of therapeutic response. In 2011 I shared the Gold Medal of the International Society of Magnetic Resonance in Medicine with John Griffiths of Cambridge University for our pioneer work on MRS of cancer. My laboratory has been developing 31P, 1H and 13C MRS methods as well as physiologically sensitive MRI techniques for monitoring metabolic changes in tumors that predict or detect therapeutic response; we generally develop these methods in perfused cells and mice and then translate them to human patients. Our focus is largely on non-Hodgkin's lymphoma (NHL) since this malignancy exhibits roughly a 50% response rate. We have recently discovered that NHL tumors in mice are guite unique in that they exhibit extremely well resolved 13C MR spectra. By monitoring the kinetics of 13C-isotope exchange and fitting these data to a metabolic network model, we can quantitate flux through specific pathways of tumor energy and phospholipid metabolism and translate this into the amount of ATP that is produced from various substrates in tumors. We are also exploring the use of hyperpolarized 13C-labeled substrates to the study of tumors. Detecting tumor response to inhibitors of signal transduction pathways is a major challenge in the clinic. We have recently demonstrated that administration of specific inhibitors of mTOR produces a marked reduction in glycolytic metabolism as a consequence of decreased expression of hexokinase-2 and other glycolytic enzymes. We can readily detect this effect by monitoring lactic acid in the tumor (in both mice and men). We are extending this approach to other signaling pathways such as ALK and PI3K/AKT inhibitors.

Selective Acidification of Melanoma by inhibition of monocarboxylic acid transporters

Melanoma is the deadliest skin cancer and the most rapidly increasing malignancy among Caucasian populations throughout the world. It can only be cured by surgical excision, but the tumor recurs in about 20% of the cases. There is currently no effective way to treat the disseminated disease. Targeted therapies are under development and show promising activity but are generally not curative since tumors exhibit a remarkable facility for circumventing these agents. We have been developing a method that does not target a specific gene or antigen but instead targets a key metabolic property of tumors – their preference for glycolytic metabolism (the Warburg effect). The end product of glycolysis is pyruvate, the majority of which is converted to lactate and transported out of the cell via monocarboxylic acid transporters (MCT). We have been using lonidamine, which is believed to inhibit MCT1, the key pathway for lactate export, thereby trapping lactic acid in the tumor cell. This decreases the intracellular pH of melanomas in mice (pHi) from about 7 to 6.4. It also dramatically decreases the ATP level in the tumor, probably by inhibiting a putative pyruvate transporter in the mitochondrial membrane (thus blocking oxidative metabolism in the tumor). These effects are remarkably specific for the tumor and produce minimal effects on normal tissues in the body. We are exploiting this selective acidification of the tumor and de-energization of tumor cells by lonidamine to dramatically increase melanoma response to two drugs, melphalan and doxorubicin, that normally are not effective against this disease but whose activity is markedly

increased under acidic conditions in tumor cells. We believe that by combining this metabolic strategy with the targeted therapies under development by pharmaceutical companies, we may be able to approach a cure of this deadly disease.

#### Imaging the Metastatic Potential of Tumors

We have also been studying the mechanism underlying tumor metastasis. We use a panel of human melanoma xenografts that vary in metastatic potential from highly indolent to highly aggressive (invasive). Using an MRI method that employs a paramagnetic contrast agent, GdDTPA, we can demonstrate that contrary to general belief, the indolent tumor is actually much better perfused (i.e., has a better blood supply) than the aggressive tumors. The aggressive tumors have a well-perfused rim but a poorly perfused central core. Using a low temperature fluorescence technique that Britton Chance developed at Penn in the 1980s, we found that the indolent tumors exhibited much higher levels of NADH that was relatively uniformly distributed throughout the tumor. Since NADH and FADH2 are the key substrates for oxidative phosphorylation, the indolent tumors were well supplied with energy. However, the aggressive melanomas showed a high level of NADH in their outer rim but a low level in their central core, which instead contained high levels of oxidized flavoproteins. In short, the aggressive tumors had a poorly perfused core in which the tumor cells were starved for substrates. We hypothesize that this highly inhospitable microenvironment in the core of the tumor provides an evolutionary pressure favoring the survival of tumor cells with the ability to move to more hospitable environments, i.e. to metastasize. It also induces these tumors to become cannibalistic and break down their own tissues to generate substrates for generating energy and to support proliferation. This phenomenon is called autophagy, and there are ways to inhibit this process and kill the tumor cells that depend on it. This theory still needs to be validated, but its implications for controlling tumor metastatic potential, the key cause of death in cancer, is considerable.

#### Carbon-13 NMR Studies of Tumor Intermediary Metabolism

We have been using 13C MRS to study the bioenergetics of melanoma tumor cells. We have been able to demonstrate that the DB1 melanoma tumor line obtains about 46% of its ATP from glycolysis and 54% from oxidative phosphorylation. The method for measuring flux through these metabolic pathways is called bonded cumomer analysis and involves the solution of ~150 differential equations. It was developed by our collaborator, Alex Shestov, at the University of Minnesota. We are extending this method to all the pathways of tumor intermediary metabolism. A key objective will be to apply this method to human cancer patients. Melanoma may not prove to be the ideal tumor for this purpose, but NHL appears to be a much better target because for reasons that are poorly understood, this tumor yields much more well resolved 13C NMR spectra. In addition, we could apply this method to any hematological cancer like leukemia since leukemic cells are routinely removed from the body and can be grown in a bioreactor. We have constructed various bioreactors for studying various types of perfused cells. Another potential application of this technology is to targeted lymphocytes that Carl June and coworkers are developing for treatment of various malignancies.

#### Lipoproteins as Marker Genes and Theranostic Agents

Since lipoproteins are naturally occurring nanoparticles, they are generally acceptable to humans and other immunocompetent animals. We have been developing lipoproteins as carriers of near infrared and NMR indicators for in vivo tracking and for delivery of drugs and photodynamic therapy agents for cancer therapy. Because lipoprotein receptors are not unique to cancer, we have been developing novel strategies for retargeting these agents to more cancer-specific receptors such as folate receptors. Much of this research has been directed against ovarian cancer, a malignancy that overexpresses folic acid receptors.

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### Casey S. Greene, Ph.D.

Assistant Professor of Pharmacology

10-131 Smilow Center for Translational Research Email: csgreene@mail.med.upenn.edu

#### **Description of Research Expertise**

Our overarching goal is to transform how we understand complex biological systems by developing and applying computational algorithms that effectively model processes by integrating multiple types of big data from diverse experiments. This allows us to infer the key contextual information required to interpret such data, and facilitates both the computationally driven asking and answering of basic science and translational research questions.

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# Judith B. Grinspan, Ph.D.



**Research Assistant Professor of Pharmacology** 

516D Abramson Center Office: (215) 590-2094 Fax: (215) 590-3709 Lab: (215) 590-5179 Email: grinspan@email.chop.edu http://www.med.upenn.edu/apps/faculty/index.php/g20000320/p6243

#### **Research Interests**

In the central nervous system, oligodendrocytes synthesize myelin as an extension of their plasma membranes. This myelin wraps axons and facilitates rapid and efficient conduction of nervous impulses as well as axonal nourishment and protection. Destruction of myelin through injury, such as birth injury leading to cerebral palsy, or disease, such as multiple sclerosis or HIV, causes loss of motor and cognitive function. Oligodendrocyte precursors and stem cells remain in the CNS following the pathology and are potentially capable of forming mature oligodendrocytes and then myelin. However, their maturation is severely limited. Reasons for this include processes such as oxidative stress and inflammation which signal to inhibitors present in the area that impede maturation. Our goal is to identify factors in the CNS that inhibit the development of mature oligodendrocytes both during development and disease. We have identified several key signaling factors that regulate developmental myelination and are increased during demyelinating disease. On-going areas of investigation in the lab include: 1) The role of white matter loss and demyelination in HIV-associated neurocognitive deficits. 2) Factors which limit myelination in perinatal white matter injury. 3) The role of lipid signaling in developmental myelination following demyelinating disease.

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### Tilo Grosser, M.D. Research Assistant Professor of Pharmacology

10-103 Translational Research Center Phone: (215) 573-7600 Email: <u>tilo@mail.med.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g275/p9176

#### **Research Interests**

Non-steroidal anti-inflammatory drugs (NSAIDs), which include both traditional NSAIDs (e.g. naproxen, ibuprofen) and NSAIDs selective for cyclooxygenase (COX)-2 (rofecoxib, valdecoxib, etoricoxib, lumiracoxib, celecoxib) relieve pain, inflammation and fever by inhibiting the formation of bioactive prostanoids. Despite their efficacy in the relief of pain and inflammation, NSAIDs may be associated with gastrointestinal complications, including serious bleeds. Selectivity for COX-2 has been shown to reduce the incidence of these serious events, but is more likely to cause serious cardiovascular events than non-selective COX inhibition.

Dr. Grosser is studying the mechanisms of these complications using genomics, proteomics, lipidomics approaches in model organisms and in proof-of-concept studies in healthy volunteers. One aim of this research is to identify approaches to the personalization of NSAID therapy.

#### **Recent Publications**

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### Chang-Gyu Hahn, M.D., Ph.D.

Associate Professor of Psychiatry

2003 Translational Research Laboratories Phone: 215-898-8793 Fax: 215-573-2041 Lab: 215-746-0684 Email: <u>hahnc@mail.med.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g275/p18424

#### Research Overview

The primary interest of my laboratory program lies with the molecular and cellular pathophysiology of psychotic and mood disorders. Directing the Neuropsychiatric Signaling Program in the department of psychiatry, my research has a special focus on identifying intracellular and molecular alterations in neural tissues derived from patients and investigating their underlying mechanisms in animal and in vitro models. Examining molecular and cellular processes occurring in patients has been one of fundamental challenges in the field. In response, my laboratory has taken a path of developing new research paradigms to address questions that could not have been otherwise.

There are two lines of research paradigms that we have developed: analyses of subcellular proteome and intracellular signaling in postmortem brains and of olfactory neuroepithelial biopsy tissues derived from patients. Postmortem brain tissues may harbor biological characteristics linked to the subjects' clinical profiles, but study of intracellular signaling in those tissues has been hampered. To that end, we have established a series of research paradigms to monitor receptor-mediated activation of intracellular signaling to isolate subcellular fractions enriched for post-synaptic density and synaptic membranes, to assess kinase activity in synaptic membranes and to capture protein complexes followed by mass spectrometer based quantitative proteomics. The olfactory neuroepithelial (OE) biopsy approach offers unique opportunities to obtain neural tissues of living patients that can be studied using ex vivo and in vitro paradigms. This paradigm permits us to address clinically relevant molecular and cellular mechanisms of neuropsychiatric illnesses, specifically pertinent to certain phase or state of illnesses. We have established olfactory neuroepithelial cell lines derived from more than 400 subjects with various psychiatric illnesses. Presently we examine these cells for various molecular pathways implicated for schizophrenia, bipolar disorder and depression using an induced neuronal cell paradigm.

#### **Recent Publications**

- Turetsky Bruce I, Hahn Chang-Gyu, Arnold Steven E, Moberg Paul J: Olfactory receptor neuron dysfunction in schizophrenia. Neuropsychopharmacology: official publication of the American College of Neuropsychopharmacology 34(3): 767-74, Feb 2009.
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### Malay Haldar, MD, PhD Assistant Professor of Pathology and Laboratory Medicine

413 BRB II/III, 421 Curie Blvd Philadelphia, PA 19104 Office: 2155739704 Fax: 2157465511 Email: <u>mhaldar@mail.med.upenn.edu</u> https://www.med.upenn.edu/apps/faculty/index.php/g275/p8840134

#### **Description of Research Expertise**

Research in our laboratory is at the intersection of innate immune system and solid tumor biology. Specifically, we study the mononuclear phagocyte system (MPS) with an emphasis on their role in the tumor microenvironment. MPS is part of the innate immune system and comprises of monocytes, macrophages, and dendritic cells (DC). These cells are functionally, phenotypically, and developmentally heterogeneous with many distinct subsets. We are interested in understanding the molecular basis of this developmental and functional heterogeneity within the MPS. A major focus in our laboratory is to understand the role of MPS within the microenvironment of a group of solid tumors known as sarcomas. DCs and macrophages are thought to play important role in cancer by modulating host-immune responses against the tumor cells, promoting metastasis, angiogenesis, etc. Additionally, the ability of these cells to regulate lymphocyte function makes them an important determinant in the success of cancer immunotherapy. Using a combination of advanced genetically engineered mouse models in conjunction with patient-derived samples, we aim to uncover the molecular pathways underlying tumor-MPS interaction with the overarching goal of targeting them for therapeutic purposes.

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- Haldar Malay, Murphy Kenneth M: Origin, development, and homeostasis of tissue-resident macrophages. Immunological reviews 262(1): 25-35, Nov 2014.



# Elizabeth A Heller, PhD

Assistant Professor of Pharmacology

10-115 Smilow Center for Translational Research 3400 Civic Center Boulevard, Building 421 Philadelphia, PA 19104 Office: 215 573-7038 Email: eheller@mail.med.upenn.edu

#### **Description of Research Expertise**

The Heller Lab studies the mechanisms by which epigenome remodeling regulates neuronal gene function and behavior. To approach this problem, we directly manipulate histone and DNA modifications at specific genes in vivo, using viral delivery of novel epigenetic editing tools, such as zinc-finger transcription factors and CRISPR/dCas9-fusion proteins. We use high-throughput sequencing to identify genes at which drug- or stress-regulation of a known epigenomic signature correlates with changes in expression. We can then target individual modifications and examine their causal relevance to transcriptional regulation and subsequent behavioral adaptations. This 'bottom-up' approach allows direct elucidation of the causal relevance of epigenetic remodeling in the brain. Because addiction and depression persist long after cessation of the harmful experience, epigenetic remodeling is an attractive underlying mechanism and presents an intriguing target for therapeutic intervention.

- Cates HM, Heller EA, Lardner CK, Purushothaman I, Peña CJ, Walker DM, Cahill ME, Neve RL, Shen L, Bagot RC, Nestler EJ.: Transcription Factor E2F3a in Nucleus Accumbens Affects Cocaine Action via Transcription and Alternative Splicing. Biol Psychiatry 84(3): 167-179, Aug 2018.
- Xu SJ, Heller EA: Single sample sequencing (S3EQ) of epigenome and transcriptome in nucleus accumbens. J Neurosci Methods 308: 62-73, Jul 2018.
- Pierce R, Fant B, Swinford-Jackson S, Heller E, Berrettini W, Wimmer M. : Environmental, genetic and epigenetic contributions to cocaine addiction. Neuropsychopharmacology 43(7): 1471-1480, June 2018 Notes: doi: 10.1038/s41386-018-0008-x.
- Aleyasin H, Flanigan ME, Golden SA, Takahashi A, Menard C, Pfau ML, Multer J, Pina J, McCabe KA, Bhatti N, Hodes GE, Heshmati M, Neve RL, Nestler EJ, Heller EA, Russo SJ. : Cell-Type-Specific Role of ΔFosB in Nucleus Accumbens In Modulating Intermale Aggression. J Neuroscience 38(26): 5913-5924, Jun 2018.
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- Hamilton PJ, Lim CJ, Nestler EJ, Heller EA.: Viral Expression of Epigenome Editing Tools in Rodent Brain Using Stereotaxic Surgery Techniques. Methods Mol Biol. Rots MG & Jeltsch A (eds.). 1767: 205-214, 2018.
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- Hu Q, Greene CS, Heller EA: Specific histone modifications associate with alternative exon selection during mammalian development. Under Review, Nucleic Acids Research 2018.
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Hu Q, Kim EJ, Feng J, Grant GR, Heller EA: Histone posttranslational modifications predict specific alternative exon subtypes in mammalian brain. PLoS computational biology 13(6): e1005602, Jun 2017.



### Marilyn Howarth, M.D.

Adjunct Associate Professor of Emergency Medicine Director, Community Outreach and Engagement Core, Center of Excellence in Environmental Toxicology Perelman School of Medicine Department: Emergency Medicine

1316a Biomedical Research Building II/III Phone: (215) 898-6221 Email: <u>marilyn.howarth@mail.med.upenn.edu</u> <u>http://www.med.upenn.edu/apps/faculty/index.php/g20001020/c2045/p10762</u>

#### **Clinical Expertise**

Occupational and Environmental Exposure Assessment

**Community Exposure Assessment** 

- Howarth MV: Chemical Exposure in the Healthcare Setting and Managing Latex Allergy. Medical Center Occupational Health and Safety. American College of Occupational and Environmental Medicine, taped CME presentation in Chicago, II April 2002.
- Marilyn V. Howarth: *The Latex Sensitive Healthcare Worker*. Occupational health in the Healthcare Industry, Clinics in Occupational and Environmental Medicine. Philadelphia, PA: Saunders, Page: 395-408, May 2001.
- Amy Behrman and Marilyn V. Howarth: *Latex Allergy*. eMedicine: Emergency Medicine. Adler J et al (eds.). Boston: eMedicine Corporation, 2001.
- Howarth MV: *The Management of Latex Allergy and Chemical Exposure in the Healthcare Setting*. Medical Center Occupational Health and Safety. American College of Occupational and Environmental Medicine, taped CME presentation in San Francisco, CA April 2001.



### Xianxin Hua, Ph.D.

Associate Professor of Cancer Biology, Departments of Cancer Biology, Cell and Molecular Biology and Pharmacology

412 Biomedical Research Building II/III Phone: (215) 746-5565 Fax: (215) 746-5525 Email: <u>huax@mail.med.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20001861/p10254

#### **Description of Research**

Our research focuses on elucidating the molecular mechanisms whereby menin, a scaffold protein interacting with multiple epigenetic regulators, regulates endocrine cells, including pancreatic beta cells, endocrine tumors, and MLL fusion protein-induced leukemia. In particular, we are interested in dissecting the function of menin, which is mutated in hereditary human tumor syndrome, Multiple Endocrine Neoplasia Type 1 (MEN1), in repressing beta cells and endocrine tumors and in promoting leukemogenesis.

1. We seek to elucidate how menin suppresses endocrine cells, such as pancreatic beta cells, via regulating histone methylations and expression of pro-proliferative genes. We are also interested in identifying menin-regulated key pathways that can be suppressed to inhibit neuroendocrine tumors.

2. Determining how menin, which acts as a tumor promoter in MLL fusion protein-induced leukemia, cooperates with wild-type MLL protein to promote leukemia and how the menin and wt MLL axis can be suppressed to improve therapy for this aggressive leukemia.

3. Understanding how inhibition of menin leads to reversal of established diabetes in mouse models and determining whether the menin pathway could be explored to ameliorate diabetes.

4. Investigating the interplay between menin, post-transcriptional modifications of menin, and TGF-ß signaling in repressing pancreatic beta cells. As both menin and TGF-ß inhibit cell proliferation, we will test whether menin and TGF-ß cooperate to suppress beta cell proliferation and the underlying mechanisms, using biochemical studies and mouse models.

These comprehensive approaches will provide novel insights into the molecular mechanisms for MEN1 tumorigenesis, regulation of beta cells, and leukemogenesis, shedding light on improving therapy against neuroendocrine tumors, leukemia, and diabetes.

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- Jing Huang, Buddha Gurung, Bingbing Wan, Smita Matkar, Natalia A. Veniaminova, Ke Wan, Juanita L. Merchant, Xianxin Hua\*, and Ming Lei\* (\*co-corresponding author): *The same pocket in menin binds both MLL and JunD, but oppositely regulates transcription*. Nature 432(7386): 542-6, 2012.
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- Yuqing Yang, Haoren Wang, and Xianxin Hua: *Deletion of the Men1 gene prevents streptozotocin-induced hyperglycemia in mice*. Exp Diabetes Res. 2010 2010.



# Harry Ischiropoulos, Ph.D.

Research Professor of Pediatrics

417 Abramson Research Center Phone: 215-590-5320 Fax: 215-590-4267 Email: <u>ischirop@mail.med.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p13832

#### **Research Interests**

Biological chemistry of nitric oxide in cardiovascular and neuronal systems. Oxidative processes in protein aggregation and neurodegeneration. Non-invasive, mass spectrometry-based discovery and validation of disease biomarkers.

#### **Research Summary**

We investigate the biological chemistry and molecular mechanisms of nitric oxide signaling. Nitric oxide is a free radical that mediates blood flow and many other physiological responses within every major organ system.

Currently mass spectrometry-based proteomic data in conjunction with structure-function analysis explore the biochemical and biophysical specificity of two nitric oxide-mediated post-translational modifications cysteine Snitrosation and tyrosine nitration. Studies explore the consequences of these modifications on protein function in metabolic processes and mitochondrial bioenergetics.

We are also generating inventories of mouse brain proteomes, phosphoproteomes, S-nitrosoproteomes and secretomes. These inventories are used to create 3D-functional landscapes of the mouse brain extracellular space and to identify signaling pathways that influence neuron physiology and neurodegeneration.

#### **Research Techniques**

Biochemical analysis of post-translational modifications; liquid chromatography-mass spectrometry; proteomics; nitric oxide detection; cell model systems of neuronal injury.

#### **Recent Publications**

- Doulias P-T. Tenopoulou M, Greene, JL, Raju, K and Ischiropoulos H. Nitric oxide regulates mitochondrial fatty acid metabolism through reversible protein S-nitrosylation. *Sci. Signal.* 6: rs1-7, 2013, PMID: 23281369, PMCID: PMC4010156
- Gould NS, Evans P, Martínez-Acedo P, Marino SM, Gladyshev VN, Carroll KS, Ischiropoulos H. Site-specific proteomic mapping identifies selectively modified regulatory cysteine residues in functionally distinct protein networks. *Chem Biol.* 22:965-75, 2015, PMID: 26165157 PMCID:PMC4515171.
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### Frances E. Jensen, MD, FACP

Professor of Neurology Chair, Department of Neurology

Email: <u>frances.jensen@uphs.upenn.edu</u> <u>http://www.med.upenn.edu/jensenlab/</u>

#### Research Overview

The primary focus of my research is to investigate pathophysiological mechanisms of epilepsy and stroke, and secondary effects on synaptic plasticity. A secondary goal is to elucidate age-dependent differences in such mechanisms, and to examine the interactions between brain development, excitotoxic brain injury, epilepsy and cognition. Neurotransmitter receptors are developmentally regulated, and we have specifically demonstrated critical roles of these receptors, as well as their upstream modulators and downstream effectors, in neuronal and glial cells that are unique to the immature, implying age-specific disease mechanisms. The overall aim is to develop new targets based on novel mechanisms for the treatment of epilepsy, stroke, and autism.

Summary of major research findings:

1. Establishment of in vivo and in vitro rodent models of neonatal seizures and perinatal hypoxic/ischemic cerebral injury for examination of cellular and molecular factors influencing age-specific susceptibility, epileptogenicity, and cellular injury.

2. Demonstration that calcium-permeable AMPA receptors are constitutively expressed on neurons and glia in developing rodent and human hippocampus and neocortex, and that these are critical to the mechanisms of seizures and ischemic injury in the developing brain.

3. First demonstration that AMPA receptor antagonists selectively block seizures in the immature brain, but not in the adult. Additional demonstration that the clinically available drugs topiramate and talampanel attenuate AMPA receptor currents and suppress neonatal seizures and stroke, including periventricular leukomalacia, in rat models.

4. Elucidation of novel calcium-mediated signaling pathways downstream from the AMPA receptor that play critical roles in the pathogenesis of epilepsy in the immature brain, and preclinical efficacy of preventative or rescue treatment in rodent models. Specific pathways include those mediated by early post-translational changes to glutamate and GABA receptors that increase synaptic excitability. First demonstration that AMPA receptor antagonists including NBQX, topiramate and talampanel can reverse these changes when administered as post-seizure treatment, and prevent long term changes.

5. Identification of novel phosphorylation sites Ser 831 and Ser 845 on the GluR1 subunit of the AMPA receptor that are required for the epileptogenic effect of early life seizures, suggesting a novel mechanism for epileptogenesis.

6. Development of novel antiepileptic and neuroprotective strategies that are permissive of neuronal plasticity and long term potentiation. These include the NMDA receptor redox site modulator pyrroloquinoline quinone, and the use-dependent, uncompetitive NMDA blocker memantine as highly protective in vivo and in vitro stroke models, without significant neurocognitive effects.

7. Identified parallel patterns of relative underexpression of the KCC2 chloride transporter versus NKCC1 transporter in human and rodent perinatal cortex during developmental period when GABA receptor agonists are ineffective as antiepileptic agents. This result is the first to strongly implicate the presence of depolarizing GABA receptors in human neonates. This date provided the preclinical target validation that was critical for translation of the use of the NKCC1 inhibitor bumetanide in an FDA approved NIH-funded ongoing clinical trial

at CHB and Partners – Phase I/II safety PK trial in neonatal seizures.

8. Elucidation of abnormal patterns of glutamate and GABA receptors, in human tissue from malformations of cortical development, such as Tuberous Sclerosis, and that these changes are associated with epileptic foci. These results are presently under evaluation with respect to the generation of new clinical treatment trials.

9. Demonstration of convergence of signaling deficits in early life seizures and autism. Alterations in canonical autism-related pathways, including mTOR, FMRP and MeCP2, occur secondary to seizures in the developing brain.

In summary, the emphasis of this translational research program is to identify age-specific mechanisms of brain injury at the cellular level using a variety of in vivo and in vitro techniques, and to use this information to explore and devise experimental therapeutic strategies with clinical potential. Several therapeutic strategies developed in the laboratory are being considered for clinical development. We have established IRBs that have created a repository of human tissue from surgical specimens and autopsy material, and routinely obtain brain tissue directly from surgery for electrophysiological investigation.

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- Engel J Jr, Pitkänen A, Loeb JA, Edward Dudek F, Bertram EH 3rd, Cole AJ, Moshé SL, Wiebe S, Jensen FE, Mody I, Nehlig A, Vezzani A.: *Epilepsy Biomarkers* Epilepsia : 2013.
- Pitkänen Asla, Nehlig Astrid, Brooks-Kayal Amy R, Dudek F Edward, Friedman Daniel, Galanopoulou Aristea S, Jensen Frances E, Kaminski Rafal M, Kapur Jaideep, Klitgaard Henrik, Löscher Wolfgang, Mody Istvan, Schmidt Dieter: *Issues related to development of antiepileptogenic therapies*. Epilepsia 54 Suppl 4 : 35-43,2013.
- Brooks-Kayal Amy R, Bath Kevin G, Berg Anne T, Galanopoulou Aristea S, Holmes Gregory L, Jensen Frances E, Kanner Andres M, O'Brien Terence J, Whittemore Vicky H, Winawer Melodie R, Patel Manisha, Scharfman Helen E: *Issues related to symptomatic and disease-modifying treatments affecting cognitive and neuropsychiatric comorbidities of epilepsy.* Epilepsia 54 Suppl 4 : 44-60,2013.
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### Kelly L. Jordan-Sciutto, Ph.D.

Chair and Professor, Department of Pathology School of Dental Medicine

Rm 312-314 Levy Building Phone: 215 898-4196 Fax: 215 573-2050 Email: jordank@upenn.edu http://www.med.upenn.edu/apps/faculty/index.php/g20000320/p4380730

#### **Research Overview**

Our laboratory investigates molecular mechanisms underlying neurodegenerative processes in the hopes of identifying common and unique players in determining neuronal dysfunction and survivall= among several neurodegenerative diseases driven by neuroinflammation. Currently we are focusing our research efforts on the role of cell cycle proteins, the endogenous antioxidant response and unfolded protein response in three neurodegenerative disorders: HIV encephalitis (HIVE), Alzheimer's disease (AD), and Parkinson's disease (PD).

While HIVE, AD, and PD exhibit different pathologic features, theories as to their etiology share common molecular mechanisms including changes in the trophic factor environment, oxidative stress, and activation of CNS inflammatory components. We hypothesize that neuronal response to these neurodegenerative stimuli includes alterations in expression and/or activity of cell cycle proteins. To this end, we and others have shown that key regulators of cell cycle progression, Retinoblastoma susceptibility gene (pRb), E2F1, and/or p53, exhibit altered levels and patterns of expression in HIVE, PD, and AD. These changes are associated with areas of pathology suggesting a role in degenerative processes. In vitro models of neurodegeneration in each of these diseases also exhibit alterations in cell cycle protein subcellular localization. We are using both human tissue and in vitro models to uncover the role of cell cycle proteins, E2F1, MDMx (a p53 and E2F1 regulatory protein), and pRb in interpreting neuroprotective vs neurotoxic stimuli in primary human, rat, and mouse neuroglial cultures stimulated with trophic factors, chemokines, dopamine, free radicals, beta-amyloid, and HIV-infected macrophage supernatant. These studies are aimed at determining how cell cycle proteins regulate neuronal survival in response to varied and conflicting stimuli. In vitro findings are then used to assess potential roles for these proteins in animal models as well as autopsy tissue relevant to each neurodegenerative condition. Our investigation of E2F1 has resulted in the discovery of a role for this protein in activation of a calpain-dependent death pathway which has not been previously described. Interestingly, neurons responding to HIV-infected macrophage supernatants (our in vitro model of neuronal response to inflammatory infiltrate which mediates HIV encephalitis) activate calpain and increase E2F1 protein levels. One of our immediate lines of investigation is testing the hypothesis that E2F1 induces neuronal death in HIV encephalitis via calpain activation, a novel pathway.

A second area of research in our laboratory is the study of the endogenous anti-oxidant response and its failure to prevent accumulation of oxidative damage and neuronal loss in neurodegenerative disorders. The two proteins of direct interest to the laboratory are Keap1 and Nrf2. Nrf2 is a transcription factor that regulates the expression of the enzymes responsible for the antioxidant response. Normally, Nrf2 is bound in the cytoplasm by the Kelch ECH associated protein 1(Keap1). However, in response to oxidative stress, sulfhydryl groups on Keap1 become oxidized releasing Nrf2 for translocation into the nucleus. We have recently shown that Nrf2 is aberrantly expressed in AD indicating it is not responding to oxidative stress in neurons of affected brain regions. Interestingly, Nrf2 does appear to be responding appropriately in neurons affected in PD. This has led us to hypothesize that the endogenous antioxidant response is aberrant in AD, but insufficient in PD. Our current studies focus on identifying differences in regulation of the endogenous antioxidant response in AD and PD. The

goal of these studies is to explore this pathway as a therapeutic target for neurodegenerative conditions. By enhancing the endogenous anti-oxidant response, neuronal toxicity may decrease leading to increased neuronal function in these patients.

A final area of interest on which our other two lines of investigation has converged is the role of the unfolded protein response (UPR). Induction of the unfolded protein response results in activation of Nrf2 and calpain, proteins activated in response to the endogenous antioxidant response and the E2F1 cell cycle protein respectively. This has led to our investigation of the UPR in neurodegenerative conditions. We are currently looking at pathways activated by the UPR in our various models of HIVE, AD, and PD. The key regulators of this response include pancreatic endoplasmic reticulum kinase (PERK), IRE1, and ATF6. We have already identified increased PERK and phosphorylation of PERK substrate eukaryotic initiation factor 2 ? in AD tissue and an in vitro model of HIVE. This is consistent with findings by Ryu, E. J., et al. (2002, J. Neuroscience 22:10690) indicating a role for UPR in an in vitro PD model. However, our results indicate that Nrf2 a PERK substrate is not activated in AD suggesting the pathway is compromised in AD. Our future investigations are to determine what parts of the pathway are aberrant in disease progression and identify small molecule inhibitors to block chronic UPR pathway activation which is contributing to neuronal dysfunction and loss.

By assessing the interaction of these three convergent pathways in neurons responding to neurodegenerative stimuli such as oxidative damage, misfolded proteins, and inflammation, we hope to gain a greater understanding of the basic mechanisms underlying neuronal damage, dysfunction and loss in neurodegenerative diseases and identify drugable targets for treatment of AD, PD, and HIVE.

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#### Carl H. June, M.D. Richard W. Vague Professor in Immunotherapy

8-123 Translational Research Center Phone: (215) 573-3269 Fax: (215) 573-8590 Email: <u>cjune@exchange.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g275/p2328

#### **Research Interests**

The June Lab is primarily responsible for developing new CARs and new vectors for current and proposed indications. This lab also fosters the development of Penn students both in doctoral and post-doctoral programs. The June Laboratory provides researchers with the tools they need to translate laboratory insights into safe and effective cancer therapies. The June Laboratory works with University of Pennsylvania faculty members interested in moving biologically-focused research ideas into clinical trials. In addition, the June Laboratory has a cadre of faculty researchers focused on developing ways to enhance the ability of the natural immune system to recognize and eliminate tumor cells. Translational research is a core unit of the The Leonard and Madlyn Abramson Family Cancer Research Institute at the Abramson Cancer Center at the University of Pennsylvania. Created in December 1997 with a \$100 million pledge from the Abramson Family Foundation, the Cancer Research Institute integrates research, education, and comprehensive patient care at the Abramson Cancer Center at the University of Pennsylvania. For more information, see the Translational Research Mission Statement.

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#### Klaus H. Kaestner, Ph.D Thomas and Evelyn Suor Butterworth Professor in Genetics

12-126 Translational Research Center Phone: 215-898-8759

Fax: 215-573-5892 Email: <u>kaestner@mail.med.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p389

#### **Research Interests**

Epigenomic rejuvenation of human pancreatic beta-cells.

The prevalence of Diabetes Mellitus has reached epidemic proportions world-wide, and is predicted to increase rapidly in the years to come, putting a tremendous strain on health care budgets in both developed and developing countries. There are two major forms of diabetes and both are associated with decreased beta-cell mass. No treatments have been devised that increase beta-cell mass in vivo in humans, and transplantation of beta-cells is extremely limited due to lack of appropriate donors. For these reasons, increasing functional betacell mass in vitro, or in vivo prior to or after transplantation, has become a "Holy Grail" of diabetes research. Our previous studies clearly show that adult human beta-cells can be induced to replicate, and - importantly - that cells can maintain normal glucose responsiveness after cell division. However, the replication rate achieved was still low, likely due in part to the known age-related decline in the ability of the beta-cell to replicate. We propose to build on our previous findings and to develop more efficacious methods to increase functional beta-cell mass by inducing replication of adult beta-cells, and by restoring juvenile functional properties to aged beta-cells. We will focus on mechanisms derived from studies of non-neoplastic human disease as well as age-related phenotypic changes in human beta-cells. In Aim 1, we will target the genes altered in patients with marked betacell hyperplasia, such as those suffering from Beckwith-Wiedemann Syndrome or Multiple Endocrine Neoplasia. Expression of these genes will be altered in human beta-cells via shRNA-mediated gene suppression and locusspecific epigenetic targeting. Success will be assessed in transplanted human islets by determination of betacell replication rate and retention of function. In Aim 2, we will determine the mechanisms of age-related decline in beta-cell function and replicative capacity, by mapping the changes in the beta-cell epigenome that occur with age. Selected genes will then be targeted as in Aim 1 to improve human beta-cell function, as assessed by glucose responsiveness. To accomplish these aims, we will use cutting-edge and emerging technologies that are already established or are being developed in our laboratories. The research team combines clinical experience with expertise in molecular biology and extensive experience in genomic modification aimed at enhancing beta-cell replication. By basing interventions on changes found in human disease and normal aging, this approach will increase the chances that discoveries made can be translated more rapidly into clinically relevant protocols.

Regulatory cascades in differentiation and proliferation of the gastrointestinal epithelium.

The mammalian gut epithelium is a highly organized and dynamic system which requires continuous controlled proliferation and differentiation throughout life. Proliferation, cell migration and cell adhesion all must be tightly controlled in order to prevent either inflammatory diseases or epithelial cancers. As with many other vertebrate organs, the digestive tract develops from heterogeneous embryonic origins. While the musculature and the connective tissue are derived from lateral plate mesoderm, the epithelium is derived from the endoderm. We have identified a novel member of the winged helix gene family termed Foxl1 which is expressed in the gut mesoderm and have begun its functional analysis in vivo through targeted mutagenesis in mice. Null mutations in the mesodermal transcription factor Foxl1 result in dramatic alterations in endoderm development, including epithelial hyperproliferation. We have now identified APC/Min and GKLF as downstream targets of Foxl1 and

have begun the analysis of these genes in gastrointestinal differentiation by tissue-specific gene ablation.

Innovative Genetic Approaches for Hepatic Repopulation

A better understanding of the liver's response to toxic injury, which includes hepatocyte proliferation, activation and differentiation of facultative hepatic stem cells ("oval cells"), and – unfortunately – an increased risk for hepatocellular carcinoma, is a prerequisite for the development of novel clinical treatments for chronic liver disease and improved cancer prevention. Likewise, cell replacement therapy, either through direct hepatocyte transplantation or in bio-artificial liver devices, needs to be improved in order to become a reliable alternative to liver transplantation. To date, investigations of hepatocyte proliferation have frequently focused on the partial hepatectomy paradigm, a "non¬injury" model that is not reflective of liver injury in humans and which has therefore failed to identify specific targets for either improved regeneration following toxic injury or for limiting proliferation in HCC in humans. In Specific Aim 1, we will determine which genes and gene combinations promote or repress hepatocyte repopulation following toxic liver injury using an innovative genetic approach. In Specific Aim 2, we will employ expression of key hepatic transcription factors to improve the differentiation of hepatic progenitor cells to functional hepatocytes. Together, these approaches will provide an improved understanding of the liver's response to toxic injury, and facilitate the discovery of new cell replacement therapies to treat chronic liver disease and liver failure.

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### Mark L. Kahn, M.D., B.A.

**Professor of Medicine** 

11-123 Smilow Center for Translational Research 3400 Civic Center Boulevard, Bldg. 421 Philadelphia, PA 19104-5159 Office: (215) 898-9007 Fax: (215) 573-2094 Email: markkahn@mail.med.upenn.edu

#### **Research Interests**

Our lab investigates signaling pathways that regulate cardiovascular biology and diseases. We are interested in both lymphatic and blood vessel regulatory pathways, and in the interactions between blood cells and vascular endothelium. Most of the pathways we investigate are known to cause human vascular diseases. We apply vertebrate genetic approaches as well as biochemical and state of the art molecular approaches to understand the function of these pathways during normal development and in disease models.

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#### Research Overview

### Marcelo G. Kazanietz, Ph.D.

Professor, Department of Pharmacology

1256 Biomedical Research Building II/III Phone: 215-898-0253 Fax: 215-476-8941 Email: <u>marcelog@mail.med.upenn.edu</u> <u>http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p5467</u>

The Kazanietz laboratory studies signaling mechanisms implicated in tumorigenesis and metastasis. A major area of research is the involvement of serine-threonine kinases of the PKC family in the control of proliferation, transformation, invasion and survival of cancer cells. PKC isozymes are the receptors for the phorbol ester tumor promoters and diacylglycerol (DAG), an important intracellular second messenger generated upon activation of tyrosine-kinase receptors and GPCRs. Our laboratory established key roles for PKCdelta and PKCepsilon in prostate and lung tumorigenesis, characterized their interactions with oncogenes and tumor suppressors, and identified kinase effectors responsible for their effects. A second area of research involves the study of small GTPases of the Rac/Rho family in cancer progression. We have recently identified the Rac-GEF P-Rex1 as a key mediator of breast cancer metastasis. Our studies found that P-Rex1 is a downstream effector of ErbB/HER receptors that is required for luminal breast cancer cell motility. A major goal is to dissect the networks, genes and effectors controlled by these cancer signaling molecules, and established their relevance as therapeutic targets for cancer and other diseases.

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### Max B. Kelz, M.D., Ph.D.

Assistant Professor, Department of Anesthesiology and Critical Care

334 John Morgan Building Phone: 215-662-3713 Fax: 215-349-5078 Email: <u>kelzma@uphs.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p4317661

#### **Research Interests**

Convergence of Sleep and Anesthesia: Insights from Narcolepsy

The wet blanket theory postulates that anesthetic drugs work non-specifically, binding promiscuously at the molecular level and globally at the neuronal (and glial) level to envelope the entire brain and comprehensively perturb brain function to enhance inhibitory signaling and inhibit excitatory signaling and consequently yield states of unconsciousness. However, alternative theories highlighting shared traits among the hypnotic states common to both NREM sleep and sub-surgical levels of many anesthetic drugs suggest that a component of the hypnotic state may arise through specific targeted actions of anesthetics upon the endogenous neural circuits that generate natural sleep.

Some of the most important clues for site-specific actions of anesthetic drugs have been provided by the clinical observation that a subset of patients suffering from narcolepsy (a primary neurological disorder in the organization of sleep and wakefulness) have problems exiting states of anesthesia. As narcolepsy is a disease that arises from a loss of orexin/hypocretin neurons confined to the hypothalamus, this finding which the Kelz lab replicated in mice, suggests that general anesthetics can and do have specific interactions with discrete populations of neurons in the CNS. Work in the Kelz lab uses combinations of molecular genetics, histochemistry, circuit mapping, electrophysiology, and behavioral assessments to phenotype the anesthetic state in multiple ways.

#### Anesthetics Enhance Firing in Endogenous Sleep-Promoting Neurons

As drugs that classically enhance inhibitory signaling and inhibit excitatory signaling, general anesthetics are not predicted to directly depolarize neurons in the CNS. However, work in the Kelz lab has found that of all the neurons that could be depolarized and increase their firing in response to anesthetics exposure, discrete populations of putative-sleep promoting neurons are indeed activated by general anesthetic drugs.

#### OptoAnesthesia

In order to localize and characterize the important features of inhaled anesthetic protein targets, we, in collaboration with the Eckenhoff lab, have found anesthetic-like activity of recently developed novel anesthetic photolabels in a variety of in vitro systems and the tadpole. Our lab is translating these findings to rodents to better understand anesthetic binding and actions in the brain and anesthetic sensitivity in mammals. This project will provide the foundation for a novel mechanism of drug action, which will ultimately lead to better anesthetic management in patients and new and better anesthetic drugs for patients.

#### Translational Studies in Humans

Together with our collaborators and other investigators in the Neurobiology of Unconsciousness group, the Kelz lab conducts volunteer studies in humans designed to reveal insights into the ways in which the human brain

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#### Peter Klein, M.D., Ph.D. Professor, Medicine and Cell and Developmental Biology

9-103 Smilow Center for Translational Research (SCTR) Phone: 215-898-2179 Email: pklein@mail.med.upenn.edu https://www.med.upenn.edu/apps/faculty/index.php/g20000320/p4546

#### **Description of Research**

This lab studies patterning in early vertebrate development, the regulation of stem cell self-renewal in the hematopoietic system, adult neurogenesis, Wnt signaling, and the molecular mechanisms in the pathogenesis and treatment of neuropsychiatric disorders. Areas of current research include:

1) Wnt signaling modifies chromatin architecture to control early development: We have found that Wnt signaling through ß-catenin establishes poised chromatin architecture at Wnt target promoters in the early embryo. We have identified Prmt2 as a histone H3 arginine-8 methyltransferase and shown that it is recruited by ß-catenin to Wnt target gene promoters and is required for dorsal-ventral patterning. We are currently examining the requirement for Prmt2 in other Wnt-regulated contexts in development and in somatic stem cell populations. We are also exploring the regulation of zygotic gene expression before the midblastula transition, focusing on the role of preMBT transcription in germ layer specification. These experiments are being carried out in Xenopus laevis embryos and in mouse hematopoietic stem cells, and involve microinjection, microsurgical procedures, molecular analysis of chromatin structure and gene expression, and biochemical analysis of the Wnt signaling pathway.

2) Wnt and GSK-3 regulation of hematopoietic stem cell (HSC) self-renewal: We are studying the roles of GSK-3 and Wnt signaling in HSC homeostasis in vivo and in primary HSC culture. We are exploring novel ex vivo culture techniques to define the signaling pathways required for and the gene expression profile associated with HSC self-renewal. In collaboration with Wei Tong at CHOP, we are also studying how JAK/STAT signaling interacts with GSK-3 and Wnts to regulate HSC renewal. These experiments are being carried out with mouse and human hematopoietic stem cells, using novel ex vivo culture techniques and stem cell transplantation assays in mice. These experiments also involve flow cytometry and cell sorting, RNA interference, and biochemical analysis of transmembrane signaling pathways. Our long-term interest is to adapt these findings to clinical applications including hematopoietic stem cell transplantation in humans and treatment of bone marrow failure disorders.

3) Neural signaling pathways that mediate the response to mood stabilizing drugs, with a focus on lithium, GSK-3, and Wnt signaling in the adult central nervous system, in order to understand the molecular pathogenesis and pharmacotherapy of bipolar disorder. This laboratory identified GSK-3 as a direct target of lithium, the most widely used and effective treatment for bipolar disorder. We are currently investigating the downstream molecular targets and the neuronal cell populations within the brain that mediate the response to mood stabilizing drugs. For these experiments, we use neural specific gene knockout and transgenic mice, multiple behavioral assays in adult mice, and in vivo analysis of neural stem cell proliferation and differentiation. In collaboration with Celeste Simon, we are examining interaction between hypoxia inducible factors, GSK-3, and the Wnt pathway in regulating neuronal stem/progenitor cells and the potential role of this cell population in mood disorders.

4) Molecular mechanisms of Wnt signaling: We are also investigating the molecular mechanisms of Wnt signaling, with a focus on how GSK-3 activity is regulated by Wnts. We have found that GSK-3 is positively regulated by the tumor suppressor APC. We are exploring the hypothesis that APC regulates multiple targets

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# Rahul M. Kohli, M.D, Ph.D

#### Assistant Professor of Medicine

502B Johnson Pavilion Division of Infectious Disease, Department of Medicine 3610 Hamilton Walk Philadelphia, PA 19104-6073

Office: 215-573-7523

Email: rkohli@upenn.edu

#### https://sites.google.com/site/kohlilabsite/home

#### **Research Overview**

Our laboratory broadly focuses on DNA modifying enzymes and pathways, particularly those that contribute to genomic plasticity. We utilize a broad array of approaches, including biochemical characterization of enzyme mechanisms, chemical synthesis of enzyme probes, and biological assays spanning immunology and virology to study the fundamental question of how a genomic diversity arises in nature.

Mutation and modification of the genome play an important role in several physiologically relevant areas and our areas of interest include:

1. Decipher the molecular basis for deamination by AID/APOBEC enzymes and perturb deaminase immunological functions

From the host immune perspective, the generation of genomic diversity is used as both a defensive and an offensive weapon. Host mutator enzymes such as Activation-Induced Cytidine Deaminase (AID) seed diversity in the adaptive immune system by introducing targeted mutations into the immunoglobulin locus that result in antibody maturation. Related deaminases of the innate immune system can directly attack retroviral threats by garbling the pathogen genome through mutator, as accomplished by the deaminase APOBEC3G, which restricts infection with HIV. Immune mutator enzymes, however, also pose a risk to the host, as overexpression or dysregulation have been associated with oncogenesis.

2. Explore the interplay of cytosine modifying enzymes on DNA demethylation

The singular genome is responsible for a wealth of different cell types, each of which can respond and adapt to environmental cues. In part, these epigenetic differences are linked to DNA modification. These modifications center around cytosine, where DNA deamination (AID/APOBEC enzymes), oxidation (TET family enzymes) and methylation (DNMTs) can all interplay and tune the genome's potential. We are interested in the enzymatic activities of these cytosine modifying enzymes, particularly in the process of DNA demethylation which plays a role in embryogenesis, gene regulation and a potential pathological role in cancer.

3. Target pathogen pathways that promote evolution and resistance.

From the pathogen perspective, alteration in key antigenic determinants at a rate that outpaces immune responses is a potent means for evasion. Further, rapid mutation may allow for the development of resistance to antimicrobials. In bacteria, adaptation and evolution are closely linked to the stress response of SOS pathway. The SOS pathway can be triggered by numerous stressors, including antibiotics, and the net result

is accelerated acquisition of drug resistance. We aim to characterize the key regulatory and effector enzymes from the SOS pathway and to target the pathway as a means to combat antibiotic resistance.

Our research program aims to understand these pathways of purposeful DNA modification and mutation. Additionally, we apply chemical biology to decipher and target these pathways, to impede the development of multidrug-resistance in pathogens or prevent the neoplastic transformations that can result from genomic mutation.

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## Hyun (Michel) Koo, DDS, MS, PhD

Professor

Department of Orthodontics

Divisions of Pediatric Dentistry & Community Oral Health

417 Levy Building

Phone: 215-898-8993

Email: koohy@dental.upenn.edu

http://www.dental.upenn.edu/departments faculty/faculty directory/hyun koo/

#### **Research Overview**

The laboratory of Dr. Koo focuses on understanding the relationship between biofilms and oral infectious diseases and seeking novel therapeutic strategies to control pathogenic biofilms, including those associated with dental caries.

Biofilms are structured communities of microbial cells that are attached to a surface and enmeshed in a selfproduced three-dimensional (3D) matrix of extracellular polymeric substances (EPS). The matrix provides an essential scaffold for the initial assembly and further development of biofilms. It promotes microbial adhesion, cohesion and protection as well as hindering diffusion. Importantly, the matrix also creates spatial and microenvironmental heterogeneities in biofilms, modulating the growth and survival of pathogens locally. The matrix is considered a key factor for the existence of the biofilm lifestyle and full expression of virulence by several bacterial pathogens.

Dr. Koo's research is particularly interested in elucidating three major questions:

- 1. How the extracellular matrix assembles dynamically in 3D. In particular, we are interested in understanding the structural organization of EPS, and how they modulate cell adhesion-cohesion, the 3D matrix-scaffold and mechanical stability of biofilms over time.
- 2. How the matrix modulates the microenvironmental heterogeneity within biofilms. Here, we focus on spatio-temporal characterization of local pH and oxygen levels, microbial organization/positioning and gene expression in situ, and how these properties influence the virulence of biofilms as a whole.
- 3. How to disrupt the EPS production and target the pathogens embedded in the matrix. We are interested in finding new strategies to prevent biofilm initiation or disrupt existing biofilms using naturally occurring molecules, as well as using in silico methods. We are also employing novel (nano/bio)technologies to create anti-biofilm materials and target the biofilm microenvironments.

To accomplish these goals, our lab uses a combination of molecular, biochemical, imaging and biophysical techniques, which include enzymatic, confocal fluorescence microscopy, AFM/rheometry, transcriptomic-proteomic and bioengineering approaches. Several in vitro and in vivo models to study the assembly of mixed-species biofilms are available in our laboratory. We also use these biofilm models to evaluate the effectiveness of novel anti-biofilm approaches.

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# Costas Koumenis, Ph.D.

Richard H. Chamberlain Professor of Research Oncology

Smilow Center for Translational Research, Rm 8-124 Phone: 215-898-0076 Fax: 215-898-0090 Email: <u>costas.koumenis@uphs.upenn.edu</u> http://www.xrt.upenn.edu/KoumenisLab.html

#### **Research Overview**

Delineation of mechanisms of resistance to tumor microenvironmental stress, with emphasis on the Unfolded Protein Response in cancer. Development of small molecule agents to target these mechanisms as novel targeted modalities. Development of novel radiosensitizers.

My laboratory is primarily interested in two broad areas:

- 1. To understand the mechanisms by which components of the microenvironment (e.g. hypoxia, low nutrient availability) interact with cellular survival/apoptotic pathways to produce a more resistant tumor phenotype. Once we understand the regulation and function of these survival pathways, we then design cell-based and assays to screen small molecule libraries for compounds that inhibit these processes and test them alone or in combination with genotoxic agents in several animal tumor models.
- 2. To increase the therapeutic effectiveness of ionizing radiation (IR) by either employing existing compounds with relatively safe toxicity profiles or employ screening strategies to identify novel and potent radiation sensitizers. We are also interested in developing novel delivery approaches for such compounds, such as biocompatible nanoparticles.

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### Mitchell A. Lazar, M.D., Ph.D.

Willard and Rhoda Ware Professor in Diabetes and Metabolic Diseases

12-102 Translational Research Center Phone: 215-898-0198 Fax: 215-898-5408 Email: <u>lazar@pennmedicine.upenn.edu</u> https://www.med.upenn.edu/lazarlab/

#### **Research Overview**

The Lazar laboratory is studying the transcriptional regulation of metabolism. We are particularly focused on the role played by nuclear receptors (NRs). In the absence of ligand, NRs bind to DNA and function as potent transcriptional repressors by recruiting corepressor complexes that include the chromatin modulating enzyme histone deacetylase 3 (HDAC3). We are studying the tissue-specific and physiological roles of the corepressor complexes using by combining genomic, genetic, proteomic, bioinformatic, and metabolic phenotyping approaches. We are especially interested in the circadian NR Rev-erb alpha, which utilizes the corepressor complex to potently repress transcription. Rev-erb alpha is a key repressive component of the circadian clock that coordinates metabolism and biological rhythms. We are also studying PPAR gamma, a nuclear receptor that is a master regulator of adipocyte (fat cell) differentiation. Ligands for PPAR gamma have potent antidiabetic activity, and thus PPAR gamma represents a key transcriptional link between obesity and diabetes. The molecular, cellular, and integrative biology of these factors are being studied in mice and humans. We also have discovered resistin, a novel hormone and target of PPAR gamma that is made by fat cells in rodents and by macrophages in humans, and are testing the hypothesis that resistin links metabolism to inflammation in human metabolic diseases.

#### **Selected Publications**

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### Edward B. Lee, M.D., Ph.D.

#### Assistant Professor of Pathology and Laboratory Medicine

613A Stellar Chance Laboratories 422 Curie Blvd Philadelphia, PA 19104 Phone: 215-898-0908 Email: <u>edward.lee@uphs.upenn.edu</u> <u>https://www.med.upenn.edu/tnr/index.shtml</u>

#### **Research Overview**

TDP-43 is the major component of pathologic inclusions in amyotrophic lateral sclerosis (ALS) and frontotemporal degeneration (FTD). TDP-43 is an RNA-binding protein which is known to regulate pre-mRNA splicing and mRNA stability. Mutations within the gene encoding FUS, another RNA-binding protein, cause ALS, and FUS-positive inclusions are seen in rare forms of FTD. Spinal muscular atrophy is caused by mutations in the gene encoding survival of motor neuron protein, an essential component of the spliceosome. Intronic hexanucleotide repeat expansions in *C9orf72* are the most common cause of ALS and FTD, implicating toxic RNA species in these clinically diverse yet mechanistically similar diseases. Clearly, ALS and FTD are RNA diseases. Our laboratory is interested in the function and dysfunction of TDP-43, FUS and *C9orf72*, and in identifying the basic molecular pathways which are relevant to human disease.

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#### **Research Overview**

### Robert J. Lee, Ph.D.

#### Assistant Professor of Otorhinolaryngology: Head and Neck Surgery

Biomedical Research Building Room 1222/1223 (lab) and 1209 (office) Phone: 215-573-9766 Email: <u>rjl@pennmedicine.upenn.edu</u> <u>http://www.robleelab.com/</u>

We study the physiology of the epithelial cells lining the upper airway (nose and sinuses) and the lower airway (lung) to understand how they sense and respond to pathogens. We combine biochemistry and molecular biology with real-time optical measurements of airway cell signaling and associated physiological responses, including ciliary beating, calcium signaling, fluid secretion, ion transport, nitric oxide production, and antimicrobial peptide secretion. Our goal is to better understand the cellular and molecular bases of airway diseases to identify novel molecular targets for new therapies.

There are two major diseases we focus on. The first is chronic rhinosinusitis (CRS), which affects 8-10% of the US population with direct healthcare costs of over 6 billion dollars annually. CRS has a major impact on individual quality of life as well as on public health; CRS accounts for 1 out of every 5 antibiotic prescriptions in adults in the US, making its treatment a major contributor to the emergence of antibiotic-resistant organisms. A continuing goal of our research is to identify new and better therapies to treat CRS and other airway diseases without the use of antibiotics, particularly through the stimulation of endogenous innate immune pathways. We also focus on cystic fibrosis (CF), the most common lethal genetic recessive disease in the US characterized by defective mucociliary transport due to altered ion transport and fluid secretion. CF is caused by mutations in the cystic fibrosis transmembrane conductance regulator (CFTR) ion channel. Our goal is to better understand the molecular basis of CF and identify novel targets to restore or enhance airway function.

The close partnership we have with physicians at the Hospital of the University of Pennsylvania and the Philadelphia VA Medical Center allows ideas generated in our lab to be directly tested or evaluated in a real clinical setting, giving our research high translational potential.

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### Virginia Lee, Ph.D.

John H. Ware 3rd Endowed Professor in Alzheimer's Research

3rd Floor Maloney Building 3600 Spruce Street Philadelphia, PA 19104-4283 Phone: 215-662-6427

Fax: 215-349-5909

Email: vmylee@upenn.edu

http://pathology.med.upenn.edu/department/people/455/virginia-man-yee-lee

#### **Research Overview**

Dr. Lee's research focuses on disease proteins that form pathological inclusions in hereditary and sporadic Alzheimer's disease (AD), Parkinson's disease (PD), frontotemporal lobar degeneration (FTLD), amyotrophic lateral sclerosis (ALS) and related neurodegenerative disorders of aging. Her work demonstrated that tau, alpha-synuclein and TDP-43 proteins form unique brain aggregates in neurodegenerative diseases and provided critical evidence that aggregation of brain proteins is a common mechanistic theme in diverse neurodegenerative diseases including AD, PD, FTLD, ALS and related disorders. Significantly, Dr. Lee's studies implicated the abnormal aggregation of tau, alpha-synuclein and TDP-43 in mechanisms that compromise neuronal viability. Most importantly, this research has opened up new avenues of research to identify targets for drug discovery to develop better treatments for these disorders.

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## Robert J. Levy, M.D.

#### **Professor of Pediatrics**

Abramson Pediatric Research Center, Rm 702D Phone: 215-590-6119 Fax: 215-590-5454

Email: levyr@email.chop.edu

http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p2954

#### **Research Overview**

Heart Valve Disease: Research programs underway concerning the developmental basis for aortic valve disease, mechanistic studies of progression of calcific aortic stenosis, serotonin mechanisms in heart valve disease, and novel biomaterials for heart valve prostheses.

Gene delivery stents are an area of major interest: plasmid or viral vectors configured in sustained release preparations onto vascular stents for site specific vascular gene therapy.

Magnetic delivery of nanoparticles for pharmaceutical and cell therapy to treat arterial disease.

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## Jon M. Lindstrom Ph.D.

**Trustee Professor of Neuroscience** 

130A John Morgan Building Phone: 215-573-2859

Fax: 215-573-2858 Email: jslkk@pennmedicine.upenn.edu

http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p7427

#### **Research Overview**

We are studying the biochemical and antigenic structure of nicotinic receptors from human muscle and Torpedo electric organ. We investigate pathological mechanisms and specific immunosuppressive therapy of experimental autoimmune myasthenia gravis in rats induced by immunization with purified receptor.

We are also studying the structure and function of neuronal nicotinic receptors. These studies primarily involve expression of cloned human receptors in Xenopus oocytes and permanently transfected cell lines.

We are also studying the effects of acute and chronic exposure to nicotine on various subtypes of nicotinic receptors. Understanding these effects is important for explaining both the effects of nicotine in tobacco and the effects of nicotinic drugs which are being developed. These structures should also reveal mechanisms through which nicotinic receptors could influence development and synaptic plasticity. Receptors are normally exposed to acetylcholine for milliseconds, but can be exposed to nicotine for hours. Nicotine, like any agonist, initially activates and then desensitizes receptors. On prolonged exposure it increases assembly of receptor subunits and decreases turnover of receptors in the surface membrane. It can be a full or partial agonist and block the cation channel. All of these effects vary depending on the receptor subtype. Combinations of these effects on various receptor subtypes in various regions are responsible for addiction to nicotine, tolerance to some of its effects, and mediating its many effects, which range from enhanced cognition to reduced anxiety and pain.

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## David Lynch, M.D., Ph.D.

**Professor of Neurology** 

502 Abramson Research Center Phone: 215-590-2242

Fax: 215-590-3779

Email: lynch@mail.med.upenn.edu

http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p6963

#### **Research Overview**

Excitotoxicity is a unique pathophysiological mechanism which is involved in cerebral ischemia, secondary damage in neuronal trauma, and neuronal damage from prolonged seizures. The deleterious effects from excitotoxicity result from calcium entry through a specific glutamate receptor, the N-methyl D-aspartate (NMDA) receptor. NMDA receptor antagonists act both as neuroprotective agents against excitotoxicity and as anticonvulsants in animals, but human clinical trials with the most potent agents have been complicated by side effects including psychosis. Much evidence indicates the presence of multiple types of NMDA receptors in the brain, and evidence from our laboratory suggests that different subtypes play different roles in physiological and excitotoxicity, one could develop therapeutic agents which are selective for the subtypes involved in excitotoxicity, one could more readily utilize NMDA receptor antagonists for treatment of human diseases.

We use a systematic approach to examine the subtype specific physiological and pharmacological properties of NMDA receptors. NMDA receptors are created in tissue culture expression systems, and their properties are studied biochemically, pharmacologically and physiologically to correlate receptor properties in these systems with such properties in vivo. We have previously shown that different NMDA receptor subtypes have distinct pharmacologies and produce different changes in intracellular calcium. In the near future we will extend these examinations of subtype specific properties to include the modulation of other intracellular messengers such as nitric oxide and examine the effect of such properties on excitotoxicity. Combined with our studies on the pharmacological specificity of NMDA receptor subtypes, this will facilitate the development of therapeutic agents directed to those NMDA receptors which play crucial roles in excitotoxicity.

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## Robert H. Mach, Ph.D.

#### Britton Chance Professor of Psychology in Radiology

Chemistry Building, Room 283 231 S. 34th St Philadelphia, PA 19104

Phone: 215-746-8233

Email: rmach@mail.med.upenn.edu

https://www.med.upenn.edu/apps/faculty/index.php/g275/p8658246

#### **Research Overview**

Current studies focus on: 1) the role of specific neurotransmitter receptors in neurological and neuropsychiatric disorders, such as dopamine D3 receptors in the mediating the behavioral effects of psychostimulants and other abused substances; 2) study of the sigmna-2 receptor/PGRMC1 as a molecular marker of cell proliferation and quiescence in tumor cells; 3) development of sigma-2 receptor ligands for the targeted delivery of cancer chemotherapeutics to tumors; 4) study of sigma-2 receptor agonists as potential chemosensitizers in the treatment of cancer; 5) development of molecular imaging agents to study the formation of reactive oxygen species/reactive nitrogen species; 6) development of PET radiotracers for imaging alpha synuclein deposits in Lewy bodies and Lewy neurites in neurodegenerative disorders.

#### **Research Techniques**

Organic synthesis; design and synthesis of small molecules targeting CNS receptors, proteins overexpressed in tumors, or mediators of oxidative stress; radiolabeling with positron-emitting radionuclides; small animal imaging studies with PET; radioligand binding studies; in vitro autoradiography; western blot analyses; cell culture of cancer cells, hippocampal neurons and microglia; microscopy; histology; radioimmunoassay; and HPLC analysis of metabolites.

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## David R. Manning, Ph.D.

**Professor of Pharmacology** 

114 John Morgan Building Phone: 215-898-1775 Fax: 215-573-7188 Email: <u>manning@mail.med.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p5067

#### **Research Overview**

The major focus of the laboratory is the process by which the binding of hormones to cell-surface receptors is translated into the regulation of target enzymes and ion channels. The Manning laboratory is specifically interested in pathways of transduction defined by heterotrimeric GTP-binding regulatory proteins (G proteins). Current studies include mapping linkages among receptors and G proteins in intact cells, defining post-translational modifications of G protein subunits that influence targeting and protein-protein interactions, and exploring the roles of novel G proteins. Considerable effort in the laboratory is devoted toward understanding the relevance of G proteins to the actions of the Hedgehog morphogens. We are currently pursuing noncanonical forms of signaling achieved by Hedgehogs using the Gi family of G proteins. We are also interested in the activation of the one or more forms of Gli transcription factors by ligands apart from Hedgehogs, and specifically through receptors that couple to the G12/13 family. Pursuit of these interests have required the development of methods to evaluate the communication of receptors with G proteins, with an emphasis placed on determinants of efficacy. The idea that ligands working through a single receptor can generate different signals (functional selectivity), or that these signals can be generated by a single ligand as function of ligand concentration, represents a common theme of the work.

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## John Matthew Maris, M.D.

**Professor of Pediatrics** 

4399 Colket Translational Research Building Phone: 215-590-5244 Fax: 267-426-0685 Email: <u>maris@email.chop.edu</u> https://www.chop.edu/cccr/labs/john-maris-laboratory

#### **Research Overview**

Researchers in the Maris Laboratory are focused on understanding the underlying molecular and genetic mechanisms that contribute to the development and progression of pediatric neuroblastoma. Also, efforts in the Maris Laboratory are dedicated to the development of new molecular diagnostic tests and less toxic, targeted cancer therapies to treat relapsed or refractory neuroblastoma. The long-term goal of the work in this laboratory is to use a multidisciplinary approach to improve existing cure rates for children with neuroblastoma.

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### Michael S. Marks, Ph.D.

#### **Professor of Pathology and Laboratory Medicine**

816G Abramson Research Center Phone: 215-590-3664 Email: <u>marksm@pennmedicine.upenn.edu</u> <u>https://www.med.upenn.edu/markslab/</u>

#### **Research Overview**

Eukaryotic cells are compartmentalized into distinct membrane-bound organelles and vesicular structures, each with its own characteristic function and set of protein constituents. Work in my laboratory is focused on understanding how integral membrane protein complexes are assembled and sorted to the appropriate compartments within the late secretory and endocytic pathways, how sorting and assembly contribute to the biogenesis of cell type-specific organelles, how these processes impact biological function in the pigmentary, blood clotting, and immune systems, and how they are thwarted by generally rare genetic diseases.

Our primary focus over the past 20 years has been on melanosomes of pigmented cells. Melanosomes are unique lysosome-related organelles present only in cells that make melanin, the major synthesized pigment in mammals. Genetic defects in melanosome constituents or in their delivery to nascent melanosomes result in ocular or oculocutaneous albinism, characterized by lack of pigmentation in the eyes and or skin and concomitant visual impairment and susceptibility to skin and ocular cancers. Melanosomes are among a number of tissuespecific lysosome-related organelles that are malformed and dysfunctional in a group of rare heritable disorders, including Hermansky-Pudlak and Chediak-Higashi syndromes. In an effort to understand the molecular basis of these diseases, we are dissecting the molecular mechanisms that regulate how different stage melanosomes are formed and integrated with the endosomal pathway. We use biochemical, morphological, and genetic approaches to follow the fates of melanosome-specific and ubiquitous endosomal and lysosomal proteins within pigment cells from normal individuals or mice and disease models. Using these approaches, we are (1) outlining protein transport pathways that lead to the formation of these unusual organelles, (2) dissecting biochemical pathways that lead to their morphogenesis, and (3) defining how these processes are subverted by genetic disease. Current efforts focus on the molecular mechanisms by which factors that are deficient in patients and mouse models of the genetic disease, Hermansky-Pudlak syndrome, impact melanosome biogenesis. We are particularly interested in how these factors contribute to the formation and dynamics of tubular connections between endosomes and maturing melanosomes that facilitate cargo transport, as well as the formation of retrograde membrane carriers that retrieve unneeded proteins from melanosomes.

In addition to these studies, we are interested in the function of individual melanosome and lysosome components and how they impact melanogenesis. For example, melanosome precursors in pigment cells harbor internal fibrils upon which melanins deposit in later stages, the main component of which is a pigment cell-specific protein, PMEL. Fibrils formed by PMEL in vitro display features common with amyloid formed in disease states such as Alzheimer and Parkinson diseases. By dissecting how PMEL forms amyloid under physiological conditions, we hope to determine how the formation of "good" and "bad" amyloid differs and thus how the formation of "bad" amyloid might be controlled. Other melanosomal proteins are transporters that impact the intralumenal environment of melanosomes to alter the type and amount of melanin that is made. Together with our collaborators we are studying the biophysical function of these transporters and how they are linked to

features such as melanosome pH.

Because genetic diseases like Hermansky-Pudlak syndrome affect multiple organ systems, we study how similar sorting processes involved in melanosome biogenesis influence other organelles in different cell types. The first involves lysosome-related organelles in platelets called dense granules and alpha granules. When platelets are activated at sites of blood vessel damage, the contents of these granules are released, leading to optimal blood clot formation and platelet activation. Like melanosomes, dense granules are malformed in Hermansky-Pudlak syndrome, and in collaboration with the Poncz, Stalker and French laboratories at CHOP and Penn we are studying how dense granule contents are delivered within platelets and their precursors (megakaryocytes). Studies in collaboration with the Poncz and French labs also address the contents and secretion of alpha granules and their disruption in human bleeding disorders.

The second cellular system is the dendritic cell, a master regulator of T cell-mediated immunity. Patients with Hermansky-Pudlak syndrome type 2 have recurrent bacterial infections, and we have found that this is at least in part due to defects in the way that dendritic cells sense bacterial infection. Normally, ingested bacteria trigger signaling by innate immune receptors present on the membrane enclosing the bacteria (the phagosome) or in the cytoplasm; signaling by both sets of receptors is defective in dendritic cells from a mouse model of the disease due to (1) impaired recruitment of the receptors and their signaling platforms on phagosomes and (2) rapid clearing of cytoplasmic receptors by autophagy. Ongoing studies aim to dissect how phagosome membrane dynamics normally lead to signaling and how this is altered in disease states.

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### David F. Meaney, Ph.D.

Solomon R. Pollack Professor and Chair of Bioengineering

120 Hayden Hall

Phone: 215-898-8501

Fax: 215-573-2071

Email: dmeaney@seas.upenn.edu

http://www.seas.upenn.edu/directory/profile.php?ID=64

#### **Research Overview**

Dave's research focuses on understanding the mechanical cues that regulate injury, repair, and growth in cells and tissues of the central nervous system. The process of mechanotransduction is critical in understanding the response of cells and tissues of the central nervous system (CNS) to traumatic injury. In this research area, experimental work is combined with mathematical modeling to provide a method to quantify the effect of physical forces on cell and tissue function. For example, some of the research combines finite element models of the brain with experimental work to estimate the tissue mechanical stress/strain associated with biological markers of injury. These models provide a starting point to relate traditional measures of stress to the microstructural constituents of the tissue. Structural models are being developed to link global mechanical deformations and the resulting deformation of cellular/subcellular microstructures in the CNS white matter. With the kinematic transformations between the macroscopic deformations and cellular components of the CNS white matter now better established, the research has expanded to determine the mechanism(s) by which a mechanical signal is converted into a biochemical signaling cascade for organotypic tissue, cultured neurons, and cultured axons. Clinical applications of his work include developing new testing standards to improve the safety of headgear and automotive restraint systems, and testing new techniques for repairing damaged tissues in the brain after injury.

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## Claire H. Mitchell, Ph.D.

Professor of Anatomy & Cell Biology

431 Levy Building Phone: 215-573-2176 Email: <u>chm@mail.med.upenn.edu</u> <u>https://www.med.upenn.edu/physiol/faculty\_mitchell.html</u>

#### **Research Overview**

My research uses physiological approaches to understand the mechanistic steps of disease. For example, the lab is currently investigating how elevated pressure leads to neuronal death, focusing on ATP release, pannexin hemichannels, P2X7 receptors, NMDA receptors and the neuroprotective actions of A3 adenosine receptors. The role of these components in cytokine release is also being probed. In addition, the lab is exploring the physiology of lysosomes, with investigations into the regulation of lysosomal pH in health and disease. Pharmacological and molecular manipulation of lysosomal CI- channels such as CFTR and CLC-7 is being used to reacidify lysosomes and improve degradative activity in aging and diseased cells.

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## Vera Moiseenkova-Bell, Ph.D.

Associate Professor of Pharmacology

10-124 Smilow Center for Translational Research Phone: 215-898-1154 Email: <u>vmb@pennmedicine.upenn.edu</u> https://moiseenkova-lab.com/

#### **Research Overview**

We are interested in understanding structure and function of Transient Receptor Potential (TRP) channels which have been implicated in a diverse range of cellular processes, including pain sensation, neuronal development, cardiovascular and renal pathophysiology, and cancer. Currently, the Moiseenkova-Bell laboratory has two main areas of research: First is to determine the structural basis of TRP channel activation, inhibition and desensitization mechanisms by utilizing cryo electron microscopy (cryo-EM). Second is to understand how TRP channels regulate cellular functions and the role of their dysregulation in human disease.

#### **Recent Publications**

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## Yael P. Mosse, M.D.

#### **Associate Professor of Pediatrics**

Colket Translational Research Building, Office 3056 Phone: 215-590-0965 Email: <u>mosse@email.chop.edu</u> <u>http://www.research.chop.edu/people/yael-p-mosse</u>

#### **Research Overview**

Despite major enhancements in therapy over the past several decades, the cure rate for patients with highrisk neuroblastoma lags significantly behind that of other childhood cancers. My lab has unwaveringly focused on neuroblastoma and on the hypothesis that discovery of its hereditary basis will provide insights that are clinically actionable and improve outcomes. Our seminal discovery that gain-of-function mutations in the Anaplastic Lymphoma Kinase (ALK) oncogene are the cause of familial neuroblastoma (Nature, 2008) highlights the insights gained from a family-based study in a rare disease and the opportunities for targeting ALK in neuroblastoma and other human cancers driven by ALK. We have led collaborative investigations that demonstrated frequent ALK activating mutations in the more common sporadic cases, the development of molecular diagnostic tools, and preclinical studies to establish the role of ALK inhibitors in the treatment of neuroblastoma and other childhood cancers. This work led to the completion of a multi-institutional pediatric phase 1 trial of crizotinib (The Lancet Oncology, 2013), demonstrating rapid translation of preclinical molecular findings into the clinic. We have positioned ALK as the only mutated oncogene tractable for targeted therapy in neuroblastoma and subsequently showed that there is differential mutation-specific sensitivity to crizotinib that results from a relative increase in ATP-binding affinity (Science Translational Medicine, 2011), data that directly impacted the design of the pediatric phase 1 trial. Additionally, we have shown that ALK is a tractable target for immunotherapy (Oncogene, 2012), setting the stage for the development of antagonistic antibodies to maximize clinical benefit.

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## Vladimir R. Muzykantov, M.D., Ph.D.

**Professor of Pharmacology** 

10-105 Smilow Translational Research Center Phone: 215-898-9823 Fax: 215-898-0868 Email: <u>muzykant@mail.med.upenn.edu</u> https://www.med.upenn.edu/apps/faculty/index.php/g5455356/p7571

#### **Research Overview**

The laboratory is focused on several projects. First is the targeting of drugs (enzymes either degrading or generating oxidants, fibrinolytics, interferon, antisense oligos and genes) to the pulmonary vascular endothelium. The purpose is to develop strategies for controlled site-specific delivery of a drug to the defined subcellular compartments of the pulmonary endothelium. For example, genetic material must be delivered into the nucleus, antioxidants must accumulate in the cytoplasm, and fibrinolytics must avoid internalization. We therefore study how carrier antibodies and their derivatives recognize endothelium, and characterize cellular trafficking and local effects of the targeted agents in cell cultures, perfused animal lungs and in intact animals. Our research includes identification of the molecules localized on the surface of endothelium useful as targets for drug delivery to either normal or pathologically challenged endothelium. Endothelium-specific antigens may serve as such targets. Affinity carriers that are currently explored in our laboratory include monoclonal antibodies (and their fragments) to: angiotensin-converting enzyme (ACE), thrombomodulin and surface adhesion molecules, ICAM, PECAM, P- and E-selectins. We have characterized carriers and their modifications providing: i) a drug with an affinity to endothelium (recognition and targeting) and, ii) drug delivery in a proper cellular compartment (sub-cellular addressing). Targeting to either surface (by non-internalizable carriers) or intracellularly has been documented in cell culture, perfused lungs and in rodents in vivo.

Secondly, we explore red blood cells (RBC) as natural carriers for drugs. We have developed an original methodology for effective conjugation of large amounts of a drug (e.g., fibrinoytic enzymes or receptors for plasminogen activators) on RBC, without loss of biocompatibility of the complex. Conjugation provides prolongation of half-life of plasminogen activators in vivo by orders of magnitude and offers specific transfer of the conjugated protein (tPA, uPA-receptor) to the pulmonary endothelium. Both mechanism of the transfer (tentatively via exchange of GPI-anchored membrane proteins between RBC and endothelium) and potential therapeutic applications of RBC-conjugated fibrinolytics (treatment/prevention of pulmonary embolism/deep vein thrombosis) are in the focus of the research. We also explore RBC as carriers for intracellular drug delivery in phagocyte cells in the reticuloendothelial tissue (liver and spleen) and endothelial cells.

#### **Selected Publications**

Brenner Jacob S, Pan Daniel C, Myerson Jacob W, Marcos-Contreras Oscar A, Villa Carlos H, Patel Priyal, Hekierski Hugh, Chatterjee Shampa, Tao Jian-Qin, Parhiz Hamideh, Bhamidipati Kartik, Uhler Thomas G, Hood Elizabeth D, Kiseleva Raisa Yu, Shuvaev Vladimir S, Shuvaeva Tea, Khoshnejad Makan, Johnston Ian, Gregory Jason V, Lahann Joerg, Wang Tao, Cantu Edward, Armstead William M, Mitragotri Samir, Muzykantov Vladimir: Red blood cell-hitchhiking boosts delivery of nanocarriers to chosen organs by orders of magnitude. Nat Commun 9(1): 2684, Jul 2018.

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### Cynthia M. Otto, DVM, PhD

Associate Professor of Critical Care

2066 Ryan Veterinary Hospital Penn Vet Working Dog Center 3401 Grays Ferry Ave Phone: 215-898-3390 Fax: 215-463-3870 Email: <u>cmotto@vet.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p3937688

#### **Research Overview**

Current Research Interests are focused on the health, genetic and behavioral aspects of performance in detection dogs. I have been following the health and behavior of the search dogs following the 9/11 response. We have established the AKC CAR Detection Dog DNA Bank to study the genetics of complex behavior. We have a DOD funded field study of the effect of different hydration strategies on performance, hydration, and inflammation in detection dogs. Opening Sept 11, 2012, the Penn Vet Working Dog Center will integrate the science and field experience to breed, select, raise and train dogs to use their noses to detect things (e.g. explosives, drugs, people, and even cancer and infectious diseases). The Penn Vet Working Dog Center will be a resource for behavioral, nutrition, development and conditioning studies in dogs being trained for detection work. In addition, the interactions between dogs and humans will be studied, focusing on 3 major groups of volunteers/interns working with the program: homeless youth, veterans, and parolees from prison dog raising programs. In addition, clinical research in emergency care of dogs and cats, sepsis and trauma continue to be of interest.

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## Park F. Cho-Park, MD, PhD

Assistant Professor of Pharmacology Smilow Center for Translational Research Room 10-104, Building 421 Office: 215-573-1190 Fax: 215-573-9135 Email: <u>pacho@pennmedicine.upenn.edu</u> <u>https://cho-park.org/</u>

#### **Research Overview**

The laboratory's long term research goal is to develop a comprehensive understanding of Proteostasis and how alterations in this process contribute to normal biological and disease processes. Although much is known about the role of transcriptional and translational control of gene expression in various human disorders, the extent to which protein degradation contributes to disease processes remains vastly unexplored.

Key to understanding protein degradation is to elucidate the mechanisms by which the 26S proteasome is regulated in vivo. While it is known that regulation of proteasome activity is intrinsically linked to its local availability and protein-protein interaction profile, detailed mechanistic insights are still lacking. Further complicating things, we know virtually nothing of the intimate relationship that must exist between protein synthesis and degradation to regulate protein homeostasis, and the effects of environmental stresses on these processes. For example, dietary restriction, aging and environmental stresses have all been linked to proteasome deregulation through an unknown mechanism. Therefore, knowledge gained from our future endeavors will not only advance the basic understanding of protein homeostasis in the broader context of biology, but will also open up new therapeutic opportunities against those diseases that arise secondary to accumulation of misfolded "toxic" proteins such as cancer, amyotrophic lateral sclerosis (ALS), Retinitis Pigmentosa, and Alzheimer's and Parkinson's diseases. As a first step towards this goal, we will take advantage of the laboratory's unique set of skills in clinical medicine, biochemistry, cell & molecular biology, and Drosophila and Mouse genetics, to further extend these lines of work using a multi-pronged interdisciplinary approach.

#### **Selected Publications**

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## Trevor M. Penning, Ph.D.

The Thelma Brown and Henry Charles Molinoff Professor of Pharmacology

1315 BRB II/III Phone: 215-898-9445 Fax: 215-573-0200 Email: <u>penning@upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p12620

#### **Research Overview**

Steroid Hormone Transforming Aldo-Keto Reductases.

The aldo-keto reductase (AKR) superfamily contains mammalian hydroxysteroid dehydrogenases (HSDs). For each sex steroid there are a pair of HSDs, which by acting as reductases or oxidases can convert potent steroid hormones into their cognate inactive metabolites or vice versa. When found in steroid target tissues they can regulate the occupancy and trans-activation of steroid hormone receptors, providing a pre-receptor regulation of steroid hormone action. Many HSDs are considered therapeutic targets. For example, aldo-keto reductase AKR1C3 (type 5 17beta-hydroxysteroid dehydrogenase) catalyses the formation of the potent androgens, testosterone and 5alpha-dihydrotestosterone, in castrate resistant prostate cancer (CRPC). CRPC is dependent upon intratumoral androgen biosynthesis that reactivate the androgen receptor and is uniformly fatal. Structure-based inhibitor design is being used to develop selective AKR1C3 inhibitors for the treatment of CRPC. In another area structure-function studies on steroid 5beta-reductase (AKR1D1)are being pursued. This enzyme catalyzes a pivotal step in bile-acid biosynthesis and natural mutations are causal in bile-acid deficiency syndromes which are often neonatal fatal. In both areas we use the following techniques: site-directed mutagenesis, x-ray crystallography, transient and steady state kinetics, and transfection studies in prostate cancer cell lines.

#### Dihydrodiol Dehydrogenases and Polycyclic Aromatic Hydrocarbon (PAH) Activation

Dihydrodiol dehydrogenases are members of the AKR superfamily. They convert PAH-trans-dihydrodiols (proximate carcinogens) to reactive and redox active o-quinones. By entering into futile redox-cycles the oquinones can amplify the production of reactive oxygen species (e.g., superoxide anion, hydrogen peroxide and hydroxyl radical). The pro-oxidant state may provide a mechanism by which PAH can act as complete carcinogens. Similar metabolic activation has been observed for the structurally related catechol estrogens and diethylstilbestrol. The cytotoxicity and genotoxicity of PAH o-quinones are being studied in human lung cells as it pertains to causality in human lung cancer. Methods include cell culture, high-resolution NMR, EPR, massspectrometry, PAH-DNA adduct chemistry, and mutagenesis paradigms.

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### **Robert Christopher Pierce, Ph.D.**

#### **Professor of Neuroscience in Psychiatry**

Center for Neurobiology and Behavior Translational Research Laboratory Phone: 215-746-8915 Fax: 215-573-7605 Email: <u>rcpierce@mail.med.upenn.edu</u> <u>http://www.piercelab.org/</u>

#### **Research Overview**

Dr. Pierce's interest in the neuropharmacology of drugs of abuse began while he was an undergraduate student at the University of Kentucky. Working with Dr. Michael Bardo in the Psychology Department, Dr. Pierce studied the effects of amphetamine on the mesolimbic dopamine system. He continued to pursue his interest in the effects of psychostimulants on brain dopamine systems through graduate school at Indiana University, where he worked with Dr. George Rebec. Dr. Pierce received post-doctoral training from Dr. Peter Kalivas at Washington State University. Their work indicated that glutamate, in a complex interaction with limbic dopamine, plays an important role in both the development and long-term expression of behavioral sensitization to cocaine, an animal model of addiction. Dr. Pierce established an independent laboratory in the Department of Pharmacology at Boston University School of Medicine in 1997. Dr. Pierce joined the Department of Psychiatry's Center for Neurobiology and Behavior in October 2008.

Currently, there are no effective therapies for cocaine addiction, which directly affects over two million people in the United States alone. This reality is the driving force for Dr. Pierce's research program. The major hurdle for abstaining from abuse of cocaine is intense drug craving, which can be triggered months and even years following the cessation of drug use. The most widely accepted model of craving in animals involves selfadministration followed by extinction and the subsequent reinstatement of drug seeking. Using this animal model, Dr. Pierce's research team pursues a strategy to identify novel neurobiological adaptations produced by cocaine. This information then can be used to formulate potential cocaine addiction therapies.

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## Mortimer Poncz, M.D.

**Professor of Pediatrics** 

317 Abramson Research Center Phone: 215-590-3574 Fax: 215-426-5476 Email: <u>poncz@email.chop.edu</u> <u>http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p5429</u>

#### **Research Overview**

My research efforts focus on the megakaryocyte-platelet-thrombus axis. The process by which hematopoietic stem cells differentiate into megakaryocytes, which then release platelets and the function of platelets in thrombosis and inflammation are the central foci of my laboratory. Many of the studies focus on the biology and pathobiology of the platelet-specific proteins, chemokines Platelet Factor 4 (PF4)/Platelet Basic Protein (PBP) and the integrin alphallb/beta3 receptor.

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# Daniel J. Powell Jr., Ph.D.

Associate Professor of Pathology And Laboratory Medicine

Smilow Center for Translational Research, Rm 8-103

Phone: 215-573-4783 Email : poda@mail.med.upenn.edu

http://www.med.upenn.edu/cci/powelllab/

#### **Research Overview**

The Powell Lab is actively investigating the application of immune-based therapy for cancer. Building on interrogations in basic T cell biology in the lab, bench-to-bedside translational immunology is being developed, with a strong focus on T cell-based therapy for ovarian cancer.

One obstacle to successful immunotherapy is the lack of highly avid, tumor-reactive T cells in multiple cancers. One current focus of the Powell lab is to generate/isolate high avidity, tumor-reactive T cells from heterogenous tumor infiltrating lymphocyte populations in traditionally "non-immunogenic" cancers utilizing novel culture conditions and T cell capture techniques. This in turn will permit downstream studies of T cell receptor (TCR) isolation, cancer antigen identification and molecular characterization of naturally occurring tumor-reactive T cells in human cancer.

A secondary field of study is the de novo generation of tumor-reactive T cells through genetic engineering methods. One approach relies on the isolation and cloning of T cell receptors (TCRs) that confer non-reactive T cells with specific and potent immune function following gene transfer via recombinant lentivirus or retrovirus. Another approach relies upon the use of chimeric antigen receptors (CARs) that confer T cells with the MHC-independent specificity of a tumor antigen-specific antibody and potent T cell activity delivered by TCR and costimulatory domains. The Powell Lab also employs the CAR approach to test the function of novel costimulatory signals in anti-tumor immunity.

Other current efforts include the exploration of immunomodulation to potentiate endogenous antitumor T cell responses, use of bispecific antibodies, pharmacological sensitization of tumor cells to immune attack, tumor vasculature targeting, preclinical validations, clinical translation and trial support.

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# Ellen Puré, Ph.D.

**Professor of Pharmacology** 

3800 Spruce Street

216E Vet

Phone: 215-573.9406

Email: epure@vet.upenn.edu

https://www.med.upenn.edu/apps/faculty/index.php/g20000343/p2386

# **Research Overview**

This laboratory is studying the cellular and molecular basis of inflammation and fibrosis, with a particular focus on the role of stromal cells and extracellular matrix (ECM), in the context of chronic inflammatory diseases and cancer. The molecular pathways currently being studied include the adhesion receptor CD44 and its principle ligand, hyaluronan, and fibroblast activation protein (FAP), a stromal cell surface protease. Studies of CD44 and FAP are being conducted in mouse models of cancer, cardiovascular disease and pulmonary fibrosis using conditional CD44 knockout mice and FAP-null mice generated in the lab. Also, the FAP promoter has been exploited to generate mice that can be used to non-invasively image reactive stromal cells in fibrotic lesions and epithelial-derived tumors, to conditionally ablate reactive stromal cells, and to manipulate gene expression specifically in fibrotic lesions and tumor stromal cells. We are studying the impact of matrix modification on cell behavior directly through regulation of receptor mediated signal transduction as well as through modulation of tissue stiffness. We are also exploring the function of CD44 and FAP in human disease.

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# Daniel J. Rader, M.D.

## Seymour Gray Professor of Molecular Medicine

11-125 Smilow Translational Research Center Phone: 215-573-4176 Fax: 215-573-8606 Email: <u>rader@upenn.edu</u> https://www.med.upenn.edu/apps/faculty/index.php/g20000343/p17778

## **Research Overview**

The Rader laboratory is focused on two major themes: 1) novel pathways regulating lipid and lipoprotein metabolism and atherosclerosis inspired by unbiased studies of human genetics; 2) factors regulating the structure and function of high density lipoproteins and the process of reverse cholesterol transport and their relationship to atherosclerosis. A variety of basic cell and molecular laboratory techniques, mouse models, and translational research approaches are used in addressing these questions. Some examples of ongoing projects are:

- The roles of sortilin (gene SORT1) and tribbles-1 (gene TRIB1) in lipoprotein metabolism and atherosclerosis. Variants at the SORT1 locus are among the most strongly associated with LDL cholesterol and (coronary artery disease) in the human genome, and variants at the TRIB1 locus are significantly associated with all major plasma lipid traits and CAD. A variety of tissue-specific deleted mouse models, gene targeting in iPS cells with differentiation to hepatocytes, and cell biologic and biochemical approaches are being employed.
- 2. Functional genomics and mechanistic studies of a number of additional genes at loci significantly associated with lipid and metabolic traits, CAD, or other cardiovascular traits. Most of these genes harbor rare coding variants associated with these traits. In addition to elucidating fundamental mechanisms by which the protein influences relevant biology, the influence of specific mutations on protein structure and function are being explored.
- 3. Molecular regulation of HDLmetabolism and reverse cholesterol transport using cells, mice, and humans.
- 4. Deep phenotyping of humans with low-frequency and rare variants in genes influencing lipid and cardiovascular traits, including the generation of iPS cells and differentiation to a variety of relevant cell types.

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# Rahim R. Rizi, Ph.D.

**Professor of Radiology** 

1 Silverstein, 3400 Spruce Street

Phone: 215-615-2426

Fax: 215-349-5115 Email: <u>rizi@uphs.upenn.edu</u>

http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p13700

# **Research Overview**

The primary mission of the Functional and Metabolic Imaging Group (FMIG) is the development and application of novel hyperpolarized MRI techniques to the diagnosis of various pulmonary and metabolic disorders. Hyperpolarization, the process of drastically increasing the population difference between nuclear spin states, provides a platform for imaging lung physiology and metabolic activity with spatial and temporal resolution unattainable with conventional MRI techniques, thus offering the potential for the earlier diagnosis of disease states and the precise monitoring of a patient's response to medical treatment. This core research theme is executed with an eye toward several ultimate goals: the identification of changes in pulmonary structure and function associated with disease, a more complete understanding of pathogenesis, and the establishment of a more sensitive testing environment to develop treatments for lung disease. To date, significant contributions in these areas include new imagining techniques for the comprehensive description of lung physiology and structure, accurate imaging of the regional pulmonary partial pressure of oxygen in both humans and large and small animals, highly developed imaging of regional ventilation, and a state-of-the-art mechanical ventilation device. Specifically, our research activities at FMIG is divided into four general branches: 1) The development of novel imaging techniques for the quantitative assessment of pulmonary structure and function: 2) The development of novel methods for real-time metabolic imaging: 3) The construction of novel polarization apparatuses: 4) The development and implementation of rapid imaging pulse sequences.

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# Michael B. Robinson, Ph.D.

**Professor of Pediatrics** 

502D Abramson Research Building Phone: 215-590-2205 Fax: 215-590-3779 Email: <u>Robinson@pennmedicine.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p9046

#### **Research Overview**

Glutamate and aspartate are the predominant excitatory neurotransmitters in the mammalian CNS. These two excitatory amino acids (EAAs) mediate most of the rapid depolarization that occurs in the CNS. In fact, the levels of these transmitters are 1000- to 10,000-fold higher than those of many other important neurotransmitters, including dopamine, serotonin, and acetylcholine. Paradoxically, these EAAs are also potent neurotoxins, both in vivo and in vitro. In fact, excessive activation of EAA receptors contributes to the neuronal degeneration observed after acute insults to the CNS, such as stroke and head trauma. We are interested in the normal physiology of EAAs and the role of these transmitters in neurodegeneration. Our laboratory has focused on understanding the regulation of extracellular levels of EAAs because it is this pool of EAAs that is toxic to neurons. Extracellular concentrations of glutamate and aspartate are normally maintained in the low micromolar range by a family of sodium-dependent high affinity transporters that are present on both neurons and glial cells. Our laboratory has developed evidence that neurons induce and maintain expression of one of the astrocytic transporters critical for limiting excitotoxicity. We have begun to define the mechanisms that contribute to this regulation. Our laboratory has also found that the function of several of the transporter subtypes can be rapidly (within minutes) altered by activation of certain kinases. This regulation is associated with a redistribution of these transporters to/or from the plasma membrane (see the image below). The long term goal of the laboratory is to develop new strategies for limiting glutamate-mediated damage by understanding the endogenous mechanisms that clear this excitotoxin.

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# Heath D. Schmidt, PhD

# Associate Professor of Psychiatry

125 South 31st Street RM 1110, Translational Laboratories Research Building Phone: 215-573-8291 Email: <u>hschmidt@nursing.upenn.edu</u> <u>https://www.nursing.upenn.edu/live/profiles/53-heath-d-schmidt</u>

# **Research Overview**

The main goal of our laboratory is to understand the neurobiological basis for drug addiction. We use a multidisciplinary approach that incorporates behavioral pharmacology and molecular biology techniques to identify novel neuroadaptations produced by chronic drug exposure. Our research program is broadly divided into three areas of focus:

- 1. Our lab is interested in understanding the biological mechanisms underlying nicotine addiction. Drug self-administration is a clinically relevant animal model that can be used to investigate the effects of potential smoking cessation medications in moderating nicotine reinforcement. Recent experiments aim to examine the role of acetylcholinesterase and nicotinic acetylcholine receptors in nicotine reinforcement and reinstatement.
- 2. Another focus of the laboratory is to integrate behavioral pharmacology and neuroscience with molecular techniques that probe drug-induced neuroadaptations at the genomic level. Specifically, our research aims to investigate the epigenetic mechanisms underlying drug craving and relapse. It is now clear that chronic exposure to drugs of abuse alters gene expression in limbic nuclei that underlies the neuronal and behavioral plasticity associated with drug taking and seeking. Our research is aimed at determining how drug-induced chromatin remodeling leads to alterations in growth factor expression following chronic cocaine.
- 3. Our previous studies have demonstrated that alterations in dopamine and glutamate transmission play a critical role in drug-taking and –seeking behaviors. Thus, one focus of our research program is to determine the molecular mechanisms that regulate plasticity in dopamine and glutamate systems and contribute to drug-seeking behavior. In collaboration with Dr. Chris Pierce, we are studying the role of protein kinase C (PKC) in cocaine priming-induced reinstatement, an animal model of relapse in human cocaine addicts. These studies also aim to understand how chronic cocaine exposure affects AMPA receptor trafficking in the nucleus accumbens.

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# Patrick Seale, Ph.D.

Associate Professor of Cell and Developmental Biology

Institute for Diabetes, Obesity and Metabolism, Room 105 Smilow Center for Translational Research, 12th Floor Phone: 215-573-8856 Fax: 215-898-5408 Email: <u>sealep@pennmedicine.upenn.edu</u> <u>http://www.med.upenn.edu/sealelab/index.html</u>

#### **Research Overview**

Obesity is the predominant risk factor for an expanding array of diseases including: type 2 diabetes, heart disease, stroke and cancer. Our lab investigates the transcriptional pathways that control the development, differentiation and function of adipose cells in normal development and in obesity. We are particularly interested in early determination and specification events; this involves the commitment of mesenchymal stem cells to a preadipose cell fate. We are also exploring pathways that determine the fate (and thus the function) of different types of fat cells.

Mammals have two main subtypes of adipose tissue, white and brown. White adipose tissue is specialized for energy storage, whereas brown adipose expends chemical energy in the form of heat. White adipose tissue is found in the subcutaneous layer and in distinct intra-abdominal depots. Excess abdominal adiposity is associated with metabolic dysfunction, insulin resistance and heart disease. By contrast, expansion of subcutaneous fat is not correlated with insulin resistance or metabolic disease.

Brown fat can counteract obesity by safely burning off excess energy. Increased brown adipose function promotes a lean and healthy phenotype. Conversely, animals lacking brown adipose develop obesity and type 2 diabetes. Recent PET-based imaging studies suggests that the amount of activated brown adipose in humans is inversely correlated with body mass index and age. These results suggest that brown adipose plays an important and unappreciated role in human energy balance. Moreover, drug or cell-based approaches that increase the amount of function of brown adipose could provide novel therapies for obesity and its metabolic complications.

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#### **Research Overview**

# Amita Sehgal, Ph.D.

## John Herr Musser Professor of Neuroscience

10-135 Smilow Center for Translational Research

Email: amita@pennmedicine.upenn.edu

http://www.med.upenn.edu/sehgal/index.shtml

The laboratory seeks to understand the molecular and cellular networks that drive behavior, in particular rhythmic behaviors such as sleep. Our studies are done largely with the fruit fly, Drosophila melanogaster, but we also translate our findings to mammalian models, especially mice. The major goals are to elucidate the mechanisms that confer a circadian (~24-hour) periodicity on much of behavior and physiology as well as understand how and why the drive to sleep is generated.

Circadian (~24-hour) clocks endogenous to most organisms drive daily rhythms of sleep:wake and of most physiological processes. Any kind of desynchrony between endogenous clocks and the environment, as is caused by travel to a different time zone or by shift work, results in a multitude of physiological disturbances. Likewise, sleep disruption, which is common in modern society, results in severe metabolic and cognitive deficits.

Our research has provided insight into mechanisms of the circadian clock, how clocks synchronize to light and how clocks interact with body systems to drive rhythms of behavior and physiology. Building upon a Drosophila model for sleep that we developed several years ago, we have also identified genes and circuits that underlie the homeostatic drive for sleep. Ongoing studies are revealing new mechanisms and cellular functions for sleep. Together our studies are providing a comprehensive understanding of how internal clocks drive body rhythms, how and why a sleep state occurs, and the extent to which clocks and sleep impact general physiology and aging.

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# Mark Sellmyer, M.D., Ph.D.

Assistant Professor of Radiology

Stellar-Chance Labs 813A Phone: 215-573-3212 Email: <u>mark.sellmyer@uphs.upenn.edu</u> <u>https://www.med.upenn.edu/sellmyerlab/</u>

#### **Research Overview**

The lab mission is to develop molecular and cellular solutions addressing important challenges in biomedical science and clinical medicine. We create small molecules, engineered proteins and cell-based tools that can "light up" and control in vivo biology using principles of chemical and synthetic biology. When possible, our technologies are translated to the clinic using nuclear medicine and molecular imaging techniques. For example, our group recently pioneered the development, preclinical testing, and human application of a new class of positron emission tomography (PET) radiotracers based on the small molecule antibiotic trimethoprim. These molecules have diverse applications in our broad fields of investigation including cancer biology, immunology, and infectious disease. If you have any questions about who we are and what we do, don't hesitate to reach out to us.

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# Sunny Shin, Ph.D.

## **Associate Professor of Microbiology**

3610 Hamilton Walk 201B Johnson Pavilion Office: (215) 746-8410 Fax: (215) 898-9557 Lab: (215) 573-4752 Email: <u>sunshin@pennmedicine.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20002980/p8421823

## **Research Overview**

My lab is interested in uncovering innate immune mechanisms used by the host to defend itself against bacterial pathogens and how bacterial pathogens evade host immunity to cause disease.

We utilize the intracellular bacterial pathogen Legionella pneumophila, causative agent of the severe pneumonia Legionnaires' disease, as our primary model. Legionella has evolved numerous mechanisms for modulating eukaryotic processes in order to facilitate its survival and replication within host cells. The ease with which Legionella can be genetically manipulated provides a powerful system for dissecting immune responses to bacteria that differ in defined virulence properties and for elucidating mechanisms of bacterial pathogenesis.

A major focus of our lab is to understand how the immune system distinguishes between virulent and avirulent bacteria and tailors appropriate antimicrobial responses. One key immune pathway involves the inflammasome, a multi-protein cytosolic complex that activates the host proteases caspase-1 and caspase-11 upon cytosolic detection of bacterial products. These caspases mediate the release of IL-1 family cytokines and other inflammatory factors critical for host defense, but overexuberant activation can lead to pathological outcomes such as septic shock. We are currently pursuing how mouse and human inflammasomes differentially respond to bacterial infection.

We are also interested in elucidating how the immune system successfully overcomes the ability of pathogens to suppress critical immune functions. We recently found that infected macrophages circumvent Legionella's ability to block host translation by selectively synthesizing and releasing key cytokines. These cytokines then instruct bystander immune cells to generate an effective immune response. We are defining additional mechanisms that facilitate communication between infected and bystander cells and promote antimicrobial defense.

We also study the evolutionarily related pathogen Coxiella burnetii, and other bacterial pathogens, with the goal of identifying shared and unique features of innate immunity and bacterial virulence. Insight into these areas will advance our understanding of bacterial pathogenesis, how the innate immune system distinguishes between virulent and avirulent bacteria and initiates antimicrobial immunity, and will ultimately aid in the design of effective antimicrobial therapies and vaccines.

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# James Shorter, Ph.D.

# **Professor of Biochemistry and Biophysics**

805B Stellar-Chance Laboratories Phone: 215-573-4256 Fax: 215-898-4217 Email: jshorter@mail.med.upenn.edu http://www.med.upenn.edu/shorterlab/index.html

#### **Research Overview**

Life demands that proteins fold into elaborate structures to perform the overwhelming majority of biological functions. We investigate how components of the proteostasis (protein homeostasis) network enable cells to achieve successful protein folding. In particular, we seek to understand how cells prevent, reverse, or even promote the formation of diverse misfolded conformers, encompassing: prions, amyloids, fibrillar structures, amorphous aggregates and toxic soluble oligomers.

Amyloid fibers are self-templating protein conformers. They self-replicate their specific 'cross-beta' conformation at their growing ends, by converting other copies of the same protein to the 'cross-beta' amyloid form. When amyloid fibers grow and divide with high efficiency they can be infectious, and are then termed prions (Cushman et al., 2010; Shorter & Lindquist, 2005; Shorter, 2010). Cells have evolved a sophisticated machinery to alleviate such aberrant protein aggregation. For example, protein disaggregases resolve protein aggregates, molecular chaperones prevent protein aggregation, osmolytes act as chemical chaperones, and degradation systems eliminate misfolded proteins (Shorter, 2008; Vashist et al. 2010).

Nonetheless, these safeguards can be breached, especially as organisms age, and the consequences are often fatal. Prion and amyloid formation are associated with some of the most devastating neurodegenerative diseases confronting humankind, including Alzheimer's disease, Parkinson's disease, variant Creutzfeldt-Jakob disease, and Huntington's disease (Cushman et al., 2010; Jackrel & Shorter, 2011). Yet, surprisingly, it is becoming increasingly clear that prions and amyloids are not always a problem. In fact, several have been harnessed during evolution for adaptive purposes and feature in some of the most revolutionary new concepts in biology and evolution, including protein-based genetic elements, long-term memory formation, melanosome biogenesis, evolutionary capacitance and the revelation of cryptic genetic variation (Shorter & Lindquist, 2005; Watt et al., 2009; Shorter, 2010). We employ biochemistry and genetics to understand the enigmatic mechanistic interfaces that exist between protein disaggregases, molecular chaperones, small molecules and amyloid/prion fibers or other misfolded species, and how these interfaces can be manipulated to divert pathogenic and promote beneficial phenotypic trajectories. Specifically, we are taking five broad approaches:

- 1. Defining the structural and mechanistic basis for Hsp104 function.
- 2. Applying Hsp104 to disease-associated protein misfolding and aggregation.
- 3. Defining the metazoan disaggregase machinery.
- 4. Defining how small molecules modulate amyloid folding trajectories.
- 5. Defining the misfolding trajectories of RNA-binding proteins bearing prion-like domains in amyotrophic lateral sclerosis and other neurodegenerative disorders.

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# Rebecca A. Simmons, M.D.

Hallman Hurt Professor of Neonatology

BRB II/III, Rm 1308 Philadelphia, PA 19104 Phone: 215-662-3269 Email: <u>rsimmons@mail.med.upenn.edu</u> https://www.med.upenn.edu/apps/faculty/index.php/g20000220/p11818

## **Research Overview**

The principal goal of our research program is to elucidate the underlying molecular mechanisms that link fetal growth retardation to the later development of obesity and type 2 diabetes in adulthood. We currently have 3 major projects and several smaller projects. The first project focuses on the relationship between oxidative stress and ß-cell dysfunction and insulin resistance. We have developed a model of fetal growth retardation in the rodent (mice and rats) which leads to the later development of diabetes and obesity in adult animals. We have established that fetal growth retardation induces progressive mitochondrial dysfunction, oxidative stress, mtDNA mutations, and electron transport defects. These defects cause abnormal ß-cell function and development, and hepatic and muscle insulin resistance. Oxidative stress decreases transcription of key genes related to ß-cell development, induces modifications of proteins of the Krebs cycle in the liver, and muscle. Pdx-1 is a critical transcription factor that regulates B-cell function and development. Transcription of this gene is permanently down-regulated in ß-cells of IUGR rats leading to a gradual reduction in ß-cell function and ß-cell replication. We have determined that oxidative stress induced by uteroplacental insufficiency in IUGR fetal pancreas induces aberrant methylation and chromatin remodeling at the Pdx-1 promoter, which in turn induces transcription silencing. The focus of the second project is to determine whether the effects of an aberrant intrauterine milieu can be reversed after birth, we have designed a number of therapeutic modalities including diet modifications and antioxidant treatment. In collaboration with Dr. Doris Stoffers, we have successfully prevented the development of diabetes in IUGR rats with several of these treatments. Administration of a pancreatic ß-cell trophic factor, Exendin-4, during the neonatal period dramatically prevents the development of diabetes in our model. Neonatal Exendin-4 treatment prevents the progressive reduction in ß-cell mass that is observed in IUGR rats over time. Expression of Pdx-1 is restored to normal levels, and islet ß-cell proliferation rates are normalized by the neonatal Exendin-4 treatment. Of major clinical significance is our finding that Exendin-4 treatment in the newborn period prevents the onset of obesity in IUGR rats. This surprising finding has stimulated a new direction for this project and we are currently determining the mechanisms by which Exendin-4 treatment reverses epigenetic modifications such as DNA methylation and histone modifications of key genes related to ß-cell development. The third project is focused on the effects of obesity during pregnancy and the long-term outcome in the offspring. The specific aims of this project are to determine the window of susceptibility of the developing organism to the effects of obesity during gestation, determining whether regulation of the adipogenic pathway is altered in offspring, and defining the molecular mechanisms responsible for enhanced adipogenesis observed in offspring of obese mothers.

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# Wenchao Song, Ph.D.

# Professor of Pharmacology

1254 BRB II/III Phone: 215-573-6641 Fax: 215-746-8941 Email: <u>songwe@upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p5289

## **Research Overview**

My research is focused on complement-mediated inflammatory, autoimmune and thrombotic vasculopathy disorders. By creating gene targeted mice, we establish mouse models of human diseases to understand disease pathogenesis and to test novel anti-complement therapies. We are also interested in the interaction of complement with other innate immune pathways such as the Toll-like receptors and with the adaptive immune system. Our long term goal is to advance basic complement immunology and to help develop new therapies for complement-mediated human diseases.

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# Timothy J. Stalker, Ph.D.

## **Research Assistant Professor of Medicine**

809 BRB II/III Phone: 215-573-3631 Email: <u>tstalker@mail.med.upenn.edu</u> https://www.med.upenn.edu/brasslab/timstalker.html

#### **Research Overview**

I have been involved with investigations in the field of thrombosis and hemostasis since joining the Brass lab at the University of Pennsylvania as a post-doctoral fellow in 2003. Since that time, the goal of my research studies has been to gain a better understanding of the mechanisms responsible for hemostasis and thrombosis, with a particular emphasis on how multiple signaling inputs present at a site of vascular injury are integrated to regulate platelet activation in vivo. The following is a brief summary of major ongoing projects performed in association with members of the Brass lab.

Project 1: Spatio-temporal regulation of platelet activation following vascular injury in vivo

We recently determined that hemostatic plugs formed following vascular injury in vivo are composed of discrete regions with variable degrees of platelet activation. Ongoing studies are investigating how multiple components of the platelet signaling network are integrated to produce this heterogeneous hemostatic plug architecture. To accomplish these goals, we make extensive use of multiple systems for examination of thrombosis in vitro and in vivo, including a spinning disk confocal intravital microscopy system for visualization of thrombosis in the microcirculation of mice. Intravital microscopy approaches also involve the use of established and novel fluorescent probes for visualizing various aspects of the hemostatic response in vivo, including fluorescently labeled antibodies, fluorescent biochemical activity sensors and genetically encoded fluorescent indicators.

Project 2: The influence of local microenvironments on hemostasis and thrombosis in vivo

In conjunction with the studies in Project 1, we have become interested in how local microenvironments within a platelet aggregate help to shape the movement and overall distribution of soluble plasma components that regulate platelet activation and coagulation. These studies couple in vivo imaging approaches measuring solute transport with in vitro and computational approaches to model and analyze the physical characteristics of the microenvironment between adjacent platelets as they become tightly packed in a hemostatic plug.

Project 3: Platelet function in the setting of trauma and other pathologic states

Platelet function is known to be perturbed in a number of pathologic settings and may contribute to the morbidity and mortality associated with these pathologies. One example is in the setting of trauma, where a subset of severe trauma patients develop a coagulopathic state characterized by abnormal blood clotting and excessive hemorrhage. We are using animal models to study platelet function in the setting of trauma-induced coagulopathy as part of a multi-institution consortium funded by the NHLBI (TACTIC).

Project 4: The role of junctional adhesion molecules in platelet biology

Another longstanding research project involves examination of the role of a family of cell adhesion molecules found on the surface of platelets, including ESAM and JAM-A, which are found at the tight junctions of other cell types (e.g. endothelial cells and epithelial cells). As platelets do not form tight junctions the role of these proteins in platelet biology is rather unclear, but they appear to be negative regulators of platelet plug formation in vivo as genetic deletion of these proteins in mice leads to a pro-thrombotic phenotype. Current studies are investigating the mechanisms by which this family of proteins influences platelet functions, as well as their role in platelet-leukocyte and platelet-endothelial cell crosstalk.

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# Doris A. Stoffers, M.D., Ph.D.

Sylvan H. Eisman Professor of Medicine

Smilow Center for Translational Research, Room 12-124 Phone: 215-573-5413 Fax: 215-898-5408 Email: <u>stoffers@mail.med.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p3556

## **Research Overview**

Research in our laboratory focuses on the embryonic development and adult regeneration of the endocrine pancreas, and the relationship of defects in these pathways to the pathophysiology of diabetes mellitus, a disease caused by a deficiency in the production or action of insulin. The beta cells of the endocrine pancreas are the only source of insulin production in the body- therefore the regulation of beta cell mass is pivotal to the development of diabetes and successful therapies aimed at correcting diabetes must impact beta cell growth and/or function. Further support for this focus derives from genetic studies linking monogenic forms of human diabetes to mutations in transcription factors that regulate the development of beta cell mass. A model example is the homeobox transcription factor, IPF-1/PDX-1, that plays critical roles in embryonic pancreas development and in differentiated islet beta cell function in the adult endocrine pancreas. Using cutting edge molecular methods, yeast two hybrid libraries, transgenic and knock-out mice, cDNA microarray, chromatin immunoprecipitation, human genetics, and genomic and proteomic approaches, our current projects include:

- Characterization of a novel PDX C-terminus Interacting Factor, PCIF1, identified in a yeast twohybrid screen. PCIF1 is a novel nuclear factor that recruits Pdx1 into a cullin3 based E3 ubiquitin ligase for polyubiquitination and proteasomal degradation. Biochemical, molecular, in vivo and human genetics approaches are being applied to elucidate the role of this novel regulatory molecule.
- 2. Examining the molecular mechanisms by which the incretin hormone GLP-1 stimulates expansion of beta cell mass, with a particular emphasis on signal transduction and the identification of molecular mechanisms whereby GLP-1 promotes beta cell regeneration and regulates PDX expression.
- 3. Elucidating molecular mechanisms underlying islet compensation for diet-induced insulin resistance.
- 4. Identifying targets of Pdx1, Pbx and Meis homeodomain factors in the pancreatic ß cell.

# Selected Publications

Juliana CA, Yang J, Cannon CE, Good AL, Haemmerle MW, Stoffers DA. A PDX1-ATF transcriptional complex governs β cell survival during stress. Mol Metab. pii: S2212-8778(18)30517-9. doi: 10.1016/j.molmet.2018.07.007. [Epub ahead of print] Aug 2018.

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# Kai Tan, PhD

# **Associate Professor of Pediatrics**

4004 Colket Translational Research Bldg. Philadelphia, PA 19104 Office: 267-425-0050 Lab: 267-425-0058 Email: <u>tank1@email.chop.edu</u> <u>http://tanlab4generegulation.org/</u>

## **Research Overview**

Gene expression variation plays a major role in driving phenotypic variation. Our lab is interested in Systems Biology of gene regulation. The advent of various bulk and single-cell omics technologies increasingly allows us to interrogate the status of a cell's components and to determine how, when, and where these molecules interact with each other. By combining omics experiments and computational modeling, we are studying gene regulatory networks in several model systems.

I. Model gene regulatory networks in development and disease

We are studying gene regulatory networks controlling development and differentiation of hematopoietic stem cells, T cells, and oncogenesis. Specific projects include:

- 1. Identify and characterize keys transcription factors and enhancers that control cell/tissue-specific gene expression.
- 2. Understand how 3-dimensional genome organization controls cell/tissue-specific gene expression.
- 3. Understand how mutations in regulatory DNA sequences contribute to pathogenesis.

II. Discover molecular networks as biomarkers for human diseases

Molecular networks are increasingly serving as tools to unravel the basis of human diseases. We are developing network-based approaches to identifying disease-related sub-networks that can serve as biomarkers for the diagnosis and prognosis of diseases and as candidates for novel therapeutics.

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# Steven A. Thomas, MD, PhD

## Associate Professor of Pharmacology

Department of Pharmacology Room 103, John Morgan Building Office: (215) 573-4950 Email: <u>sathomas@mail.med.upenn.edu</u> https://www.med.upenn.edu/apps/faculty/index.php/g20000343/p18120

#### **Research Overview**

Broadly, the lab studies the development and physiology of the mammalian brain. One goal is to define the systems that contribute to specific behaviors, and to understand the mechanisms that underlie these behaviors. Such knowledge may ultimately permit the prevention and treatment of mental illness. Gene-targeting allows the analysis of specific genetic alterations in the context of the whole organism. The ability to add, delete or modify genes is particularly useful in the analysis of complex organ systems such as the brain, where half of all genes are thought to be uniquely expressed.

The lab focuses on the adrenergic nervous system in which norepinephrine (NE) and epinephrine are the classic neurotransmitters. By genetically eliminating the biosynthetic enzyme for NE, dopamine beta-hydroxylase (DBH), mutant mice (Dbh-/-) that completely lack NE and epinephrine were created. These mice are conditional mutants in that NE can be restored to the adrenergic terminals by supplying a synthetic amino acid precursor of NE, L-DOPS. The lab is pursuing several fundamental observations that resulted from the creation of these mutant mice. These include the roles of NE in learning and memory, as well as the neuronal physiology and signaling that underlie these effects. They also include the role of NE in the effects of stress. For each of these, potentially important interactions with other transmitters and hormones is also being explored. Finally, Dr. Thomas is pursuing several novel genetic approaches for producing complementary models to the Dbh-/- mice toward a more complete understanding of CNS adrenergic function.

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# Wei Tong, Ph.D.

# **Assistant Professor of Pediatrics**

310D Abramson Research Center
Phone: 267-426-0930
Fax: 267-426-5476
Email: tongw@email.chop.edu
http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p8146029

## **Research Overview**

Our lab focuses on molecular hematology-oncology with an emphasis on studying signal transduction in normal blood cell development and hematological malignancies. We use genetically-engineered mouse models, bone marrow transplantation, tissue culture cells, gene transcriptional profiling, protein complex purification and mass spectrometric identification, coupled with extensive usage of molecular, cellular, and biochemical technologies.

Hundreds of billions of blood cells have to be replenished everyday. Cytokines and cytokine receptors play important roles in blood cell formation, a process known as hematopoiesis. The amplitude and duration of cytokine receptor signaling is a highly regulated process that is crucial for cytokine- governed hematopoiesis. Dysregulation of these complex signaling networks can predispose to myeloproliferative diseases and myeloid leukemia.

We previously identified the adaptor protein, Lnk, as a novel negative regulator of cytokine receptor signaling. Lnk deficiency in mice results in an enhanced proliferative capacity of hematopoietic stem cells (HSCs) and progenitor cells of multiple lineages. Lnk loss-of-function leads to hyper-sensitivity to thrombopoietin (Tpo) and erythropoietin (Epo), which regulate platelet and red blood cell formation, respectively. Our results also implicate a new mechanism for rapidly downmodulating cytokine signaling: Lnk negatively regulates cytokine receptor induced JAK2 activity in a phosphorylation-dependent manner. We are interested in:

- 1. Elucidating molecular mechanisms of Lnk regulatory functions in cytokine receptor signaling
- 2. Understanding both normal and oncogenic cytokine receptor signaling processes that control hematopoietic stem and progenitor cell numbers and development in vivo
- 3. Undertaking studies to identify novel signaling components in the receptor/JAK2 signaling complex that lead to oncogenic transformation, as JAK2 is the central kinase governing many cytokine receptor signaling, and has been found mutated in some patients with myeloproliferative diseases.
- 4. Understanding ubiquitination and de-ubiquitination in regulation of cytokine signaling and hematopoietic stem cell expansion.
- 5. Investigating cytokine signaling in Acute Lymphoblastic Leukemia.
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## Andrew Tsourkas, Ph.D.

**Professor of Bioengineering** 

210 S. 33rd Street, 240 Skirkanich Hall Office: 215-898-8167 Email: atsourk@seas.upenn.edu https://www.seas.upenn.edu/~atsourk/index.html

#### **Research Overview**

Developing targeted imaging and therapeutic agents designed to improve the detection and treatment of cancer. Specific research interests include (i) developing new nanoformulations that are capable of carrying extremely high payloads of drugs, radiosensitizing agents, and/or contrast agents; (ii) investigating new targeting strategies that maximize specificity and sensitivity; and (iii) developing new bioconjugation techniques that enable the highly efficient, site-specific labeling of antibodies and other targeting ligands and that allow for the rapid production of bispecific antibodies.

#### **Recent Publications**

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## Patrick M Viatour, Pharm.D, PhD

## Assistant Professor of Pathology and Laboratory Medicine

Colket Translational Research Building, Rm 4064 Philadelphia, PA 19104 Office: 267-425-3004

Email: pviatour@pennmedicine.upenn.edu

Web: http://www.med.upenn.edu/apps/faculty/index.php/g275/p8466377

#### **Research Overview**

The long-term goal of my lab is to determine the mechanisms that transform adult stem cells into the cell of origin for many types of cancer. In particular, we study the epigenetic mechanisms that drive tumor initiation and progression upon loss of major tumor suppressor genes such as the Rb genes family.

This family, which includes Rb, p130 and p107, plays a central role in the regulation of cell cycle activity by sequestering E2F transcription factors. Cellular exposure to mitotic stimuli leads to the functional inactivation of Rb family proteins. Consequently, E2F factors are released and transactivate a large set of genes that collectively promote the progression through cell cycle. Genetic and epigenetic events targeting various components of the Rb pathway have been identified in the vast majority of cancers. A common and important consequence of these events is the permanent inactivation of Rb family, therefore establishing Rb family genes as major tumor suppressor genes. However, besides aberrant proliferation, the mechanisms that drive tumorigenesis upon Rb family inactivation remain mostly unknown.

To determine these mechanisms and identify critical drivers of tumorigenesis for translational purposes, we have generated new mouse models that recapitulate the acute Rb family inactivation observed in cancer and have chosen hematopoiesis and the liver as experimental systems. Our recent data (Cell Stem Cell 2008, JEM 2011 & 2013) have demonstrated that stem cells, in contrast to terminally differentiated cells, are particularly sensitive to Rb family loss. Indeed, Rb family deficient stem cells rapidly exhibit a complex phenotype including proliferation, biased differentiation and tumorigenesis. Complementary molecular approaches have started to unravel new and surprising means for E2F factors, including the recruitment of complex epigenetic mechanisms, to activate important oncogenic features that drive tumor progression.

Our current research effort aims at identifying these epigenetic mechanisms and developing compoundbased strategies to inactivate them and impair tumor development. To this end, we are developing several mouse models and using a combination of bioinformatic analysis, as well as in vitro, ex vivo and in vivo approaches.

#### **Selected Publications**

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# Benjamin Voight, Ph.D.

## Associate Professor of Pharmacology

10-126 Smilow Center for Translational Research Phone: 215-746-8083 Email: <u>bvoight@pennmedicine.upenn.edu</u> <u>http://coruscant.itmat.upenn.edu</u>

#### **Research Overview**

The central aim in my lab is to understand the genetic, biological, and evolutionary basis of metabolic and cardiovascular phenotypes in human populations. To build this understanding, the lab constructs computational and statistical tools grounded in principles of population biology and quantitative genetics. These tools are then applied to genetic data collected across thousands of whole human genomes.

My research has answered population genetic questions about recent demographic and selective events in human populations, and work to develop new statistics to identify selective pressures is ongoing. Recent work in the lab has focused on statistical models which capture variability in the rate of mutation in the human genome.

I have an active interest in mapping risk alleles for common diseases, particularly type-2 diabetes and coronary heart disease, but perhaps more importantly, to identify the causal variant, gene, and mechanism that influences risk to these diseases from existing non-coding associations identified by genome-wide association studies.

I continue to utilize the framework of Mendelian Randomization, to perform causal inference studies between genetically-heritable biomarkers and complex diseases. Work in the lab is toward applications, but also development of novel methodologies.

In the coming years, the lab activities will focus on several key areas of interest, which includes:

- Developing statistical models to capture variability in the rate of mutation in human genomes, with application to identifying de novo mutations and rare variation related to human disease

- Computational methods and functional characterization of the causal variants and genes related to non-coding associations for type 2 diabetes and heart disease

- Developing informational and statistical tools which interrogate human genetic association data together with other sources of 'omics data to construct credibly actionable information on pathways responsible for disease susceptibility

- Population genetic methods to identify loci in the human genome which are targets of natural selective pressures, and to further identify the causal variants and genes responsible

- Genomics in Arachnids to understand the structure and function of spider silk genes

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# Kirk J. Wangensteen, M.D., Ph.D.

Assistant Professor of Medicine

BRB II/III, Rm 910 Office: 215-573-7314 Email: <u>wkirk@upenn.edu</u> <u>https://www.med.upenn.edu/wangensteenlab/</u>

## **Research Overview**

Our lab is conducting exciting research on the genetics of liver repopulation and hepatocellular carcinoma (HCC). We have developed two highly innovative in vivo genetic screening paradigms to elucidate genetic pathways involved in carcinogenesis and liver repopulation in the setting of toxic injury. We aim to discover pathways that lead to drug sensitivity and resistance in HCC. One of our assays involves CRISPR activation screening in vivo in the liver, the first-ever use of this type of screening in live mice.

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## Franz Weber, Ph.D.

**Assistant Professor of Neuroscience** 

10-132 Smilow Research Center Office: 215-898-0254 Email: <u>fweber@pennmedicine.upenn.edu</u> <u>https://www.med.upenn.edu/weberlab/</u>

## **Research Overview**

We are interested in the neural and homeostatic mechanisms controlling REM sleep and the functional role of this brain state in emotional memories and behaviors. We study REM sleep and its functional roles in the mouse model. Our lab employs a wide range of methods including optogenetics, in vivo electrophysiology, calcium imaging, viral tracing and quantitative modeling to disentangle the neural and homeostatic mechanisms controlling REM sleep. We further seek to develop a circuit-based understanding of how REM sleep affects emotional behaviors in health and disease.

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# David Weiner, Ph.D.

Emeritus Professor of Pathology and Laboratory Medicine

The Wistar Institute Phone: 215-898-0381 Email: <u>dweiner@wistar.org</u> <u>https://wistar.org/our-scientists/david-weiner</u>

## **Research Overview**

Dr. Weiner's research focus is in the area of Molecular Immunology. His group has focused extensively on the development of gene-based vaccines, immune therapies and molecular interventions for the treatment of human and animal disease. His laboratory is one of the founders of the field of DNA vaccines, and importantly, was the first to move DNA vaccines to human clinical studies establishing their initial safety and immunogenicity opening up this area for clinical development. First study in HIV immune therapy conducted in 1995, and first immune therapy for cancer (CTCL) in 1995. The first DNA trial in normal healthy HIV+ patients occurred in 1997.

Other clinical trials of DNA, conducted in collaboration with the HIV Vaccine Trials Network (HVTN) are: HVTN 070, study of DNA vaccine against HIB including cytokine genes, and HVTN 080, study of DNA vaccine for HIV by adaptive electroporation with IL12. In 2009, collaboration with a biotechnology company resulted in VGX 3100, a study of a DNA vaccine for cervical cancer and immune therapy.

His group was the first to show that a DNA based approach could impact an HIV model challenge in nonhuman primates. Based on these accomplishments Dr. Weiner contributed to the initial 'Points to Consider' guidance document for the FDA on moving gene based approaches through the Clinic. He has created many new technologies for treatment of human disease and has been awarded more than 50 patents on his laboratory's work. His lab is instrumental in the recent resurgence of interest in the DNA vaccine field due to the lab and collaborators developing new vectors and delivery approaches that improved their immune potency in humans. He is very active in teaching and training of students and fellows and junior faculty. He chairs the popular Gene Therapy and Vaccines Program at the University of Pennsylvania, and co directs the Tumor Virology Program of the Abramson Cancer Center at the University of Pennsylvania.

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# Aalim M. Weljie, Ph.D.

## **Research Assistant Professor of Pharmacology**

10-113 Translational Research Center Phone: 215-573-8085 Email: <u>aalim@upenn.edu</u> <u>https://www.med.upenn.edu/weljielab/</u>

## **Research Overview**

The Weljie Lab is located in the Department of Systems Pharmacology and Translational Therapeutics within the Perelman School of Medicine at the University of Pennsylvania. Our lab is at the forefront of metabolomics technologies to examine biological problems in a translational medicine context, particularly related to sleep and circadian rhythms.

Metabolomics is a growing sub-field of systems biology centered on the study of small biological molecules in biological fluids and tissues. Recent research suggests that analysis of metabolite concentrations in living systems is useful in disease diagnosis, prognosis, and predicting drug efficacy in a personalized medicine context.

There is an intrinsic link between metabolism and function of the innate circadian clock system in numerous organisms and disease states, but the exact mechanism by which the clock controls mammalian metabolism is poorly understood. Our work seeks to fill this knowledge gap along with a particular emphasis on understanding the relationship of the clock with cancer and environmental health.

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## Rebecca Wells, M.D.



#### **Professor of Medicine**

905 BRB II/III Phone: 215-573-1860 Fax: 215-573-2024 Email: <u>rgwells@mail.med.upenn.edu</u> http://www.wellslab.com/

#### **Research Overview**

My research focuses on the mechanism of hepatic fibrosis. Liver fibrosis results from the deposition of excess, abnormal extracellular matrix by myofibroblasts derived from non-fibrogenic cells that undergo "activation" in the context of chronic liver injury. Fibrosis in the bile duct is a similar matrix-driven process, although the identity of the myofibroblast populations and the chronic vs. acute nature of the injury are not known.

We are investigating the mechanisms of fibrosis in three ways: a) by studying the matrix, mechanical, and soluble factors that influence fibrosis, including the activation of myofibroblast precursor populations; b) by identifying new fibrogenic cell populations and new means of studying previously identified cells; and c) by applying the results of our experiments with isolated cells to whole animal models and to the study of human diseases, including hepatocellular carcinoma and biliary fibrosis.

We have demonstrated in rat models of fibrosis that increased liver stiffness precedes matrix deposition and that fibrosis and liver stiffness are not linearly related. The early increases in liver stiffness are important because hepatic stellate cells and portal fibroblasts, the major myofibroblast precursors of the liver, require increased stiffness to become fibrogenic. Our recent work has examined liver mechanics in more detail, and we have attempted to determine the components of the liver responsible for various mechanical properties. We have found that livers strain soften and compression stiffen, in contrast to biopolymers like collagen. Our work suggests that proteoglycans and other matrix components as well as cell-matrix interactions are the reason for these mechanical properties. Our theory collaborators have developed a new constitutive model for the tissue that is in good agreement with our data.

This work led to an ongoing project examining the mechanics of the cirrhotic liver and their impact on the development of hepatocellular carcinoma (HCC). Using a variety of matrices, animal models, and human and animal cells, we are studying the impact of various mechanical properties on liver cell behavior with the goal of understanding the remarkable propensity of HCC to develop in a highly mechanically abnormal environment.

We have not studied liver mechanics in isolation, but also study various matrix components, including fibronectin splice variants and proteoglycans, and are examining their effects on liver cell function, fibrosis, and liver mechanics.

Human model diseases of interest to our studies of the mechanism of fibrosis include biliary atresia. We are part of an international group that has recently identified a plant toxin that causes biliary atresia. We have developed model mammalian cell systems to study its mechanism of action and are testing structurally similar compounds in an attempt to identify critical structural groups, which may lead us to compounds of relevance to

humans. Additionally, as part of a general interest in biliary fibrosis, we are studying potential myofibroblast precursor populations in the extrahepatic bile duct, the impact of acute vs. chronic cholangiocyte injury, mechanisms of liver fibrosis post bile duct obstruction, and differences between intra- and extra-hepatic cholangiocytes.

Overall, our goal is to develop a unified and comprehensive model of liver fibrosis that incorporates multiple cell types, soluble and secreted factors, matrix proteins, and local and regional mechanical factors.

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# Alexander S. Whitehead, D.Phil.

## Professor, Department of Pharmacology

159 Johnson Pavilion Phone: 215-898-2332 Fax: 215-573-9135 Email: <u>aswhiteh@mail.med.upenn.edu</u> http://www.med.upenn.edu/apps/faculty/index.php/g20000343/p17480

## **Research Overview**

- 1. Biosynthetic control and molecular genetics of major acute phase proteins
- 2. Mechanisms and mediators of inflammation
- 3. Inherited defects of folate metabolism and their role in hyper-homocysteinemia, cardiovascular disease, neural tube defects, and other pathological conditions
- 4. Pharmacogenetics of commonly prescribed drugs that target, or interact with, components controlling homocysteine and folate metabolism

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## Hao Wu, Ph.D.

**Assistant Professor of Genetics** 

547A Clinical Research Building Office: 215-573-9360 Email: <u>haowu2@pennmedicine.upenn.edu</u> <u>https://www.med.upenn.edu/apps/faculty/index.php/g275/p8878781</u>

#### **Research Overview**

DNA cytosine methylation (5-methylcytosine) is an evolutionarily conserved epigenetic mark and has a profound impact on transcription, development and genome stability. Historically, 5-methylcytosine (5mC) is considered as a highly stable chemical modification that is mainly required for long-term epigenetic memory. The recent discovery that ten-eleven translocation (TET) proteins can iteratively oxidize 5mC in the mammalian genome represents a paradigm shift in our understanding of how 5mC may be enzymatically reversed. It also raises the possibility that three oxidized 5mC bases generated by TET may act as a new class of epigenetic modifications.

Interestingly, key epigenetic enzymes such as TET family of DNA deoxygenate and JmjC-domain-containing histone demethylase directly utilize oxygen and some major metabolites as their cofactors to modify epigenetic marks on DNA or histone, supporting the notion that cells in multicellular organisms can rapidly adapt to changing environmental inputs or metabolic states by dynamically modifying their epigenome and gene expression programs.

Our laboratory uses high-throughput sequencing technologies, bioinformatics, mammalian genetic models, as well as synthetic biology tools to investigate the mechanisms by which proteins that write, read and erase DNA and histone modifications contribute to mammalian development and relevant human diseases. To achieve this goal, we are also interested in developing new genomic sequencing and programmable epigenome-modifying methods to precisely map and manipulate these DNA modifications in the complex mammalian genome.

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# Gary Wu, M.D.

Ferdinand G. Weisbrod Professor in Gastroenterology

915 BRB II/III Phone: 215-898-0158 Email: <u>gdwu@mail.med.upenn.edu</u> <u>http://www.med.upenn.edu/apps/faculty/index.php/g345/p8790</u>

## **Research Overview**

The research programs in the Wu laboratory focus on the mutualistic interactions between the gut microbiota and the host with a particular focus on metabolism. Growing evidence suggests that diet impacts upon both the structure and function of the gut microbiota that, in turn, influences the host in fundamental ways. Current areas of investigation include the effect of diet on the composition of the gut microbiota and its subsequence effect on host metabolism related to nitrogen balance as well as its impact on metabolic pathways in the intestinal epithelium, principally fatty acid oxidation. Through a UH3 roadmap initiate grant, he is helping to direct a project investigating the impact of diet on the composition of the gut microbiome and its relationship to therapeutic responses associated with the treatment of patients with Crohn's disease using an elemental diet. Finally, Dr. Wu is leading a multidisciplinary group of investigators using phosphorescent nanoprobe technology to examine the dynamic oxygen equilibrium between the host and the gut microbiota at the intestinal mucosal interface.

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## Xiaolu Yang, Ph.D.

## **Professor of Cancer Biology**

650 BRB II/III Phone: 215-573-6739 Fax: 215-573-6725 Email: <u>xyang@pennmedicine.upenn.edu</u> <u>https://www.med.upenn.edu/yanglab/</u>

#### **Research Overview**

The Yang Lab studies the molecular and cellular mechanisms that protect against major diseases, including cancer and neurodegeneration. Our current projects are focused on three areas: 1) apoptosis pathways, 2) the tumor suppressor p53, and 3) the cellular systems that degrade misfolded proteins. Our experimental strategies include molecular and cell biology techniques, biochemical techniques, metabolic analysis, cell culture, genomics, mouse disease models, and human patient samples.

Apoptosis is a physiological process of cell auto-destruction that eliminates unwanted, damaged, or harmful cells. Dysregulation of apoptosis is associated with many diseases such as cancer, neurodegeneration, and immunodeficiency. Apoptosis is executed by the caspase family of cysteine proteases. We previously pioneered a paradigm for the activation of caspases, whereby initiator caspase activation is controlled by oligomerization. We are investigating the regulation of caspase activation in various apoptosis pathways. Paradoxically, some caspases are also involved in cell proliferation. We are studying the proliferative role of caspases to better understand the interplay between cellular life and death processes.

p53 plays a preeminent role in blocking tumor formation and is the single most frequently mutated gene in human tumors. p53 is activated by various tumor-promoting stresses and effectuates a range of anti-proliferative and repair responses. We are investigating the regulation and functions of p53, as well as its structural homologue p73. We previously identified a complex that stabilizes the principal p53 antagonist Mdm2 and are now examining how this complex controls p53 activation. We also revealed a role for p53 family proteins in modulating cellular metabolism, particularly the production of NADPH, the reducing equivalent required for biosynthesis and anti-oxidant defense. We are further studying how these proteins act as both sentinels and regulators for metabolism, coordinating metabolism with cell fate decision, and how these functions may be compromised in tumor cells. We are also investigating other metabolic alterations in tumor cells that enable their survival, proliferation, and metastasis.

Proteins are the most abundant macromolecules in the cell and are critical to virtually all physiological processes. However, proteins are prone to misfolding, and accumulation of misfolded proteins is genetically and pathologically linked to neurodegenerative diseases and cancer. Cells ultimately rely on degradative systems to maintain protein quality. We recently identified a cellular system that selectively degrades misfolded proteins through sequential SUMOylation and ubiquitination, and protects against neurodegeneration. We are further defining the mechanism of this novel protein quality control system, as well as its dysregulation in human diseases.

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## Zhaolan (Joe) Zhou, Ph.D.

## **Associate Professor of Genetics**

452A Clinical Research Building Office: 215-746-5025 Fax: 215-573-7760 Email: <u>zhaolan@pennmedicine.upenn.edu</u> <u>https://www.med.upenn.edu/zhoulab/#/</u>

#### **Research Overview**

A fundamental question in Genetics and Neuroscience is how the brain executes genetic programs while maintaining the ability to adapt to the environment. The underlying molecular mechanisms are not well understood, but epigenetic regulation, mediated by DNA methylation and chromatin organization, provides an intricate platform bridging genetics and the environment, and allows for the integration of intrinsic and environmental signals into the genome and subsequent translation of the genome into stable yet adaptive functions in the brain. Impaired epigenetic regulation has been implicated in many neurodevelopmental and neuropsychiatric disorders.

The Zhou laboratory is interested in understanding the epigenetic mechanisms that integrate environmental factors with genetic code to govern brain development and function, elucidating the pathophysiology of specific neurodevelopmental disorders with known genetic causes such as Rett syndrome and CDKL5 deficiency, and illuminating the pathogenesis of selective neuropsychiatric disorders with complex genetic traits such as autism and major depression. We use a variety of cutting-edge genomic technologies, together with cellular and physiological assays in genetically modified mice, to pursue our interests. We aim to ultimately translate our findings into therapeutic development to improve the treatment for neurodevelopmental and neuropsychiatric disorders.

## 1. Defining the stress-induced epigenetic code underlying depressive-like behaviors

The genetic underpinnings of neuropsychiatric disorders are highly complex, involving multifaceted interactions between risk genes and the environment. It is known that environmental factors such as adverse early life events or chronic traumatic experience confer significantly greater susceptibility to psychiatric conditions later in life. However, the pathogenic mechanisms by which environmental factors interact with genetic programs in the nervous system to trigger psychiatric illness remain poorly understood. Thus, we have developed novel genetically modified mice, and plan to employ the next-generation sequencing and single cell sequencing technologies to identify the stress-induced epigenetic modifications from neuronal cell types of interest, to employ CRISPR-mediated genomic and epigenomic editing techniques to evaluate the causal relationship between stress-induced epigenetic changes and maladaptive behaviors, and to elucidate the key signaling pathways that mediate gene-environment interactions in the brain.

#### 2. Elucidating the molecular basis of Rett Syndrome

Rett Syndrome (RTT) is a neurodevelopmental disorder characterized by developmental regression, motor dysfunction, and cognitive deficits. The majority of RTT cases are associated with mutations on an X-

linked gene encoding MeCP2, a methyl-CpG binding protein involved in organizing chromatin and modulating gene expression. To understand the molecular pathogenesis of RTT, we have developed mouse models recapitulating RTT-associated mutations. We found that mice with RTT-associated missense mutations, such as R106W, T158M and T158A, develop RTT-like phenotypes and show deficits in neural circuitry. These mutations decrease the binding of MeCP2 to methylated DNA and concomitantly reduce MeCP2 protein stability, leading to gene expression and cellular morphological changes in a neuronal cell type-specific manner (Ref). We aim to define the role of methyl-DNA binding of MeCP2 in protein stability, delineate the cellular origin of impaired neural circuitry, and elucidate the mechanisms by which MeCP2 modulates neuronal cell-type specific function.

3. Understanding the pathogenic mechanisms of CDKL5 deficiency

CDKL5 deficiency is a disorder caused by genetic defects in the the X-linked gene encoding cyclindependent kinase-like 5 (CDKL5). Patients with CDKL5 dysfunction show early onset intractable seizures and severe neurodevelopmental impairment, and are frequently diagnosed with a number of disorders including Infantile Spasms, West Syndrome, Lennox-Gastaut, atypical Rett Syndrome, and autism. To gain insight into the pathogenic mechanisms underlying CDKL5-related disorders, we have developed mouse models in which the CDKL5 gene is ablated or modified. We found that loss of functional CDKL5 disrupts multiple signal transduction pathways, impairs hippocampal event-related potentials, and leads to autisticlike phenotypes in mice. We plan to identify the molecular targets of CDKL5, dissect the signaling cascades responsible for cardinal autistic-like phenotypes, and investigate the neural mechanisms by which CDKL5 dysfunction leads to early onset seizures and cognitive deficits.

4. Exploring the coding and decoding of the methylome in neurons

Cytosine methylation (5mC), mostly at CpG dinucleotides in mammals, is a central epigenetic mark essential for development. While we can now profile genome-wide DNA methylation at single-base resolution (sequencing methylome), how the methylome is established and maintained, and how the cell interprets the methylome to affect gene expression and chromatin structure remain poorly understood. Moreover, recent studies have challenged the stability of the methylome in postmitotic neurons and have coupled changes in DNA methylation at specific loci to adaptive behaviors. We are interested in understanding how DNA methylation is coded and decoded genome-wide but with locus-specificity in neurons. Given the high abundance of hydroxymethylcytosine (5hmC) in the brain, we set up to address the functional significance of 5mC and 5hmC in neural development, the role of the methylome in the establishment of neuronal identity, and the molecular mechanisms by which the methylome modulates genome function in the brain.

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