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Message from the Chairman

It is a great pleasure for me to welcome you to the Sue Golding Graduate Division (SGGD) and our Department of Microbiology and Immunology at the Albert Einstein College of Medicine. Our laboratories in the Department of Microbiology and Immunology cover a wide range of topics spanning the fields of virology, bacteriology, host immune responses to infection and cancer, inflammation and autoimmune disease. The department warmly and enthusiastically welcomes PhD candidates and postdoctoral fellows who are interested in pursuing research projects and potentially developing careers in these areas. I welcome all new students in the SGGD and postdoctoral candidates to contact me or any of the department's faculty directly to explore the terrific range of opportunities available to you in the Department of Microbiology and Immunology.

My best wishes for success in your new adventure!

A handwritten signature in black ink, appearing to read 'Steven Porcelli'.

Professor & Chairman  
Department of  
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## MICROBIOLOGY AND IMMUNOLOGY

### FACULTY 2019 – 2020

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**MICROBIOLOGY AND IMMUNOLOGY**

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**2017 – 2018**

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## **DR. JOAN W. BERMAN**

Dr. Berman's laboratory examines the mechanisms that mediate HIV entry into the CNS and how viral and inflammatory mediators damage neurons and other CNS cells. More than 40 million people worldwide are HIV infected. As a result of antiretroviral therapies, HIV infected people are living longer. HIV enters the CNS early after infection and despite therapy, persists within the CNS. Prevalence of NeuroAIDS and its associated cognitive impairment is increasing. An understanding of mechanisms that mediate these effects are critical to the development of therapeutic strategies.

HIV infection of the CNS can have devastating consequences, often resulting in cognitive impairment and severe neurological complications. The basis of this impairment is poorly understood. Although its development is associated with early viral infiltration of the CNS, the number of activated monocytes/macrophages within the CNS appears to be a better indicator of neurologic compromise than viral load, suggesting that leukocyte infiltration and cognitive impairment are tightly correlated. How infected monocytes cross the blood brain barrier (BBB) and infiltrate the CNS is not well understood. This process is critical to the development of NeuroAIDS as it brings leukocytes into the brain where they activate and infect microglia, and effect damage to the BBB and other CNS cells. The mechanisms of HIV-infected monocyte transmigration across the BBB have only been minimally characterized. We are characterizing several of the steps in this transmigration process using a tissue culture model of the human BBB. We analyze the mechanisms that mediate attachment and diapedesis of HIV-infected monocytes across the BBB to identify markers that contribute to brain infection and BBB disruption, such as adhesion molecules, tight junction and adherens proteins, chemokines and their receptors. The lab has a major translational component, examining sera and CSF from HIV infected individuals for predictors of cognitive impairment, as well as patient cells for unique markers of this impairment and for their ability to transmigrate across the blood brain barrier. We examine tissue from HIV-infected individuals for altered proteins. The overall goal is to identify targets for therapeutic intervention to limit the entry of HIV into the CNS.

Many HIV-infected people who abuse drugs have more extensive CNS damage associated with significant cognitive impairment. As many drugs of abuse cause an increase in extracellular dopamine, we examine the effects of dopamine on HIV infection of macrophages. We demonstrated that dopamine increases HIV infection of human macrophages and are addressing the mechanisms by which dopamine causes this increase as well as alterations in macrophage function. We also study the impact of buprenorphine and methadone, therapies for Opiate abuse, in the context of NeuroAIDS.

## **PUBLICATIONS**

Eugenin EA, Martiney JA, Berman JW. (2019) The malaria toxin hemozoin induces apoptosis in human neurons and astrocytes: potential role in the pathogenesis of cerebral malaria. *Brain Res.* 2019 Jul 2;146317. doi: 10.1016/j.brainres.2019.146317. PMID: 31276637

Williams, DW, Calderon, TM, Lopez, L, Carvallo, L, Gaskill, PJ, Eugenin, EA, Moregillo, S, Berman, JW. (2013) Mechanisms of HIV Entry Into the CNS: Increased Sensitivity of HIV Infected CD14+CD16+ Monocytes to CCL2 and Key Roles of CCR2, JAM-A, and ALCAM in Diapedesis. *PLOS One.* Jul 26;8(7):e69270.

Williams, DW, Eugenin, EA, Calderon, TM, Berman, JW. (2012) Monocyte Maturation, HIV

Susceptibility, and Transmigration Across the Blood Brain Barrier are Critical in HIV Neuropathogenesis. *Journal of Leukocyte Biology*, Mar;91 (3):401-15.

Buckner CM, Calderon TM, Williams DW, Belbin TJ, Berman JW. (2011) Characterization of monocyte maturation/differentiation that facilitates their transmigration across the blood-brain barrier and infection of HIV: Implications for NeuroAIDS. *Cell Immunol*; 267(2):109-23.

Eugenin E.A., Clements J.E, Zink M, and Berman J.W.(2011) HIV infection of human astrocytes disrupts blood brain barrier integrity by a gap junction dependent mechanism. *The Journal of Neuroscience*. 31(26):9456-65.

King JE, Eugenin EA, Hazleton JE, Morgello S and Berman JW (2010) Mechanisms of HIV Tat Induces phosphorylation of NMDA Receptor Subunit 2A in Human Primary Neurons: Implications for NeuroAIDS Pathogenesis. *Am.J Pathology*, June17:2819-30.

Roberts TK, Eugenin EA, Morgello S, Clements JE, Zink MC and Berman JW, (2010) PrP<sup>C</sup>, the Cellular Isoform of the Human Prion Protein, is a Novel Biomarker of HIV-Associated Neurocognitive Impairment and Mediates Neuroinflammation, *Am. J.Pathology*, Oct 2010; 177(4):1848-60.

Gaskill PJ, Calderon TM, Luers AJ, Eugenin EA, Javitch JA, Berman JW, (2009) Human Immunodeficiency Virus (HIV) Infection of Human Macrophages Is Increased by Dopamine. A Bridge between HIV-Associated Neurologic Disorders and Drug Abuse., *Am J Pathol*. September 175(3):1148-59.

Eugenin EA, Osieki K, Lopez L, Goldstein H, Calderon TM, Berman JW, (2006) CCL2/Monocyte chemoattractant protein-1 mediates enhanced transmigration of human immunodeficiency virus (HIV)-infected leukocytes across the blood-brain barrier: a potential mechanisms of HIV-CNS invasion and NeuroAIDS. *J Neurosci* 26(4):1098-1106.

## Dr. Michael Berney

The Berney lab seeks to understand how the human pathogen *Mycobacterium tuberculosis* adapts bioenergetically and metabolically to the host environment. Using an integrated approach of genetic engineering, metabolomics, biochemical assays, transcriptomics and animal experiments we are pursuing fundamental questions such as which nutrients and energy sources do pathogenic microorganisms use in the host, or how do aerobic pathogens survive in host tissues that are hypoxic. Our goal is to identify vulnerable pathways that can be exploited for drug discovery.

### **Suffocating *M. tuberculosis***

In recent years the energy generating machinery of *M. tuberculosis* has received considerable attention as a new drug target space resulting in the discovery of some promising new (and old) drug candidates. The most promising candidate drugs are inhibitors of the ATP synthase (Bedaquiline) and *bc<sub>1</sub>*-cytochrome *c* reductase (Q203). However, these drugs have relatively low to no early bactericidal activity (first 7 days) and we hypothesized that this is partially due to cytochrome *bd* oxidase and its ability to uncouple electron flux from proton pumping. Recently we demonstrated that inactivation of the terminal oxidase Cyt-*bd* ( $\Delta$ cydAB) leads to rapid killing and clearance of *Mtb*  $\Delta$ cydAB in mouse lungs treated with the inhibitor Q203 (Kalia et al. 2017, *PNAS*). Our goals are now to understand the role of Cyt-*bd* in TB pathogenesis and to develop drugs that exploit this synthetic lethality.

### **Trapping *M. tuberculosis* in its nutritional autonomy.**

Co-evolution of pathogens and host has led to many different metabolic strategies employed by intracellular pathogens to deal with the immune response and the scarcity of food during infection. Therefore, it is not a surprise that maintenance of metabolic homeostasis contributes to the virulence of intracellular pathogens. Recently we identified a metabolic vulnerability of *M. tuberculosis* that leads to persister-free killing *in vitro* and *in vivo* (Berney et al. 2015, *PNAS*). We could show that methionine biosynthesis, a branch of the aspartate family amino acid biosynthesis (the “aspartate pathway”), is essential for host infections, because *M. tuberculosis* is unable to scavenge methionine from the host. The aspartate pathway is a core anabolic pathway that provides the cell with the proteinogenic amino acids lysine, threonine, isoleucine and methionine, the peptidoglycan precursor diaminopimelate and S-adenosylmethionine, the main cofactor in cellular methyltransferase reactions. Sensing and regulating the abundance of these essential intermediates allows *M. tuberculosis* to integrate information from cell wall biosynthesis, translation and one carbon metabolism to maintain cellular homeostasis. Interestingly, aspartate and glutamate, the two essential precursors of this pathway are both thought to be taken up from the host, which links the regulation of this pathway to external signals from the host. Such metabolic interplay between *M. tuberculosis* and the host are still poorly understood. In this project we study the metabolic regulation and vulnerability of the aspartate pathway during active and latent mouse infections, determine intermediates that are exchanged in crosstalk with the host and investigate the allosteric and transcriptional control that is needed to maintain pathway homeostasis and guarantee balanced growth of *M. tuberculosis*.

## Publications

*Mycobacterium tuberculosis'* capacity to survive iron-starvation might enable it to persist in iron-deprived microenvironments of human granulomas.

Kurthkoti K, Amin H, Marakalala MJ, Ghanny S, Subbian S, Sakatosb A, Livnye J, Fortune SM, **Berney M**, Rodriguez GM.

*mBio* (2017 IN PRESS)

Exploiting the synthetic lethality between terminal respiratory oxidases to kill *Mycobacterium tuberculosis* and clear host infection.

Kalia NP, Hasenoehrl EJ, Ab Rahman NB, Koh VH, Ang MLT, Sajorda DR, Hards K, Grüber G, Alonso S, Cook GM, **Berney M**<sup>\*,+</sup>, Pethe K<sup>\*,+</sup>.

*Proceedings of the National Academy of Sciences* (EE June 26<sup>th</sup> 2017) (+equal contributions, \*corresponding author)

*Mycobacterium tuberculosis* in the face of host-imposed nutrient limitation.

**Berney M**\* & Berney-Meyer L.

In *Tuberculosis and the Tubercle Bacillus, Second Edition*, ASM Press. (2017) Jun;5(3).

*OXPHOS as a new target space for tuberculosis: success, failures, and future directions*

Cook GM, Hards K, Greening C, Heikal A, Dunn E, Nakatani Y, Pethe K, Crick D, **Berney M**.

In *Tuberculosis and the Tubercle Bacillus, Second Edition*, ASM Press. (2017) Jun;5(3).

*Central Role of Pyruvate Kinase in Carbon Co-Catabolism of Mycobacterium tuberculosis.*

Tahel Noy, Olivia Vergnolle, Travis E Hartman, Kyu Y Rhee, William R Jacobs Jr., **Michael Berney**\*, and John S Blanchard\*

*Journal of Biological Chemistry* (2016) 291/13: 7060–7069

*Essential roles of methionine and S-adenosylmethionine in the autarkic lifestyle of Mycobacterium tuberculosis*

**Berney M**\*, Berney-Meyer L, Wong K, Chen B, Chen M, Kim J, Wang J, Chan J, Wang F, Jacobs WR\*.

*Proceedings of the National Academy of Sciences* (2015) 112: 10008–10013

Featured with a spotlight article in *Trends in Microbiology*

*An obligately aerobic soil bacterium activates hydrogen production to survive reductive stress during hypoxia*

**Berney M**\*, Greening C, Conrad R., Jacobs WR, Cook GM.

*Proceedings of the National Academy of Sciences* (2014) 111: 11479-11484

Featured with an interview in *The Pathologist* (<https://thepathologist.com/issues/0114/the-survival-artists/>)

**Full publist:** <https://www.ncbi.nlm.nih.gov/myncbi/michael.berney.1/bibliography/40584568/public/>

## DR. ROBERT BURK

### **Human Papillomavirus (HPV) and Microbiome Translational Science: Molecular Epidemiology, Pathogenesis and Evolution.**

The main focus of the Burk laboratory is to understand viral-host evolution and the emergence of HPV types that are highly pathogenic and cause multiple cancers in humans (e.g., cervix and oropharynx). In addition, the lab is also testing hypotheses on the role of epigenetic changes in the viral and host (human) genome and its relationship to precancer and cancer development. Concomitant with viral-host relationships is a new emerging area of interest, the cervical microbiome/mycobiome and its relationship to viral-host interactions and other outcomes. These investigations extend from clinical studies where we obtain exfoliated cervix cellular material (Pap cells) and evaluate the HPV genome, CpG methylation and the composition of the microbiome to cell based biochemistry studies of viral proteins and molecular evolution of viral sequences.

Papillomaviruses are 8.0 kb double stranded DNA viruses readily amenable to amplification and sequencing, making this system ideal as a model for DNA virus evolution and identification of pathogenic genetic signatures. Over 200 HPV types exist and further characterization of HPVs infecting the population (i.e., from our large sample repository) have allowed us to explore the virus as a species, characterization of the frequency and heterogeneity of HPV types and variants in the population, and the role of viral evolution in pathogenicity. The lab uses phylogenetic methods and other analytic strategies to test hypotheses about the relationship and characteristics of HPV genomes and disease. Exploration of natural selection of papillomaviruses has led us to the conclusion that the viruses are evolving through complex means yet to be discovered. Our major collaboration with investigators at the National Cancer Institute, NIH has provided an ideal translational team of world-class epidemiologists, biostatisticians and clinical investigators. In combination with evolutionary biologists at the American Museum of Natural History, our integrative group provides a unique perspective for intellectual growth of students that want to “think outside the box”. More recently, we have investigated epigenetic changes to the HPV genome and have demonstrated very significant results on the association of these changes with neoplastic progression. The identification of HPV in specific biological niches has challenged us to explore the microbiome through barcoding and parallel sequencing using Next-Gen methods. We have recently developed the methodologies and computer software to test hypothesis on the influence of the microbiome on cervix cancer development in HPV positive women.

Other research areas include a human genetic project to identify the gene(s) for hyperhidrosis (excessive sweating). This is a fascinating disorder that is strongly associated with a family history of excessive sweating. There seems to be at least two phenotypes, excessive sweating from the palms and soles, and excessive sweating from the underarms, body, face and groin areas. The analyses of families with this disorder suggest genetic and/or allelic heterogeneity. To date, we have collected over 1500 DNA samples from affected individuals and families. We are in the process of exome-sequencing the coding regions using Next-Gen technologies to identify candidate mutations associated with this disorder.

Lastly, as part of our goal to understand genes and cancer, we have for many years studied the von Hippel-Lindau (VHL) gene that is a driver of kidney cancer. We investigate the function of the VHL protein, in part, an oxygen sensor. Our recent observations indicate that intact VHL is required for primary cilia formation and function in renal cells. We have localized VHL and other

proteins known to interact to cilium. Further studies will investigate the function of VHL in the cilium.

## PUBLICATIONS

Amaro-Filho SM, Gradissimo A, Usyk M, Moreira FCB, de Almeida LM, Moreira MAM, Burk RD. HPV73 a nonvaccine type causes cervical cancer. *Int J Cancer*. 2019 Apr 9. doi: 10.1002/ijc.32315. PMID: 30963559

Ho, G.Y.F., Bierman, R., Beardsley, L., C.J. Chang, and **Burk, R.D.** Natural history of cervicovaginal papillomavirus infection in young women. *N. Engl. J. Med.* 338:423-428, 1998.

Chen, Z., Terai, M., Fu, L., Herrero, R., DeSalle, R. and **Burk, R.D.** Diversifying selection in human papillomavirus type 16 (HPV16) lineages based on complete genome analysis. *J. Virol.* 79:7014-7023, 2005.

Schiffman, M., Herrero, R., DeSalle, R., Hildesheim, A., Wacholder, S., Rodriguez, A.C., Bratti, M.C., Sherman, M.E., Morales, J., Guillen, D., Alfaro, M., Hutchinson, M., Wright, T.C., Solomon, D., Chen, Z., Schussler, J., Castle, P.E. and **Burk, R.D.** The carcinogenicity of human papillomavirus types reflects viral evolution. *Virology* 337:76-84, 2005.

Bottalico, D., Chen, Z., Dunne, A., Ostoloza, A., McKinney, S., Sun, C., Schlecht, N.F., Fatahzadeh, M., Herrero, R., Schiffman, M. and **Burk, R.D.** The oral cavity contains abundant known and novel Human papillomaviruses from the *Betapapillomavirus* and *Gamma papillomavirus* genera. *J. Inf. Dis.* 204:787-792, 2011. PMID: 21844305; PMCID: PMC3156102.

Chen, Z., Schiffman, M., Herrero, R., DeSalle, R., Anastos, K., Segondy, M., Sahasrabudhe, V., Gravitt, P.E., Hsing, A. and **Burk, R.D.** Evolution and taxonomic study of HPV16-related *Alphapapillomavirus* variant genomes: HPV31, HPV33, HPV35, HPV52, HPV58 and HPV67. *PLoS ONE* 6(5): e20183. PMID:2167391.

Smith, B., Chen, Z., Reimers, L., van Doorslaer, K., Schiffman, M., DeSalle, R., Herrero, R., Yu, K., Wang, T. and **Burk R.D.** Sequence imputation of HPV16 genomes for genetic association studies. *PLoS ONE* 6(6):e21375. Epub 2011 Jun 23. PMID:21731721.

Smith, B.C., McAndrew, T., Chen, Z., Harari, A., Barris, D.M., Viswanathan, S., Rodriguez, A.C., Castle, P., Herrero, R., Schiffman, M. and **Burk, R.D.** The cervical microbiome over 7 years and a comparison of methodologies for its characterization. *PLoS One.* 2012;7(7):e40425. PMID: 22792313.

**Burk, R.D.**, Harari, A. and Chen, Z. Human papillomavirus genome variants. *Virology* 445:232-243, 2013. PubMed PMID: 23998342; PMCID: PMC3979972.

Mirabello, L., Frimer, M., Harari, A., McAndrew, T., Smith, B. Chen, Z., M., Wentzensen, Wacholder, S., Castle, P.E., Raine-Bennett, T., Schiffman, M. and **Burk, R.D.** HPV16 methyl-haplotypes determined by a novel next-generation sequencing method are associated with cervical precancer. *Int. J. Cancer* 136:E146-53, 2015. PMID: 25081507.

Van Doorslaer, K., DeSalle, R., Einstein, M.H. and **Burk, R.D.** Degradation of Human PDZ-

proteins by Human Alphapapillomaviruses represents an evolutionary adaptation to a novel cellular niche. *PLoS Pathog.* 2015 Jun 18;11(6):e1004980. PubMed PMID: 26086730.

Harari, A., Chen, Z. and **Burk, R.D.** Human papillomavirus genomics: past, present and future. *Curr. Probl. Dermatol.* 45:1-18, 2014. PubMed PMID: 24643174; PMCID: PMC4430864.

Stern, J.M., Moazami, S., Qiu, Y., Kurland, I., Chen, Z., Agalliu, I., Burk, R., Davies, K.P. Evidence for a distinct gut microbiome in kidney stone formers compared to non-stone formers. *Urolithiasis.* 2016 PubMed PMID: 27115405.

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## DR. JOHN CHAN

Our lab studies how *Mycobacterium tuberculosis* (Mtb), the causative agent of tuberculosis (TB), interacts with the host; on-going studies include:

**Tuberculous latency and reactivation:** Gene profiling studies have identified a set of Mtb genes (the dormancy regulon) that are regulated by exposure to low oxygen tension and nitric oxide, two latency-promoting environmental signals. Deletion of a dormancy regulon gene, *rv2623* (a member of the USP [universal stress protein] family), results in hypervirulence in infected hosts. *Rv2623* also regulates Mtb growth in vitro. The growth-regulating attribute has been linked to the ATP-binding capacity of *Rv2623*. Understanding how *Rv2623* regulates the growth of Mtb and how members of the dormancy regulon promote latency is a focus of our laboratory.

We are collaborating with JoAnn Tufariello to study the role of the five Mtb Rpf proteins, putative peptidoglycan hydrolyases, in regulating tuberculous latency and reactivation. Mutagenesis studies showed that Mtb doubly deficient for RpfA and RpfB displays defects in persistence and reactivation, both in in vivo and in vitro models of tuberculous latency and disease recrudescence. Studies have been initiated to characterize how Mtb Rpf's regulate mycobacterial growth.

**The mechanisms that regulate the granulomatous reaction:** Our Studies using the B cell-deficient  $\mu$ MT mouse model and specific Fc $\gamma$  receptor knockout mice have shown that humoral immune response regulates the tuberculous granulomatous reaction and is required for optimal control of Mtb. There is also evidence that B cells can regulate T cell response in infected hosts. We are conducting experiments aimed at characterizing the roles of B cells in regulating the host granulomatous response to Mtb.

TNF is essential in controlling TB. However, TNF also contributes to the development of immunopathology. TNF neutralization reactivates TB in both mice and humans with persistent infection. We are using this TNF neutralization reactivation model to study the role of TNF in regulating the tuberculous granulomatous reaction. We are also generating cell-specific conditional TNF knockout mouse strains that will be used to decipher the relative contribution of cell-specific TNF in the protective immunity and immunopathogenesis of this cytokine in the host.

**TB vaccines:** We will apply the knowledge gained from the above-listed investigation to rationally design safe and effective TB vaccines in collaboration with the Jacobs and Porcelli labs. For example, understanding how to manipulate the humoral response to the advantage of the host may lead to the development of vaccines with increased efficacy. Knowing how Mtb regulates host production of TNF may lead to the design of Mtb-derived vaccines with enhanced immunogenicity.

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## **DR. KARTIK CHANDRAN**

As our world grows more interconnected and humans impinge on the few remaining wild habitats, infections caused by the accidental transmission of viruses from their natural animal hosts to humans are increasingly of concern. The unprecedented 2013–2015 Ebola virus disease epidemic in western Africa provides a particularly apt example. Few specific antiviral treatments are available for Ebola and other emerging agents, and our ability to develop them is challenged by a poor understanding of exactly how viruses co-opt our own cells at the molecular level.

The Chandran Lab at Einstein strives to understand this molecular warfare between virus and cell, and to apply what we learn to the development of antiviral treatments. Filoviruses, such as Ebola virus and Marburg virus, and hantaviruses, such as Sin Nombre virus and Hantaan virus, are major topics of study in our group. Working collaboratively with our partners on three continents, we have helped uncover critical host factors required for cell invasion by Ebola virus, including the long-sought viral receptor, Niemann-Pick C1 (NPC1). One of our recent interests is to decipher how genetic variation in host-encoded factors—in NPC1, for example—can influence the susceptibility of humans and animals to viral infection and the likelihood of animal-to-human 'host-jumping' events. Our ongoing efforts also include translational studies to develop anti-Ebola drugs, including small molecule and antibody therapeutics, targeting host factors critical for viral invasion.

## **SELECTED PUBLICATIONS**

### **Mechanism of Ebola virus entry and infection:**

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## DR. JOHANNA P. DAILY

Our primary research interest is in pathogenesis in the *Plasmodium falciparum*. Patients infected with this parasite can be completely asymptomatic or develop severe disease resulting in death. The goal of our research has been to define the molecular mechanisms that underlie this variation in disease outcomes in *P. falciparum*. Toward this goal, we have developed a new pathogenesis model through the analysis of *in vivo* parasite biology and associated host factors using a whole genome approach. We have identified novel parasite biology when it resides in the human host; this biology has not been reported under *in vitro* cultivation and may play a role in enhanced virulence and/or transmission capacity. Using longitudinal studies we have characterized individual responses to malaria during a severe and subsequent mild infections to understand how patient's immune responses may change and lessen immunopathology. The long term goal is to identify parasite and host processes involved in disease to serve as targets for vaccine or chemotherapeutic development. We carry out field based translational studies in cohorts infected with malaria in Africa and these inform our experimental work using molecular biology, whole transcriptional, metabolomic and cellular approaches in the laboratory.

- I. Define factors that protect against parasite sequestration to human brain microvasculature.
- II. Define host immunity associated with protection from clinical disease.
- III. Comprehensive analysis of host and parasite small molecules to study pathogenesis and develop biomarkers of cerebral malaria associated brain swelling.

### Selected Publications

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## DR. TERESA DiLORENZO

Type 1 diabetes is an organ-specific autoimmune disease characterized by T cell-mediated destruction of the insulin-producing beta cells of the pancreatic islets. While insulin therapy allows for continuation of life, it neither cures the disease nor prevents its devastating complications. Studies utilizing the nonobese diabetic (NOD) mouse model of the disease have shown that T cells, recognizing autoantigenic peptides bound to major histocompatibility complex (MHC) molecules, are absolutely required for disease development. T cells specific for beta cell antigens can also be detected in the peripheral blood and islets of type 1 diabetes patients. Our laboratory utilizes an extensive collection of mouse models to investigate the antigenic specificities, pathogenicity, and immunobiology of T cells in type 1 diabetes. These models are also being used to develop and optimize therapeutic strategies. New, increasingly “humanized” mouse models are continually in development in our group, as are strategies to utilize human samples to translate our findings to patients.

Our research program seeks to develop an improved understanding of the immunopathogenesis of type 1 diabetes, with the objective of applying new knowledge to the goals of improved diagnostic, monitoring, and therapeutic strategies for this disease. Our efforts have resulted in several important contributions in this area. Our laboratory was the first to identify islet-specific glucose-6-phosphatase catalytic subunit-related protein (IGRP) as a major beta cell antigen recognized by CD8 T cells in NOD mice. In work that was inspired by our discovery in NOD mice, peptides derived from IGRP were subsequently shown to be T cell targets in patients. Our group has also been a leader in characterizing humanized NOD-based models of type 1 diabetes. Our study of HLA-A\*02:01-transgenic NOD mice led to the identification of new T cell epitopes of IGRP and insulin, several of which have since been shown to be markers of beta cell autoreactivity in HLA-A\*02:01-positive patients. We developed and characterized models in which HLA-A\*02:01 expression is accompanied by reduced thymic expression of insulin, as is seen in patients, resulting in improved humanized models for type 1 diabetes. We discovered that mature human CD8 and CD4 T cells can be “reprogrammed” to be beta cell-specific upon transduction with a lentivirus encoding a T cell receptor that recognizes a beta cell antigen; this will allow human T cells to be incorporated into future models of type 1 diabetes. We were the first to explore the potential of delivery of beta cell antigens to steady-state dendritic cells *in vivo* in NOD mice for the purpose of inducing tolerance. Using antigen-linked anti-DEC-205, we showed that transferred T cell receptor-transgenic T cells could be deleted, and endogenous beta cell-specific T cells reduced in number, even in the context of ongoing autoimmunity in NOD mice having known T cell tolerance defects. We identified undersized peptides as previously unknown targets of autoreactive CD8 T cells and devised a strategy for their identification as antigens in autoimmune disease. Two United States patents related to our work have been granted.

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## DR. DAVID FOOKSMAN

The goals of my laboratory are to understand the regulation of plasma cell differentiation, migration, survival and function. Plasma cells are terminally-differentiated B cells that secrete high-affinity antibodies constitutively, following immunization and exposure to a pathogen. The quality, magnitude and longevity of the antibody response are dependent upon the differentiation and survival of these cells, which involves many signaling factors and auxiliary cell types. We have used intravital two-photon imaging to study plasma cell differentiation and migration in the lymph node and have found that these cells exhibit a highly linear migration that is independent of  $g_{\alpha i}$  chemotaxis. This migration is unique among lymphocytes and enables these cells to travel long distances crossing heterogeneous microenvironments to reach niches critical for their survival. In some cases, plasma cells may undergo malignant transformation during differentiation leading to neoplasms in humans such as multiple myeloma. Despite their critical role in immune function and disease, many fundamental questions remain regarding the physiology of plasma cells in vivo. We are using two-photon intravital imaging in combination with modern cellular and immunological tools to visualize and better understand the physiology of these cells under normal and pathological conditions. The current topics in the laboratory are focused on:

1. Plasma cell differentiation. What factors regulate selection and differentiation of germinal center B cells to plasma cell?
2. What factors control plasma cell migration to the bone marrow and subsequent long-lived survival and retention?
3. What factors control myeloma cell retention and migration in the bone marrow, which enables tumor progression?

## PUBLICATIONS

(\* corresponding author, # senior author)

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## **DR. NIKOLAOS FRANGOIANNIS**

Our laboratory studies the cell biological processes and the molecular pathways involved in cardiac repair, remodeling and fibrosis. The adult mammalian heart has negligible regenerative capacity and heals through formation of a collagen-based scar. Repair of the infarcted heart is dependent on induction and timely suppression of inflammatory signals, and on recruitment of reparative cells (fibroblasts and vascular cells). Dysregulation of the inflammatory and fibrotic responses causes adverse remodeling of the heart and results in heart failure. Using cell-specific genetic manipulations, established mouse models of cardiac injury and remodeling, and cell biological assays (using isolated cardiomyocytes, fibroblasts and macrophages), we explore the molecular circuitry of myocardial repair and fibrosis. Ongoing studies address the following questions:

### **1. What are the signals implicated in suppression and resolution of the post-infarction inflammatory reaction?**

Timely inhibition and spatial containment of inflammatory signaling are critical for cardiac repair. We study the role of macrophage-specific inhibitory signals in suppression and resolution of the post-infarction inflammatory reaction.

### **2. Which the molecular signals are responsible for fibroblast activation and de-activation in infarcted and remodeling hearts?**

In the infarcted heart, fibroblasts critically regulate cardiac repair by transdifferentiating into myofibroblasts and by producing extracellular matrix proteins. However, excessive or dysregulated activation of fibroblasts results in extension of fibrosis and causes diastolic ventricular dysfunction. We study the molecular signals that activate and de-activate fibroblasts in cardiac repair, focusing primarily on the role and regulation of the TGF-beta cascade.

### **3. How does the extracellular matrix modulate the phenotype of cells involved in repair and fibrosis?**

The extracellular matrix is not simply a structural scaffold, but actively participates in transduction of signaling responses. Specialized components of the matrix are induced following injury and modulate cytokine and growth factor-mediated responses, signaling through integrins or syndecan receptors. Our lab is particularly interested in the biology of these “matricellular proteins” in cardiac repair and remodeling.

### **4. How does metabolic disease cause cardiac fibrosis?**

Diabetes and obesity are associated with profound alterations in cardiac function causing diastolic heart failure. Our lab studies the effects of metabolic dysregulation on cardiac fibroblasts and explores the mechanisms of fibrosis and capillary rarefaction in diabetic hearts.

### **5. What is the fate and role of pericytes in the infarcted and remodeling heart?**

Pericytes are abundant in the mammalian heart and may regulate angiogenic and fibrogenic responses. Our lab will study the fate and role of pericytes in myocardial infarction and in diabetic cardiomyopathy using lineage tracing strategies and cell-specific loss-of-function approaches.

The ultimate goal of our research is to identify therapeutic targets for attenuation of adverse remodeling following cardiac injury, thus preventing the development of heart failure.

## **PUBLICATIONS**

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## DR. DAVID GOLDMAN

The medical community has long recognized fungi as important allergens for patients with asthma. Interestingly, fungal sensitization is more common in children and has been linked to severe asthma resulting in death. The accepted paradigm is that fungal sensitization occurs as a result of recurrent, transient environmental exposures. Yet, increasing evidence suggests that fungi may interact with people in unrecognized ways to promote asthma. My lab is interested in understanding the role of subclinical fungal infections in asthma and their potential contribution to the high prevalence of asthma in urban areas.

We have demonstrated that the majority of Bronx children older than 2 years have serologic evidence of cryptococcal infection. *Cryptococcus neoformans* is an encapsulated fungus that is well suited to serve as co-factor in urban asthma. *C. neoformans* colonizes pigeon droppings and is endemic to urban areas. Once inhaled, this fungus causes persistent, subclinical infections. Cryptococcal infection induces TH2 inflammation in animal models. In a rat model, we have shown that cryptococcal pulmonary infection acts a co-factor to enhance allergic inflammation to allergen challenge and promotes airway hyper-responsiveness, both hallmark features of asthma. Pulmonary cryptococcosis also induces chitinase expression, which has recently been implicated as an essential mediator of allergic inflammation.

In addition to fungal studies, my lab is interested in anthrax pathogenesis. *Bacillus anthracis* is widely recognized as a potential agent of bioterrorism as evidenced by the 2001 anthrax attack. The toxins of *B. anthracis* are essential to virulence. In collaborations with Drs. Arturo Casadevall and Jurgen Brojatsch, we have studied the mechanisms by which *Bacillus anthracis* toxins contribute to host death. We have identified a previously unrecognized protease in human serum that inactivates the protective antigen component of lethal toxin *in vitro*. The precise protease and its role in the host response and susceptibility to anthrax remain to be determined. We have also identified a potential role for platelet activating factor (PAF) in mediating the lethal effects of toxin, including the alterations in vascular permeability which is characteristic of anthrax. Together, these observations may have important implications in developing new approaches to the treatment of anthrax.

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cannot produce infectious virus. To evaluate the efficacy of immune system “hacking” strategies to deplete the HIV reservoir, we have established a novel humanized mouse model consisting of highly immunodeficient NSG mice intrasplenically injected with CD4<sup>+</sup> memory T cells isolated from HIV-infected patients who are virally suppressed by ART treatment (viral loads <50 copies/ml) which include a population of latent HIV-infected cells. We demonstrated that the transplanted HIV reservoir was activated *in vivo* as reported for ART-suppressed individuals during treatment interruption. These mice displayed plasma viremia within 1 week after injection which rapidly rose over the next month. We will be using this mouse model to examine the effects of the aforementioned immune amplification strategies to reduce the HIV reservoir as indicated by elimination of viremia, temporal delay in the onset of the viremia and/or reduction in the amplitude of the viremia. We have also developed another humanized mouse model infectible with an infectious HIV expressing a luciferase reporter that enables us to serially visualize HIV infection in live mice by the intensity of the luciferase signal (see Figure).

The mechanisms by which HIV infection and meth disrupt the blood-brain barrier (BBB), stimulate migration of HIV infected monocytes into the CNS and induce neuroinflammation and the impact of ART on these processes are not fully delineated. This is a highly significant area of research relevant to NIH high priority topics of HIV/AIDS research, understanding the basic biology of HIV pathogenesis causing immune dysfunction and chronic inflammation and addressing the impact of HIV-associated comorbidities including neurological complications. We are also using a novel transgenic mouse we developed, hu-CD4/R5/cT1 mice, which circumvents major entry and transcription blocks preventing murine HIV-1 infection by targeting transgenic expression of human CD4, CCR5 and cyclinT1 genes to CD4<sup>+</sup> T cells and myeloid-committed cells. These mice develop disseminated HIV-1 infection after intravenous HIV-1 injection and local HIV-1 infection after intravaginal inoculation. We are utilizing these mice to evaluate the *in vivo* efficacy of novel HIV-1 vaccines. In addition, we are using these transgenic mice to evaluate the mechanisms by which co-infection facilitates HIV-1 acquisition and to determine the efficacy of different preventive therapies. By crossing the hu-CD4/R5/cT1 mice with another novel transgenic mouse line we developed, which expresses a full-length HIV provirus that produces infectious HIV, we are investigating the effect of drugs of abuse on disrupting the BBB and facilitating the entry of HIV-infected inflammatory cells into the brain and evaluating the capacity of antibodies to adhesion molecules to prevent the transmigration of HIV-infected inflammatory cells into the brain

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## **DR. CLAUDIA GRAVEKAMP**

Our laboratory is focused on the development and testing of cancer immunotherapy and non-immune-based cancer therapies. Since most cancer deaths occur by metastases (primary tumors can often be removed by surgery, chemotherapy, or radiation), our therapies are focused on the treatment of metastases. We have developed various therapies using different novel approaches, in preclinical mouse tumor models with metastatic breast and pancreatic cancer. For instance, we use an attenuated bacterium *Listeria monocytogenes* as a platform for the delivery of anticancer agents to the tumor microenvironment and into tumor cells such as radioactivity, tumor-associated antigens, or small molecules like alphagalactosylceramide, or we kill tumor cells through cryoablation by freezing and thawing tumor cells, combined with various adjuvants targeting myeloid-derived suppressor cells (MDSC) such as stimulator of interferon genes (STING)-ligand cyclic di-guanylate (c-di-GMP, Curcumin, and AMD3100. Since MDSC play a major role in immune suppression in the tumor microenvironment, MDSC are an important target in cancer immunotherapies. We also focus on the age factor since most cancer patients are old and elderly react less efficient to vaccines than young adults. The MDSC are present in blood of patients and mice with cancer. This MDSC population is strongly increased in the tumor microenvironment particularly at older age, and contributes to the age-related T cell unresponsiveness.

### **Listeria-based cancer vaccines**

Attenuated *Listeria monocytogenes* is a weakened facultative anaerobic bacterium (non-toxic and non-pathogenic) and has been used to deliver antigens into antigen-presenting cells. We developed various *Listeria*-based constructs expressing tumor-associated antigens including Mage-b, Survivin, p53 etc and tested these constructs in mice with metastatic breast and pancreatic cancer, and demonstrated a significant reduction in metastases and tumor growth. In addition, we have further improved the efficacy of the *Listeria*-Mage-b vaccine with help of MDSC-targeting adjuvants like c-di-GMP and Curcumin. However, in 2009 our lab discovered that *Listeria* infects and kills tumor cells by the generation of reactive oxygen species (ROS) through the activation of the NADPH-oxidase pathway, and left healthy tissues unharmed. Based on this tropism for the tumor microenvironment we started using *Listeria* as a platform for the selective delivery of anti-cancer agents to the tumor microenvironment. For more detail see Kim et al, Cancer Res 2009; Chandra et al, Cancer Immunology Research, 2014.

### **Mechanisms that contribute to the selective survival and multiplication of *Listeria* in the tumor microenvironment**

We have analyzed potential mechanisms explaining why *Listeria* survived and multiplied in the TME and not in healthy tissues. We discovered that *Listeria* is protected from immune clearance in the TME through strong immune suppression, but is rapidly killed in healthy tissues that lack immune suppression. In addition, we found that MDSC play an important role in the selective delivery and survival of *Listeria* in the tumor microenvironment. MDSC are selectively attracted by the primary tumor through the production of attractants such as granulocyte macrophage-colony stimulating factor (GM-CSF), interleukin (IL)-6, A100. *Listeria* infects, survives and multiplies in MDSC of tumor-bearing mice, and is protected from immune clearance because of the immune suppressive character of MDSC. We have shown that *Listeria*, once at the tumor site, infects (and kills) tumor cells directly or spreads from MDSC into tumor cells through the cell-to-cell spread mechanism specific for *Listeria*. For more detail see Quispe-Tintaya et al, PNAS 2013; Chandra et al, BJC, 2013.

## **Radioactive Listeria for the treatment of pancreatic cancer**

Ninety six percent of patients diagnosed with pancreatic cancer have only 6 months to live, despite aggressive treatments. This underlines the urgent need for new effective therapies. In collaboration with Dr. Ekaterina Dadachova (Department of Radiation, Einstein), we developed a radioactive Listeria for the treatment of pancreatic cancer, by coupling  $^{188}\text{Re}$  to anti-Listeria antibodies followed by incubation with Listeria bacteria. This resulted in the synergistic destruction of cancer cells through Listeria-induced ROS and through ionizing radiation of the  $^{188}\text{Re}$ . The number of metastases was reduced by 50% in mice treated with Listeria alone, and by 90% in mice treated with Listeria- $^{188}\text{Re}$ . This correlated with the accumulation of radioactivity in the metastases. This was the first time that a live attenuated bacterium was successfully used to deliver radioactivity selectively to the tumor microenvironment. The potential of the radioactive Listeria for the treatment of pancreatic cancer was discussed in several high profile journals like Science, Nature, as well as lay Journals like The Economist, Forbes Magazine and many others. Currently, we are testing Listeria with other radioisotopes. For more detail see Quispe-Tintaya et al, PNAS 2013. Recently, we developed Listeria- $^{32}\text{P}$  by incorporating  $^{32}\text{P}$ -phosphorus directly into the Listeria during culture. Most likely of the longer half-life of  $^{32}\text{P}$  (14 days) than of  $^{188}\text{Re}$  (16.9 hrs), Listeria- $^{32}\text{P}$  was also highly effective against tumors and metastases in syngeneic and transgenic mouse models of pancreatic cancer. For more detail see Oncotarget 2017.

## **Listeria incorporated with alphagalactosylceramide**

In collaboration with Dr. Steven Porcelli (Department Microbiology and Immunology, Einstein), we incorporated alphagalactosylceramide ( $\alpha\text{GC}$ ) into the Listeria bacteria simply during culture. This method was originally developed for mycobacteria.  $\alpha\text{GC}$  is a marine sponge that activates natural killer T cells (NKT) cells, which in turn stimulates other immune cells like natural killer (NK) cells and T cells. We demonstrated that Listeria expressing tumor-associated antigen Mage-b incorporated with  $\alpha\text{GC}$  created an immune-stimulating environment that attracted the NKT cells to the metastases, resulting in improved activation of CD8 T cells to Mage-b and a dramatic reduction in the number of metastases in a mouse model of metastatic breast cancer (4T1). For more detail see Singh et al, BJC 2014.

## **Cryoablation combined with adjuvants**

Cryoablation involves killing of tumor cells through freezing and thawing, resulting in recruitment of tumor-specific T cells. Since MDSC strongly inhibits these T cells we have the cryoablation combined with MDSC-targeting adjuvants like STING ligand c-di-GMP, Curcumin, and AMD3100. c-di-GMP reduces the number of MDSC and converts a subpopulation of MDSC into an immune-stimulating phenotype producing IL-12 (stimulates T cells). Curcumin reduces IL-6 produced by MDSC and breast tumors. IL-6 strongly inhibits T cells in the tumor microenvironment. AMD3100 is a small molecule that prevents the interaction of CXCR4 on MDSC and stromal cell-derived factor (sdf-1) on tumor cells. Currently, these combination therapies are under investigation in mice with metastatic breast cancer in collaboration with the Anticancer Fund (Brussels, Belgium). Preliminary results are extremely promising. Cryoablation and Meriva (Curcumin derivate) significantly delayed the onset of metastases and eliminated completely the primary tumor, prolonged the survival rate compared to the control groups in correlation with improved CD8 T cell responses to multiple tumor-associated antigens. For more detail see Chandra et al, Onolmmunology 2015.

## Feasibility of cancer vaccination at older age

Cancer is a disease of the elderly. When cancer becomes metastatic, it often needs aggressive second-line treatment, for which the options are limited. This is particularly challenging for frail, elderly cancer patients in which comorbidity plays an antagonistic role. Immunotherapy is the most promising and benign option for preventing or curing metastatic cancer in such patients. Unfortunately, cancer immunotherapy is less effective at old than at young age, due to T cell unresponsiveness, especially in the tumor microenvironment (TME). Various causes have been described for T cell unresponsiveness at old age, such as lack of naïve T cells at older age, deficiency in the upregulation of co-stimulatory molecules on aged dendritic cells (DCs), and most recently, the increase in the population of MDSC in the TME of old compared to young mice, among other age-related immune impairments. As mentioned above, *Listeria* has an intimate relationship with MDSC. We have shown that *Listeria*-based vaccination was equally effective in young and old mice with metastatic breast cancer by targeting MDSC. The *Listeria* killed the tumor cells directly through ROS, and *Listeria*-activated T cells killed the infected tumor cells presenting the *Listeria* antigens. For more detail see Chandra et al, BJC, 2013.

## Most recent peer-reviewed publications relevant to the field of cancer vaccination and cancer therapies selected out of 54

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### **Most recent invited publications relevant to the field of cancer vaccination at older age selected out of 16**

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## **RESEARCH IMPACT**

**Commentary on paper about Radioactive Listeria by Quipe-Tintaya et al. in PNAS 2013. Stritzker J, and Szalay AA. Single-agent combinatorial cancer therapy.** [www.pnas.org/cgi/doi/10.1073/pnas.1305832110](http://www.pnas.org/cgi/doi/10.1073/pnas.1305832110).

### **Websites of Journals and magazines that discussed the impact of the radioactive Listeria for therapeutic treatment of pancreatic cancer:**

<http://www.nature.com/nrgastro/journal/vaop/ncurrent/full/nrgastro.2013.81.html>

<http://news.sciencemag.org/sciencenow/2013/04/radioactive-microbes-nuke-tumor-.html>

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<https://www.sciencenews.org/article/microbes-can-redeem-themselves-fight-disease>

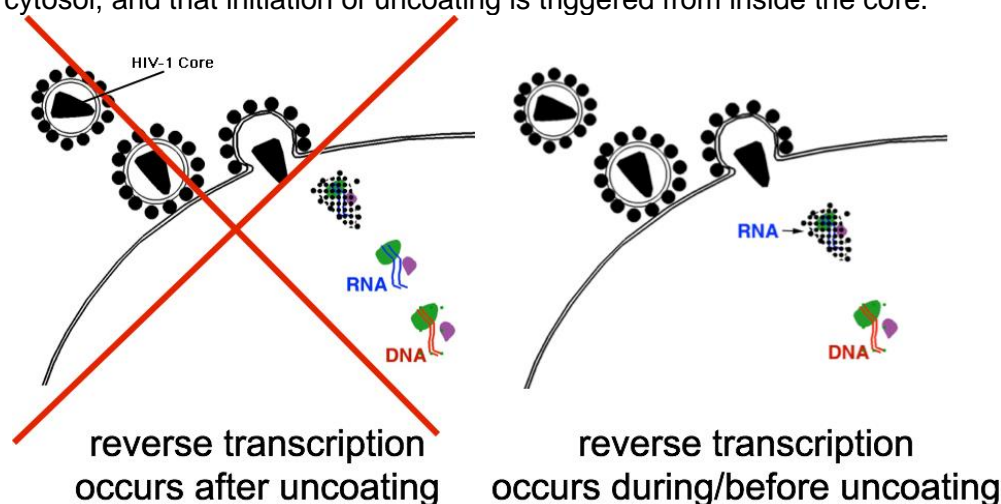
## DR. FELIPE DIAZ-GRIFFERO

**key words: HIV-1 uncoating and reverse transcription, restriction factors TRIM5alpha TRIMCyp, transportin-3 (TNPO3), CPSF6, SAMHD1, MxB, SERINC5, elite controllers, and HIV-1 T cell restriction factors.**

My research program is focused on understanding early events of HIV-1 infection such as uncoating, reverse transcription and nuclear import. To this end, we have exploited a group of proteins that are expressed by the host, and block HIV-1 infection at early stages. These proteins, known as restriction factors, have allowed us to understand fundamental processes in the HIV-1 life cycle. Besides assisting the understanding of fundamental problems on HIV-1 biology, restriction factors represent a new frontier in the search for an effective HIV-1 cure. The following sections explain our past findings, ongoing and planned research.

### 1) HIV-1 Uncoating

HIV-1 uncoating occurs early in infection, and is the shedding of monomeric capsid from the HIV-1 core, which is composed of 1500 monomers of capsid protein assembled into a conical structure containing the RNA viral genome. Our investigations revealed, contrary to an old dogma, that HIV-1 reverse transcription occurs before or during uncoating but not after (Roa et al., 2012)(Fig. 1). Furthermore, we demonstrated that genetic or pharmacological inhibition of reverse transcription inhibits the uncoating process during infection (Yang et al., 2012). These experiments suggested that internal rearrangements inside the core start the uncoating process. In agreement, we found that cytosolic extracts stabilized the HIV-1 core during infection in vivo and in vitro (Fricke et al., 2013a). Overall, our work suggests that HIV-1 cores are stable in the cytosol, and that initiation of uncoating is triggered from inside the core.



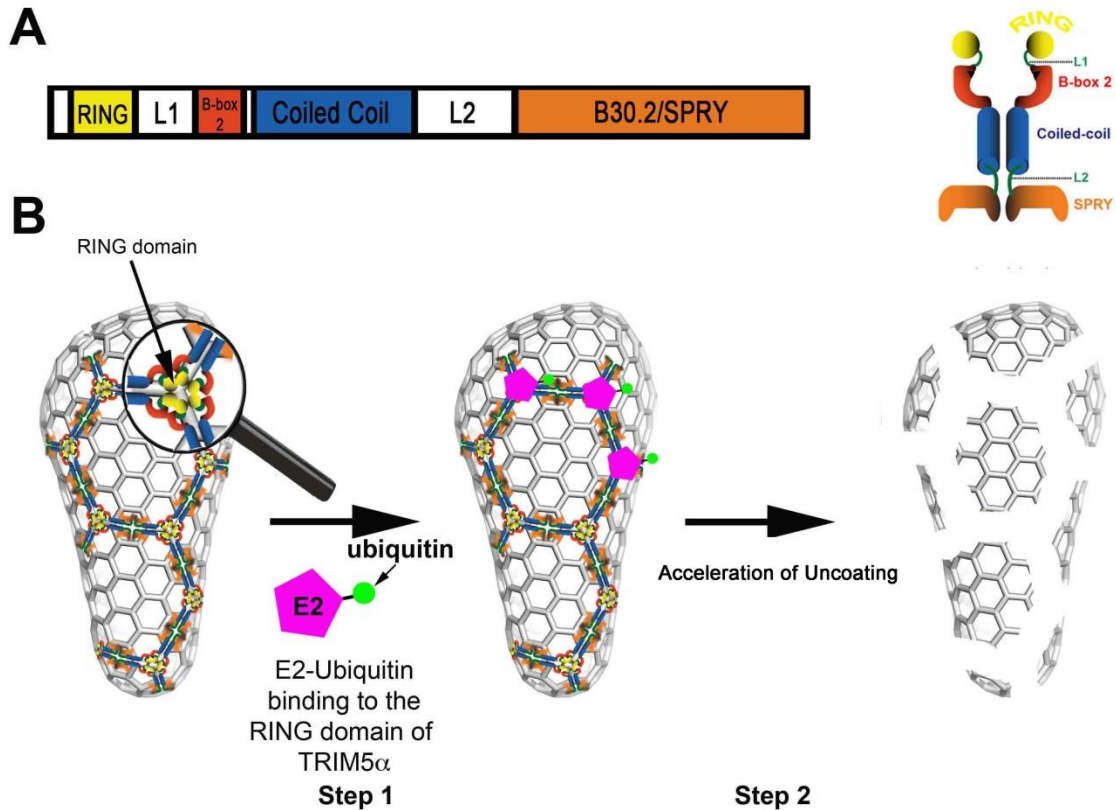
**Figure 1. Current model for the occurrence of HIV-1 reverse transcription and uncoating.** Our investigations showed that HIV-1 reverse transcription is completed inside the viral core during/before uncoating. This is in stark contrast of a past dogma that suggested that reverse transcription occurs after uncoating.

The study of HIV-1 uncoating in vitro has been hindered by the unstable nature of the HIV-1 core outside the cellular environment. This evidence together with work mentioned above

suggests that the HIV-1 core is stabilized by cellular factors. Future work on this area will use biochemical and genetic approaches to identify factors that stabilize the HIV-1 core in the cellular environment. To this end, we will biochemically isolate HIV-1 cores from infected cells and identify the proteins associated to the core by mass spectrometry. We will compare the protein content of HIV-1 cores stabilized by different conditions: using reverse transcription inhibitors (Yang et al., 2012), viruses containing a defective reverse transcriptase enzyme (Yang et al., 2012), the microtubule disruptive drug nocodazol (Lukic et al., 2014; Malikov et al., 2015), cells expressing cytoplasmic CPSF6(Fricke et al., 2013b), and cells expressing MxB/Mx2(Fricke et al., 2014). As a negative control, we will mock isolate cores from cells expressing rhesus TRIM5a, which accelerates uncoating (Diaz-Griffero et al., 2007a; Perron et al., 2007; Stremlau et al., 2005). The assays we have developed to study capsid stability in vitro and in vivo will be used to confirm these interactions(Fricke et al., 2013a). Finally, the contribution to uncoating and infection will be evaluated in cells where the candidate proteins are knockout using the Cas9/CRISPR technology that is already working in our lab. Finding proteins that stabilize the HIV-1 core during infection will provide fundamental understanding on the uncoating process of HIV-1.

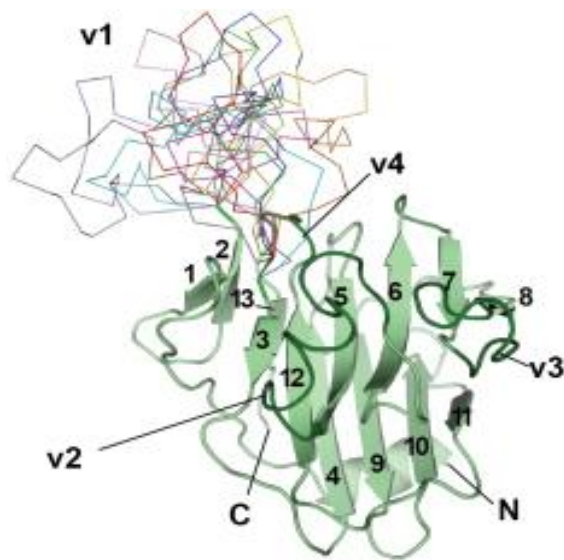
## 2) TRIM5 $\alpha$

The HIV-1 restriction factor TRIM5 $\alpha$  is composed of four domains: RING, B-box-2, coiled-coil and PRYSPRY domains (Fig. 2A). To understand the contribution of these different domains to restriction, we have solved the structure of the RING, B-Box-2 and PRYSPRY domains (Biris et al., 2013; Diaz-Griffero et al., 2009; Lienlaf et al., 2011; Roa et al., 2012). Our structure-function studies revealed: 1) the RING domain provides E3 ligase activity, which is necessary for restriction(Lienlaf et al., 2011; Roa et al., 2012), 2) the B-box-2 domain regulates the ability of TRIM5a to form higher-order complexes(Diaz-Griffero et al., 2009; 2007b), which is an essential function for the ability of TRIM5 $\alpha$  to form an array of protein in the surface of the core (Fig.2B)(Ganser-Pornillos et al., 2004). 3) the PRYSPRY domain is the domain that comes in direct contact with the HIV-1 core (Yang et al., 2014). In summary our findings suggested that the rhesus macaque protein TRIM5 $\alpha$  binds to the surface of the HIV-1 core by forming an array protein (Fig. 2B). Formation of this complex recruits Ubc13, which is an E2 enzyme required for restriction(Pertel et al., 2011). Subsequently, an unknown activity leads to acceleration of uncoating (Diaz-Griffero et al., 2007a; Stremlau et al., 2006). Although, we have recently solved the structure of Ubc13 interacting with the RING domain (Yudina et al., 2015), the mechanism and energy source by which this complex leads to acceleration of uncoating is unknown (Fig.2B).



**Figure 2. Inhibition of HIV-1 infection by TRIM5 $\alpha$ .** (A) The different domains of TRIM5 $\alpha$  are shown, and a small cartoon depicting the TRIM5 $\alpha$  protein is shown on the right side. (B) TRIM5 $\alpha$  proteins assembled forming a hexagonal pattern on the surface of the HIV-1 core, and the RING domain of TRIM5 $\alpha$  recruits an E2 enzyme (Ubc13). Subsequently the core is disassembled (acceleration of uncoating) and infection is aborted. The mechanism and source of energy for this process is unknown.

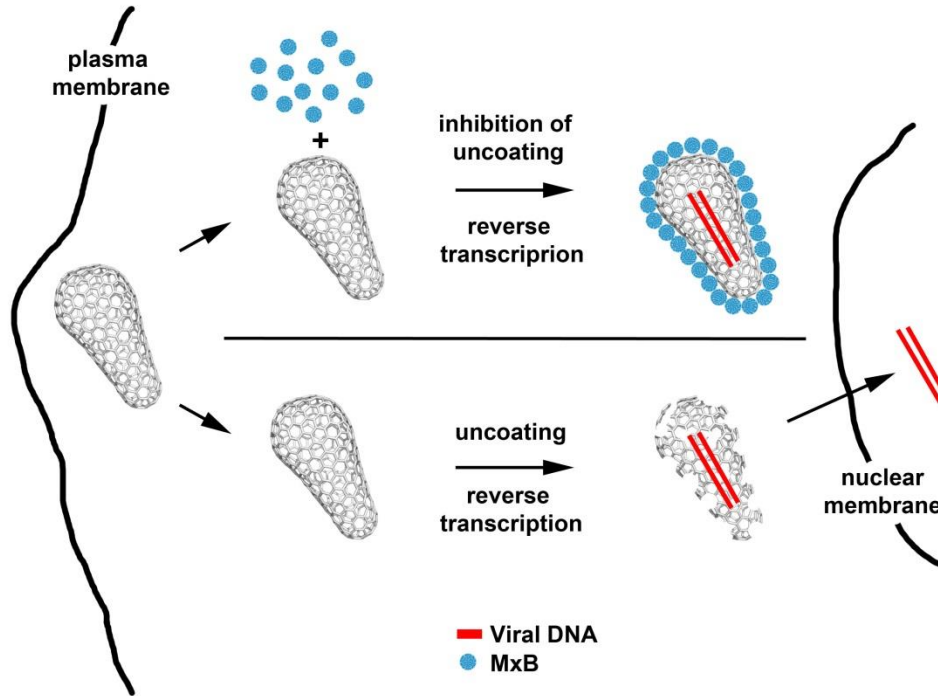
Interestingly, the structure of the PRYSPRY domain, which is the domain that directly interact with the HIV-1 core, exhibit a flexible loop in the region that interacts with the HIV-1 core (Fig. 3), as established by genetic experiments (Li et al., 2006; Yap et al., 2005). These observations suggested that movement of the loop is providing the energy necessary for the complex to accelerate uncoating. Future experiments will test the hypothesis that a flexible loop is required for acceleration of uncoating. To this end, we will identify TRIM5 $\alpha$  mutations on the PRYSPRY domain that decrease the flexibility of the loop but preserve binding to the HIV-1 core. These particular variants will be tested for their ability to block HIV-1 and accelerate uncoating in human cells. These studies will be complemented by experiments that will measure the ability of the PRYSPRY domain mutants in solution to disassemble in vitro assembled HIV-1 CA complexes (Fricke et al., 2013a). Overall these experiments will sort out the role of loop flexibility in acceleration of uncoating.



**Figure 3. Structure of the PRYSPRY domain of rhesus monkey TRIM5 $\alpha$ .** The structure of the PRYSPRY domain is shown. The four variable loops of the protein are indicated as V1, V2, V3 and V4. The V1 loop, which directly interact with the HIV-1 core, exhibited hundred of different conformations, as indicated by the strands in different colors. These observations suggested that the PRYSPRY domain of TRIM5 $\alpha$  exhibit great plasticity, which might allow the binding to different epitopes on the surface of the HIV-1 core. In addition, the movement of the V1 loop might be the energy necessary for accelerating the uncoating process of HIV-1.

### 3) MxB/Mx2

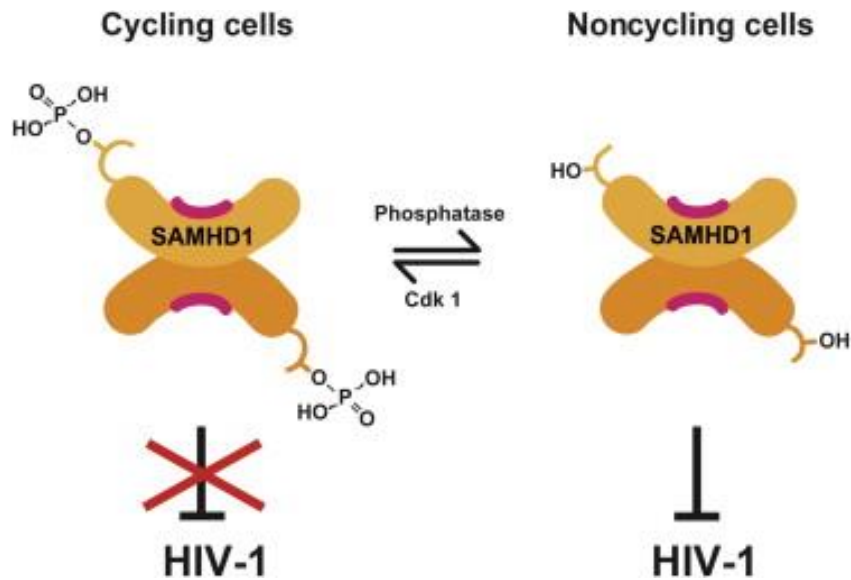
The restriction factor MxB is an interferon- $\alpha$  inducible protein that blocks HIV-1 infection in T cells (Goujon et al., 2013; Kane et al., 2013; Liu et al., 2013). Our investigations revealed that MxB blocks HIV-1 infection by inhibiting the uncoating process of HIV-1 (Fricke et al., 2014) (Fig. 4). We found that MxB directly interacts with the HIV-1 core by using a triple arginine in the N-terminal domain of MxB (Schulte et al., 2015). Our studies also showed that oligomerization of MxB is essential for the ability of MxB to bind to the HIV-1 core and restrict HIV-1 (Buffone et al., 2015). Overall, these results suggested that MxB binding to the core is forming an array on the surface of the HIV-1 core. Future experiments will test the hypothesis that MxB forms an array of protein on the surface of the HIV-1 core, which leads to inhibition of uncoating. To this end, we will perform Electron Microscopy of pure MxB protein overlaid on in vitro assembled HIV-1 CA that forms flat sheets. These experiments will show whether MxB cages the HIV-1 core in order to prevent HIV-1 uncoating. We are currently testing our purified MxB protein from human cells for its ability to interact with HIV-1 cores.



**Figure 4. Inhibition of HIV-1 by MxB/Mx2.** Our investigations revealed that MxB directly interacts with the HIV-1 core and prevents the uncoating process of HIV-1 terminating infection.

#### 4) SAMHD1

The restriction factor SAMHD1 prevents HIV-1 infection of macrophages, dendritic cells, and resting T cells (Baldauf et al., 2012; Hrecka et al., 2011; Laguette et al., 2011). Our investigations revealed that SAMHD1 is regulated by phosphorylation of T592 (White et al., 2013a; 2013b) (Fig. 5). The unphosphorylated form of SAMHD1 potently blocks HIV-1 infection. By contrast the phosphorylated form does not affect HIV-1 infection. These investigations suggested that the ability of SAMHD1 to block HIV-1 infection can be modulated. To this end, we are currently investigating in human primary cells the regulation of phosphorylation by different cytokines. We recently found that SAMHD1 is S-glutathionylated, and that this post-translational modification is essential for the ability of SAMHD1 to block HIV-1 infection. We are currently investigating the contribution of SAMHD1 S-glutathionylation to restriction. Although we have performed extensive biochemical and cellular characterization of SAMHD1 (Brandariz-Nuñez et al., 2013; 2012; Ryoo et al., 2014; St Gelais et al., 2014; Welbourn et al., 2012; White et al., 2013b; 2014), we have not explored the role of SAMHD1 in immunity. Efficient lentiviral infection of macrophages in old world monkeys correlates with a strong adaptive immunity (Schaller et al., 2012).



**Figure 5. Regulation of SAMHD1 anti-HIV-1 activity by phosphorylation.** Our investigations revealed that phosphorylation of SAMHD1 at T592 modulates the ability of this restriction factor to block HIV-1 infection of macrophages.

We are currently testing the hypothesis that SAMHD1 is involved in adaptive immunity. To this end, we will study adaptive immunity in the SAMHD1 knockout mice by testing antibody response, and the ability of the mice to prevent the growth of diverse pathogens. We will initially test pathogens that are known to be inhibited by SAMHD1, such as HSV-1/2 (Kim et al., 2013) and mycobacterium tuberculosis (our unpublished preliminary studies). These investigations will help us understand the role of SAMHD1 in the immune system.

## PUBLICATIONS

(h-index=27, total citation=2618). Total papers = 69

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## DR. BETSY HEROLD

Dr. Herold's lab focuses on identifying molecular mechanisms that contribute to the HIV-HSV syndemic and translating these findings into the clinic with the goal of developing novel therapeutic or prevention modalities. In collaboration with William Jacobs, PhD, the lab developed a paradigm shifting live attenuated HSV-2 vaccine candidate by deleting the immunodominant envelope glycoprotein D, which has been the primary component of subunit vaccines. Subunit vaccines induce high titer neutralizing antibodies but failed to protect against HSV in clinical trials. In contrast, the gD deletion virus vaccine provided 100% protection against vaginal, skin, and neurological infections with a panel of clinical isolates of HSV-1 and HSV-2 in mice and guinea pigs, completely prevented the establishment of HSV latency, and elicited high titer antibodies that are rapidly transported into mucosal sites and facilitate antibody-dependent cell mediated cytotoxicity (ADCC) and antibody-dependent phagocytosis. Collaboratively, the Herold and Jacobs labs are now actively engaged in studies to define why deletion of gD skews the immune response towards non-neutralizing FcR activating antibody responses and conversely, why gD elicits neutralizing antibody responses. They are also actively engaged in advancing this vaccine into the clinic and using the deletion virus as a vector to engineer vaccines against other pathogens including HIV.

A second major goal of the lab is identifying the signaling pathways that HSV-2 usurps for entry and immune evasion: Genital herpes infections are a major global health problem and a substantial co-factor for HIV infection. Development of new approaches to prevent and ultimately eradicate HSV requires an understanding of the molecular and cellular events critical for the establishment of infection and latency and how the virus evades host immunity. To identify novel targets, the Herold lab has focused on cellular signaling pathways usurped by the virus to promote infection. Current work from the laboratory demonstrates that HSV activates Akt and calcium signaling pathways and these signaling pathways play critical roles in the establishment of infection and in cell-to-cell spread. Notably, HSV triggers the translocation of Akt from the inner to the outer plasma membrane where it interacts with the viral envelope glycoprotein B to activate calcium signaling and promote viral entry. In immune cells, viral induced Akt activation promotes apoptosis. We recently identified several drugs that block HSV-induced Akt signaling and prevent infection in several preclinical models.

The lab is also actively engaged in studies to understand the biology behind the HIV-HSV syndemic. Specifically the lab has found that defensins and secretory leukocyte protease inhibitor (SLPI) inhibit HSV and HIV infection in vitro and contribute to the endogenous antiviral activity of genital tract secretions. However, HSV-2 down-modulates the expression of these antimicrobial peptides, which may facilitate HIV and HSV infection and spread. In addition, HSV-2 induces the expression of proinflammatory cytokines and recruits immune cells to sites of HSV replication to promote HIV acquisition and transmission. HSV also has immunomodulatory effects on immune cells. HSV-2 interferes with dendritic cell (DC) function in vitro by inducing apoptosis, which may allow HSV to escape immune surveillance, but the cytokines and chemokines secreted by DCs in response to HSV promote HIV replication. Many of the in vitro and murine findings were recapitulated in clinical samples comparing genital tract mucosal immunity (genital tract secretions, cytobrushes, and vaginal or skin biopsies) in HIV-infected women who are HSV-2 seropositive or seronegative. Surprisingly, they also found that coinfection with HIV and HSV-2 is associated with significant changes in the phenotype and function of peripheral blood CD4 T cells that may contribute to the HIV reservoirs. Specifically they found that IL-32, which is decreased in HSV-2+ vs HSV-2 seronegative women blocks the effects of latency reversal stimuli being studied for HIV eradication and cure.

Finally the lab is also focused on the development of topical pre-exposure prophylaxis products (PrEP) for HIV and HSV prevention: In collaborative studies, their research team has developed an intravaginal ring that delivers tenofovir disoproxil fumarate (TDF), the more potent prodrug of tenofovir. The greater potency reflects significantly increased tissue and cellular uptake of TDF. The TDF ring prevented 100% of macaques from SHIV infection and retained activity when macaques were pretreated with high dose medroxyprogesterone, which provides a rigorous model of SHIV Infection by increasing susceptibility of NHP to Infection. Notably, a 0.3% TDF gel provided significantly greater protection than 1% tenofovir gel against HSV-2 in wild-type mice and against HIV and HSV-2 in transgenic mice (expressing human CD4, CCR5 and cyclin T1 to render them susceptible to HIV). The lab recently completed a Phase 1 clinical trial in the Bronx. The TDF ring was safe, and the tissue drug levels exceeded those associated with protection against HIV. A more expanded Phase 1 study in sexually active young adults in the US and Kenya is planned.

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5. Taneva E, Crooker K, Park SH, Su JT, Ott A, Cheshenko N, Szleifer I, Kiser PF, Frank B, Mesquita PM, **Herold BC**. Differential mechanisms of tenofovir and tenofovir disoproxil fumarate cellular transport and implications for topical pre-exposure prophylaxis. Antimicrob Agents Chemother. 2015 Dec 28;60(3):1667-75. PMC4775922
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**WILLIAM R. JACOBS JR., Ph.D.**

**Strategies to Sterilize Infections of the Latent Pathogens *Mycobacterium tuberculosis* and Herpes Simplex Viruses**

The Jacobs lab focuses on diseases that affect the developing world. Tuberculosis, caused by *M. tuberculosis*, causes 1.5 million deaths every year and over 9 million cases are reported each year. In fact, the World Health Organization (WHO) reports that 1 in 3 people on planet Earth have latent *M. tuberculosis* infections. Herpes viruses, caused by herpes simplex virus 1 (HSV-1) or herpes simplex virus 2 (HSV-2), cause significant latent infection around the globe, but can cause death or deformities in newborn children and severe infections or infections in the population. Although one pathogen is caused by a bacterium and the other by a virus, they share the common property that they can cause lifelong infections in humans. The Jacobs Lab use genetic approaches to elucidate the mechanisms by which these two pathogens cause latent infections. A major focus of the work is to develop novel vaccine candidates by engineering specific defects in the causative pathogenic agents. For *M. tuberculosis* the Jacobs Lab developed the first tools to move DNA into *M. tuberculosis*. The key to this success was using viruses that affect *M. tuberculosis*. By genetically engineering a mycobacterial virus, Dr. Jacobs made a shuttle phasmid, a chimeric vector that replicates in *E. coli* as a causent and in mycobacteria as a phage. These shuttle phasmids led to the development of the first transformation systems, efficient transposon delivery systems, and reporter mycobacteriophages that could readily asses drug susceptibilities in clinical isolates of *M. tuberculosis*. An effort to understand how *M. tuberculosis* evades killing by the immune system or bactericidal antibiotics is a major effort of the Jacobs group. For herpes viruses Dr. Jacobs has collaborated with Dr. Betsy Herold and engineered a deletion mutant of HSV-2 deleted for the gene encoding the major immunodominant antigen and entry protein named gD. Surprisingly immunization of mice or guinea pigs with HSV-2  $\Delta$ gD provides sterilizing immunity against HSV-2 or HSV-1. Notably, protection from this deletion mutant is mediated by a special class of antibodies that mediate antibody dependent cell-mediated cytotoxicity (ADCC). Current efforts in the Jacobs lab are focused on elucidating the mechanism of the astonishing immunity and attempting to achieve a more efficacious TB vaccine.

See <http://www.aecom.yu.edu/tbresearch/> for lab updates.

**Recent Publications:**

1. **Foreman, T., Mehra S., LoBato, D., Malek, A., Alvarez,X., Golden, N., Bucşan, A., Didier, P., Doyle, L., Russell-Lodrigue, K., Roy, C., Blanchard, JL., Kuroda, A., Lackner, A., Chan, J., Khader, S., Jacobs, Jr. WR., and Kaushal, D.**(2016) "CD4+ T cell-independent mechanisms suppress reactivation of latent tuberculosis in a macaque model of HIV co-infection" *PNAS*. (Accepted).
2. **Petro CD, Weinrick B, Khajouinejad N, Burn C, Sellers R, Jacobs WR Jr, Herold BC.** (2016). "[HSV-2  \$\Delta\$ gD elicits FcyR-effector antibodies that protect against clinical isolates.](#)" *JCI Insight* (12). pii: e88529. PMID: 27536733

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4. Olsen A, Chen Y, Ji Q, Zhu G, De Silva AD, Vilchèze C, Weisbrod T, Li W, Xu J, Larsen M, Zhang J, Porcelli SA, Jacobs WR Jr, Chan J. (2016). "[Targeting \*Mycobacterium tuberculosis\* Tumor Necrosis Factor Alpha-Downregulating Genes for the Development of Antituberculous Vaccines.](#)" *MBio*. 7(3). pii: e01023-15. PMID: 27247233.
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9. Pope, W.H., Bowman, C.A., Russell, D.A., Jacobs-Sera, D., Asai, D.J., Cresawn, S.G., Jacobs, W.R., Jr., Hendrix, R.W., Lawrence, J.G., Hatfull, G.F. (2015) Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. *eLife* PMCID PMC 4408529.
10. Hartman, T., Weinrick, B., Vilcheze, C., Berney, M., Tufariello, J.M., G. M. Cook., and W. R. Jacobs, Jr. (2014) Succinate dehydrogenase is the regulator of respiration in *Mycobacterium tuberculosis*. *PLoS Pathogens*. 10(11):e1004510. PMCID PMC 4161257.
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11. **DR. WILLIAM R. JACOBS, JR.**

## DR. GANJAM V. KALPANA

### **Molecular Genetic Analysis of Tumor Suppressor INI1/hSNF5 in HIV-1 Replication and Cancer**

INI1/hSNF5 is a component of the chromatin remodeling SWI/SNF complex. It is an interacting partner for HIV-1 integrase (IN) and also a tumor suppressor biallelically mutated in rhabdoid tumors, a rare but highly aggressive pediatric malignancy. The two major areas of focus in the laboratory are: (i) understanding the role of INI1 in HIV-1 replication and exploring its potential as a drug target for intervention of AIDS; and (ii) understanding the mechanism of tumor suppression by INI1/hSNF5 and developing novel and effective therapeutic strategies for rhabdoid tumors.

**INI1 in HIV-1 replication:** We have found that INI1/hSNF5 directly binds and recruits components of Sin3a-histone deacetylase (HDAC) complex into the HIV-1 virions and this HDAC1 complex appears to be required for viral infectivity. We are currently isolating and characterizing IN and INI1 mutants defective for binding to HDAC1 complex and testing their effect on HIV-1 replication. We have found that HIV-1 harboring IN mutants defective or binding to INI1 are severely compromised for replication. Furthermore, we have found that INI1 mutants defective for binding to HDAC1 complex dominant negatively inhibit HIV-1 but not SIV replication. These studies are likely to open up a new paradigm for role of INI1 in HIV-1 replication and may provide novel strategies to inhibit viral replication.

**Mechanism of Tumor suppression by INI1/hSNF5:** By using a series of genetic systems developed in our laboratory and by isolating cancer-associated mutations of INI1, and a wealth of protein-protein interaction defective mutants of INI1, we are dissecting the exact mechanism of INI1-mediated G0/G1 cell cycle arrest, mitotic arrest, and senescence and tumor suppression. Furthermore, characterizing the INI1-associated HDAC1 complex has revealed an unanticipated role of INI1 in interferon signaling and tumor suppression.

**Development of targeted therapies for rhabdoid tumors based on INI1 function:** One of the goals of our laboratory is to develop molecularly targeted therapies based on the understanding of genesis of rhabdoid tumors. Majority of rhabdoid tumors have biallelic inactivation of *INI1* gene. Our previous studies demonstrated that Cyclin D1 is a direct downstream target of INI1 mediated repression and that rhabdoid tumors are exquisitely dependent on Cyclin D1 for genesis and survival. Our preclinical studies have provided proof of principle for our hypothesis that targeting Cyclin/cdk axis is an effective means of inhibiting rhabdoid tumors *in vitro* and *in vivo*. The current goal is to develop novel strategies to facilitate clinical translation of laboratory findings to establish an effective therapy for these tumors. For this purpose, we are using non-invasive imaging technology such as microPET to monitor the therapeutic efficacy in primary mouse tumor models, developing novel drugs to target these tumors and investigating the interaction between *Cyclin D1*, the cdk pathway and *Ini1* in mouse models.

Identification of downstream pathways regulated by *INI1* has been instrumental in novel biomarkers and therapeutic targets for these tumors. *Aurora A* is repressed by *INI1* and it is down-repressed in rhabdoid tumors due to loss of *INI1*. We have found that *Aurora A* is a novel therapeutic target as siRNA-mediated depletion of this gene resulted in potent mitotic catastrophe and cell death in rhabdoid tumors.

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**DR. LIBUSHA KELLY**  
<http://www.kellylab.org/>

Microbial populations are dynamic, transactional social networks of paramount importance to human health. The collection of microbes living in and on our bodies (the 'microbiome') is influenced by top-down and bottom-up regulation and these processes are poorly understood. For example, the availability of resources produced by other microbes ('public goods') can inhibit or support the growth of particular microbes (bottom-up). Administering a drug or viral predation can remodel microbial community structure (top-down). Our research program focuses on how microbial populations in the human body respond to perturbations such as diet, disease, and drugs, and how these responses are linked to health outcomes. The overall goal of our work is to empower patients to improve their health via targeted control of their microbiome. Towards this end we study how microbial communities are influenced by top-down and bottom-up regulation with a focus on three main biological questions: 1) How does microbial metabolism of drugs influence treatment outcomes in patients? Here we develop pretherapy analysis protocols to identify patients with high-risk microbiomes; we propose novel prebiotic approaches to influence microbial drug metabolism; and we predict new microbiome/drug interactions. 2) How do interactions between bacteria and archaea at the bottom of the microbial food chain influence access to dietary substrates? We endeavor to increase access to beneficial dietary compounds and we study how aging influences food processing in the gut. 3) How do virus/host interactions influence population-level metabolism in the gut? We predict viral influences on microbiome health and function and we identify new viruses that infect microbial populations in the human gut. Our approaches borrow from many fields and include metabolomics, high throughput genomics, information theory, synthetic chemistry, flow sorting, and imaging. Taken together, my research program forms the foundation of a new field of targeted microbiome manipulation for personalized health care.

### **Complete Publication List:**

<https://scholar.google.com/citations?user=sq7-rm4AAAAJ&hl=en>

### **Selected Publications and Products:**

† Indicates that authors contributed equally to the publication

#### *Xenobiotic metabolism and the human microbiome*

Leah Guthrie, Sanchit Gupta, Johanna Daily, **Libusha Kelly**. "Human microbiome signatures of differential colorectal cancer drug metabolism". Accepted, Nature Biofilms and Microbiomes.

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### Phage and bacterial genomics and metagenomics

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## DR. GREGOIRE LAUVAU

### **Immune effector cell differentiation & protective host responses against microbial pathogens and tumors *in vivo***

Microbial pathogens invasion usually triggers potent host immune responses, however efficient protection and pathogen killing require the presence of effector cells and combinations of inflammatory signals that are ill-defined in most infections. Tumor often escape immune responses through a variety of mechanisms including immune suppression.

Our work therefore focuses on precisely defining these events in various settings *in vivo*. Specifically, we investigate (i) the inflammatory signals and related pathways, and innate immune cells that regulate T and innate cell differentiation, and (ii) the cross-talks between memory T cells and innate immune cells. Innate immune cells include monocytes, macrophages, dendritic cells and lymphocytes. We use various models of acute microbial pathogen infections in mice, namely the bacteria *Listeria monocytogenes*, *Streptococcus pneumoniae*, the viruses Vesicular Stomatitis virus and Murine Cytomegalovirus. We study the immune response to the parasite of malaria *Plasmodium* in surrogate mouse models and in human patients. We also investigate the role of poor prognosis mutations found in breast cancer patients on immune cells functions. We take advantage of a range of advanced fluorescent-tracer based methodologies and intravital microscopy to monitor and visualize immune cells *in situ*. We use cell transfer experiments and novel genetically modified mice models in which dynamic cell functions can be monitored and/or in which functional subsets of immune cells can be selectively eliminated. We also make use of the latest cutting edge approaches to analyse immune cell expression and epigenetic programming, as well as high end cytometry by time of flight. Overall, the goal of my laboratory is to improve our fine understanding of the factors that orchestrate antimicrobial and antitumoral host protective immune responses *in vivo*. We believe that our work will contribute to better immune cell-mediated preventive and therapeutic vaccination strategies.

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## DR. THOMAS S. LEYH

My laboratory is focused on understanding the molecular basis of life. Our interdisciplinary pursuit of this issue has provided a broad experimental platform for our work and has proven a recipe for discovery. For example, my group discovered the link between sulfur biology and GTPase function; a linkage that rests with the enzyme ATP sulfurylase, which allosterically couples the chemical potential of GTP hydrolysis to the synthesis of activated sulfate (APS, adenosine 5'-phosphosulfate), an essential sulfur metabolite. Our inquiries in this area have revealed further that this same enzyme forms a complex with its partners in the cysteine biosynthetic pathway, and, remarkably, that new catalytic function emerges from this complex - the hydrolysis of ATP. In this case, it is the energy of ATP hydrolysis that is linked to the synthesis of APS. This finding underscores how cellular components can combine in synergistic ways to create hierarchies of function. Such hierarchies, whose behaviors are rooted in the reduction of entropy, are not well understood, and are of keen interest to us. First principles of chemistry and enzymology suggested that ATP sulfurylases that are not linked to an external energy source, such as ATP or GTP hydrolysis, might transfer APS directly to the active site of the next enzyme in the metabolic pathway, APS kinase. We have shown that in a spectacular display of the interplay of structure and function, certain sulfate activating complexes transfer APS directly between the active-sites of ATP sulfurylase and APS kinase *via* a 75Å-long groove that opens and closes in response to the position of the nucleotide within the groove.

Transfer of the sulfuryl-moiety ( $-\text{SO}_3^-$ ) from activated sulfate to biological acceptors is used widely by the cell to regulate metabolism, and the extent to which a particular metabolite is sulfated is determined by the balance of the *in-vivo* activity of the sulfotransferase (which transfers the sulfuryl-group) and sulfatase (which hydrolytically removes it). Compelling, disease-relevant biology pivots on the activities of each of the six known cytosolic sulfotransferase isozymes. Our laboratory has concentrated primarily on estrogen sulfotransferase (EST), which sulfates estrogen and thereby prevents it from binding to and activating the estrogen receptor. Aberrant sulfation of estrogen is tightly, causally linked to cancer in primary estrogen-dependent breast tumors. We have recently determined the first transition-state structure of an enzyme catalyzed sulfuryl-transfer reaction – that of EST. While it is quite gratifying to “see” precisely how the electronic structure of the bonds involved in the transfer reorganizes as enzyme-bound substrate moves between their ground- and transition-states, the structure is also of considerable practical value in that it defines the target for the design and synthesis of sulfuryl-transfer transition-state inhibitors (a perfect transition-state mimic is expected to inhibit with picomolar affinity).

*Streptococcus pneumoniae*, a multiple-drug resistant organism, is estimated to take the lives of 3600 people daily, the majority of whom are children and the elderly. We discovered recently that mevalonate kinase, an essential enzyme in the isoprenoid biosynthetic pathway in *Streptococcus pneumoniae*, is potently allosterically inhibited by diphosphomevalonate (DPM), a downstream intermediate in the pathway, and that the human isozyme is not. Genetic and animal studies of this multiple-drug resistant organism have taught us that the mevalonate pathway is essential for the survival of *S. pneumoniae* in the lung, and human serum. Consequently, we have undertaken a major research effort to develop novel antibiotics that target these enzymes in gram-positive bacteria. The program, carried out under the auspices of the *NIAID*, brings together an interdisciplinary team of faculty, postdoctoral fellows and graduate students in the areas of high-resolution NMR-spectroscopy, crystallography, synthetic chemistry, and biochemistry to explore fundamental issues of allostery, catalysis, and inhibition in these systems. I am pleased to report that our recent efforts have produced inhibitors that act with nanomolar affinity at each of multiple points in the pathway, and are capable of killing infectious *S. pneumoniae* in rich media at ~ 25 µg/ml.

The three projects outlined above comprise the core of our research activities; however, we are also expanding into two new areas. The etiology of how *M. tuberculosis* emerges from dormancy in the lung tubercle is not yet well understood. We are beginning to define the molecular logic of this transition with Prof. John Chan, an expert mycobacteriologist who has isolated a mutation that activates growth by derepressing dormancy. While the protein that harbors this mutation has not yet been assigned molecular function, we now know that it co-purifies with one-equivalent of adenine nucleotide bound to it, that it slowly hydrolyses ATP, and that its sequence identifies it as a possible element of a signaling network – we are currently testing this hypothesis using genetic and biochemical assays. In a final program, we are collaborating with a single molecule spectroscopist, and biological chemist at Columbia University to better understand and control the ribosomal editing functions of the protein-synthetic machinery toward mis-acylated tRNA. Editing protects against disease by recognizing and rejecting misacylated tRNA; controlling editing gives way to regiospecific incorporation of non-natural amino acids into proteins, which will facilitate myriad scientific endeavors including single-molecule exploration of the cellular milieu.

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## DR. JOSHUA D. NOSANCHUK

**Key Words:** *fungus, histoplasmosis, cryptococcosis, candidiasis, melanin*

- *Histoplasma capsulatum*: Research on this fungus pertains to the development of active and passive immunotherapeutics. Since individuals with severe histoplasmosis [such as AIDS patients with disseminated disease] often lack effective cell-mediated immune responses, induction of an effective humoral response or passive administration of antibody has tremendous therapeutic potentials. My laboratory is the first to identify protective monoclonal antibodies for the treatment of *H. capsulatum* infection. We are studying the mechanisms of antibody efficacy and are testing the recombinant antigens as a potential prophylactic and therapeutic vaccine. Also, we have embarked with the Nathenson and Almo labs to study the impact of co-stimulation on histoplasmosis and have demonstrated that the PD-1/PDL pathway is critically important to disease pathogenesis. Antibodies can interfere with this negative co-stimulation pathway and prevent lethal histoplasmosis.

- *Candida parapsilosis*: This is the newest fungus to the laboratory. The incidence of *C. parapsilosis* infections has exploded in recent years and very little is known about its virulence. We developed the first efficient method for targeted gene deletion for *C. parapsilosis* and are actively pursuing targets to define what makes this fungus pathogenic, with a particular emphasis on secreted hydrolytic proteins and lipid metabolism. We are also targeting virulence associated genes in *C. albicans* and studying their role in pathogenesis.

- *Cryptococcus neoformans*: We are primarily using this pathogen to elucidate the impact of melanin in pathogenic fungi. Melanin is a complex polymer of unknown structure that is prevalent throughout the biological kingdoms. Ongoing investigations are examining mechanisms of melanin synthesis and rearrangement by molecular, physical, and immunological methods. This work is in collaboration with Dr. Arturo Casadevall, Departments of Microbiology & Immunology and Medicine.

Additional areas of special emphasis:

Methamphetamine: This drug has increasingly become a major scourge on our society. Although the behavioral impact of methamphetamine is well understood, there is a dearth of data on the effect of the drug on immune function. We have established that methamphetamine significantly adversely regulates diverse aspects of immunity. We have an ongoing program to further elucidate the mechanisms and impact of this dysregulation.

Nitric oxide releasing nanoparticles: We are exploring the therapeutic potential of this novel compound for the treatment of diverse infectious diseases, including bacterial and fungal diseases. This work is in collaboration with Dr. Joel Friedman, Departments of Medicine and Physiology & Biophysics.

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## **DR. LIISE-ANNE PIROFSKI**

The focus of the Pirofski laboratory is on antibody and B cell immunity to encapsulated microbes using *Streptococcus pneumoniae* (Pneumococcus) and *Cryptococcus neoformans* (Cryptococcus) as examples. Both of these microbes cause disease in normal and immunocompromised people, particularly those with HIV infection, AIDS, B cell and antibody defects. The laboratory conducts translational studies of the serological, cellular, and molecular response to these microbes in normal and immunocompromised patients and basic scientific studies of microbial pathogenesis and host-microbe interaction. The goals of this research are to understand how innate and acquired antibody and B cell immunity to these microbes confers resistance to disease and to translate this knowledge into novel approaches to treatment and prevention of pneumococcal and cryptococcal disease.

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## DR. STEVEN PORCELLI

### **Improving T cell responses for vaccination and disease prevention**

Our laboratory studies the control of acquired immune responses by T cells, which we view as the master regulators and key effectors of host defense and immune tolerance. In broad terms, our research can be divided into two interrelated areas. The first is to understand the role of regulatory T cells, with particular emphasis on the activities of a specialized T cell subset known as CD1d-restricted NKT cells. These T cells have the highly unusual property of responding to specific glycolipid antigens, and we are studying ways to control their regulatory and effector functions in various mouse models of disease. A second second major research area is the study of T cell responses against pathogenic microorganisms, especially *Mycobacterium tuberculosis*. We have recently made significant progress in understanding how mycobacteria block effective host T cell responses, and we are now working to incorporate our findings into the rational and intelligent design of a new tuberculosis vaccine. In the short term, we hope to broaden our understanding of how organisms like *M. tuberculosis* successfully evade eradication by the immune system. Our major long term goal is to create a genetically or chemically modified live attenuated *M. tuberculosis* strain that will be safe and effective as a vaccine against tuberculosis. The laboratory has also recently developed interests in novel cancer vaccines, tumor-specific immunotherapies and immunity against emerging viral threats such as Ebola and Zika viruses, and is pursuing several projects in these areas.

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## DR. VINAYAKA PRASAD

Research in our laboratory is focused on three areas of HIV/AIDS: HIV associated neurocognitive disorders (HAND), HIV replication mechanisms and RNA aptamers targeted to HIV.

**HIV associated Neurocognitive Disorders (HAND):** The severe form of HAND, the HIV associated dementia (HAD), is common among clade-B HIV-infected individuals in the US, but less common among individuals infected with clade-C HIV-1 in India, suggesting clade-specific differences in neuropathogenicity. Understanding clade-specific determinants of neuropathogenesis may shed light on the disease mechanism and help develop targeted drugs for HAD. We previously demonstrated that due to a C31S polymorphism, clade C Tat lacks the chemokine function of Clade B Tat that plays a crucial role in an increased brain infiltration of monocytic phagocytes in HAD. We studied neuropathogenesis induced by two HIV-1 clades B and C using SCID mouse HIV encephalitis (SCID-HIVE) model and reported that while the introduction of clade B HIV-1<sub>ADA</sub> into SCID mouse brain recapitulates the key features of human HAD disease, mice exposed to similar inputs of HIV<sub>Indie-C1</sub> (clade C) made fewer memory errors than those exposed to HIV-1<sub>ADA</sub> (clade B). HIV-1<sub>ADA</sub> also caused greater astrogliosis and loss of neuronal network integrity.

Work from many groups has shown that clade C HIV-1 in Southern Africa can induce HAD at much higher incidence than in India. We hypothesized that such variation is due to polymorphism in the neuropathogenesis determinants in Tat or gp120, the two major neurotoxicity determinants of HAND. With respect to Tat, we observed that the percentage of HIV isolates with dicysteine motif in Tat is 2-3% on the Indian subcontinent while in the Southern African countries, they ranged from 19-26%. These data broadly correlate with the HAD frequencies reported from India, South Africa and Botswana (3-4%, 25% and 38% respectively). This finding has been corroborated using a Zambian HIV-1C isolate that displays a C31 residue and thus an intact dicysteine motif. Our in vitro and SCID-HIVE results clearly indicate that Tat dicysteine motif determines neurovirulence. If confirmed in population studies, it may be possible to predict neurocognitive outcomes of individuals infected with HIV-1C by genotyping Tat.

Since Tat is not the only neurovirulence determinant in HIV-1, we examined whether gp120 exhibits intra-clade differences between India and Southern Africa. Our findings indicate that gp120 can also display region-specific differences. For example, the Southern African HIV isolates appear to contain more robust neurovirulence determinants than those in the Indian isolates. Thus, two different viral genes in India appear to show determinants of low neurotoxicity. These results suggest that clinical studies studying the incidence of HAD or HAND to correlate viral genetic differences must examine both Tat and gp120. *Ongoing work in our laboratory is attempting to identify the neurovirulence signatures of gp120 in clade C and clade B virus isolates and exploring the role of exosomes in neurovirulence.*

**Anti-HIV RNA aptamers hematopoietic gene therapy:** We previously developed and tested the efficacy of novel, anti-HIV-1 RNA aptamers to inhibit HIV-1 replication. Aptamers are sequences isolated by the iterative process of SELEX and are highly specific to their targets. The most efficacious aptamers identified in our laboratory as well as combinations of them could be tested in nonhuman primates (macaques). We will introduce such aptamers into hematopoietic stem cells, which will then be used in bone marrow transplantation followed by challenge with chimeric, pathogenic SHIVs. We have thoroughly characterized anti-RT aptamers and generated aptamers to HIV-1 Gag MA and NC proteins. Perturbation of HIV-1 Gag and viral RNA interaction using

anti-Gag aptamers has provided new insights showing that preventing Gag-RNA binding causes down-modulation of viral RNA thus inhibiting virus production. Most recently, we developed high affinity aptamers ( $K_d = 1\text{nM}$ ) to HIV-1 protease. *We are currently characterizing the Nef aptamers to understand the specific Nef functions in HIV replication that are affected by each aptamer.*

**HIV Replication Mechanisms:** We have a long-standing interest in elucidating the mechanistic basis of key steps in HIV-1 replication. In earlier work, we delineated the determinants of polymerase processivity, fidelity of DNA synthesis and strand displacement synthesis by HIV-1 RT. *Our current work is focused on the role of beta chemokines in HIV-1 budding.*

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## DR. CHAIM PUTTERMAN

Systemic lupus erythematosus (SLE) is a prototypical autoimmune disease that typically affects women in their reproductive years. Involvement of the kidneys, or lupus nephritis, appears in about 50% of lupus patients during the course of their disease. Despite medical treatment, morbidity and mortality from renal disease are common in lupus patients. The overall increase in the incidence of lupus and in the number of deaths from the disease reported in the United States are additional reasons for significant concern.

Anti-double stranded (ds) DNA antibodies are a serologic hallmark of patients with SLE. In recent years it has been increasingly clear that not only are anti-dsDNA antibodies an important diagnostic marker for lupus, but that these autoantibodies are also instrumental in the pathogenesis of lupus nephritis. The mechanisms by which anti-dsDNA antibodies induce renal injury, however, are not completely understood. It has been suggested that anti-dsDNA antibodies bind DNA in the circulation followed by non-specific deposition of these immune complexes in the kidney, or that in-situ immune complexes are formed in the kidney by binding of anti-dsDNA antibodies to nuclear antigens deposited on the glomerular basement membrane. Alternatively, some anti-dsDNA antibodies may cause injury by penetrating into living cells and affecting unidentified metabolic pathways. Finally, we and others have generated evidence that strongly suggests that at least some anti-dsDNA antibodies are pathogenic not by virtue of their affinity for DNA, but rather by direct cross-reactivity with renal antigen.

The long-term goals of the laboratory are to study the antigenic triggers and renal pathogenicity of anti-dsDNA antibodies. We want to understand which antigen(s) can trigger pathogenic anti-dsDNA antibodies, and whether protein antigens can induce a lupus like anti-DNA response. We are determining the cross-reactive kidney antigen bound by anti-DNA antibodies in human lupus and in mouse models of the disease to understand what determines the nephritogenic potential of these antibodies. Understanding the renal pathogenicity of cross-reactive anti-dsDNA antibodies by identifying the target antigen for these antibodies in the kidney would improve our understanding of a key manifestation of lupus, and would facilitate the development of serological tools to better predict the onset and severity of renal involvement in patients with SLE. Furthermore, identification of the triggering and/or target antigen in lupus will allow us to develop novel approaches to the treatment of lupus, by blocking the effects of anti-DNA antibodies on target organs or by specifically tolerizing pathogenic B cells.

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## **DR. XINGXING ZANG**

(Immune Checkpoint and Immunotherapy lab: <http://www.einstein.yu.edu/zang>)

Our laboratory focuses on new pathways and immunotherapies of T cell costimulation and coinhibition. We have recently discovered new members of the T cell costimulatory/coinhibitory B7 family and CD28 family, including B7x, HHLA2 and TMIGD2, and are using a variety of experimental approaches (gene knock-out mice, transgenic mice, monoclonal antibodies, crystal structure, etc) to understand how new B7/CD28 family members regulate T cell activation and tolerance. Current emphasis in the lab is placed in the following areas:

- 1) Novel drugs development: Translational medicine of T cell costimulation and coinhibition;
- 2) In vivo functions of new B7/CD28 pathways;
- 3) Human cancer-associated new B7/CD28 pathways and cancer immunotherapy;
- 4) New B7/CD28 pathways in autoimmune diseases/metabolic diseases and immunotherapy;
- 5) Relationship between new B7/CD28 pathways and infection;
- 6) Functional and structural characterization of new members of the Ig superfamily.

Our goal is to elucidate the mechanisms by which costimulation and coinhibition regulate T cells in peripheral non-lymphoid organs, and to translate the lessons learned in these studies towards developing new therapeutic strategies for immune-mediated diseases such as cancers, autoimmune disorders, metabolic diseases, infectious diseases, and transplantation rejection. Our research has won extensive attention from biopharmaceutical industry including some of the biggest drug companies.

Since 2008 the lab has mentored total 31 trainees of graduate students, postdoctoral fellows, clinical fellows, and visiting scientists. Many of trainees have subsequently developed independent careers in academic universities, medical centers, biopharmaceutical industry, and US government.

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