



Office of Education, Division of Intramural Research  
National Heart, Lung, and Blood Institute

## FELLOWS NEWSLETTER

The Fellows Newsletter is published monthly by the Office of Education, Division of Intramural Research, National Heart, Lung, and Blood Institute and distributed to NHLBI DIR members to promote the interest of DIR Fellows.

### Office of Education, DIR, NHLBI

Herbert M. Geller, Ph.D., Director  
Angela N. Theofilos, Program Coord.  
Aurora J. Taylor, Program Coord.

[DIREDucation@nhlbi.nih.gov](mailto:DIREDucation@nhlbi.nih.gov)

Building 10, Room 2N242

Tel: 301-451-9440

### Fellows Advisory Committee

Joshua Anzinger, TMB

Kjetil Ask, TMB

Arianna Biesso, LBC

Allen Chang, LB

Kang Chen, LBC

Ashvin George, LB

Mohit Kashyap, LMI

Cory Lago, TMB

Jonathan Lam, TMB

Yuan Le, LCE

Ashvin George, TMB

Mark McDermott, LKEM

Yrina Rochman, LMI

Shiwei Song, LMB

Aibin Wang, LMC

Lu Wang, LMI

Zhibin Wang, LMI

Thomas Winkler, HB

Julie Wu, TMB

Zheng You, LB

Yingfan Zhang, LMC

Hang Zhao, LB

### ***From the Director of the Office of Education***

Spring is officially here in Bethesda. I hope many of you got to visit our local cherry blossoms in the Kenwood neighborhood very near campus. If you enjoyed them, you will have another chance at sightseeing over the next week as the azaleas bloom, and Kenwood is a great place to see them.

This is a special DIR Retreat Issue of the Newsletter. Over 200 NHLBI scientists, including Fellows, Staff Scientists, and PIs have registered for the retreat. We have 114 scientific posters and 14 scientific talks in addition to our Keynote speaker. A special feature will be the Mentored Lunch on Thursday where you will have a chance to practice your "elevator talk". Finally, we will present the Outstanding Mentoring awards and the Best Poster Awards at our Friday awards banquet. I intend to visit each of your posters, and so I hope to interact with each of you.

## **8th Annual NHLBI DIR Scientific Retreat**

**Featuring:**

**-Bob Kocher, M.D., Keynote Speaker**

**-Gerald Shulman, Ph.D., M.D., Scientific Speaker**

**-Peter Walter, Ph.D., Scientific Speaker**

**April 14-16, 2010**

**The Baltimore Tremonts  
Baltimore, MD**



**Recent Publications by NHLBI Fellows**

- Brzeska, H., **Guag, J.**, **Remmert, K.**, Chacko, S., & Korn, E. D. (2010). An Experimentally Based Computer Search Identifies Unstructured Membrane-binding Sites in Proteins APPLICATION TO CLASS I MYOSINS, PAKS, AND CAR-MIL. *J. Biol. Chem.* 285, 5738-5747.
- Frank, L. H., **Yu, Q.**, **Francis, R.**, **Tian, X.**, Samtani, R., Sahn, D. J., Leatherbury, L., & Lo, C. W. (2010). Ventricular Rotation Is Independent of Cardiac Looping: A Study in Mice With Situs Inversus Totalis Using Speckle-Tracking Echocardiography. *J. Am. Soc. Echocardiogr.* 23, 315-323.
- Park, M. K.**, Fontana, J. R., Babaali, H., Gilbert-McClain, L. I., Stylianou, M., Joo, J., Moss, J., & Manganiello, V. C. (2009). Steroid-Sparing Effects of Pentoxifylline in Pulmonary Sarcoidosis. *Sarcoidosis Vasc. Diffuse Lung Dis.* 26, 121-131.
- Pasapera, A. M.**, Schneider, I. C., Rericha, E., Schlaepfer, D. D., & Waterman, C. M. (2010). Myosin II activity regulates vinculin recruitment to focal adhesions through FAK-mediated paxillin phosphorylation. *J. Cell. Biol.* 188, 877-890.
- Phillips, D.**, ten Hove, M., Schneider, J. E., Wu, C. O., Sebag-Montefiore, L., **Aponte, A. M.**, Lygate, C. A., Wallis, J., Clarke, K., Watkins, H., Balaban, R. S., & Neubauer, S. (2010). Mice over-expressing the myocardial creatine transporter develop progressive heart failure and show decreased glycolytic capacity. *J. Mol. Cell. Cardiol.* 48, 582-590.
- Rinschen, M. M., **Yu, M. J.**, Wang, G. H., Boja, E. S., **Hoffert, J. D.**, Pisitkun, T., & Knepper, M. A. (2010). Quantitative phosphoproteomic analysis reveals vasopressin V2-receptor-dependent signaling pathways in renal collecting duct cells. *Proc. Natl. Acad. Sci. U. S. A* 107, 3882-3887.
- Um, J. H.**, **Park, S. J.**, **Kang, H.**, Yang, S. T., Foretz, M., McBurney, M. W., Kim, M. K., Viollet, B., & Chung, J. H. (2010). AMP-Activated Protein Kinase-Deficient Mice Are Resistant to the Metabolic Effects of Resveratrol. *Diabetes* 59, 554-563.
- Xie, L. K., **Hoffert, J. D.**, Chou, C. L., **Yu, M. J.**, Pisitkun, T., Knepper, M. A., & Fenton, R. A. (2010). Quantitative analysis of aquaporin-2 phosphorylation. *Am. J. Physiol. Renal Physiol.* 298, F1018-F1023.

**Featured CORE:  
Proteomics Core**

Marjan Gucek, PhD, Director

The mission of the NHLBI Proteomics Core Facility is to provide investigators at the NHLBI access to mass spectrometry and gel based proteomics for identification and quantitation of proteins and their posttranslational modifications (PTM). We have state-of-the-art equipment, including latest additions of Orbitrap Velos and 5800 MALDI TOF/TOF.

Our workflows for relative protein quantitation are based on DIGE, label-free and iTRAQ approaches. We can also help you identify and quantify protein posttranslational modifications, including phosphorylation, nitrosylation, acetylation, etc. We provide training in

proper sample preparation and lead the researchers through mass spectrometric analysis to data searching and interpretation. Users have access to a variety of proteomics software platforms (Sequest, Mascot, Proteome Discoverer, Scaffold, Protein Pilot) for researching the data or viewing the results. In addition to helping the NHLBI investigators, we develop new approaches for PTM characterization and absolute protein quantitation.

The Proteomics Core Facility for NHLBI investigators was established in 2002 and I have taken it over in 2009. It's been a challenging and rewarding experience so far. I worked in a similar setup at Johns Hopkins before joining NHLBI. I find the environment here very supportive and I hope to generate renewed excitement for proteomics and

mass spectrometry. Our main lab is in building 10/8C214, we also have one instrument in 6N116 and gel capabilities in 5D08. The Proteomics Core Steering Committee currently consists of Drs. Elizabeth Murphy (Chairwoman), Maurice Burg, Stewart Levine and Joel Moss.

In proteomics core, it's all about the instruments. They all have names like Velos, Orbitrap, Typhoon and they can do amazing things. You might hear us say: We scanned your gel on Typhoon and analyzed the digested proteins on Orbitrap Velos. Translation: It's all good!

I've been in the mass spectrometry field for 15 years and the performance of these instruments has taken a giant leap forward in terms of sensitivity, speed and mass accuracy. Things that were

top notch a few years ago are now routine. Some challenges still remain – my hope is one day mass spectrometry will become as sensitive as western blots – if you can see your protein in a western blot, we can get you the identification. (Currently, the mass spectrometry is sensitive enough to identify proteins after silver or coomassie blue staining.)

Trypsin is the biggest enzyme in mass-spectrometry based proteomics. For the majority of projects, we would digest your proteins into smaller tryptic peptides, which are separated on reverse phase liquid chromatography and analyzed by a mass spectrometer. The main challenge is to ionize these peptides (charge them). Once charged, they fly into vacuum where we measure their m/z ratio. We can also fragment the peptides and the fragmentation pattern can then reveal the peptide se-

quence and consequently pinpoints to the protein. It is a wonderful technique for identification and quantitation – relative and absolute – of proteins. We can also characterize post-translational modifications (PTM), including but not limited to phosphorylation, nitrosylation and acetylation. PTMs can be challenging because of the low abundance so some type of enrichment is needed, either antibody based or taking advantage of some special physicochemical property of the modification.

We have an excellent team of proteomics specialists who will guide you through the experimental design, sample preparation and data analysis. The team in the core is: Angel Aponte, Yong Chen and Guanghui Wang – they are all experts in the field and very motivated. We usually help our users in experimental design, we guide them

through the sample preparation and downstream analysis. If you are interested in learning about the instruments and mass spectrometry, we can help you with that as well. Learning about mass-spectrometry-based proteomics can be very useful for the fellows using the core because you gain the skills that can later help you getting a job in the field.

For a successful project, it is beneficial to have as much interaction with users and their PIs as possible. There is a project meeting before the project starts. We organize monthly users meeting where we present latest developments in the core. We have covered various topics so far, including quantitative proteomics, post-translational modifications and data analysis. It's fun for us and I count on your continued support.

---

## **The Fellows Seminar Series presents:**

# **Mechanisms of Plaque Macrophage Removal During Regression and Stabilization of Mouse Atherosclerotic Lesions**

**Gwendalyn Randolph, Ph.D.**  
**Professor of Gene and Cell Medicine**  
**Mount Sinai School of Medicine**

**Tuesday, April 13th, 2010**  
**11:00am to 12:00pm**  
**Building 50, room 1328/1334**