New Center Seminar Series – Call for Speakers!

The Center is beginning a Research In Progress (RIP) Seminar series with the first meeting from 12:30 PM – 1:30 PM on Friday, June, 2, 2017. These seminars will be open to the public and will continue in the Fall on the first Friday of each month. Each RIP meeting will feature two speakers and a pizza lunch beginning at 12:20 PM. We ask all Investigators and/or their senior staff; Core and Core Section Directors and/or their senior staff, and Pilot Project Grantees – both past and current to present the results of their research and their future plans. We encourage all Center members and interested researchers to participate in this important Center activity. To facilitate their participation, the Center will cover travel expenses for speakers who are non-Yale investigators or their senior staff. In addition, there also will be a few non-Center speakers in areas of particular interest. Please email the name of the speaker, draft title of their talk, and first and second choices for dates to the Co-Directors, Angus and Ken. We also welcome suggestions for non-Center speakers.

Targeted Parallel Reaction Monitoring (PRM)

The PRM technology that is available from the Targeted Proteomics Core obviates the stochastic nature of LC/MS/MS analyses by quantifying the *same* proteins in each analysis. As described in a review by Dr. Navin Rauniyar (Int. J. Mol. Sci. **2015**, 16: 28566-28581) who works with Dr. TuKiet Lam, Director, Discovery Proteomics Core; PRM offers several advantages over the MRM technology that was used, for example, in Cates *et al* (J. Neurosci., **2014**, 34:11461-11469) to quantify a very low extent (0.56%) of *in vivo* phosphorylation at Thr 149 in ΔFosB that was isolated from mouse striatal extracts by SDS PAGE without prior enrichment. Should the need arise in your research to quantify individual proteins and/or their extent of phosphorylation (or other PTMs), we believe that PRM will provide similar sensitivity as MRM together with a >200 fold increase in mass resolution and 50-fold increase in mass accuracy that will provide greatly increased selectivity and confidence in protein identification. A single 90 min scheduled LC/PRM assay can quantify ~400 peptides. Assuming that each target protein is interrogated by ~6 transitions/peptide from 3 "light", naturally occurring and 3 matching "heavy" stable isotope labelled, internal standard synthetic peptides/protein, that is, 36 data points/protein;

a 90 min scheduled LC/PRM assay can interrogate the "absolute" expression of ~66 or the relative expression of ~133 targeted proteins or their PTM-proteoforms. Dr Nairn's laboratory are leveraging these capabilities to design a PRM assay for ~50 proteins enriched within the Post-Synaptic Density that will soon be available to Center Investigators. For more information on PRM or the PRM/PSD assay contact Co-Directors Angus & Ken.

Pilot Projects Grants Opportunity

The Center is delighted to announce that six Pilot Project grants have been awarded in the current Grant Year 12 (Table 1) and is now accepting applications for Pilot Projects for Grant Year 13 that begins 6/1/17. The goals of this program are to encourage young investigators in our Center's laboratories to embark on careers in substance abuse research, disseminate the Center's core technologies to researchers investigating the neurobiology of addiction who are not yet using neuroproteomics technologies, and to expand the technical abilities of the Center. Pilot Grants provide short term funding to obtain preliminary data so applicants can apply for longer term grant support. These awards provide $7,500 D.C. to help pay for the cost of preparing samples for analysis in the Center's Cores and free access to all of the Center's Cores. Applications are accepted from: 1) Center investigators and 2) their Postdoctoral Fellows and higher level research staff, 3) non-Center investigators expert in substance abuse with interests in initiating research in neuroproteomics, 4) non-Center investigators with expertise in cellular and molecular aspects of neuronal signaling with interests in initiating neuroproteomics research. Awards will be for one year for research that is directly related to the Center's theme of the "Proteomics of Altered Signaling in Addiction" and that propose to apply existing technologies from the Cores or to develop new technologies. Awards to non-Center investigators will be accompanied by Center membership for the term of the award. Priority will be given to new projects that are related to our Center's theme, to collaborative projects involving multiple investigators, and to Technology Development projects. The receipt deadline for applications is May 1, 2017. Additional information: **http://medicine.yale.edu/keck/nida/general/pilot_grants.aspx**. Please contact the Co-Directors, Angus & Ken, to ensure that new projects and potential pilot project proposals qualify for Center support!

Proteome Software Scaffold Training

The Discovery Proteomics Core now has Scaffold: http://www.proteomesoftware.com/products/scaffold/ Scaffold helps visualize and validate complex MS/MS proteomics experiments. Mascot data files are directly input into a licensed version of Scaffold by staff in the Discovery Core. After this point, Center users may download a free viewer to process the data remotely at any PC or Mac computer. The software is highly intuitive. Scaffold offers three alternative scoring systems for judging the significance of peptide identifications – including a new LFDR method that uses a Bayesian approach to estimate Local False Discovery Rate. Scaffold provides several statistical tests including T-Test, Fisher's Exact Test, ANOVA, and Coefficient of Variance to assess the significance of observed differences in expression. Scaffold also has other useful capabilities such as Volcano and Pie charts. If you would like assistance using Scaffold – either directly at Yale or indirectly via use of the free viewer please contact the Co-Directors, Angus & Ken.

Table 1: Grant Year 12 Pilot Projects

PI	Title	Institution	Center Lab	Project Title
T. Cijsouw	Postdoctoral Scholar	Tufts U.	Thomas Biederer	Mapping the proteome of the synaptic cleft through peroxidase-based reporter proteins
Ryan Logan	Assistant Professor	U. Pittsburgh	N.A.	Identifying circadian regulated proteins in specific cell types of the Nucleus Accumbens involved in cocaine reward
Megan Miller	Postdoctoral Associate	Yale U.	Marina Picciotto	A systematic evaluation of high-affinity α4β2 nicotinic acetylcholine receptor phosphorylation
Melissa Monsey	Postdoctoral Associate	Yale U.	Jane Taylor	Profiling the neuronal proteome of the lateral amygdala following cocaine-cue memory retrieval and systemic garcinol administration
Rebecca Taugher	Postdoctoral Fellow	U. Iowa	N.A.	Role of ASIC1A in regulating the NAc proteome in both the drug naïve and cocaine withdrawn states
Elsa Yan	Professor	Yale U.	N.A.	Role of dimerization in modulating sensitivity and dynamic range of ligand sensing in family CG protein coupled receptors

Table 2: Yale/NIDA Neuroproteomics Center Cores
We are delighted to announce that Angus Nairn has been named Director of the BBC.

Core	Name	Role	Email
Administrative	Angus Nairn	Co-Director/PI	angus.nairn@yale.edu
	Kenneth Williams	Co-Director/PI	kenneth.williams@yale.edu
Discovery Proteomics	TuKiet Lam	Core Director and Protein Identification and Profiling	tukiet.lam@yale.edu
	Pietro DeCamilli	Phosphoinositide Analysis	pietro.decamilli@yale.edu
	Ewa Folta-Stogniew	Biophysics	ewa.folta-stogniew@yale.edu
Targeted Proteomics	Kenneth Williams	Core Director	kenneth.williams@yale.edu
Bioinformatics and Biostatistics Core (BBC)	Angus Nairn	Core Director	angus.nairn@yale.edu
	Robert Bjornson	High Performance Computing	robert.bjornson@yale.edu
	Kei-Hoi Cheung	Yale Protein Expression Database (YPED)	kei.cheung@yale.edu
	Mark Gerstein	Bioinformatics	mark.gerstein@yale.edu
	Hongyu Zhao	Biostatistics	hongyu.zhao@yale.edu
Pilot Research Projects	Marina Picciotto	Core Director	marina.picciotto@yale.edu