

**ProteinSociety.org**

**THE 23<sup>rd</sup> SYMPOSIUM OF THE  
PROTEIN SOCIETY**

**Program & Exhibit Addendum**

Printed as of July 13, 2009

**July 25-29, 2009**

**Boston Marriott Copley Place**

**Boston, MA**

# ADDENDUM TO THE PROGRAM/ABSTRACT VOLUME

**ITINERARY BUILDER:** Go to the following URL and click on "Itinerary Builder" to plan your daily schedule:  
<http://submissions.miracd.com/tps2009/Itinerary/Login.asp>

## SESSION CHAIRS

### CONCURRENT MORNING SYMPOSIA #2 TRAFFICKING

9:00 AM – 12:15 PM

Salon E, 4<sup>th</sup> Floor

Session Chair: Christopher Hill, *The University of Utah*

### CONCURRENT AFTERNOON SYMPOSIA #8 DRUG RESISTANCE

3:15 PM – 5:45 PM

Salon F, 4<sup>th</sup> Floor

Session Chair: Michael Kay, *The University of Utah*

### CONCURRENT AFTERNOON SYMPOSIA #4 CYTOSKELETON DYNAMICS

1:45 PM – 5:00 PM

Salon E, 4<sup>th</sup> Floor

Session Chair: Jeanne Hardy, *University of Massachusetts, Amherst*

### CONCURRENT AFTERNOON SYMPOSIA #10 DYNAMIC COMPLEXES AND NETWORKS

3:30 PM – 6:45 PM

Salon F, 4<sup>th</sup> Floor

Session Chair: Andrej Sali, *University of California, San Francisco*

### CONCURRENT MORNING SYMPOSIA #12 TRANSLOCATION AND TRANSPORTATION

9:00 AM – 12:15 PM

Salon F, 4<sup>th</sup> Floor

Session Chair: Linda Randall, *University of Missouri*

## SUNDAY – July 26

### \*\*\*ROOM CHANGE\*\*\*

### EDUCATOR'S LUNCHEON WORKSHOP: INTERACTIVE, COLLABORATIVE, QUANTITATIVE BIOCHEMISTRY EDUCATION IN THE 2.0 ERA

12:15 PM – 1:45 PM

**This session will take place in Salon J, on the 4<sup>th</sup> floor**

#### PRESENTER CHANGE

Program #115 (Board #54) 2<sup>nd</sup> Author Dawn Herrick presenting

Program #166 (Board #105) 4<sup>th</sup> Author Anthony Mittermaier presenting

#### POSTER RELOCATION

Program #407 (Board #121) Author Seema Mittal presenting (previously scheduled Tuesday, July 28)

#### ABSTRACT WITHDRAWAL

Abstract Withdrawal Program #142 (Board #81) (Author Eleonora Presman)

Abstract Withdrawal Program #145 (Board #84) (Author Srinivas Annavarapu)

Abstract Withdrawal Program #95 (Board #34) (Author Andrey Gorin)

Abstract Withdrawal Program #65 (Board #4) Author Jin-Ryoun Kim)

## **NEW ABSTRACT**

### **Board #67 Partially folded equilibrium intermediate of the villin headpiece HP67 defined by $^{13}\text{C}$ relaxation dispersion**

Nichole O'Connell<sup>1</sup>, Michael Grey<sup>1</sup> Yuefeng Tang<sup>2</sup>, Pallav Kosuri<sup>1</sup>, Vesselin Miloushev<sup>1</sup>, Daniel Raleigh<sup>2</sup>, Arthur Palmer<sup>1</sup>

<sup>1</sup>Biochemistry & Molecular Biophysics, Columbia University, 650 W. 168th St., Black Building 511, New York, NY, 10032, <sup>2</sup>Department of Chemistry, State University of New York at Stony Brook, Stony Brook Rd., Stony Brook, NY, 11794

Identification and characterization of ensembles of intermediate states remains an important objective in describing protein folding in atomic detail. The 67-residue villin headpiece, HP67, consists of an N-terminal subdomain (residues 10-42) that transiently unfolds at equilibrium under native-like conditions and a highly stable C-terminal subdomain (residues 43-76). The transition between folded and unfolded states of the Nterminal domain has been characterized previously by  $^{15}\text{N}$  NMR relaxation dispersion measurements [Grey et al., *J. Mol. Biol.* (2006) **355**, 1078]. In the present work,  $^{13}\text{C}$  spin relaxation is used to further characterize backbone and hydrophobic core contributions to the unfolding process. Relaxation of  $^{13}\text{C}$  spins was measured using the Hahn echo technique at five static magnetic fields (11.7, 14.1, 16.4, 18.8, and 21.1 T) and the Carr-Purcell-Meiboom-Gill (CPMG) relaxation dispersion method at a static magnetic field of 14.1 T. Relaxation of methyl  $^{13}\text{C}$  spins was measured using CPMG relaxation dispersion experiments at static magnetic fields of 14.1 and 18.8 T. Results for  $^{13}\text{C}$  and  $^{15}\text{N}$  spins yielded a consistent model in which the partially unfolded intermediate maintains residual structure for residues near the unprotonated His41 imidazole ring and in the interface between the N- and C-terminal subdomains. In addition, a second faster process was detected that appears to represent local dynamics within the folded state of the molecule and is largely confined to the hydrophobic interface between the N- and C-terminal subdomain

## **NEW ABSTRACT**

### **Board #81 Structure and function of a bacterial organelle: proteins from the shell of the ethanolamine utilization microcompartment in *E. coli***

Shiho Tanaka<sup>1</sup>, Michael Sawaya<sup>2</sup>, Todd Yeates<sup>1,3</sup>

<sup>1</sup>DOE Institute for Genomics and Proteomics, <sup>2</sup>Howard Hughes Medical Institute, UCLA, 611 Charles Young Dr. East, Los Angeles, CA, 90095-1570, <sup>3</sup>Department of Chemistry and Biochemistry, UCLA, 611 Charles Young Dr. East, Los Angeles, CA, 90095-1569

Many bacteria produce intracellular microcompartments that serve as simple organelles for carrying out specific metabolic processes. These giant structures, roughly a thousand Angstroms across, are comprised of enzymes surrounded by a protein shell reminiscent of a viral capsid. Their structures and functions are only partly understood. Previous biochemical, genetic, and bioinformatic studies have identified a few different kinds of microcompartments dedicated to distinct metabolic functions across the bacterial kingdom. Different kinds of bacterial microcompartments encapsulate different enzymes, but in all cases their outer shells are composed primarily from a few thousand copies of proteins from the same conserved family of BMC-type proteins. Depending on the microcompartment, between three and seven BMC paralogs are present, apparently performing specialized architectural, biochemical or transport roles in the shell. In previous studies we have elucidated the structures of BMC proteins from the shell of the carboxysome, which is arguably the simplest microcompartment, encapsulating just two enzymes, carbonic anhydrase and RuBisCO, as part of a mechanism for enhancing CO<sub>2</sub> fixation in all cyanobacteria. The eut (ethanolamine utilization) microcompartment is a more complex organelle. It is present in common laboratory microbes such as *E. coli* and *Salmonella enterica*, where it serves to metabolize ethanolamine in a sequestered space inside the cell. Ethanolamine is metabolized by way of acetaldehyde, a volatile and potentially cytotoxic intermediate. The eut microcompartment provides a space inside which ethanolamine can be fully metabolized without release of acetaldehyde. There are most likely five or more proteins carrying out at least four enzymatic reactions inside. The eut microcompartment presents a paradox: bulky cofactors such as ado-B12 and coenzymeA must presumably cross the shell without allowing loss of small molecules (i.e. acetaldehyde). Precisely how this is accomplished is not understood, but the shell proteins must play key roles. We have crystallized all four of the BMC-type shell proteins (or parts thereof) from the eut microcompartment shell in *E. coli*. The structures provide new insights into shell architecture, conformational change, and gated transport through protein pores. Current findings will be reported.

## MONDAY – July 27

### NEW SPEAKER

#### CONCURRENT AFTERNOON SYMPOSIA #10 DYNAMIC COMPLEXES AND NETWORKS

*Haiyuan Yu*, Harvard Medical School will replace Marc Vidal for the following talk:

#### **Interactome Networks and Human Disease**

Time of Talk - 6:15 PM

### PRESENTER CHANGE

**Program #199 (Board #8) 5<sup>th</sup> Author Victor Naumov presenting**

**Program #166 (Board #105) 3<sup>rd</sup> Author Anthony Mittermaier presenting**

### POSTER RELOCATION

**Program #327 (Board #97) Author Kenneth Mills presenting (previously scheduled Tuesday, July 28)**

**Program #412 (Board #31) Author Marc Elsiger presenting (Topic: Accomplishments and Prospects of the NIH Protein Structure Initiative)**

### ABSTRACT WITHDRAWAL

**Abstract Withdrawal Program #222 (Board #31) (Author Gurcharan Kaur)**

**Abstract Withdrawal Program #288 (Board #97) (Author Stephanie Serniwnka)**

**Abstract Withdrawal Program #255 (Board #64) (Author Pavarthi Ramakrishnan)**

## TUESDAY – July 28

#### CONCURRENT MORNING SYMPOSIA #12 TRANSLOCATION AND TRANSPORTATION

9:00 AM – 12:15 PM

Salon F, 4<sup>th</sup> Floor

Session Chair: Linda Randall, *University of Missouri*

### PRESENTER CHANGE

**Program #388 (Board #66) 2<sup>nd</sup> Author Dooyoung Ahn presenting**

### ABSTRACT WITHDRAWAL

**Abstract Withdrawal Program #356 (Board #34) (Author Fei Xu)**

**Abstract Withdrawal Program #338 (Board #16) (Author Patrick McDevitt)**

**Abstract Withdrawal Program #357 (Board #35) (Author Daniel Hsieh)**

### NEW ABSTRACT

#### **Board #122 N-Myristoyl Transferase-Mediated Modification of the Protein N-Terminus**

Chethana Kulkarni, David Tirrell

Division of Chemistry and Chemical Engineering, Caltech, 1200 E. California Blvd., MC 210-41, Pasadena, CA, 91125

We are developing new methods for in vivo labeling of the protein N-terminus with the eukaryotic enzyme, N-myristoyl transferase (NMT). While NMT normally labels substrate proteins with a 14-carbon fatty acid (myristic acid), our lab and others have shown that it will tolerate reactive analogs, including an azide variant (12-azidododecanoic acid). Furthermore, NMT recognizes only the first 8-10 residues of most substrate proteins, and will thus modify proteins other than its substrates if they bear an appropriate recognition sequence. Through standard cloning methods, we have created a plasmid encoding green fluorescent protein (GFP) carrying the first nine residues of the Fyn protein, an NMT substrate. Bacterial co-expression of this Fyn-GFP construct and human NMT-2 in the presence of 12-azidododecanoic acid produces Fyn-GFP bearing an azide at its N-terminus in quantitative yield. Additionally, we have demonstrated that this method is both specific for the N-terminus and selective for a single protein, Fyn-GFP, in the presence of crude *E. coli* cell lysate. Currently, we are exploring bioconjugation applications of this approach to N-terminal protein modification; we are also initiating directed evolution experiments to create mutant NMTs with altered fatty acid and protein specificities.

## GRADUATE PROGRAM FAIR

**Date:** Sunday, July 26  
**Time:** 12:00 PM – 1:30 PM  
**Location:** Foyer, 4<sup>th</sup> Floor

### *ORGANIZATIONS IN ATTENDANCE*

**Boston University**  
**City of Hope Beckman Research**  
**Cold Spring Harbor Lab**  
**Johns Hopkins University**

**Johns Hopkins University Program in**  
**Molecular Biophysics**  
**UC San Diego**  
**University of Massachusetts, Amherst**  
**Yale University**

### **THE PROTEIN SOCIETY IS PLEASED TO ANNOUNCE** **THE RESULTS OF ITS 2009 ELECTION:**

#### **Councilors**

James Bowie (*University of California, Los Angeles*)  
Carol B. Post (*Purdue University*)  
Janet L. Smith (*University of Michigan*)

Three-year terms for the new officials commence on July 29, 2009, upon the close of the 23<sup>rd</sup> Annual Symposium of The Protein Society (July 25-29, 2009 in Boston), and continue until August 9, 2012, upon the close of the 26<sup>th</sup> Annual Symposium (August 5-9, 2012 in San Diego). The Society welcomes these new additions to its governance.

## **SPONSORS**

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*\*Funding for this conference was made possible (in part) by NIH Grant 1R13GM088990-01 from the National Institute of General Medical Sciences. The views expressed in written conference materials or publications and by speakers and moderators do not necessarily reflect the official policies of the Department of Health and Human Services; nor does mention by trade names, commercial practices, or organizations imply endorsement by the U.S. Government.*

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The Protein Society acknowledges the 2009 Corporate Members for their continued generosity

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The Protein Society acknowledges the generous support of its Award sponsors

*The Carl Brändén Award*, Rigaku Corporation  
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*The Stein and Moore Award*, The Protein Society  
*The Hans Neurath Award*, The Hans Neurath Foundation  
*The Christian B. Anfinsen Award*, The Aviv Family Foundation  
*The Emil Thomas Kaiser Award*, The Protein Society and Dr. Bonnie Kaiser  
*The Irving Sigal Young Investigator Award*, The Merck Research Laboratories  
*The Student Poster Awards*, Eli Lilly and Company

## ***The 2009 Finn Wold Travel Award Contributors as of July 9, 2009***

*The Protein Society acknowledges these individuals for their support for the 2009 Finn Wold Travel Awards*

### **Mrs. Finn Wold**

**Dr. Spencer Anthony-Cahill**, Western Washington University  
**Dr. Leonard Banaszak**, University of Minnesota  
**Dr. Linda Chapman**, University of Missouri, Columbia  
**Dr. David P. Goldenberg**, University of Utah  
**Dr. Blake Hill**, Johns Hopkins University  
**Dr. Susan Marqusee**, University of California, Berkeley  
**Dr. Marie-Claire McKenna**, Siemens Medical Solutions Diagnostics  
**Dr. C. James McKnight**, Boston University School of Medicine  
**Dr. Arthur G. Palmer**, Columbia University  
**Dr. Daniel P. Raleigh**, SUNY, Stony Brook  
**Dr. George D. Rose**, Johns Hopkins University  
**Dr. Madeline A. Shea**, University of Iowa  
**Dr. Charles W. Sokolik**, Denison University  
**Dr. Cynthia V. Stauffacher**, Purdue University  
**Dr. Donald F. Steiner**, University of Chicago  
**Dr. Marc S. Wold**, University of Iowa  
**Dr. Beulah M. Woodfin**, University of New Mexico

## EXHIBIT ADDENDUM

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### **RELOCATION**

FiberCell Systems Inc. moved to **Booth 100**

### **EXHIBITOR**

• **Pressure BioSciences, Inc.**                      **Booth 211**

Norfolk Avenue

South Easton, MA 02375

Phone: 508 230-1828

Fax: 508 230-1829

Web: [www.pressurebiosciences.com](http://www.pressurebiosciences.com)

Email: [info@pressurebiosciences.com](mailto:info@pressurebiosciences.com)

Pressure BioSciences, Inc. (PBI) markets products based on pressure cycling technology (PCT). PCT uses alternating cycles of ambient and high pressure to control molecular interactions, including the safe, rapid, and reproducible extraction of DNA/RNA/proteins/small molecules from a wide variety of cells and tissues, and the significant acceleration of protein digestion.

## EXHIBITOR WORKSHOP

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### **NEW TITLE AND DESCRIPTION**

**Sunday, July 26**

#### **Novel Dip and Read™ Platform for ELISA and Label-Free Kinetic Characterization**

FortBio, Inc.

1360 Willow Road, Suite 201

Menlo Park, CA 94025

Phone: 650 322-1360 Fax: 650 322-1360

Web: [www.fortebio.com](http://www.fortebio.com)

12:00 Noon – 1:00 PM – Salon C/D

**Presenter:** Sriram Kumaraswamy, Ph..D., ForteBio, Inc.

Abstract: Fortebio's Octet platform provides instruments, biosensors, reagents and assay kits for biomolecular interactions analysis in 96- and 384-well microplate format. These systems utilize proprietary Biolayer Interferometry (BLI) to enable real-time, label-free and accurate determination of affinity, kinetics and concentration. The Octet platform enables hands-free multi-step ELISA assays within 15 minutes versus 3-4 hours for traditional methods.

## EXHIBITOR WORKSHOP

**Tuesday, July 28**

### **Characterizing Proteins, Macromolecules and Nanoparticles using Various Types of Light Scattering**

Brookhaven Instruments Corporation  
750 Blue Point Road  
Holtsville, NY 11742  
Phone: 631 758-3200  
Web: [www.bic.com](http://www.bic.com)

12:00 Noon – 1:00 PM – Salon B

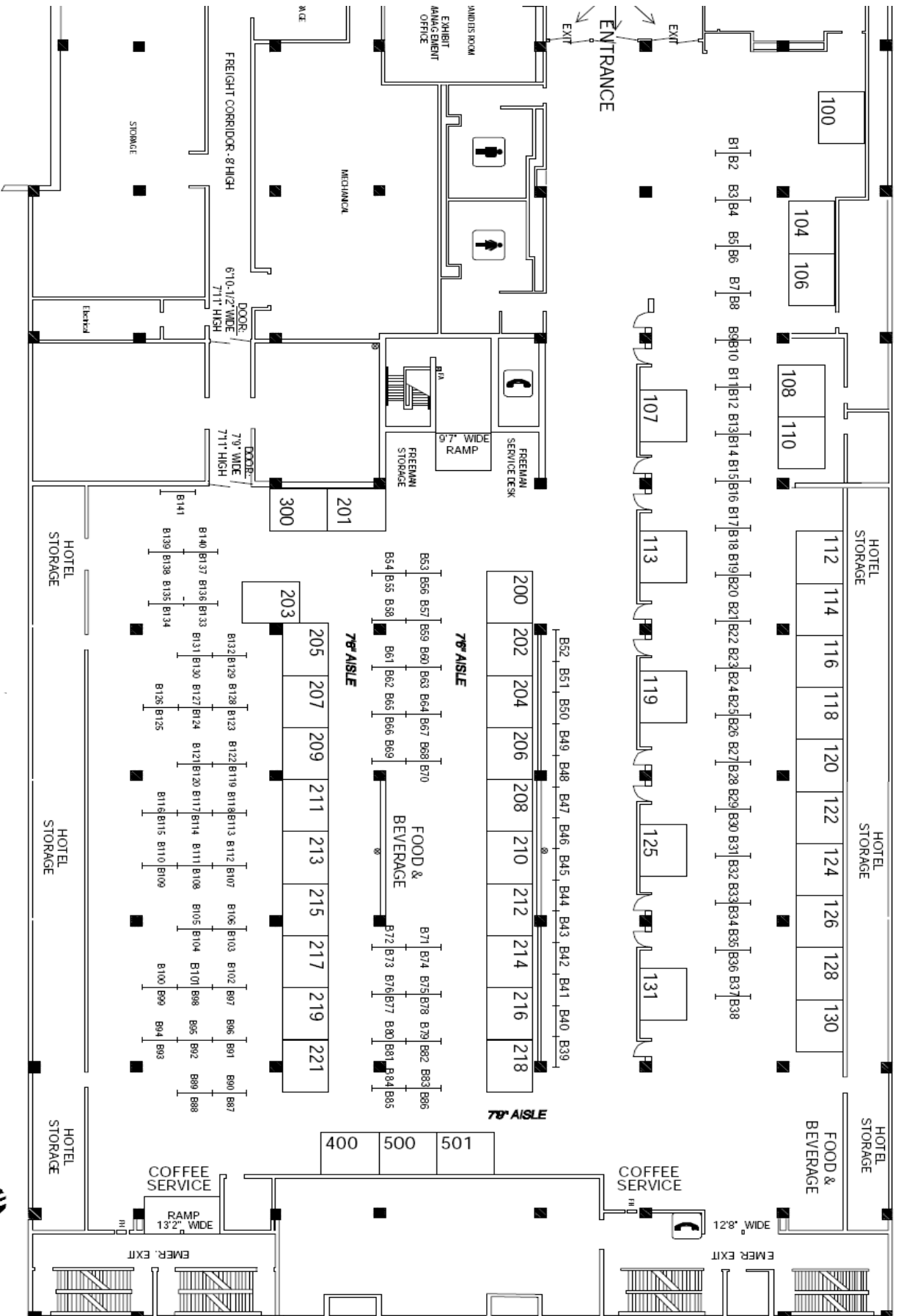
**Presenter:** Ian M. Herzberg, Ph.D.

Light scattering techniques can be used to characterize fundamental properties of suspended particles and dissolved macromolecules, including size, molecular weight, and charge. The techniques available for these applications include dynamic and static light scattering, and electrophoretic and/or phase analysis light scattering. Several of these techniques can be applied to proteins in batch or chromatographic modes. This workshop will present an introduction to the theoretical basis for these techniques, and include a discussion of practical aspects of their application, citing relevant examples of the use of Brookhaven Instruments' equipment for studies of protein conformation, assembly and aggregation.

#### **Disclaimer**

Participation in the Exhibits Program does not constitute an endorsement by the participating societies of the claims, products, or services offered

# EXHIBIT HALL FLOORPLAN



The Protein Society  
 July 25 – 29, 2009  
 Back Bay Exhibit Hall, 3<sup>rd</sup> Floor  
 Boston Marriott Copley Place, Boston, MA  
 Revised July 2, 2009

