

Meeting Organizer:

Patricia L. Clark, *University of Notre Dame*

Program Committee:

Connie Jeffery, *University of Illinois at Chicago*

Lisa Lapidus, *Michigan State University*

Conference Venue:

Notre Dame Conference Center

McKenna Hall

University of Notre Dame

574-631-6691

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Department of Chemistry & Biochemistry, University of Notre Dame
Thomas R. Kissel Endowment for Excellence in Chemistry

12th Midwest Conference on Protein Folding, Assembly and Molecular Motions

Notre Dame Conference Center – McKenna Hall – University of Notre Dame

April 29, 2017

8:00 – 8:55 *Coffee, juice, and pastries*

8:55 – 9:00 *Opening Remarks* – Patricia L. Clark

Binding and Catalysis

Chair: Brendan Mahoney, Peng Laboratory

9:00 – 9:20 *Bringing mutant enzymes back to life: restoring structure to restore function*
Shahir S. Rizk¹, Somnath Mukherjee², Akiko Koide^{3,4}, Shohei Koide^{2,3,5} and
Anthony A. Kossiakoff²

¹Department of Chemistry and Biochemistry, Indiana University South Bend, Department of
Biochemistry and Molecular Biology, Indiana University School of Medicine, South Bend,
²Department of Biochemistry and Molecular Biology, University of Chicago, ³Perlmutter Cancer
Center, New York University Langone Medical Center, New York, ⁴Department of Medicine,
New York University School of Medicine, New York, ⁵Department of Biochemistry and
Molecular Pharmacology, New York University School of Medicine, New York

9:20 – 9:40 *Human Miro 1/2 GTPase structures suggests ligand binding domains are
required for proper folding and Parkin ubiquitin ligase recognition*

Kyle P. Smith¹, Julian L. Klosowiak¹, Pamela J. Focia², Sungjin Park¹, Srinivas
Charkravarthy³, Cheng-Tsung Lai⁴, Sarah E. Rice¹, Douglas M. Freymann²

¹Department of Cell & Molecular Biology, Northwestern University; ²Department of
Biochemistry & Molecular Genetics, Northwestern University; ³Biophysics Collaborative Access
Team, Advanced Photon Source, Argonne National Laboratory; ⁴Department of Chemistry,
Northwestern University

9:40 – 10:00 *Live-cell RNA-protein binding affinity and kinetics by fast relaxation imaging*
Caitlin M. Davis, Irisbel Guzman, David Gnutt and Martin Gruebele

Center for the Physics of Living Cells, University of Illinois, Urbana, IL 61801

10:00 – 10:20 *Reconstitution of ATP-dependent membrane protein degradation in phospholipid
bicelles*

Yiqing Yang¹, Miyeon Kim¹, Ruiqiong Guo¹, Kristen Gaffney² and Heedeok
Hong^{1,2}

¹Department of Chemistry & ²Department of Biochemistry and Molecular Biology, Michigan
State University, East Lansing, MI 48824

10:20 – 10:50 *Coffee Break*

Proteins *In Vivo*

Chair: Shahar Sukenik, Gruebele Laboratory

10:50 – 11:10 *Developing Realistic Simulations of Co-translational Protein Folding*

Ian M. Walsh¹, Shuxiang Li², Adrian H. Elcock² & Patricia L. Clark¹

¹Department of Chemistry and Biochemistry, University of Notre Dame, Notre Dame, IN 46656;

²Department of Biochemistry, University of Iowa, Iowa City, IA 52242

11:10 – 11:30 *Stress-triggered phase separation, tuned by unusual features of an intrinsically disordered region, promotes cellular fitness during stress*

Joshua Riback¹, Chris Katanski², Jamie L. Kear-Scott², Tobin R. Sosnick^{2,3}, D. Allan Drummond²

¹Graduate Program in the Biophysical Sciences, University of Chicago; ²Department of Biochemistry and Molecular Biology, University of Chicago; ³Institute for Biophysical Dynamics, University of Chicago

11:30 – 11:50 *MspI is a membrane protein dislocase for tail-anchored proteins*

Matthew L. Wohlever, Agnieszka Mateja, Philip T. McGilvray, Kasey J. Day, Robert J. Keenan

Department of Biochemistry and Molecular Biology, The University of Chicago, 929 East 57th Street, Chicago, IL 60637

11:50 – 1:20 *Lunch*

1:20 – 3:00 *Poster Session*

Protein Motions and Assemblies

Chair: Chris Katanski, Drummond Laboratory

3:00 – 3:20 *Dynamical and structural differences in apo and inhibitor-bound neurolysin revealed by molecular dynamics and machine learning*

Arzu Uyar^a, Vardan Karamyan^b and Alex Dickson^{a,c}

(a) Department of Biochemistry and Molecular Biology, Michigan State University, East Lansing, MI, 48824; (b) Department of Pharmaceutical Sciences, School of Pharmacy, Texas Tech University Health Sciences Center, Amarillo, TX, 79106; (c) Department of Computational Mathematics, Science and Engineering, Michigan State University, East Lansing, MI, 48824

3:20 – 3:40 *The Transthyretin-Related Protein of Escherichia coli as a Potential Modulator of Functional Amyloid Formation*

Maya Deshmukh, Margery L. Evans, Neha Jain, Matthew R. Chapman

Department of Molecular Cellular and Developmental Biology, University of Michigan, Ann Arbor, Michigan

3:40 – 4:00 *Multisite λ Dynamics Enables Efficient Calculation of Mutational Folding Free Energy in T4 Lysozyme*

Ryan L. Hayes and Charles L. Brooks III

Department of Chemistry, University of Michigan, Ann Arbor, Michigan

- 4:00 – 4:20 *Coffee Break*
- 4:20 – 4:40 *Insights into the Mechanism of Cystatin C Oligomer and Amyloid Formation and its Interaction with Beta-Amyloid*
Tyler J. Perlenfein, Jacob D. Mehlhoff, Regina M. Murphy
Department of Chemical and Biological Engineering, University of Wisconsin, Madison, WI 53706
- 4:40 – 5:10 **Closing Plenary Speaker:**
Designing highly specific allosteric biosensors of small molecules
Vatsan Raman
Departments of Biochemistry & Bacteriology, University of Wisconsin, Madison, WI
- 5:10 – 5:15 *Closing Remarks – Connie Jeffery*
- 5:15 – 6:30 *Closing Reception*