
October 3, 2020
6 pm – 8:15 pm CDT (UTC -5)

Virtual Saturday Night Thermo
Event for trainees only

(the Zoom link for this session will be sent separately to all who registered for SNT)

Organizers:

Kacey Mersch, University of Iowa
Ari Paiz, UT-Southwestern
Vince J. LiCata, Louisiana State University
Susan Pedigo, University of Mississippi

Moderators:

Kacey Mersch, University of Iowa
Ari Paiz, UT-Southwestern

6:00 – 7:00 pm **Flash Talks**

- 1. Tradeoff between Thermostability and DNA-binding Function in Engineered Variants of EnHD**
Lily Schumacher ([McCully Lab](#)), Santa Clara University
- 2. Domain Interactions Determine the Conformational Ensemble of SurA**
Mathis Leblanc ([Fleming Lab](#)), Johns Hopkins University
- 3. Conformational analysis of the structural ensemble of the SARS-CoV-2 nucleocapsid protein**
Jasmine Cubuk ([Soranno Lab](#)), Washington University in St. Louis
- 4. Development of a Thiol Exchange- and Mass Spectrometry-Based Technique for the Evaluation of Protein Folding Stabilities**
Aurora Cabrera ([Fitzgerald Lab](#)), Duke University
- 5. Pressure Effects on the Conformational Transitions of tRNA^{Lys3}**
Jinqiu Wang ([Royer Lab](#)), Rensselaer Polytechnic Institute
- 6. Composition-dependent thermodynamics of intracellular phase separation**
Joshua Riback ([Brangwynne Lab](#)), Princeton University

Short Break

7:15 – 7:45 pm **Career Panel**

- 7. Jackie Thompson Dillon, Ph.D.**
Associate Scientific Manager at Benson Hill
- 8. Alexandra Schnoes, Ph.D.**
Associate Director of Career and Professional Development iBiology, Inc.
- 9. Donald M. Engelman, Ph.D.**
Chairman of the Scientific Advisory Board of pHILIP, inc.
Eugene Higgins Professor of Molecular Biophysics and Biochemistry, Yale University

7:45 – 8:15 pm **Career Panel Q&A and open discussion**

8:15 – **Open mixer**

Sunday ♦ October 4, 2020
1 pm – 5 pm CDT (UTC -5)

- 12:40 pm **Zoom link goes live**
- 1:00 – 1:05 pm **Opening Comments by Organizers**
- 1:05 – 1:10 pm **President's Welcome by Kathleen Hall, Washington University Saint Louis**

12th Annual Gary K. Ackers Lecture

- 1:10 – 1:20 pm **Introduction to the Gary K. Ackers Lecture in Biothermodynamics**
Bertrand García-Moreno, Johns Hopkins University
- 1:20 – 2:10 pm **12th Annual Gary K. Ackers Lecture**
Using statistical thermodynamics to understand protein stability and bioinformatics
Doug Barrick, Johns Hopkins University
- 2:10 – 2:20 pm **Ackers Lecture Q&A**
- 2:20 – 2:25 pm **Short Break**

Session I

- Moderator Drake Jensen, [Galburt Lab](#), Washington University Saint Louis
Co-moderator Ryan Mahling, [Shea Lab](#), University of Iowa
- 2:25 – 2:45 pm **Unusual van't Hoff and Arrhenius Barriers to Steps of Transcription Initiation at the \square PR Promoter**
Dylan Plaskon, [Record Lab](#), University of Wisconsin-Madison
- 2:45 – 3:05 pm **Energetic dependencies dictate folding mechanism in a complex protein**
Xiuqi Chen, [Kaiser Lab](#), Johns Hopkins University
- 3:05 – 3:35 pm **Protein Folding and Aggregation in the Cellular Environment**
[Silvia Cavagnero](#), University of Wisconsin-Madison

- 3:35 – 3:40 pm **Short Break**

Session II

- Moderator Michael Baxa, [Sosnick Lab](#), University of Chicago
Co-moderator Mayank Boob, [Gruebele Lab](#), University of Illinois at Urbana-Champaign
- 3:40 – 4:00 pm **How is phase behavior encoded in the sequence of low-complexity domains?**
Anne Bremer, [Mittag Lab](#), St. Jude Children's Research Hospital
- 4:00 – 4:20 pm **Prolyl isomerase Ess1 engages bivalent RNAPII CTD substrates in a length-dependent manner**
Tongyin Zheng, [Castañeda Lab](#), Syracuse University
- 4:20 – 4:50 pm **Understanding functions of dysfunctional proteins**
[Elizabeth Rhoades](#), University of Pennsylvania
- 4:50 – 5:00 pm **Concluding remarks for the day**
- 5:15 – 6:00 pm **Virtual Social.** *A separate Zoom meeting link will be provided via email to all registrants. Breakout rooms will be set up for discussion.*
- 7:00 – 9:00 pm **Virtual Posters.** *See page 10 for details.*

Monday ♦ October 5, 2020
1 pm – 5 pm CDT (UTC -5)

12:40 pm **Zoom link goes live**

1:00 – 1:10 pm **Announcements**

Session III

Moderator Emery Usher, [Showalter Lab](#), Penn State University
Co-moderator Melissa Stuchell-Brereton, [Soranno Lab](#), Washington University Saint Louis

1:10 – 1:30 pm **Exploring the biophysics of protein-surface interactions**

Gabriel Ortega, [Plaxco Lab](#), University of California Santa Barbara

1:30 – 1:50 pm **Thousand-fold nearest-neighbor cooperativity in ligand binding by the dodecameric ring-shaped gene-regulatory protein, Bha TRAP**

Weicheng Li, [Foster Lab](#), The Ohio State University

1:50 – 2:20 pm **Examining equilibria through conformational ensembles**

Lisa Warner, Boise State University

2:20 – 2:25 pm **Short Break**

Session IV

Moderator Robb Welty, [Walter Lab](#), University of Michigan
Co-moderator Miranda Mecha, [Cavagnero Lab](#), University of Wisconsin

2:25 – 2:45 pm **MELD-Bracket: May the best ligand win!**

Emiliano Brini, [Dill Lab](#), Stony Brook University

2:45 – 3:05 pm **Peptide Anchor Modification Allosterically Modulates T Cell Recognition in a TCR Dependent Fashion**

Angela R. Smith, [Baker Lab](#), University of Notre Dame

3:05 – 3:35 pm **Biophysics at DOE National Labs**

Nathan Baker and Wendy Shaw, Pacific Northwest National Laboratory

3:35 – 3:40 pm **Short Break**

34th Annual Gibbs Conference Keynote Lecture

3:40 – 3:50 pm **Introduction to the 34th Annual Gibbs Conference Keynote Speaker**

Timothy Lohman, Washington University Saint Louis

3:50 – 4:40 pm **Keynote Lecture**

But does it bind? RNA, proteins, and salt

[Kathleen Hall](#), Washington University Saint Louis

4:40 – 4:50 pm **Keynote Q&A**

4:50 – 5:00 pm **Closing Remarks by Organizers and President, Liskin Swint-Kruse, University of Kansas Medical Center**

5:15 – 6:00 pm **Virtual Social.** *A separate Zoom meeting link will be provided via email to all registrants. Breakout rooms will be set up for discussion.*

7:00 – 9:00 pm **Virtual Posters.** *See page 10 for details.*

◆ **Virtual Posters** ◆
Sunday, October 4 and Monday, October 5, 2020
7 pm – 9:30 pm CDT (UTC -5)

Organizers:

Jim Horn, Northern Illinois University
Lydia Kisley, Case Western Reserve University
Ashley De Lio, University of Illinois at Urbana-Champaign
Suman Shrestha, University of Texas at Arlington

Virtual Posters will be presented in Zoom breakout rooms. Sessions I and II will be held on Sunday evening and will feature posters from presenters with last names P to Z; Session I will also feature posters from presenters who are nearing graduation and seeking postdoctoral positions. Sessions III and IV will be held on Monday evening and will feature posters from presenters with last names A to O. Both nights will start at 7:00 pm and conclude at 9:30 pm, with the first session running from 7:00-8:30 and the second session running from 8:00-9:30 pm. Details about how to join the poster session during Gibbs34 will be sent to all conference registrants.

Poster Session I (Posters 1 - 19)

October 4, 2020

7 pm – 8:30 pm CDT (UTC -5)

Presenting Authors: Job Seekers (**, students looking for a postdoc)
and Last Names Starting with Y to Z

- 1** Syeda Tajin Ahmed
Design rules for tuning protein adsorption on grafted zwitterionic thin films
- 2** Mayank Boob
TMAO: protecting proteins from feeling the heat
- 3** Aurora Cabrera
Development of a Thiol Exchange- and Mass Spectrometry-Based Technique for the Evaluation of Protein Folding Stabilities
- 4** Ellen Gagliani
A Drosophila model of Adams-Oliver Syndrome reveals Notch cofactor titration as a mechanism underlying developmental defects
- 5** Pooja Goswami
Potential G1/S Transcription Factor Feedback Loop in the Start Transition of Budding Yeast Probe by Scanning Number and Brightness
- 6** Taranpreet Kaur
Regulation of Interactions at the Surface Dictates Multi-phasic Architecture of Protein-RNA condensates
- 7** Aaron Morgan
Kinetics of Nucleotide Binding to the gp16 ATPase
- 8** Cristian M Pis Diez
Persulfide-sensing in a dithiol-based transcriptional regulator impair DNA-binding by the formation of a tetrasulfide crosslink with minor structural perturbation
- 9** Meredith Rickard
The Impact of Local Environment on Simulated Metabolite Conformations
- 10** Suman Shrestha
Evolutionary changes in caspase folding landscape

11. Yanxing Yang
Binding of amyloid peptides to lipid bilayers: effects of ions and lipid content
- 12** Liqi Yao
The Evolution and Mechanism of Enzyme Specificity in Caspase-3
- 13 Alexander Yarawsky
*Determining the mechanism of the Zn-mediated assembly of a functional amyloid-forming protein from *Staphylococcus epidermidis**
- 14 Shawn Yoshida
Characterizing the simulated anomalous diffusion of proteins in relation to the nanoporous structure of extracellular matrix-relevant hydrogels
- 15 Feng Yu
The Dimensions of Intrinsically Disordered Proteins Determine their Solution Sensitivity
- 16 Yafan Yu
*The structural basis for natural competence in *Acinetobacter**
- 17** Yifan Zhang
*Iron acquisition by *Streptococcus pneumoniae*: PiuA specifically recognizes tetradentate catechol FeIII complexes*
- 18 Siwen Zhang
Probing pressure effects on core packing of a repeat protein using ¹³C-1H NMR
- 19** Xinji Zhu
Salt Dependence of the Stability of a Psychrophilic DNA Polymerase

Poster Session II (Posters 20 - 39)

October 4, 2020

8 pm – 9:30 pm CDT (UTC -5)

Presenting Authors: Last Names Starting with P to W

- 20 Niyati Patel
Using VHH Single Domain Antibodies as Modules for Protein Thermostability Enhancement
- 21 Marko Popovic
A thermodynamic insight into viral infections: do viruses in a lytic cycle hijack cell metabolism due to their low Gibbs energy?
- 22 Julien Roche
Thermodynamic stability of hnRNP A1 low complexity domain revealed by high-pressure NMR
- 23 Riya Samanta
Investigation of an Allosteric Mechanism from an Evolutionary Perspective
- 24 Emma Schoch
Stabilization of Dimeric Fbxw7 by Fusion to its Binding Partner Skp1
- 25 Lily Schumacher
Tradeoff between Thermostability and DNA-binding Function in Engineered Variants of EnHD
- 26 Catherine Scull
Co-transcriptional folding of riboswitches
- 27 Sambuddha Sen
*Characterization of a H₂S stress regulator FisR from *Acinetobacter baumannii**

- 28 Hossain Shadman
A Comparison of the Structural Features of Mammalian and Fish Protamines: a Molecular Dynamics Simulation Study
- 29 Corinne Soutar
Amphotericin B Interactions with Cell Membrane Sterols Revealed by Solid-State NMR
- 30 Helena Spikes
Group 14 Metallfluorenes as Solvatochromic Probes of Membrane order
- 31 Grace Sullivan
Unfolding Thermodynamics of an Intramolecular DNA Kissing Complex
- 32 Sydney Tippelt
How Hox Proteins Regulate DNA Binding
- 33 Eric Tomko
Functional distinctions between human and yeast TFIIH kinase modules and XPB/Ssl2 dsDNA translocase
- 34 Matias Villarruel
Characterization of the interaction between a truncated hemoglobin and membranes in Mycobacterium tuberculosis
- 35 Yuhan Wang
Quantifying protein-protein binding interaction in vitro and in cells
- 36 Jinqiu Wang
Pressure Effects on the Conformational Transitions of tRNALys3
- 37 Jordan Webb
Structural Characterization of a Novel Interaction Between the Coregulator NCoA1 and the Notch Transcriptional Activation Complex
- 38 Chamitha Weeramange
The Cra-FruK complex alters regulation of central metabolism of γ -proteobacteria
- 39 Riley Workman
Conformational entropies of aqueous and condensed-phase glycine-rich pentapeptides following liquid liquid phase separation

Poster Session III (Posters 40 – 58)

October 5, 2020

7 pm – 8:30 pm CDT (UTC -5)

Presenting Authors: Last Names Starting with J to O

- 40 Amanda Jons
Immobilizing Split GFP Biosensors in Protein Materials: Salt Tunes Analyte Binding and Release
- 41 Grant Keller
Determinants of Antigenicity in Tumor Neopeptides for the Development of Personalized/Multiple Peptide Vaccines
- 42 Irine Khutsishvili
Unfolding Thermodynamics of an RNA Pseudoknot and its DNA Analogs
- 43 Tom Laue
IgG Charge

- 44 Patrick Laughlin
Redirecting Self-Assembly of a Virus Capsid: Capsid Assembly Modifiers Stabilize Hexameric Lattice while Destabilizing Native Icosahedral Symmetry
- 45 Tosha Laughlin
Engineering Multidirectional pH Dependent Protein-Ligand Interactions using Ionizable Triggers Within a Linked Dimer Interface
- 46 Taeho Lee
Temperature Dependency of CLC-ec1 dimerization in membranes
- 47 Josephine Liess
Structure and Function of Clostridium perfringens Type IV Pili
- 48 Jiaqi Ma
Dynamic allostery controls the peptide sensitivity of the Ly49C natural killer receptor
- 49 Upasana Mallimadugula
A Parallel Ratchet-Stroke Mechanism Leads to an Optimum Force for Molecular Motor Function
- 50 Justin Marsee
Assessing the Classification of putative PHB depolymerase from B. paraperthus
- 51 Meranda Masse
Contribution of nascent polypeptides of increasing length to the apparent stability of the bacterial ribosome
- 52 Miranda Mecha
Optimal prevention of aggregation is achieved when client proteins fold on the surface of the Hsp70 chaperone: a computational study
- 53 Alexander Meyer
Structure and Function of Clostridium perfringens Type IV Pili
- 54 Pinaki Misra
Early events in light chain aggregation at physiological pH reveal new insights on assembly, stability, and aggregate dissociation
- 55 Tushar Modi
Information propagation in time through allosteric signaling
- 56 David Moses
Probing the Hidden Sensitivity of Intrinsically Disordered Proteins
- 57 Sarah Mosure
Structural basis for heme-dependent NCoR binding to the transcriptional repressor REV-ERB β
- 58 Kari Olson
The Energetic and Structural Characterization of Dystrophin Spectrin Repeats

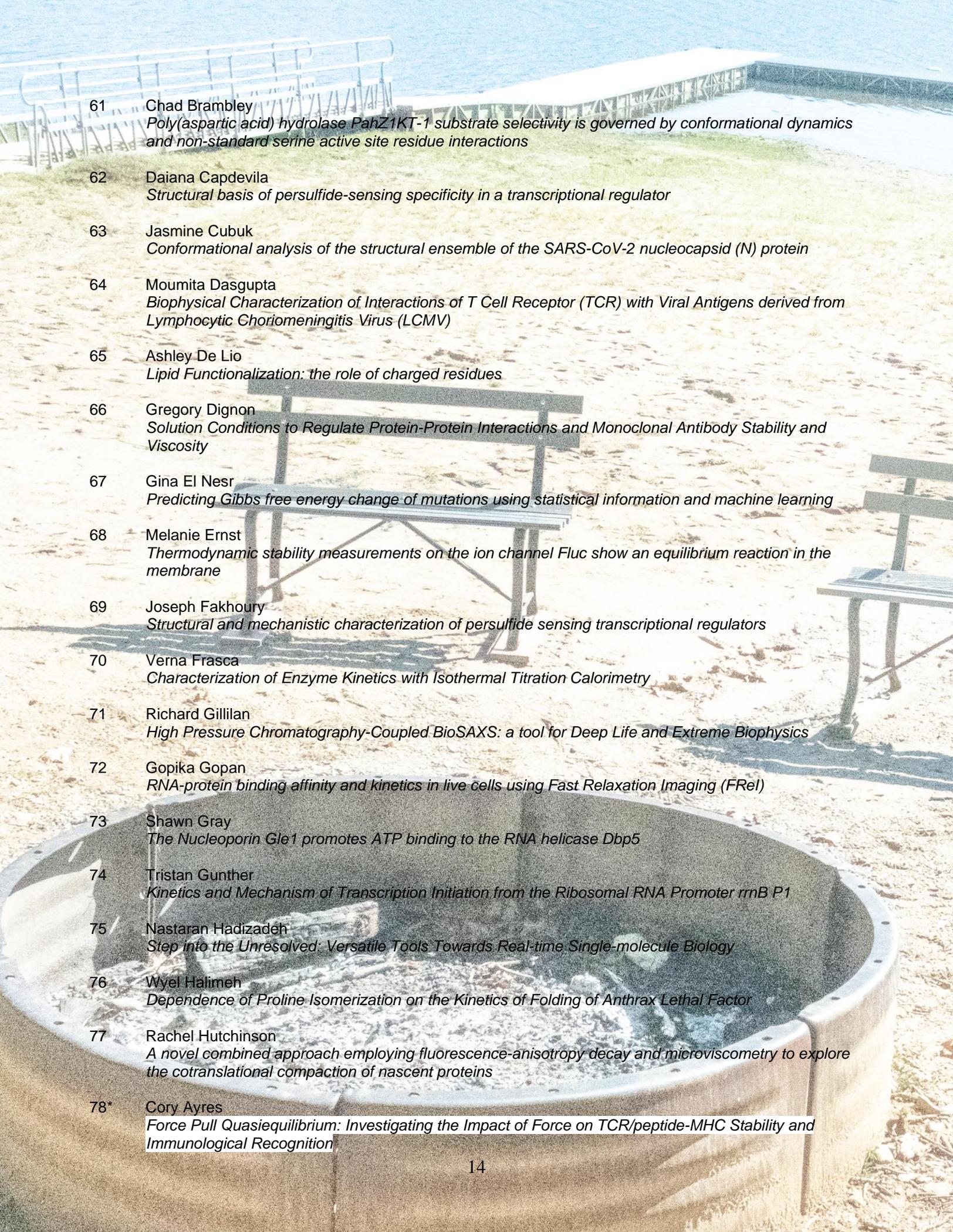
Poster Session IV (Posters 59 - 80)

October 5, 2020

8 pm – 9:30 pm CDT (UTC -5)

Presenting Authors: Last Names Starting with A to H and late-breaking posters

- 59 Ibraheem Alshareedah
Phase transition of RNA-protein complexes into ordered permeable hollow condensates
- 60 Jhullian Alston
Phase separation propensity of the SARS-CoV-2 nucleocapsid protein

- 
- 61 Chad Brambley
Poly(aspartic acid) hydrolase PahZ1KT-1 substrate selectivity is governed by conformational dynamics and non-standard serine active site residue interactions
- 62 Daiana Capdevila
Structural basis of persulfide-sensing specificity in a transcriptional regulator
- 63 Jasmine Cubuk
Conformational analysis of the structural ensemble of the SARS-CoV-2 nucleocapsid (N) protein
- 64 Moumita Dasgupta
Biophysical Characterization of Interactions of T Cell Receptor (TCR) with Viral Antigens derived from Lymphocytic Choriomeningitis Virus (LCMV)
- 65 Ashley De Lio
Lipid Functionalization: the role of charged residues
- 66 Gregory Dignon
Solution Conditions to Regulate Protein-Protein Interactions and Monoclonal Antibody Stability and Viscosity
- 67 Gina El Nesr
Predicting Gibbs free energy change of mutations using statistical information and machine learning
- 68 Melanie Ernst
Thermodynamic stability measurements on the ion channel Fluc show an equilibrium reaction in the membrane
- 69 Joseph Fakhoury
Structural and mechanistic characterization of persulfide sensing transcriptional regulators
- 70 Verna Frasca
Characterization of Enzyme Kinetics with Isothermal Titration Calorimetry
- 71 Richard Gillilan
High Pressure Chromatography-Coupled BioSAXS: a tool for Deep Life and Extreme Biophysics
- 72 Gopika Gopan
RNA-protein binding affinity and kinetics in live cells using Fast Relaxation Imaging (FRel)
- 73 Shawn Gray
The Nucleoporin Gle1 promotes ATP binding to the RNA helicase Dbp5
- 74 Tristan Gunther
Kinetics and Mechanism of Transcription Initiation from the Ribosomal RNA Promoter rrnB P1
- 75 Nastaran Hadizadeh
Step into the Unresolved: Versatile Tools Towards Real-time Single-molecule Biology
- 76 Wyel Halimeh
Dependence of Proline Isomerization on the Kinetics of Folding of Anthrax Lethal Factor
- 77 Rachel Hutchinson
A novel combined approach employing fluorescence-anisotropy decay and microviscometry to explore the cotranslational compaction of nascent proteins
- 78* Cory Ayres
Force Pull Quasiequilibrium: Investigating the Impact of Force on TCR/peptide-MHC Stability and Immunological Recognition

79* Stephen Fried
Non-Refoldability is Pervasive across the E. coli Proteome

80* Paul Campitelli
Substitutions at Non-Conserved Rheostat Positions Modulate Function by Re-Wiring Long-Range, Dynamic Interactions

81* Mathis Leblanc
Domain interactions determine the conformational ensemble of the periplasmic chaperone SurA

* Late-Breaking Poster

