Shake, Rattle, and Roll **Virus Dynamics Workshop**

April 17 DLR 131 @ 10am – 3pm \rightarrow MRGN 121 3:30pm – 5pm



Purdue Institute of Inflammation, Immunology and Infectious Disease

KEYNOTE PRESENTATION Ganesh Anand

Penn State, Eberly College of Science



INVITED SPEAKERS





Washington

Ted Pierson

NIH, VRC

Rob Stahelin Purdue University





Laren Ann Metskas Purdue University



Adam Zlotnick Indiana Universitv



Carol Post Wen Jiang Purdue University



Marc Morais Indiana University Purdue University

Purdue University



Virus breathing, metastability and epitope dynamics by integrative mass spectrometry and cryo-EM

RNA viruses are metastable macromolecular assemblies that respond to environmental changes through dynamic breathing motions. Cryo-Electron Microscopy and Amide hydrogen/exchange mass spectrometry (HDXMS) offer powerful insights into dynamics of whole viral particles in solution. I will describe dynamics of viral surface regions and core ribonucleoprotein in two model viruses: Dengue and Turnip Crinkle Virus (TCV). We have identified a broad neutralizing antibody, C10 that induces altered 'breathing' dynamics in dengue viral particles and shows unique stoichiometry-specific responses. Deconvolution analysis of HDXMS has enabled us to identify residues on the surface that mediate altered interraft and intraraft interactions at different temperature perturbations and C10 stoichiometries. Cryo-EM of expanded TCV reveals strong interactions between the capsid proteins and the RNA genome correspond to asymmetric ribonucleoprotein core packing observed near a unique 5-fold vertex in the expanded particle, which is the specific point of egress for the genomic RNA into the host. Our results highlight an active role of genomic RNA-protein core as environmental sensors and controlling capsid uncoating and RNA release inside hosts. A combination of HDXMS and cryo-EM has been invaluable in uncovering the significance of essential asymmetries in icosahedral virus assemblies. I will conclude my talk by sharing our insights into Spike dynamics across the SARS-CoV-2 variants and share perspectives on integration of biophysical insights of viruses with antibody recognition.