BIOCHEMISTRY SEMINAR

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"Identifying protein misfolding inhibitors through directed evolution"

Abstract: Protein folding is an essential process for both basic biology and biotechnology. Impaired folding of a protein will pose barriers to its engineering and utility; misfolding is also associated with numerous diseases. My research group builds tools to study protein (mis)folding through high throughput frameworks and apply these tools to identify agents that promote the folding or inhibit the misfolding of a target protein. I will describe our recent efforts to use genetically encoded biosensors to study the aggregation of amyloid proteins and to identify both cyclic peptides and antibody mimetics that bind to different species generated in the amyloid aggregation cascade.

Bio: Tina is a native of Rochester, NY and received her B.S. in chemistry at Caltech, where worked in the labs of Robert Grubbs and John D. Roberts. She completed her PhD at Yale University with David A. Spiegel, where she developed chemical tools to study protein glycation. She then joined David R. Liu's lab at the Broad Institute for her postdoctoral studies, where she worked on developing phage-assisted continuous evolution methods for evolving proteins with improved soluble expression. Tina joined the Department of Chemistry at UW–Madison in the fall of 2019, where she is currently an Assistant Professor. Her research group focuses on studying protein folding using synthetic biology and protein engineering approaches.