UMD Department of Chemistry & Biochemistry
Fall 2020 Seminar Series
Friday, October 2, 2020
3:00 p.m. Remote

Dr. Katie Dunleavy

Postdoctoral Fellow, West Virginia University
host: Dr. Anne Hinderliter

Hydration Environment Characterizations of the Folding of IA3, an Intrinsically Disordered Protein

The intrinsically disordered protein (IDP), IA3, found in Saccharomyces cerevisiae has been previously shown to adopt α-helical secondary structure through the N-terminus when bound to yeast proteinase A (YPRA). The helical structure of IA3 can be stabilized in the absence of YPRA, by using the secondary structure stabilizer, 2,2,2 – trifluoroethanol (TFE). To characterize the TFE induced disordered to ordered states of this IDP, site directed spin labeling (SDSL) and electron paramagnetic resonance spectroscopy (EPR) were used. Cysteine scanning throughout IA3 results in varied degrees of helicity dictated by labeling position, most sensitive within the N-termini. These SDSL – EPR studies, combined with structural characterization using circular dichroism spectroscopy have identified labeled variants that weaken, mimic, or strengthen the TFE induced ordered states of IA3, or overall helical propensity. IA3 labeled variants with differing degrees of helical transitions have further been utilized to assess local hydration dynamics surrounding the disordered and ordered state of this IDP in the absence and presence of TFE, respectively. Overhauser dynamic nuclear polarization (ODNP), a combined EPR and nuclear magnetic resonance spectroscopy technique was used to probe hydration dynamics (i.e. water diffusivity) at the surface of these IA3 variants. Results from ODNP studies suggest significant fluctuations in hydration behavior dependent on both the presence of TFE and the varying degrees of structure found within the N- and C-termini of IA3.