Characterizing order-disorder transitions in natively disordered proteins

Prof. David Weis

Prof. Weis's research focuses on understanding how protein conformation fluctuates over time (dynamics) and how conformation and dynamics change in response to the binding of a ligand. The ligand might be a small molecule, another protein, or DNA. While much research over the past hundred years has demonstrated the importance of protein structure to its function, much more recently it has become apparent that natively disordered proteins play an equally important role. Natively disordered proteins have one or more regions that lack any secondary or tertiary structure under physiological conditions yet retain important biological activity. Mass spectrometry, when combined with H/D exchange labeling technique, is a sensitive probe of disorder in proteins. Research in the Weis lab during the REU program will focus on the characterization of order/disorder transitions proteins following ligand biding. REU projects will focus on some aspect of this research including mass spectrometry, HPLC, expression and purification of recombinant proteins, and protein-protein interaction studies. In the past ten years, Professor Weis has mentored over a dozen undergraduate researchers. Since arriving at KU in 2007, Prof. Weis has mentored four undergraduate students.

This work has resulted in three publications with undergraduate co-authors:

Keppel, T. R., Jacques, M. E., and Weis, D. D. (2010) The use of acetone as a substitute for acetonitrile in analysis of peptides by liquid chromatography/electrospray ionization mass spectrometry, Rapid Commun. Mass Spectrom. 24, 6-10.

Keppel, T. R., Jacques, M. E., Young, R. W., Ratzlaff, K. L., and Weis, D. D. (2011) An efficient and inexpensive refrigerated LC system for H/D exchange mass spectrometry, J Am Soc Mass Spectrom 22, 1472-1476.

Keppel, T. R., Howard, B. A., and Weis, D. D. (2011) Mapping unstructured regions and synergistic folding in intrinsically disordered proteins with amide H/D exchange mass spectrometry, Biochemistry 50, 8722-8732.