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Implementation of Multiple Spectroscopic Techniques to Simultaneously Observe Native and Mutated Protein Unfolding BRENNAN CULL, KELTY BEN, JUSTIN LINK, Xavier University, Cincinnati, OH — A protein's natural, correctly folded structure can determine the protein's ability to carry out its function. If the unfolding process of proteins can be observed, then the relative stability can be better understood between native and mutated proteins. A global picture of the unfolding process may be completed through the studies of strategically mutated proteins using tryptophan as a probe. Horse heart cytochrome c, a thoroughly studied, model protein was used in our investigation to explore this idea. Various spectroscopic techniques such as circular dichroism (CD), absorbance, and fluorescence were simultaneously applied while slowly unfolding our protein by increasing the concentration of a chemical denaturant, guanidine hydrochloride. This provided us information about the thermodynamic properties of the protein and several mutants which can then be interpreted to gain relative stability information among mutations. Efforts to utilize these techniques on native and mutated proteins in comparison to current scientific unfolding theories will be presented in this session.

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