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Multiple Spectroscopic Techniques Simultaneously Observe Native and Mutated Protein Unfolding of Horse Heart Cytochrome c[1]

MARIO CRIBARI, BRENNAN CULL, JUSTIN J. LINK, Xavier University, Cincinnati, OH — Understanding of how a protein folds is a topic that has been plaguing various scientific fields for decades. Proper folding is integral to a protein's function, and so knowledge of that folding is pertinent for medical conditions involving malfunctioning proteins, among other things. Some understanding of protein folding can be gained by analyzing the denaturation of a model protein through spectroscopic techniques; specifically, circular dichroism (CD), absorbance, and fluorescence. Wild-type and 13 mutant versions of the model protein horse heart cytochrome c in the oxidized form were analyzed using these techniques. By mutating the protein such that the single fluorescent amino acid tryptophan was present in different regions of the protein, specific information about each region and its folding process was acquired. Combining the information of each region allowed for the development of a global picture of the protein folding, including a possible ordering of the folding of each region. Further analysis about the characteristics of the various regions of the protein and the order in which they fold can allow for a deeper understanding of the protein folding of horse heart cytochrome c.

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