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Development of a Protocol to Study the Conformational Stability of Protein Using the Model Protein Cytochrome c[1] JESSICA STAVOLE, BENJAMIN OPPERMAN, Department of Biology, Xavier University, JUSTIN LINK, Department of Physics, Xavier University — The function of a protein is inherently dependent upon the proper folding and the resulting tertiary structure of the molecule. The development of an unfolding procedure is desirable so that the structural stability of a protein molecule can be determined through the change in thermodynamic properties of the unfolding reaction. The protein cytochrome*c* has long been used in protein structural studies and monitored by circular dichroism (CD), absorption, and fluorescence spectroscopic techniques. Single amino acid mutations of wild type cytochrome *c* were unfolded both chemically and thermally using the developed protocol and the unfolding was monitored by CD spectroscopy. Thermodynamic properties such as Gibbs free energy, enthalpy and melting temperature were used to interpret the results. The mutant proteins were calculated to have different thermodynamic properties than that of the native cytochrome *c* during the unfolding process. When denatured at a lower pH, the proteins thermally unfolded more readily. The objective of this session is to present recent work addressing the denaturation of wild type and mutant proteins.

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