

CMC – Structure Initiative Protocols

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### **Differential scanning calorimetry (DSC).**

In DSC experiments thermal unfolding of proteins monitored *via* changes in the heat capacity. These changes are believed to originate from the disruption of the forces stabilizing native protein structure (such as van der Waals, hydrophobic and electrostatic interactions, hydrogen bonds, etc.) and the hydration of the exposed residues. Therefore, protein denaturation profiles and thermodynamic parameters obtained from DSC experiments, such as calorimetric enthalpy ( $\Delta H$ ) and denaturation temperature ( $T_m$ ) are sensitive to the structural state of proteins. Presence of the sharp transition(s) in DSC scans indicates that the target protein has a tertiary structure and thus, folded. Changes in the protein conformation would affect the position and the shape of the transition(s) in DSC scans.

#### *SAMPLE GUIDELINES:*

DSC is sensitive to the buffer base. Acetate, Phosphate and Pipes are generally used for DSC. Hepes and Heppso can be also used. However some batches of these buffer sometimes create baseline artifacts. All other buffers (Tris, Mops, TES, etc.) are not suitable. No reducing agents (DTT, etc.). Presence of some organic solvents (DMSO) is tolerated why other (EtOH) cause artifacts. 700 $\mu$  l of  $\geq 0.4$ mg/ml protein is required for one DSC scan.