

Properties of DNA duplex 'melting' and Protein denaturation

Process	Contributions	
	Enthalpic	Entropic
DNA Duplex → Single Strands	Base-Pairing, $\Delta H_{bp} > 0$ Base-Stacking, $\Delta H_{bs} > 0$	Chain Configuration, $\Delta S_{conf.} > 0$ Mixing (non self compl. strands), $\Delta S > 0$ Dissociation, $\Delta S > 0$ Symmetry (self compl. strands), $\Delta S > 0$
Protein Native → Denatured	H-bonds, $\Delta H_{hb} > 0$ Electrostatic Interactions $\Delta H_{Elec.}$ either $<$ or $>$ 0 van der Waals, $\Delta H > 0$	Chain Configuration, $\Delta S_{conf.} > 0$ Hydrophobic Interactions, $\Delta S_{hyd.} < 0$

For protein unfolding:

$$\Delta C_P = C_P(\text{denatured}) - C_P(\text{folded}) > 0,$$

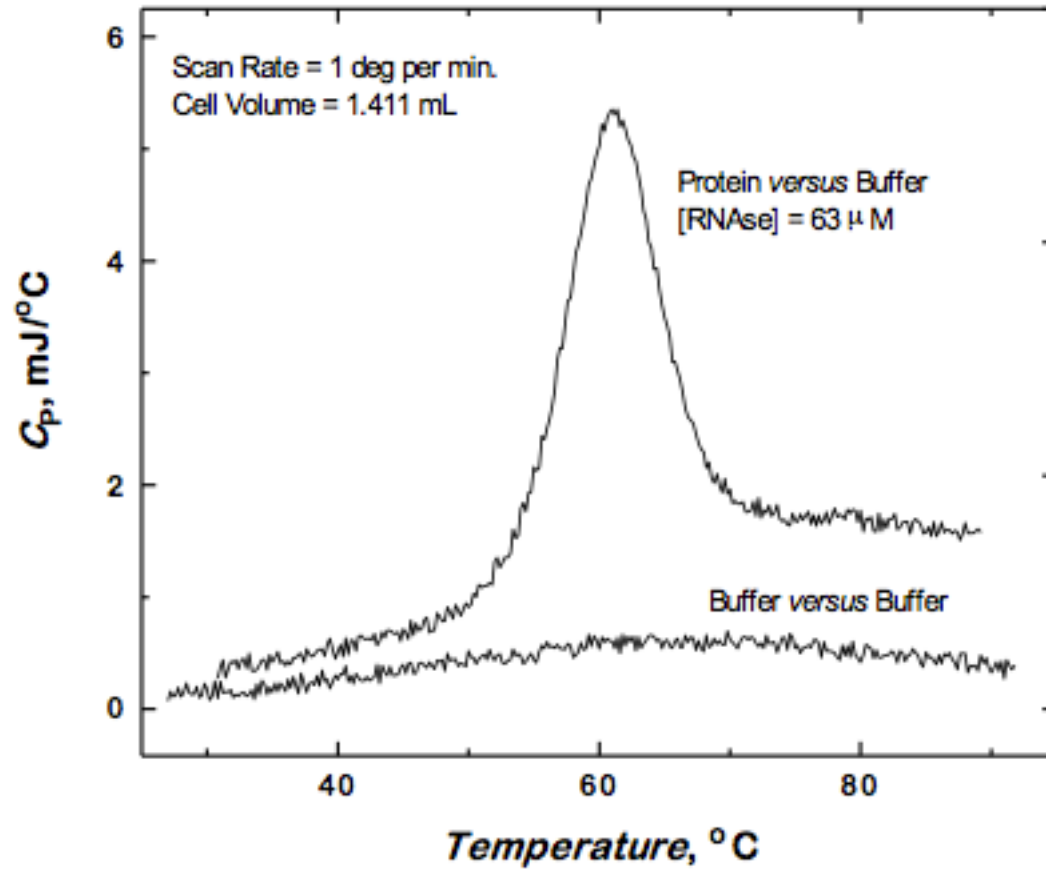
and approximately constant.

For DNA duplex melting:

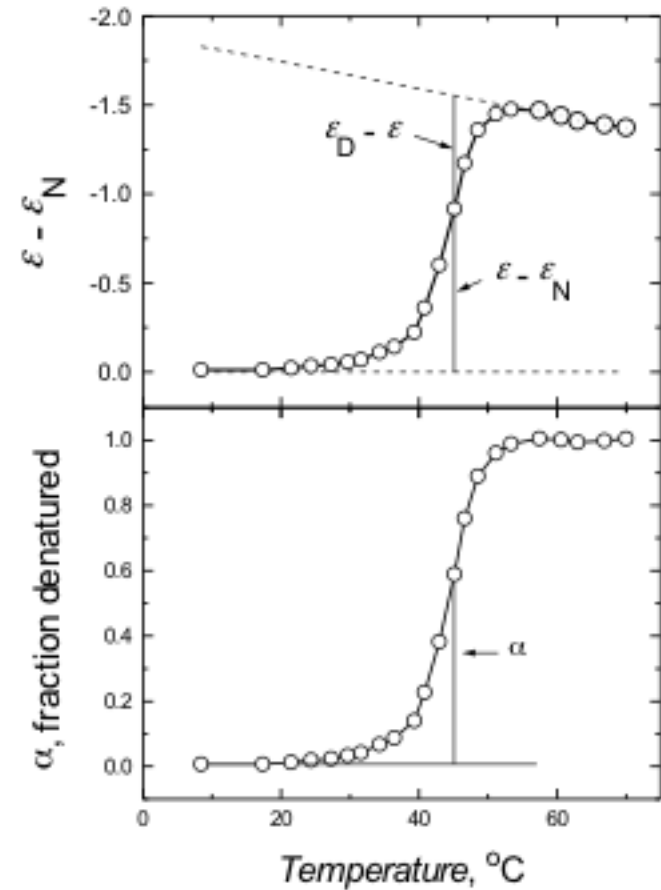
$$\Delta C_P = C_P(\text{ss DNA}) - C_P(\text{dsDNA}) \sim 0.$$

Experimental Measurements of Protein Denaturation

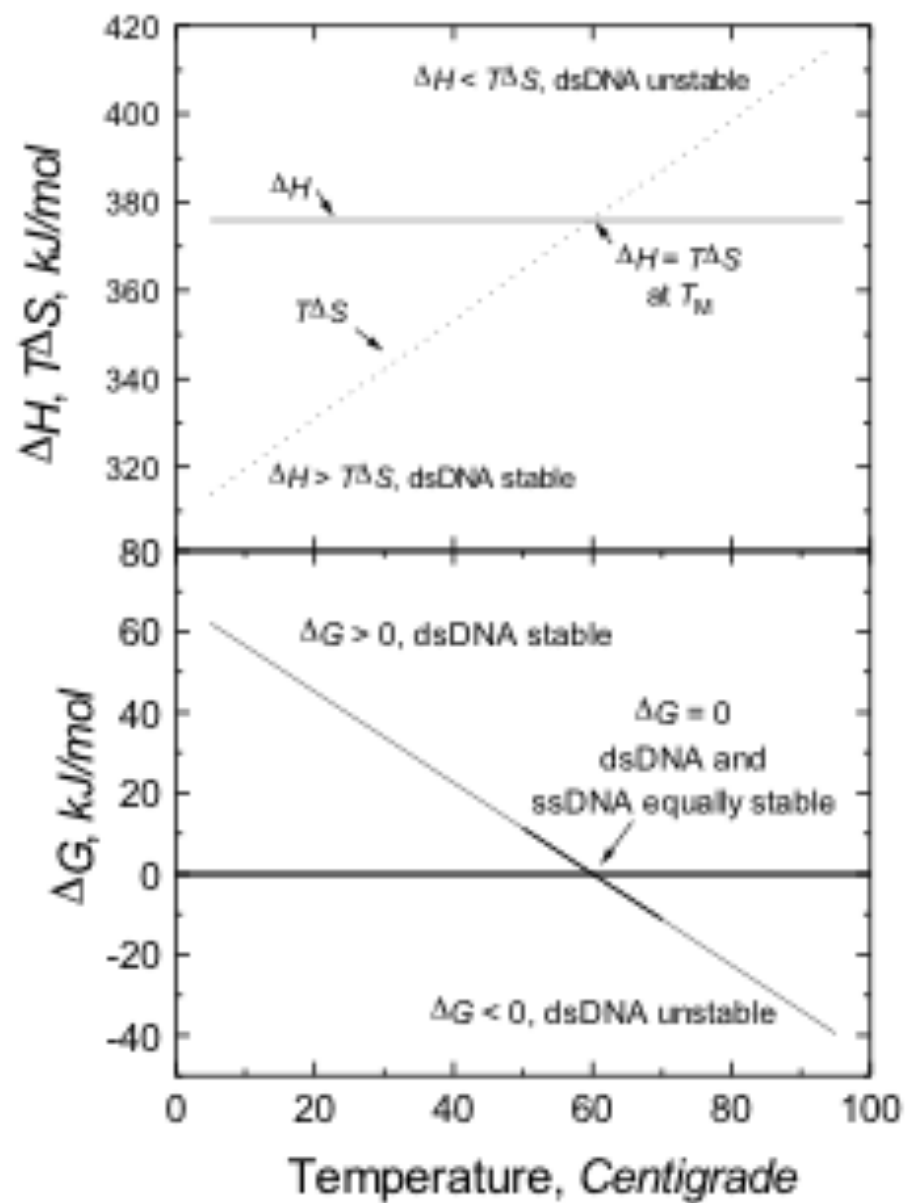
Calorimetry



Tryptophan Abs.



$$\Delta G(T) = \Delta H_M - T\Delta S_M$$



$$\Delta G(T) = \Delta H_M + \Delta C_p(T - T_M) - T \left\{ \Delta S_M + \Delta C_p \ln \left(\frac{T}{T_M} \right) \right\}$$

