

Assignments for Week-9

Q1. The dipole moment of water is

- a. 1.45 Debye
- b. 2.40 Debye
- c. 1.80 Debye
- d. 1.85 Debye

Q2. For protein folding

- a. $\Delta C_p < 0$
- b. $\Delta C_p > 0$
- c. $\Delta C_p = 0$
- d. $\Delta C_p = \infty$

Q3. In the DSC plots, the mutated protein shows higher T_m value compared to that its wild type form. It means that

- a. Mutation has provided conformational stability to the protein
- b. Mutation has destabilized the conformational stability of the protein
- c. Mutation has strengthened intra-molecular hydrophobic interactions.
- d. Mutation has broken down the salt bridges, if any

Q4. The DSC scan of a protein shows an endotherm. This suggests that

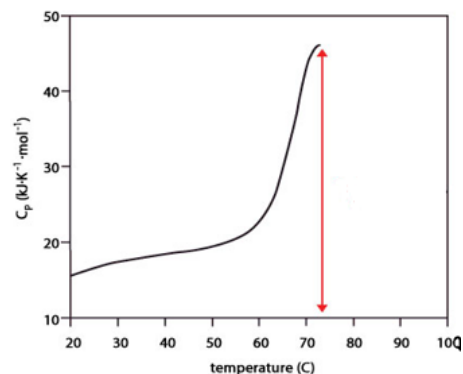
- a. Heat is generated due to co-operativity of the process
- b. Heat is required to break hydrogen bonds and hydrophobic interactions
- c. pH of the protein solution changes because of heating
- d. entropy of the system increases

Q5. If on reheating the protein sample in a DSC experiment, no endotherm is observed, it suggests that:

- a. The protein unfolding is reversible
- b. All the protein solution has evaporated.
- c. The protein unfolding is irreversible
- d. All the bonds in the protein have broken down

Q6. In the following figure the temperature indicated represents

- a. 100% denatured protein
- b. Beginning of protein unfolding
- c. Partially folded protein
- d. 50% denatured protein



Q7. At $T_{1/2}$, the value of ΔS° for a two-state transition is given by

- (A) $\Delta H^\circ/T_{1/2}$
- (B) $\Delta H^\circ + T_{1/2}$
- (C) $\Delta G^\circ - \Delta H^\circ$
- (D) $\Delta G^\circ/\Delta H^\circ$

Q8. The binding of a drug to a target protein generally leads to

- (A) increase in its thermal stability
- (B) decrease in its thermal stability
- (C) no change in its thermal stability
- (D) denaturation of the protein

Q9. The DSC profile of a pure protein can be used to

- (A) estimate the purity of newly isolated same protein
- (B) estimate the extent of exposure of hydrophobic content of the protein to the solvent
- (C) estimate the extent of breakage of covalent bonds in the protein
- (D) estimate the amount of heat required to denature the protein

Q10. The structure of liquid water is

- (A) strictly tetrahedral network of hydrogen bonds
- (B) strictly monomeric water molecules with hydrogen bonding to small extent
- (C) mixture of monomeric and tetrahedral network of hydrogen bonds
- (D) square planar network of hydrogen bonds