

1.

a. Complete the following sketch by drawing an amino acid R-group that would interact favorably with each of the side chains shown.

i) Amino acid: Amino acid:

ii) Interaction: Interaction:

b. Under the R-groups you have drawn, i) identify the amino acid and ii) indicate the type of interaction (i.e. force or bond) pictured.

c. Indicate here which of the two interactions is the stronger:

d. For the stronger interaction you chose, indicate whether it can contribute to the stabilization of protein

1) primary structure: Y or N

2) secondary structure: Y or N

3) tertiary structure: Y or N

4) quaternary structure: Y or N

2. Leu 118 is a buried residue in wild type T4 lysozyme, "T4L (WT)". Using in vitro mutagenesis techniques, *Eriksson et al. changed Leu 118 to Ala. The structures of the proteins showed that a large cavity had been created in the hydrophobic core of the mutant enzyme. The thermodynamic parameters for the unfolding reaction were measured and found to be:

	T _m (°C)	DH (kJ/mol)
T4L (WT)	51.8	497
T4L (Leu 118Ala)	39.6	316

1. Calculate DS for the unfolding of each protein at their respective T_m's.
2. Calculate DDG, the decrease in protein stability, due to the Leu 118--> Ala substitution, at 46°C (i.e. about halfway between the two T_m's).
3. Calculate DDG at 27°C. What fraction of each protein is unfolded at this temperature?
4. Of the total DG of stabilization for T4L at 27°C, what fraction was lost by the Leu 118-->Ala substitution?