1. (12 points)

a) and b) The following were good possibilities for interactions with the Asp and Ser side chains:
Asp: Lys+ or Arg+ (charge interaction) or any polar amino acid (D-H, H-bond interaction).
[2 pts for each correct structure; 1 pt for name; 1 pt for interaction]

Ser: Most polar (incl charged) amino acids could donate (D-H) or accept (A) H-bonds.

For both Asp & Ser, a nonpolar R-group could also be drawn (van der Waals interaction).

c) Details differ depending on the two interactions depicted; the order of strength is: [2 pts]
Charge > H-bond > van der Waals

d) 1) None of the interactions shown could affect primary structure. [0.5 pts each]

2) Most would not contribute much to secondary structure.

3) and 4) R-group interactions are the most significant factors for both tertiary and quaternary structure. [0.5 pts each]

2.
a) DS = DH/Tm
T4L (WT) = 497/(273 + 53.5) = 1.53 kJ/mol-K
T4L (Leu118Ala) = 316/(273 + 39.6) = 1.01 kJ/mol-K
b) At 46°C, DG = DH - TDS = DH - (273 + 46)DS (unfolding)
T4L (WT) 8.87 kJ/mol
T4L (Leu118Ala) -6.46 kJ/mol
DGWT - DGmutant = DDG (unfolding) = 15.33 kJ/mol
c) At 27°C, DG = DH - 300*DS (unfolding)
T4L (WT) 37.92 kJ/mol
T4L (Leu118Ala) 12.72 kJ/mol
DGWT - DGmutant = DDG (unfolding) = 25.2 kJ/mol

	Keq = exp (-DG/RT)	Fu = Keq/(1+Keq)
T4L (WT)	2.40*10-8	2.4*10-7
T4L (Leu118Ala)	6.05*10-3	6.01*10-3

d) Fraction lost = DDG/DGWT = 0.66