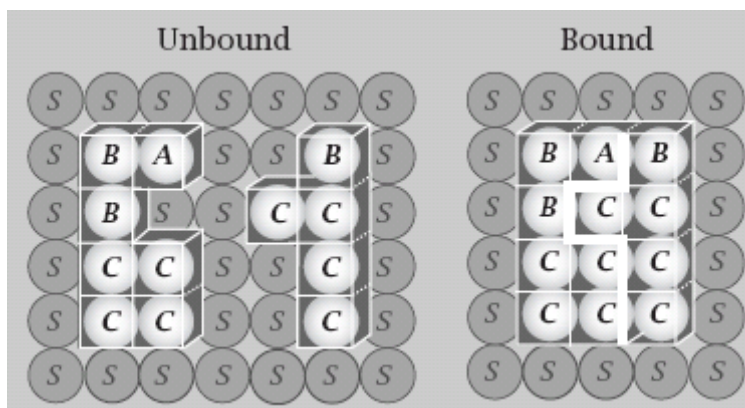


**20.110/2.772/5.601 Fall 2005**  
**Recitation # 16**  
**11/10/2005**

1. In class we studied the mixing of species A and B, assuming both of them as polar substances (such that they make hydrogen bonds with each other and also with their own kind). Now assume that we have a three species system, A, B and C. Assume that for such a lattice model,  $N = n_A + n_B + n_C$ . All sites are filled.

- a. Write an expression for entropy of mixing.
- b. Using the mean field ("Bragg-Williams") approximation, where we assume that the particles on a lattice are mixed as uniformly and randomly as possible, write an expression for the energy of mixing ( $\Delta U_{\text{mix}}$ ) in terms of the binary interactions parameters chi ( $X_{AB}$ ,  $X_{AC}$ ,  $X_{BC}$ ).
- c. Write an expression for the free energy of mixing (in Helmholtz free energy).
- d. Write an expression for the chemical potentials of substances A, B and C.
- e. Now assume that the species A is polar, while species B and C are nonpolar and form very weak inter-species (AC, BC etc) bonds. What do you think will happen to the free energy of the system, relative to the situation when all species were polar? What would happen to the entropy of the system?

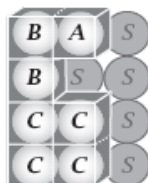
2. (D&B) You have a two-dimensional molecular lock and key in solvent *s*, as shown in the figure below. Different parts of each molecule have different chemical characters, *A*, *B*, or *C*.



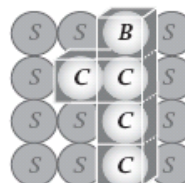
a. In terms of the different pair interactions, ( $\omega_{AB}$ ,  $\omega_{AC}$ ,  $\omega_{AS}$ , ... etc.) write an expression for the binding constant  $K$  (i.e., for association).

b. Which type of pair interaction ( $AB$ ,  $AC$ ,  $BC$ ) will dominate the attraction?

Unbound

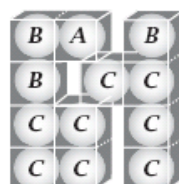


Break 2AS 1BS 3CS  
 Make 6SS



Break 1BS 5CS  
 Make 6SS

Bound



Make 1AB 2AC 1BC 3CC

3. Let's compare the magnitude of entropic forces that favor unfolding of proteins (gain in chain conformations) to the entropic forces favoring folding (hydrophobic ordering of water around exposed nonpolar side chains):

Consider a protein of 200 amino acid units. Let's estimate the entropy gain due to chain conformations when the chain goes from a compact, unique folded state to a random coil. Using the lattice model approximation, we showed in lecture that one could estimate the number of states for a random coil on a 3D lattice as:

$$\Omega = z^N$$

Where  $N$  is the number of repeat units (200). If we take the folded state as a unique single state for the folded protein, we have the following for the entropy change on denaturation:

$$\Delta S_{chain\ freedom} = k_B \ln \left( \frac{\Omega_{unfolded}}{\Omega_{folded}} \right) = k_B \ln \left( \frac{z^N}{1} \right) = k_B N \ln z$$

$$\Delta S_{chain\ freedom} = 1.381 \times 10^{-23} \frac{J}{K} (200) \ln(6) = 4.95 \times 10^{-21} \frac{J}{K} = 2979 \frac{J}{K \cdot mol}$$

Now, from measurements of individual amino acids, we can approximate that the average entropy loss when a nonpolar amino acid is exposed to water as 100 J/mole K. Using this value, what fraction  $f$  of amino acids in the protein chain would need to be nonpolar in order to provide enough 'hydrophobic entropy loss' to exactly balance the entropy gain from chain conformations during unfolding?