

**Discussion 8 -- Practice Problems: Nucleic Acids and DNA Protein interactions**

1. (From *Lehninger Principles*, 6th ed., p. 309 #2) One strand of a double-helical DNA has the sequence (5') GCGCAATATTTCTCAAAATATTGCGC (3').

- A. Write the base sequence of the complementary strand below the sequence of the given strand.
- B. What special type of sequence is contained in this DNA segment?
- C. Does the double-stranded DNA have the potential to form any alternative structures?

2. Restriction-modification systems are important components of prokaryotic defense mechanisms against foreign genetic material. They comprise of two distinct enzymatic activities: a restriction endonuclease and a methyltransferase.

The restriction endonuclease recognizes and cleaves foreign DNA sequences at specific sites, while methyltransferase transfers methyl groups to the same specific DNA sequence to the C-5 carbon or the N4 amino group of cytosine or to the N6 amino group of adenine.

What is the purpose of the methyl-transfer reaction? How is the purpose accomplished?

3. Two complementary strands of DNA can exist in solution in the form of a duplex (double-stranded form) or can exist as separate strands ("random coils"), depending on the position of the equilibrium shown below.

**Double-stranded form      < = = >      single strands ("random coil")**

- A. In the table below, for the process of strand separation (the direction written above), list and explain 2 different types of interactions that contribute to the  $\Delta H$ ; and list and explain 2 different types of interactions that contribute to the  $\Delta S$  for the duplex-random coil transition. For each contribution to  $\Delta H$  and for each contribution to  $\Delta S$ , state whether that thermodynamic contribution favors the *double-stranded* or the *single-stranded* form of DNA.

	<b>specific types of interactions responsible, with brief explanation</b>	<b>Form of DNA favored (double-stranded, or single-stranded)</b>
<b><math>\Delta H</math> (enthalpy change)</b>		
<b><math>\Delta H</math> (enthalpy change)</b>		
<b><math>\Delta S</math> (entropy change)</b>		
<b><math>\Delta S</math> (entropy change)</b>		

- B. Explain why hydrogen bonds between bases in the base pairs in double-stranded DNA make relatively little contribution to the stability of the double-stranded form of DNA.
- C. How do the thermodynamic contributions involved in establishing the equilibrium of the folded to unfolded state of proteins? ( $\text{Protein}_{\text{folded}} \rightleftharpoons \text{Protein}_{\text{unfolded}}$ ) compare to the individual thermodynamic contributions to the equilibrium between duplex and single stranded DNA?

Protein	Specific type of interaction and whether it favors folded or unfolded state of protein, and how that compares with DNA duplex – single strands equilibrium)
$\Delta H_{\text{internal interactions}}$	
$\Delta H_{\text{H-bonds to water}}$	
$\Delta S_{\text{hydrophobic effect}}$	
$\Delta S_{\text{conformational}}$	