Chapter 3 Solutions

1) The pK_a of the ε-amino group ($R\text{-}NH_3^+$) on the lysine side chain is 10.79. RNH_3^+ will typically not bind to a metal ion (M^{n+}), even though RNH_2 might. For lysine to bind to a metal ion, the ε-amino group would need to be deprotonated, which is difficult at physiological pH. Thus, the ε-amino group does not commonly serve as a ligand for a metal ion in a metalloprotein under physiological conditions.

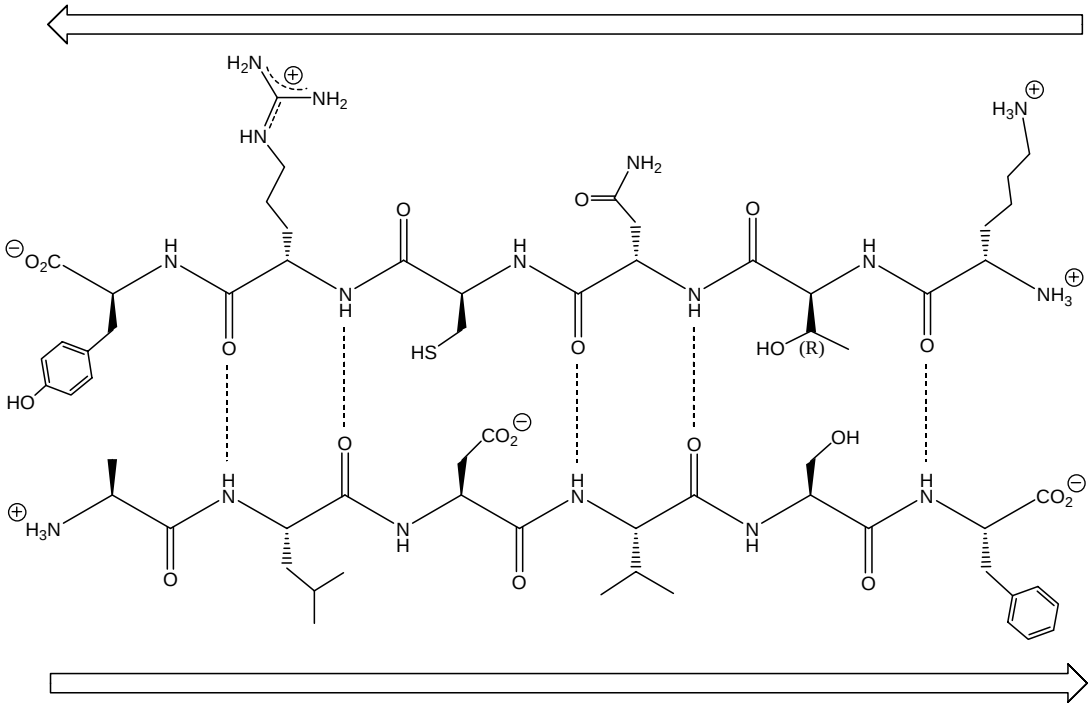
2) Double-stranded DNA typically forms a B-type helix, whereas double-stranded RNA prefers an A-type. Additionally, the backbone for DNA has one fewer hydroxyl unit per nucleotide unit than RNA has. Furthermore, DNA utilizes thymine whereas RNA utilizes uracil. Transcription factor IIIA binds to double-stranded DNA, presumably by recognition and interaction with the aforementioned motifs. Double-stranded RNA, which does not contain the same motifs, will be a poor binding target for TFIIIA.

3) In a peptide backbone, each amino acid has 2 freely-rotatable bonds. Thus, a 100mer peptide will have 200 such bonds. If each bond can be in one of 3 possible orientations, then the total number of possible configurations for the peptide is $3^{200} = 2.66*10^{95}$.

In a polynucleotide backbone, each nucleotide unit contains 5 freely-rotatable bonds. Thus, a polynucleotide chain containing 100 nucleotide units will have 500 such bonds. If each bond can be in one of 3 possible orientations, then the total number of possible configurations for the polynucleotide is $3^{500} = 3.64*10^{238}$.

Even though many possible conformations exist, most proteins and polynucleotides have unique tertiary structures. Deviation from the native folding of such a species can disrupt or destroy its function (with potentially lethal effects). Presumably, the unique tertiary structure is the most favorable conformation due to optimal intramolecular hydrogen-bonding and hydrophobic interactions.

4)



5) H-E-L-P-M-E-I-M-T-R-A-P-P-E-D-I-N-A-G-E-N-E; red letters indicate soft metal-binding sites.