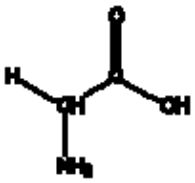
Name: _____

Understanding Protein Structure

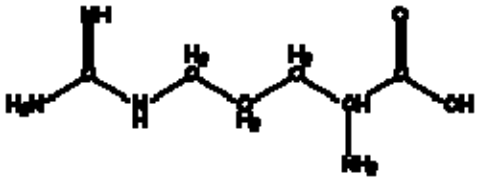
Atoms to Ecosystems

Part 1: Primary Protein Structure

1. Examine the structures of glycine and arginine, two of the 20 amino acids biological organisms use to build their proteins.



Glycine

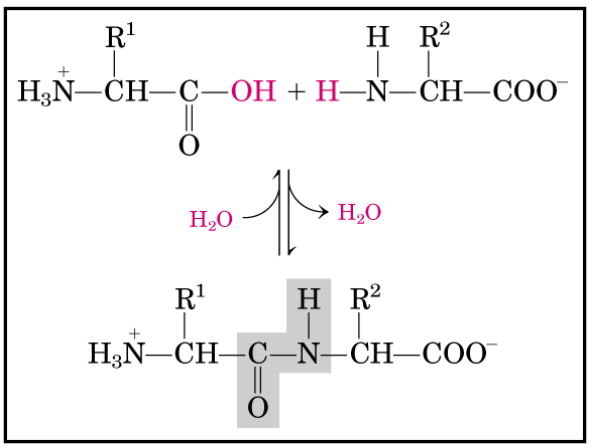


Arginine

a. What do these two structures have in common? Draw a common structure for an amino acid.

b. What makes these two structures different?

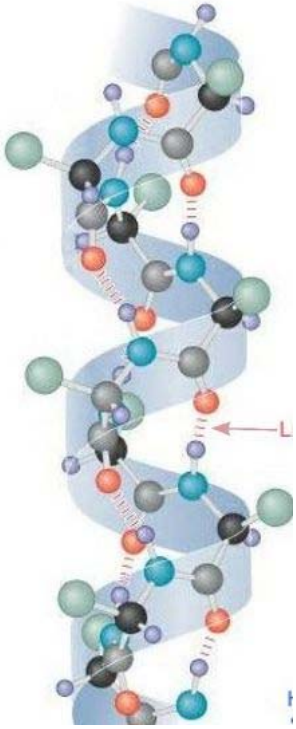
2. The first step in producing a protein in a cell is to link the amino acids together to form a polypeptide. This linkage reaction is known as a *condensation reaction* (shown at right) and is catalyzed, in biological systems, by the ribosome.



a. In the space below, draw out the condensation reaction that would take place were you to join glycine and arginine together in a dipeptide.

b. Examine your drawing. Are the two ends of the dipeptide molecule identical? Biochemists often refer to the amino terminus (or end) and carboxy terminus. Label the amino terminus and carboxy terminus on your dipeptide from part 2a. Try building the structure using the model kits to help you visualize the molecules!

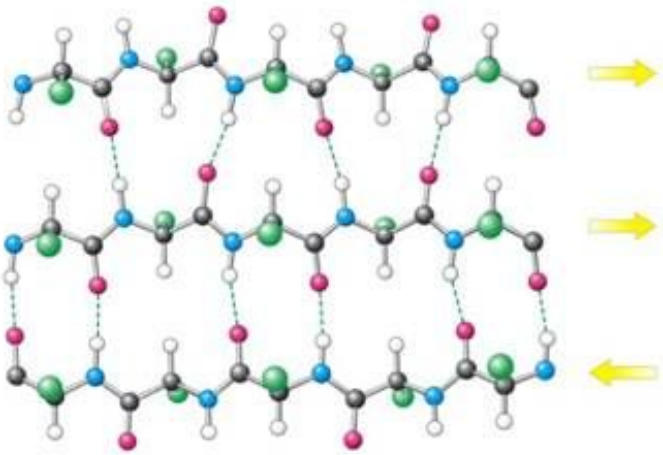
Part 2: Secondary Protein Structure



Once a series of amino acids have been linked together to form a polypeptide, that polypeptide (the protein's primary structure) is free to interact to form secondary structures. The two most common secondary structures are alpha helices and beta sheets. If you have internet access, check out the protein structures at http://webhost.bridgew.edu/fgorga/proteins/default.htm.

a. Examine the alpha helix at right. What kind of molecular interactions hold this structure together?

b. Between which two atoms do these bonds form? Indicate them on your dipeptide on the previous page.

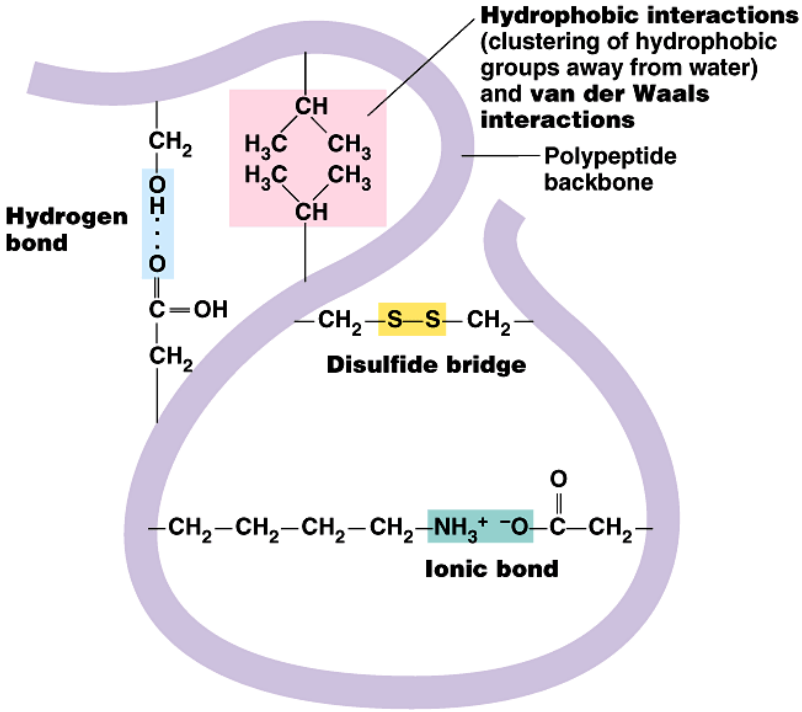


c. Examine the beta sheet at left. Are these the same forces anchoring these polypeptides together? Between which atoms do they occur?

d. Do you expect these secondary structures, alpha helices and beta sheets to hold their shape at high temperature? Why or why not?

Part 3: Tertiary Protein Structure

Regions of a polypeptide not involved in alpha helices or beta sheets are also free to interact, forming a protein's tertiary structure. The primary force driving their interactions is the *hydrophobic effect;* this occurs as hydrophobic and hydrophilic amino acids stabilize.



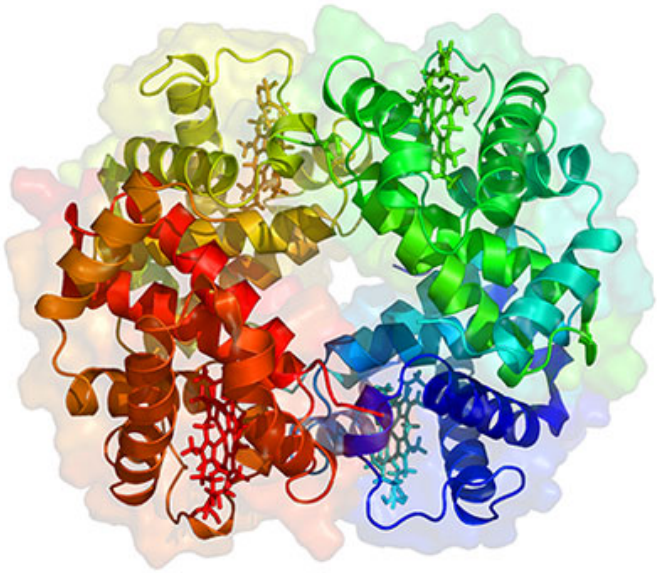
a. In the space below, draw the tertiary structure you expect to see in a globular protein containing long stretches of hydrophobic and hydrophilic regions. (Note that you don't need to draw individual molecules, just represent how you expect the various regions to behave.)

b. The diagram above illustrates the various interactions that can stabilize a protein's tertiary structure. Which of these interactions do you expect to be most thermostable and why?

Part 4: Quaternary Protein Structure

In some proteins, two or more polypeptides (each with their own primary, secondary, and tertiary structures) must interact to make a functional molecule. Two or more peptides interacting make up the quaternary structure of a protein.

a. Examine the quaternary structure of hemoglobin, at right. Hemoglobin is the protein that transports oxygen in our red blood cells. How many polypeptide chains make up a functional hemoglobin molecule?



b. Can you identify any secondary structures in this representation? Label them!

c. Sickle Cell Disease is a genetic condition that results from the substitution of valine for glutamic acid in one of the hemoglobin polypeptides, as indicated at right. Examine the structures of these two amino acids in the chart on the next page. Based on just their structures, do you expect this single amino acid substitution to have an effect on this protein's structure? Why or why not?

HBB Sequence in Normal Adult Hemoglobin (Hb A):

Nucleotide	CTG	ACT	CCT	GAG	GAG	AAG	TCT
Amino Acid	Leu	Thr	Pro	Glu	Glu	Lys	Ser
	3			6			9

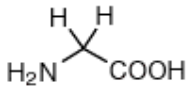
HBB Sequence in Mutant Adult Hemoglobin (Hb S):

Nucleotide	CTG	ACT	CCT	GTG	GAG	AAG	TCT
Amino Acid	Leu	Thr	Pro	Val	Glu	Lys	Ser
	3			6			9

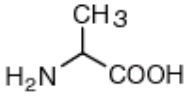
d. The substituted amino acid described in 4c occurs at the outer surface of the folded protein. How do you expect its location to affect protein structure? (Hint: revisit part 3!)

The 20 Biologically Important Amino Acids:

Small

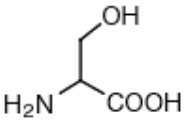


Glycine (Gly, G)
MW: 57.05

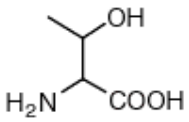


Alanine (Ala, A)
MW: 71.09

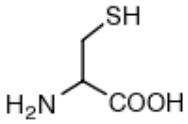
Nucleophilic



Serine (Ser, S)
MW: 87.08, pK_a ~ 16

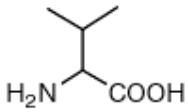


Threonine (Thr, T)
MW: 101.11, pK_a ~ 16

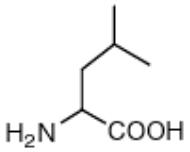


Cysteine (Cys, C)
MW: 103.15, pK_a = 8.35

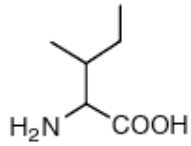
Hydrophobic



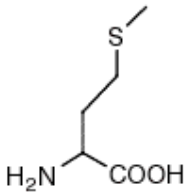
Valine (Val, V)
MW: 99.14



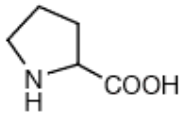
Leucine (Leu, L)
MW: 113.16



Isoleucine (Ile, I)
MW: 113.16

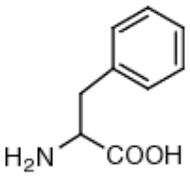


Methionine (Met, M)
MW: 131.19

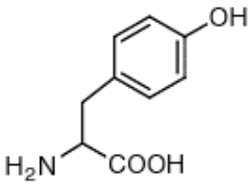


Proline (Pro, P)
MW: 97.12

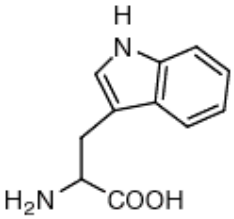
Aromatic



Phenylalanine (Phe, F)
MW: 147.18

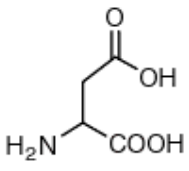


Tyrosine (Tyr, Y)
MW: 163.18

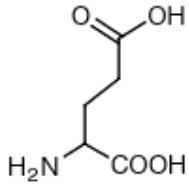


Tryptophan (Trp, W)
MW: 186.21

Acidic

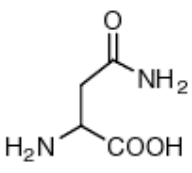


Aspartic Acid (Asp, D)
MW: 115.09, pK_a = 3.9

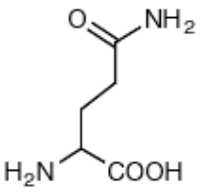


Glutamic Acid (Glu, E)
MW: 129.12, pK_a = 4.07

Amide

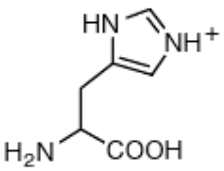


Asparagine (Asn, N)
MW: 114.11

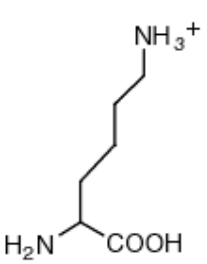


Glutamine (Gln, Q)
MW: 128.14

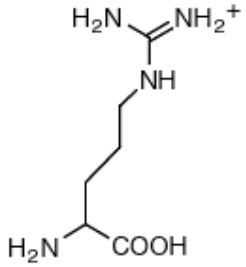
Basic



Histidine (His, H)
MW: 137.14, pK_a = 6.04



Lysine (Lys, K)
MW: 128.17, pK_a = 10.79



Arginine (Arg, R)
MW: 156.19, pK_a = 12.48