**Modeling Protein Structure with Pipe Cleaners and Beads**

Each color of bead represents one of the 20 possible amino acids:

Red **=** methionine(met)

Orange = leucine (leu)

Yellow = cysteine (cys)

Green = threonine (thr)

Pink = histidine (his)

Blue = glutamic acid (glu)

Find the chart of amino acids in your text. Look at the R group on each of the following amino acids, and identify each as nonpolar, polar, negatively charged, or positively charged.

Red (methionine) =

Orange (leucine) =

Yellow (cysteine) =

Green (threonine) =

Pink (histidine) =

Blue (glutamic acid) =

Now, attach two pipe cleaners together so they form a straight line. Then, build a polypeptide by placing beads that represent the appropriate amino acids in the following order (spread the beads out evenly on the pipe cleaners):

Met-Leu-Leu-Glu-Leu-His-Cys-Thr-Cys-Leu-Met-Glu-Glu-Thr-Cys-His

1. What you just made is called the primary conformation – just a string of amino acids connected by \_\_\_\_\_\_\_\_\_ bonds. It is this primary structure – the order of the amino acids – that will determine the protein’s ultimate form and its \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_.
2. Next, find one place to add a beta pleat (an accordion fold), and another place to do an alpha helix (spiral twist). The polypeptide is now in the secondary conformation; the pleats and helices are due to \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ bonds.
3. The tertiary conformation is where the peptide looks like a globular protein. Here are the rules to follow when forming the tertiary structure
	1. In a watery environment, polar amino acids want to have contact with \_\_\_\_\_\_
	2. In a watery environment, nonpolar amino acids want to be near each other \_\_\_\_\_ from water
	3. Positively charged amino acids are \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ to negatively charged amino acids
	4. Cysteine side chains want to be near each other because they can form stabilizing \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ bridges
	5. When you think you have folded the protein correctly, show your teacher.
4. For some proteins, the tertiary conformation is its functional form. However, for some proteins to function, they need to associate with other tertiary structures (called subunits) creating what is called the \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ conformation. How could you model that?

Why are some of the structures formed in the class different? How does this relate to chaperonins?

How does mad cow disease relate to protein folding?