Protein Modeling Lab Activity

Objective:

Use a flexible model to illustrate the first three levels of protein folding.

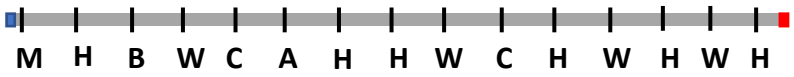
Procedure:

1. Using the amino acid side chain chart, sort the 22 amino acids into the five different structural categories: hydrophilic, hydrophobic, acidic, basic, and cysteines.

2. Straighten the 4-foot mini toober (foam covered wire) that is in your kit. Place a blue endcap on one end and a red endcap on the other end. The blue endcap represents the amino terminus (N-terminus, beginning) of the protein. The red endcap represents the carboxy terminus (C-terminus, end) of the protein.

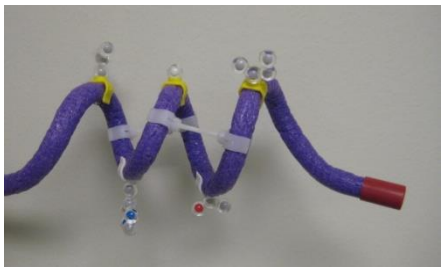
3. Choose 15 side chains to use in your protein. You should include 1 methionine, 6 hydrophobic, 1 acidic, 1 basic, 2 cysteines, and 4 hydrophilic side chains.

4. **Primary Structure:** Using a ruler or meterstick, clip the side chains onto the mini toober every three inches as shown below, starting one inch from the N terminus.



M = Methionine **H = Hydrophobic**
B = Basic **C = Cysteine**
A = Acidic **W = Hydrophilic**

5. **Secondary Structure:** Coil the last 18 inches of mini-toober (including the last 5 amino acid side chains) into an alpha helix as shown here. Use the two-ended plastic clips to represent the hydrogen bonds that hold the secondary structure together. (If done correctly, the three hydrophobic side chains should all be on the same side of the helix.)



6. **Tertiary Structure:** (Remember: protein folding takes place in the watery environment of the cell.)

a. Start by folding the mini-toober so that all of the hydrophobic side chains are facing the interior of the molecule where they will be hidden from water molecules in the cytoplasm.

b. Fold the mini-toober so that the 2 cysteine side chains face one another. These will form a disulfide bond to help stabilize the structure.

c. Bend the mini-toober to bring the acidic and basic side chains to within one inch of each other. These will form an ionic bond which will also help stabilize the protein.

d. Continue to fold the mini-toober so that all of the hydrophilic side chains face the exterior of the molecule where they can hydrogen bond with water molecules.

Now, watch the demonstration video below to see how Professor Flick's model turned out.

https://monroecommunity.zoom.us/rec/share/_YfaAJlqKK085TRdxD9NBOtxoZXbDyBYAaN8y1u7j2qBoToHIFaRUJYMyTZU4Mfb.BLbU18kW6rIvxkr4?startTime=1610480481000

Questions:

1. Pause Professor Flick's demo video at 0:46 and 05:46 and examine each of the amino acid side chains and identify which atoms are present (gray = carbon, red = oxygen, blue = nitrogen, yellow = sulfur, white = hydrogen). Answer the following questions:

A. Hydrophobic side chains primarily contain which two elements?

B. Acidic side chains contain two _____ atoms. These are part of a carboxyl group.

C. Basic side chains contain _____ which is part of an amino group.

D. Which side chains are likely to position themselves on the interior of a protein where they are shielded from water?

E. Would two basic side chains be attracted to one another? Why or why not?

2. Primary Structure: record the three letter abbreviations for the amino acids used in Professor Flick's model on the diagram below (start at 8:10 in the video).

3. Tertiary Structure: sketch the final shape of Professor Flick's protein below, indicating the disulfide and ionic bonds.

4. Suppose amino acid #4 (hydrophilic) was replaced with a hydrophobic amino acid as a result of a genetic mutation. How would the protein structure change? Sketch a new structure below.

5. Do you think this mutation will affect protein function? Why or why not?