Pipe Cleaner Protein Modeling

Modified from C. Kohn, Waterford WI

Purpose: To visualize how a protein is constructed and understand the structure is related to the function.

Introduction:

The function of a protein is determined by its shape, and the shape of the protein is determined by its amino acids. Because proteins are smaller than microscopic, we would have a pretty hard time doing a hands-on lab on this topic. However, we can explore proteins in an indirect way through modeling so that we can better understand it.

In this case, you will be using pipe cleaners, beads, and cut up straws to model how proteins fold, and how mutations affect the shape of proteins. Each team will be responsible for completing their own sheet, normal protein, and mutated protein.

Background:

There are 3 basic rules of protein folding based on the R-group:

1. **Hydrophobicity** –
   a. Hydrophobic (*water hating*) amino acids will always try to get to the inside of a protein. On the other hand, hydrophilic (*water loving*) amino acids try to get further into the water because they love it so much.

Red beads will represent hydrophobic amino acids; Blue beads will represent hydrophilic amino acids

2. **Charge** – amino acids can have one of three charges – positive, negative, or neutral
   a. Like opposite sides of a magnet, positively and negatively charged amino acids attract each other
   b. Like the same pole of a magnet, amino acids with similar charges (positive and positive, or negative and negative) will try to move as far apart from each other as they can.
   c. Neutral amino acids remain largely unaffected

Yellow beads will be the positively charged amino acids, whereas Pink beads will be the negatively charged amino acids. (We won't bother with neutral amino acids). Yellow and Pink beads near each other should attract.

3. **Cysteine Bonds** –
   a. Cysteine amino acids are like the obnoxious couple in the hallway –they just can't bear to be apart! Cysteine amino acid pairs will move toward each other and form strong covalent bonds between the sulfur atoms.

Green beads will represent the amino acids cysteine.

Complete Q1, Q2 and Q3 on your student answer sheet.

Amino Acid	Code	Bds	Charge	Hydrophobicity
Alanine	Ala	1	Neutral	Hydrophobic
Arginine	Arg	2	**Positive**	*Hydrophilic*
Asparagine	Asn	1	Neutral	*Hydrophilic*
Aspartic acid	Asp	2	**Negative**	*Hydrophilic*
Cysteine	Cys	GRN	Neutral	*Hydrophilic*
Glutamine	Glu	2	**Positive**	*Hydrophilic*
Glutamic acid	Gln	2	**Negative**	*Hydrophilic*
Glycine	Gly	1	Neutral	Hydrophobic
Histidine	His	2	**Positive**	*Hydrophilic*
Isoleucine	Ile	1	Neutral	Hydrophobic

Amino Acid	Code	Bds	Charge	Hydrophobicity
Leucine	Leu	1	Neutral	Hydrophobic
Lysine	Lys	2	**Positive**	*Hydrophilic*
Methionine	Met	1	Neutral	Hydrophobic
Phenylalanine	Phe	1	Neutral	Hydrophobic
Proline	Pro	1	Neutral	Hydrophobic
Serine	Ser	1	Neutral	*Hydrophilic*
Threonine	Thr	1	Neutral	*Hydrophilic*
Tryptophan	Trp	1	Neutral	Hydrophobic
Tyrosine	Tyr	1	Neutral	Hydrophobic
Valine	Val	1	Neutral	Hydrophobic

1. Use the amino acid characteristic chart to create a polypeptide that is 18 amino acids long. You may use any amino acids and in any order your team chooses to create your PRIMARY STRUCTURE.

IMPORTANT TIPS!!!

a. Some amino acids will have multiple beads! For example, Arginine is both positively charged (yellow) and hydrophilic (blue). As such, you would use both a blue and yellow bead together to represent this amino acid.

b. Be sure to have a cut up straw between each amino acid so that you know where one ends and the next begins! You may need multiple pipe cleaners to fit all of your amino acids!

Complete Q4, Q5 and Q6 on your student answer sheet.

2. SECONDARY STRUCTURE of a protein results when parts of the polypeptide coil or fold. Take your string of beads and fold the strand back and forth accordion style for a short section. Next coil another section around your pencil to form a spiral.

Complete Q7 and Q8 on your student answer sheet.

1. Next, fold your protein into the TERTIARY STRUCTURE. This requires that you consider the "R group" of the amino acid involved (the rules we discussed in the intro). Start by moving your red and blue beads to represent hydrophobicity. Next connect your opposite charges (wrap them around each other using the pipe cleaner). Finally, if you have more than one cysteine, wrap those together to form a strong bond. If your finished protein looks like a hot mess...GOOD JOB!

Complete Q9, Q10 and Q11 on your student answer sheet.

Student Answer Sheet Names:

Q1. Draw and identify two different amino acids. Highlight the portions the amino acids have in common. Circle the R-group for each amino acid.

Name:	Name:	Name: Cysteine

Q2. Identify which colors we will use to represent the different characteristics of amino acid R-groups:

Hydrophilic =	Hydrophobic =	Positive (+) =	Negative (-) =	Cysteine =

Q3. What type of amino acids should cluster in the inside of the protein in a watery environment like the cell or body?

_____

Q4. What process (reaction) binds these amino acids together to form this polypeptide chain?

_____

Q5. What bonds are represented by the straws? _____

Q6. Is the structure you just built a protein? Explain.

_____

Write out the abbreviation of your amino acid chain in order:

Q7: What are the names of the sections you just formed? _____

Q8. What holds the parts of the secondary structure together? _____

Q9. In a watery environment (like your body), polar amino acids want to have contact with _____, whereas nonpolar amino acids want to huddle near the _____, far away from it.

Q10. Cysteine side chains want to be near each other because they can form stabilizing _____ bridges.

(See page 83 in Campbell textbook for help).

Q11. Some proteins are an association of two or more polypeptides aggregated into one. Give the 2 examples listed in your book of such proteins. _____ and _____.

Have your protein approved by the teacher. Answer the extension question!