

Key Teaching Points for the Amino Acid Starter Kit[®]

Overall Student Learning Objective: What Dictates How a Protein Will Fold?

- Proteins are made up of amino acids.
- Different R groups (or side chains) have unique chemical properties.
- There are two major types of protein secondary structure: alpha helices and beta sheets.
- Proteins fold following basic laws of chemistry including:
 - The hydrophobic side chains are buried in the interior of a globular protein.
 - The hydrophilic side chains are usually exposed on the surface of a globular protein.
 - Acidic and basic amino acids can form salt bridges, or electrostatic interactions.
 - The cysteine amino acids can form disulfide bonds.
- Secondary structures stabilize the tertiary structure of the protein.

★ We recommend showing the students a 3D model of a protein to begin the activity.

For a more complete lesson guide, please visit:

<http://www.3dmoleculardesigns.com/Teacher-Resources/Amino-Acid-Starter-Kit.htm>

Side Chain Properties

Sort the side chains and place them in the appropriate place on the circular amino acid pie chart. You may use the Amino Acid Side Chain Chart[®] to help you sort.

- Notice that some of the side chains have a **YELLOW** band around the bottom. These side chains are **hydrophobic** and DO NOT like water.
- Notice that some of the side chains have a **WHITE** band around the bottom. These side chains are **hydrophilic** and DO like water.
- Notice that some side chains have a **RED** band around the bottom. These side chains are **acids** and carry a negative charge.
- Notice that some side chains have a **BLUE** band around the bottom. These side chains are **bases** and carry a positive charge.
- Notice that some side chains have a **GREEN** band around the bottom. These side chains are **cysteines** and are able to form a covalent disulfide bond between each other (they like to pair together).

1. What pattern can you observe in the structure of the hydrophobic side chains as compared to the hydrophilic side chains?

Folding a Protein

Modeling the Primary Structure



- Pick the two cysteine side chains (**green**).
- Pick the two acidic side chains (**red**).
- Pick the two basic side chains (**blue**).
- Pick any three hydrophilic amino acids (**white**).
- Pick any six hydrophobic amino acids (**yellow**).
- **Randomly** distribute them on the TOOPER. (If you space them about three inches apart, you will get an even distribution).

The sequence of amino acids in a protein (from N-terminus to C-terminus) is called its primary structure.

Modeling the Tertiary Structure

Fold your protein according to these chemical principles:

- The hydrophobic side chains are buried in the interior of a globular protein.
- The hydrophilic side chains are usually exposed on the surface of a globular protein.
- Acidic and basic amino acids can form salt bridges, or electrostatic interactions.
- The cysteine amino acids can form disulfide bonds

The final folded, 3D shape of your protein is called its tertiary structure.



2. Are all of the proteins folded the same way?

3. Why or why not?

4. How many different sequences of amino acids could be generated in your protein if there were an unlimited number of amino acids available for each of the 15 positions?

A protein's shape (structure) determines the function. Changing an amino acid side chain could alter the protein's shape, thus its function could be impaired or even enhanced.

Change one of the side chains in your sequence.

5. How might your protein be affected by a change in the side chain?

Modeling the Secondary Structure

- Unfold your protein and remove the amino acid side chains.
- Use the toober to fold the backbone of a protein. Incorporate a three-stranded beta sheet and two alpha helices in your structure.
- Shake the protein noting that the protein maintains its basic shape.
- Create an active site on the surface of your protein by adding three amino acid side chains – a serine, a histidine and a glutamic acid.
- The three amino acid side chains that make up your protein's active site may bind with a substance.
- Now, unwind your folded protein keeping the amino acids in their original position.

6. Where are the amino acids positioned on the protein backbone relative to each other?

Fold the protein again making the active site, but this time **do not** incorporate any alpha helices or beta sheets into the structure. Shake the protein you have just folded.

7. What happened to the shape of the protein when you shook the protein without the alpha helices and beta sheets incorporated into the overall structure?

8. Why are alpha helices and beta sheets important in protein structure?

The secondary structure of a protein consists of alpha helices and/or beta sheets. Proteins can be described as a series of alpha helices and beta sheets, joined by loops of less regular protein structure.

The Amino Acid Starter Kit[©] can be borrowed from the MSOE Model Lending Library (<http://cbm.msOE.edu/teachRes/library>) or purchased from 3D Molecular Designs (www.3dmoleculardesigns.com).