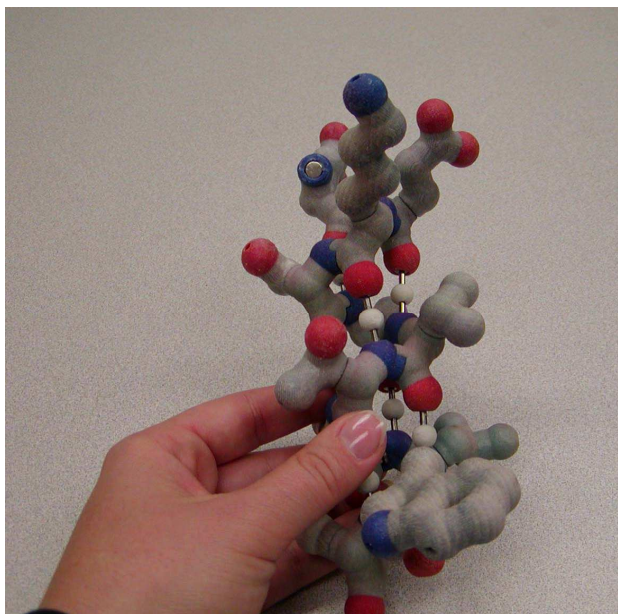


SMART Teams

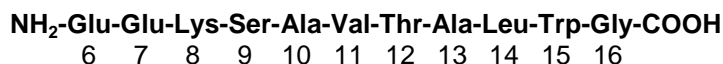
*Exploring the
Molecular World*

Modeling Helix A of β -Globin



Activity

1. Using the sidechains provided, construct helix A (residues 6-16) from β -globin, a subunit of hemoglobin.



2. One of the major driving forces of protein folding is the interaction of the amino acids with the environment. Examine the helix you just built. Can you determine what effect water has on the folding of these amino acids? *Note that the uncharged amino acids (gray amino acid side chains) lie primarily on one side of the helix, and the polar amino acids (containing red O and blue N) lie on the opposite side of the helix. The hydrophobic side lies on the inside of the protein, away from water, and the polar side is exposed on the outside of the protein.*

3. Sickle Cell Anemia is caused by a single mutation in the β -globin gene. Amino acid #7 (glutamate) is replaced with another amino acid (valine). This mutation leads to deformed red blood cells, resulting in anemia. Using your construction Kit, replace the glutamate at position 7 with a valine. What effect does this mutation have on the structural properties of the helix? *This portion of the helix changes from charged to hydrophobic, creating a hydrophobic 'patch' on the surface of the protein. This causes the hemoglobin proteins to 'clump' as the hydrophobic valine seeks to hide from the water surrounding the protein.*

****Possible misconceptions to be aware of when using working with these models:**

Amino acids are not assembled by backbone pieces first and followed by the addition of the sidechains. Physiologically, amino acids are constructed as individual units, which are then linked together during translation to form peptide bonds. The sidechains are separate in this kit to allow for exploration of the different structures of sidechains and to allow for just peptide backbones.