

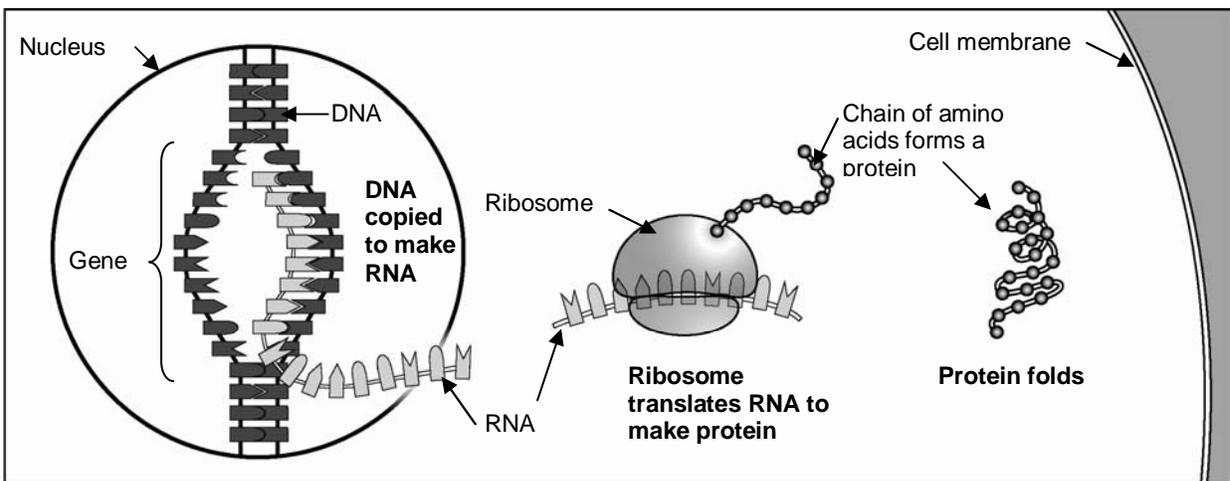
From DNA to Protein

Structure and Function

The nucleus of every cell contains chromosomes. These chromosomes are made of DNA molecules. Each DNA molecule consists of many genes. Each gene carries coded information for how to make one type of protein.

Your body makes many different kinds of proteins. Every protein in your body has a specific shape. It is this specific shape that allows each protein to perform a specific job. The combination of specific proteins that your body makes gives you your traits.

During protein synthesis, DNA is copied in the nucleus to make RNA. The RNA then moves to the cytoplasm where it attaches to a ribosome. The ribosome translates the coded information from the RNA to create a protein molecule with a specific sequence of amino acids. The protein folds into a particular shape that enables it to perform a specific function.



To help you understand how proteins are produced and how they function, you will model the processes of protein synthesis and protein folding.

Your Tasks:

- Model the processes of protein synthesis and protein folding.
- Relate the three dimensional (3-D) shape of proteins to their functions.

A. Modeling Protein Synthesis and Protein Folding

1. Use the *From DNA to Protein – Record Sheet* in your lab kit. The illustration in **Step A** of this worksheet represents a small part of the DNA code in a gene that carries instructions for making one kind of protein.
2. DNA molecules and genes cannot leave the nucleus. To carry the instructions to the ribosomes (protein factories) in the cytoplasm, the coded information in a gene (DNA) base sequence is transcribed (copied) to make messenger RNA (mRNA) molecules with complementary (opposite) base sequences.
3. Use the base pairing chart below to determine the base sequence code on the mRNA that would be produced when the DNA molecule is transcribed to make mRNA. The first few mRNA bases have been provided as samples. Write your answer on the mRNA line on the diagram (**Step B** of your worksheet).

Base on DNA	Complementary Base on mRNA
A	U
T	A
G	C
C	G

4. The mRNA then leaves the nucleus and attaches to a ribosome in the cytoplasm. In the ribosome, the mRNA base sequence is translated to determine the sequence (order) of amino acid building blocks in a protein.
5. Use the mRNA base sequence on your diagram and the genetic code chart provided to translate the mRNA code into a sequence of amino acid building blocks in a protein (also called a polypeptide). Each amino acid will be represented by a circle. The colors for the amino acids (yellow, blue, red or white) are indicated on the genetic code chart.
 - Write the name of the amino acids in the protein in the box above the circle (**Step C** of your worksheet).
 - Color each circle with the appropriate color as shown in the example. If you do not have colored pencils, you may write the color in the space below each of the circles.

6. Proteins are made of amino acids hooked end-to-end like beads on a necklace. To simulate a protein, you will make a model of your protein using a long chenille stem (the fuzzy covered wire) and colored beads. Refer to the sequence of 15 amino acids (the colored circles on **Step C** of your worksheet) and arrange beads of the appropriate colors on the chenille stem. The beads should be approximately evenly spaced the along the chenille stem.
7. The model that you have created represents the unfolded, **primary structure** of a protein – which is the sequence of amino acids in a protein.
8. Proteins do not remain straight and orderly. They twist and buckle, folding in upon themselves to form 3-dimensional (3-D) shapes. Twist one half of your protein model around a pencil to make a spiral. This spiral region is called an “alpha-helix.”
9. Bend the other half of your protein molecule into a zig-zag shape by making a bend in the opposite direction at each bead. This zig-zag region is called a “beta-pleated sheet.”
10. The alpha-helix and beta-pleated sheet represent the **secondary structure** of a protein. Make a drawing to show the secondary structure of your protein model (**Step D** of your worksheet). Label the alpha helix region and the beta-pleated sheet region on your drawing.
11. Twist your protein into a 3-D shape according to these protein folding rules:

Amino Acid (Bead) Color (based on chemical properties)	Protein Folding Rules
Yellow	These are fatty <u>hydrophobic</u> (water fearing) amino acids that should be clustered on the inside of the protein
Blue	These are <u>negatively charged</u> basic amino acids that are attracted to red (positively charged) amino acids on the protein
Red	These are <u>positively charged</u> acidic amino acids that are attracted to blue (negatively charged) amino acids on the protein
White	These are <u>hydrophilic</u> (water loving) amino acids that should be clustered on the outside of the protein

12. The resulting twisted structure is called the **tertiary structure** of a protein. Make a drawing to show the tertiary structure of your protein model (**Step D** of your worksheet). Note: Do the best you can to make your 2-dimensional drawing look like your 3D model.

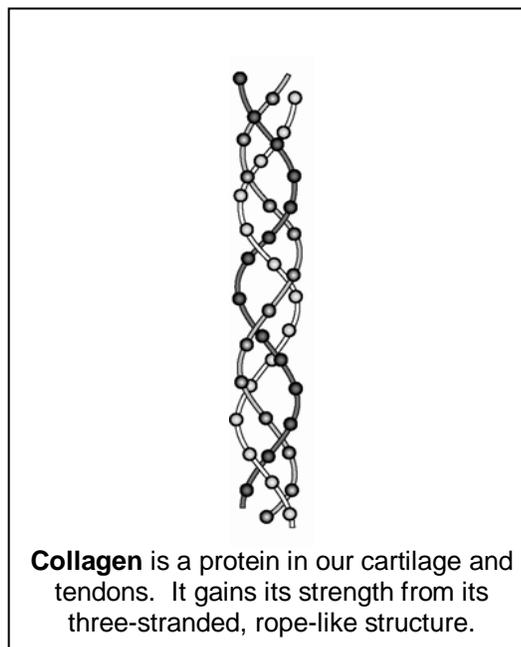
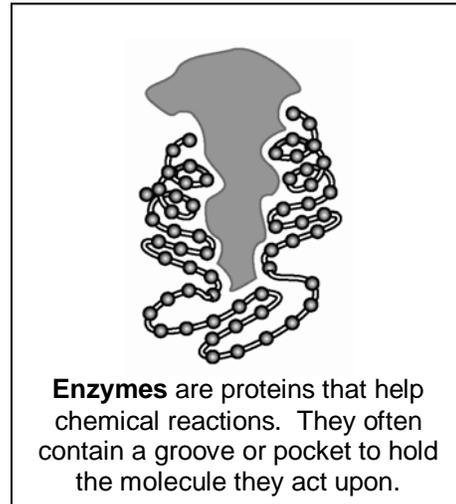
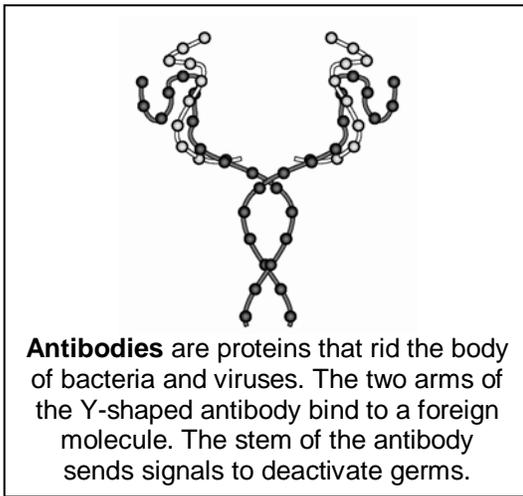
13. Some protein chains are attracted to other protein chains. Work with a partner and try putting your protein model next to their protein model in a way that still follows the rules of protein folding. This represents the **quaternary structure** of a protein.

14. Make a drawing to show the quaternary structure of your protein model (**Step D** of your worksheet).

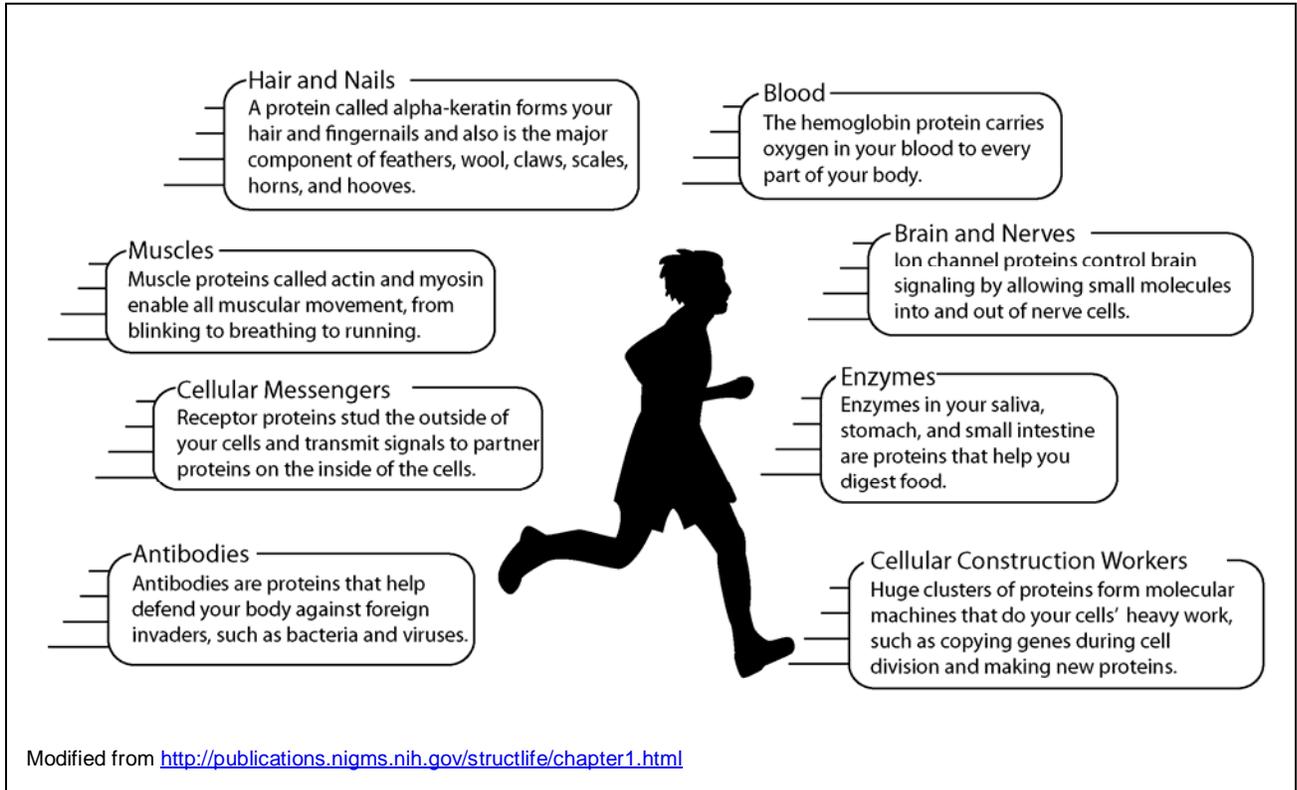
B. Protein Shape and Function

The 3-D folded model that you created represents only a small part of a protein. Actual proteins are huge molecules made of hundred or thousands of amino acids. The primary structure of actual proteins consists of hundreds of amino acids hooked together into a long chain that are then twisted, bent, and folded into a protein with a specific 3-D shape.

Just like the shape of a tool determines its function, the final shape of a protein enables it to accomplish its functions in your body. Each different type of protein in your body has a shape that is specific for its function. The diagrams below show some examples of the shapes of different kinds of protein.



The protein that you eat in food is digested into amino acids. These amino acids are then used by your cells to build many different kinds of new proteins. These proteins are worker molecules that are necessary for virtually every activity in your body. Proteins have many different functions in our bodies.



Different kinds of proteins have different shapes that are essential for their function. The shape of a protein is essential for its function. By studying the structures of proteins, we are better able to understand how they function normally and how some proteins with abnormal shapes can cause disease.

The forces that hold a protein into its 3-D shape are weak and easily disrupted by changes in temperature or exposure to strong acids or bases. When this happens the protein denatures (it unfolds and untwists).

1. Use your protein model to show what would happen to a protein in your body that denatures. Pull the ends to of your protein model to straighten the amino acid chain.
2. How will denaturing a protein affect its ability to carry out its function?

3. What might happen to a person if each of the following proteins became denatured? Be specific. (Hint: Refer to the diagram on page 6.)

- Muscle proteins:

- Antibodies:

- Enzymes:

- Ion channel proteins in the brain and nerve cells:

- Receptor proteins on the outside of cells:

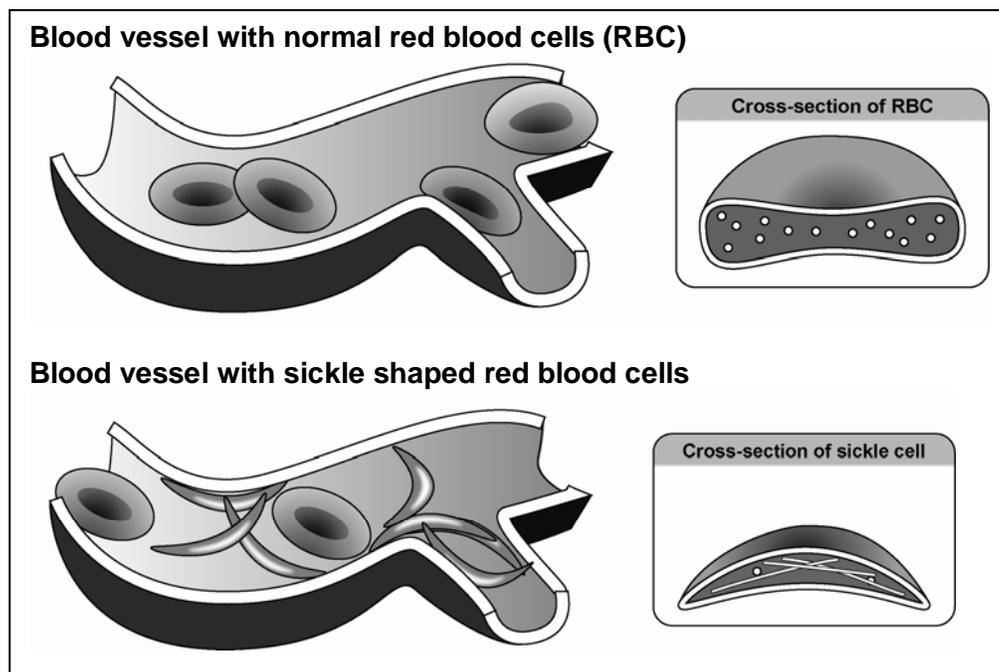
C. Sickle Cell Anemia – An Error in Protein Structure and Function

Hemoglobin is a protein molecule found in red blood cells. The hemoglobin protein binds to oxygen and carries the oxygen to cells throughout the body. Sickle cell anemia is a blood disease that affects the ability of hemoglobin to bind to oxygen. People with sickle cell anemia inherit a mutation in the DNA base code that carries the information for how to make hemoglobin protein. This DNA mutation leads to a change in the sequence of the amino acids for hemoglobin. In sickle-cell anemia, one amino acid in the hemoglobin protein is incorrect.

1. To model the effect of a change in the amino acid sequence of a protein, replace one of the yellow beads on your protein molecule with a red bead. Follow the “protein folding rules” on page 5 to refold your protein model.

2. How does changing the amino acid sequence on your model affect the protein model?

The change in the shape in the hemoglobin protein molecules causes them to stick together into long rods that distort the shape of the red blood cells. Instead of the normal smooth, round shape, the red blood cells become sickle shaped (shaped like the letter “C”). The sickle-shaped red blood cells are stiff and stick together, forming clumps in the blood vessels. These clumps block the normal flow of blood to the limbs and organs, causing symptoms such as pain and swelling, infections and organ damage.



3. Explain how changing the shape of the hemoglobin proteins affects the hemoglobin function.

4. Explain how the change in hemoglobin function affects the structure and function of red blood cells.

5. Explain how the change in red blood cell structure and function results in the symptoms of sickle cell anemia.

6. Arrange the following phrases in order to indicate the sequence of events that would occur as a result of a gene mutation in the gene that codes for hemoglobin protein.

- 1 Gene mutation (change in the DNA code in the gene for hemoglobin)
- 2 Change in the mRNA code
- ___ Change in the amino acid sequence of the hemoglobin protein
- ___ Change in the structure or function of body cells or tissues
- ___ Change in the shape of a hemoglobin protein
- ___ Change in the ability of the hemoglobin protein to function properly
- 7 Change in characteristics and symptoms of a genetic disease