

Proteins

Learning objective 1.7.A Describe the structure and function of proteins.

Name:

Date:

Period:

Use the tool **Sequence Becomes Shape**. On the **Fold a protein** tab you press R groups to write a sequence and the chain folds itself. Do Parts 1 to 3 there, then switch to **Predict the effect** for Part 4.

Part 1 • Predict, then check

Build each of these three sequences, twelve residues long, and record how compact the tool says the result is. Predict first.

Sequence of R groups	I predict	What the tool says	R group interactions
12 × Hydrophobic			
12 × Ionic + (all the same charge)			
Alternating Ionic + and Ionic –			

1. Explain why the all-hydrophobic chain and the all-positive chain end up so differently, even though both are twelve amino acids long.

Part 2 · The parts and the bond

Press **Load an example protein** and open the panels underneath the bench to answer these.

2. Describe the parts of a single amino acid.

3. Identify the process that forms the covalent peptide bonds joining amino acids into a polypeptide, and state which two groups the bond forms between.

4. Name the three chemical categories an R group can fall into.

5. Name the four interactions that hold tertiary structure together, and state which one is covalent.

Part 3 · Break it

With the example protein loaded, press **Heat it** and watch. Then cool it again and press **Change the pH**. Record the R group interaction count each time.

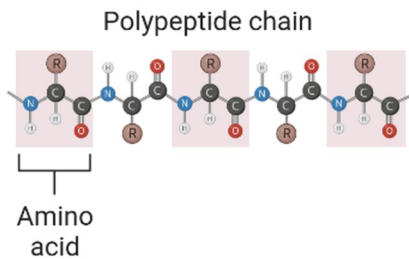
Condition	R group interactions	How compact	Disulfide bridges
Normal			
Heated			
pH changed			

6. Explain why heating leaves the disulfide bridges in place while the other interactions are lost.

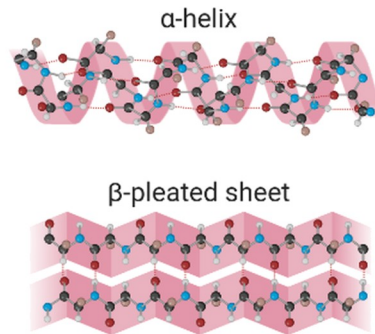
Part 4 • Predict the effect

Switch to **Predict the effect** and work the cards. Then answer these on your own, in complete sentences.

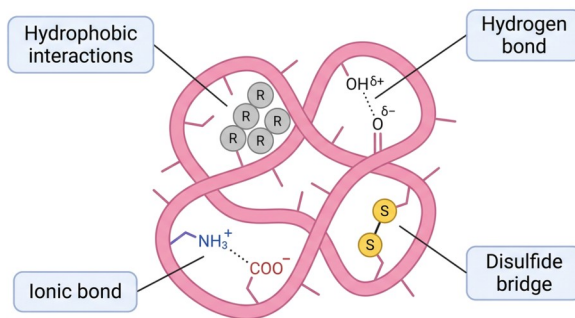
Primary structure



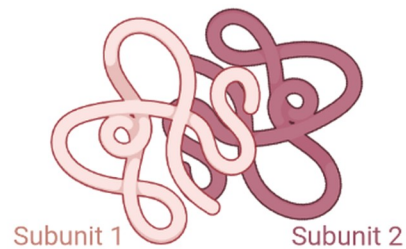
Secondary structure



Tertiary structure



Quaternary structure



The four levels of protein structure. Panels are not drawn to the same scale. Use it with the questions in this part. Created in BioRender.

7. Connect the primary structure of a protein to its overall shape.

8. A receptor has two amino acids replaced, putting charged R groups where hydrophobic ones used to be. Explain why the receptor changes shape, and predict the effect on its function.

9. Place an X next to each level of protein structure you would expect to be altered by that substitution, and briefly justify each choice.

What the model simplifies

The protein folds in two dimensions. Real proteins fold in three, so a real hydrophobic core can be fully enclosed where this one can only approximate that.

Amino acids are drawn as colored beads labeled by the chemical category of their R group. The CED states that the molecular structure of amino acids is beyond the scope of the AP Exam, so this tool models R group properties and their interactions rather than drawing structures.

Secondary structure — the alpha-helices and beta-pleated sheets formed by hydrogen bonding along the backbone — is described in the tool but not drawn. The bench shows tertiary folding driven by R group interactions.