AP BIOLOGY · UNIT 1 · TOPIC 1.7

# 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

Predict how compact each of these three sequences will be. Then build each one, twelve amino acids long, and record what the tool reports.

| Sequence of R groups | I predict | How compact (tool readout) | R group interactions |
|---|---|---|---|
| 12 × Hydrophobic | | | |
| 12 × Ionic + (all the same charge) | | | |
| Alternating Ionic + and Ionic − | | | |

**1. The all-hydrophobic chain and the all-positive chain are both twelve amino acids long. Explain why the two chains fold so differently.**

## Part 2 · The parts and the bond

Press **Load an example protein**. Then open the panels under the heading The four levels to answer these questions.

**2. Describe the parts of a single amino acid.**

**3. (a) Identify the process that forms the peptide bonds joining amino acids into a polypeptide.**

**(b) Identify the two groups between which a peptide bond forms.**

**4. Identify the three chemical categories of R groups.**

**5. (a) Identify the four interactions that stabilize tertiary structure.**

**(b) Identify which of these interactions is covalent.**

## Part 3 · Break it

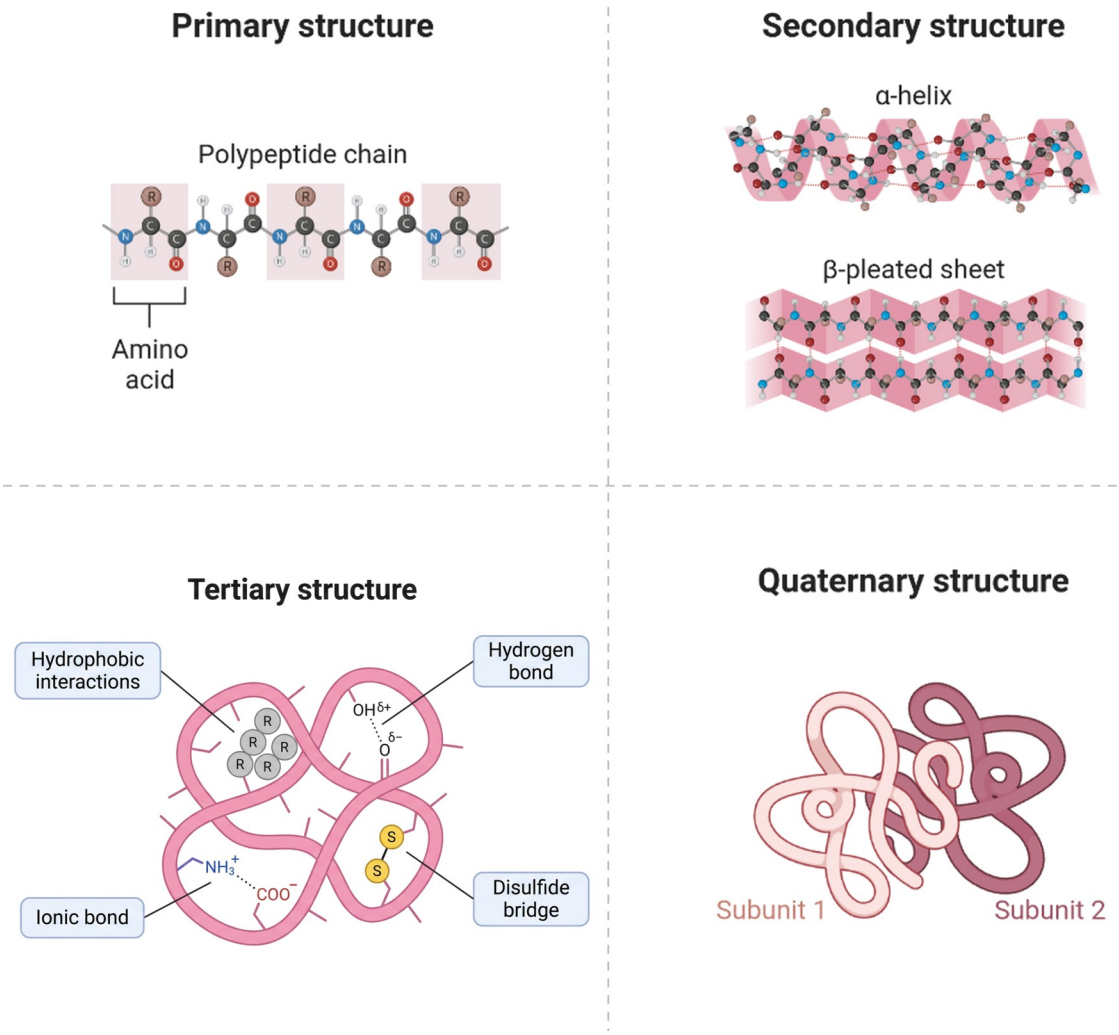
With the example protein loaded, record the Normal row. Then press **Heat it** and record the Heated row once the protein settles. Next, press Load an example protein again and then press **Change the pH**. Record the pH changed row.

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

**6. Explain why heating disrupts the hydrogen bonds, hydrophobic interactions and ionic interactions but leaves the disulfide bridges intact.**

## Part 4 · Predict the effect

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




*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. Explain how the primary structure of a protein determines its overall shape.**

**8. In a receptor protein, two amino acids with hydrophobic R groups are replaced by amino acids with charged R groups.**
**(a) Explain why the receptor changes shape.**

**(b) Predict the effect of the change on the receptor's function. Justify your prediction.**

**9. The receptor in question 8 is a single polypeptide.**
**(a) For each of the four levels of protein structure (primary, secondary, tertiary and quaternary), determine whether the substitution would alter it.**

**(b) Provide reasoning to justify each determination in part (a).**

## 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.