Four levels, four different questions

These are levels of description, not four separate ingredients. Start with sequence, then describe local patterns, the whole chain and, where present, an assembly of chains.

1. PRIMARY

Which amino acid comes next?

The specific order of amino acid residues in a polypeptide. Covalent peptide bonds join neighbouring residues.



2. SECONDARY

How does a local region fold?

Regular local backbone arrangements, including alpha helices and beta pleated sheets. Hydrogen bonds stabilise these patterns.



3. TERTIARY

What is the shape of one whole chain?

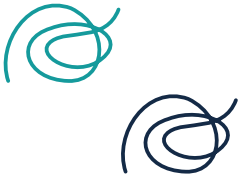
The overall three-dimensional conformation of one polypeptide, including its helices, sheets, turns and other regions.



4. QUATERNARY

How do separate chains fit together?

The arrangement and interactions of two or more polypeptide subunits in one protein. It does not mean exactly four chains.



Schematic key: circles are residues; each continuous folded line is one chain. Shapes illustrate the level, not an experimentally determined protein structure.

Supporting reading: OpenStax Biology 2e, 3.4 Proteins.

Scope: Cambridge Biology 9700 syllabus, section 2.3, outcome 2, p. 18.

Secondary means local pattern

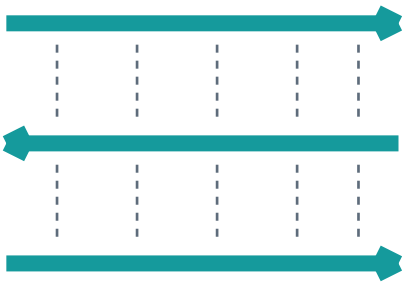
The peptide backbone can form repeating structures. An alpha helix is coiled; a beta pleated sheet contains aligned, extended strands. Both are secondary structure.

α helix



Coiled backbone

β pleated sheet



Adjacent backbone strands

Dashed lines: hydrogen bonds

Schematic views, not atomic models. Sheet arrows show strand direction; a strand is a stretched region of a chain, not necessarily an entire separate polypeptide.

1. IDENTIFY WHAT HYDROGEN-BONDS

Hydrogen bonds form between backbone C=O and N-H groups. They are not the covalent peptide bonds that link successive amino acids, and do not require bonds between R groups.

2. LOCAL PATTERNS CAN SHARE ONE CHAIN

Different regions of one polypeptide may form helices and sheets, connected by turns or loops. A sheet can involve segments of the same chain folding back alongside one another.

Key distinction: recognising a sheet does not, by itself, prove quaternary structure. Count separate polypeptide chains, not the visible arrows or coils.

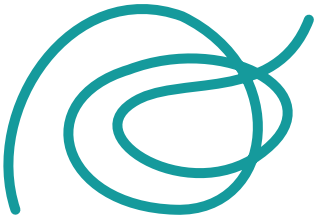
Supporting reading: Alberts et al., Molecular Biology of the Cell, protein structure.

Scope: Cambridge Biology 9700 syllabus, section 2.3, outcome 2, p. 18.

One chain or several subunits?

Tertiary structure describes one complete folded polypeptide. Quaternary structure describes how multiple polypeptides associate. A single-chain protein has no quaternary structure.

TERTIARY



One folded chain

QUATERNARY



Four chains in this example

One protein can contain several subunits; each subunit has its own sequence.

1. SEQUENCE HELPS DETERMINE FOLDING

The order of residues places R groups along the chain. Their chemistry influences folding and the shape of binding sites. A sequence change may affect function, but not every substitution has a large effect.

2. AN ASSEMBLY IS NOT JUST A BIG FOLD

Adult haemoglobin has two alpha and two beta polypeptide chains: their association is quaternary structure. A very long single chain is still only one chain. Detailed haemoglobin structure comes later.

3. QUICK IDENTIFICATION GUIDE

Order of residues: primary. A local helix or sheet: secondary. Whole-chain shape: tertiary. Arrangement of separate chains: quaternary. The next lesson examines the interactions that stabilise these structures.

Supporting reading: OpenStax Biology 2e, 3.4 Proteins.

Scope: Cambridge Biology 9700 syllabus, section 2.3, outcome 2, p. 18.