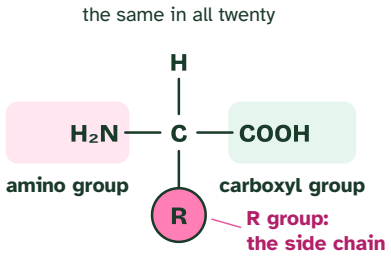
Proteins: shape is *function*

What to know, what to draw and what to say. Nothing else.

THE ONE IDEA

The sequence of amino acids decides how a chain folds, and the folded shape decides what the protein can do.



Draw it like this. A central carbon with four things on it. Only the R group changes.

1.7.A START HERE

Twenty monomers, *one pattern*

- Every protein is built from **amino acids**. All twenty kinds share one pattern: a central carbon carrying an **amino group**, a **carboxyl group**, a hydrogen atom and a side chain.
- The side chain, the **R group**, is the only part that differs. It gives each amino acid its chemistry, and it decides how a chain folds.
- You do not need the structure of any particular amino acid: know the pattern, and the kinds of R group.

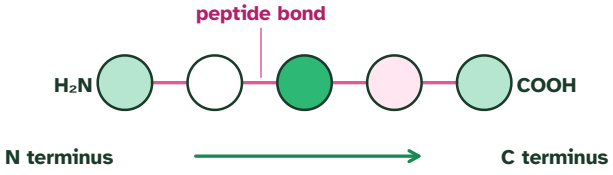
WHAT PROTEINS DO

E Enzymes	speed up reactions
C Channels	and pumps cross membranes
A Antibodies	defend the body
F Fibers	collagen and keratin

1.7.A PEPTIDE BONDS AND DIRECTION

A chain with a *beginning* and an end

- Amino acids join by dehydration synthesis: the carboxyl group of one meets the amino group of the next, and an OH and an H leave as water. The covalent bond is a **peptide bond**.
- Many amino acids joined make a **polypeptide**. It has direction: a free amino group at the **N terminus** and a free carboxyl group at the **C terminus**.
- Each new amino acid is added at the carboxyl end, so a chain grows from N to C. The order along it is the **sequence**.
- R groups are not part of the bond: they hang off the backbone.



Each circle is one amino acid. The arrow shows the way the chain grows.

20
kinds of amino acid

20^{10}
ways to order a chain of only ten

1.7.A WHAT DECIDES THE FOLD

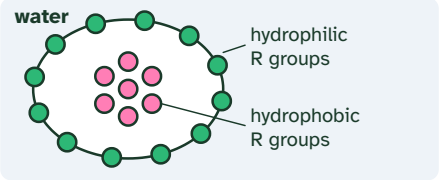
R groups: three kinds

NONPOLAR
Hydrophobic
Mostly carbon and hydrogen. In water they cluster together, away from it.

POLAR
Hydrophilic
Carry OH or other partial charges. They hydrogen bond with water and each other.

CHARGED
Ionic
Acidic ones become negative, basic ones positive. Opposite charges attract.

- In water, a protein's surface is mostly hydrophilic and charged R groups; its **core is mostly hydrophobic**.



1.7.A SEQUENCE, SHAPE, FUNCTION

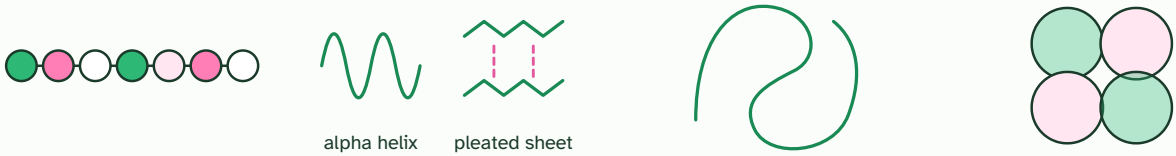
One amino acid can *change everything*

- Change the sequence and the chain may fold differently: a new shape, and a changed or lost function.
- **Sickle cell disease:** one charged amino acid in a chain of hemoglobin is swapped for a hydrophobic one. The molecules stick together when oxygen is low and distort the red blood cell.
- **Shape is function**: an enzyme's active site, a receptor's binding site and a channel's pore are all pockets made by folding.

Four levels of *structure*, and how to lose them

1.7.A FOUR LEVELS OF STRUCTURE

Each level is built on the *one before*



	PRIMARY	SECONDARY	TERTIARY	QUATERNARY
What it is	The **sequence** of amino acids. It decides everything that follows.	Local folding of the backbone into an **alpha helix** or a **beta pleated sheet**.	The whole chain's **three-dimensional shape**, set by its R groups.	How the chains fit together in a protein of **two or more polypeptides**.
Held by	**Peptide bonds** Covalent.	**Hydrogen bonds** Between C=O and N–H of the backbone, not between R groups.	**R group interactions** A hydrophobic core, hydrogen bonds, ionic bonds and disulfide bridges.	**The same interactions** This time between chains.
Denatured	Kept: only hydrolysis breaks peptide bonds.	Lost.	Lost.	Lost.

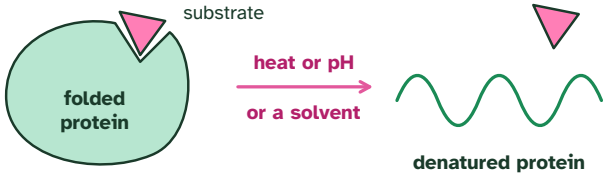
Hemoglobin has four chains; collagen has three, wound into a rope.

A **disulfide bridge** is a covalent bond between the sulfur atoms of two cysteines

1.7.A

Denaturing: unfold it and it stops working

- The interactions that hold the shape are weak. Break them and the protein unfolds: it is **denatured**.
- It **keeps its full sequence** but loses its shape, so an enzyme's active site no longer fits its substrate.
- Unfolded chains expose their hydrophobic R groups and clump, as egg white does in a pan. Clumped protein rarely refolds.
- Each protein works best where it evolved: most human proteins near 37 °C and pH 7, the enzymes of the stomach near pH 2.



CAUSE 1
Heat
The chain vibrates until hydrogen bonds snap.

CAUSE 2
Acid or alkali
Charges on R groups change, so ionic and hydrogen bonds fail.

CAUSE 3
Solvents
Ethanol and other solvents loosen the hydrophobic core.

WATCH OUT

Five mistakes that *cost points*

- ✕ **Peptide bonds join the backbone.** R groups are not part of the bond: they hang off the chain.
- ✕ **Secondary structure is hydrogen bonds in the backbone.** Bonds between R groups are tertiary.
- ✕ **Not every protein has quaternary structure.** Only those made of two or more polypeptides.
- ✕ **Denaturing is not hydrolysis.** The peptide bonds and the sequence stay; only the shape goes.
- ✕ **Amino acids are not only C, H, O and N.** Two of the twenty carry sulfur in their R groups.

COVER THE SHEET

Can you *answer these?*

1. Draw an amino acid and label its four parts.
2. Describe how a peptide bond forms.
3. Identify the two ends of a polypeptide.
4. Predict where hydrophobic R groups lie in water.
5. Describe what holds an alpha helix in shape.
6. Explain how one changed amino acid can alter function.
7. Explain why a denatured enzyme stops working.
8. Explain why boiling does not hydrolyze a protein.

IN THE EXAM

Follow the chain of cause: sequence, then R group interactions, then shape, then function. Name the level of structure and the bond that holds it.

GO FURTHER

Animated figures, a dry lab and a marked Check are in the full guide online.