REVISION GUIDE

Twenty amino acids, and the shape that *does the work*

Proteins

A chain of amino acids folds into an enzyme, a channel or a strand of silk, and one changed amino acid can change the whole shape. How a sequence becomes a shape, and what happens when the shape is lost.

6 chapters · a dry lab

The interactive guide, with every animation:

biologybybradford.com/guides/ap-biology-unit-1-proteins

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	Answers	26

By the end you can

- [ ] Describe the parts of an amino acid and explain how dehydration synthesis joins them by peptide bonds into a chain with an amino (N) end and a carboxyl (C) end 1.7.A
- [ ] Explain how the chemistry of R groups, hydrophobic, hydrophilic, charged or polar, gives each amino acid its properties 1.7.A
- [ ] Describe primary, secondary, tertiary and quaternary structure and the bonds or interactions that hold each 1.7.A
- [ ] Explain how a change in the sequence of amino acids can change the shape, and so the function, of a protein 1.7.A
- [ ] Explain how heat, pH and solvents denature a protein, and why a denatured protein no longer works 1.7.A

Tick each one when you can do it without the book.

01 Twenty monomers, one *pattern*

1.7.A AMINO ACIDS

Proteins do most of the work in a cell: enzymes speed up its reactions, channels and pumps move things across its membranes, antibodies defend it, and fibers such as collagen and keratin hold it together. Every one is built from the same monomers, **amino acids**.

All twenty kinds share one pattern. A central carbon carries four things: an **amino group** (NH_2), a **carboxyl group** (COOH), a hydrogen atom, and a side chain called the **R group**. Only the R group differs from one amino acid to the next, and it gives each its chemistry.

You do not need to know the structures of particular amino acids for the exam. You do need the pattern, and how R groups are sorted by what they do (chapter 3).

KEY POINTS

- Same in every amino acid: amino group, carboxyl group, hydrogen.
- Different: the R group.

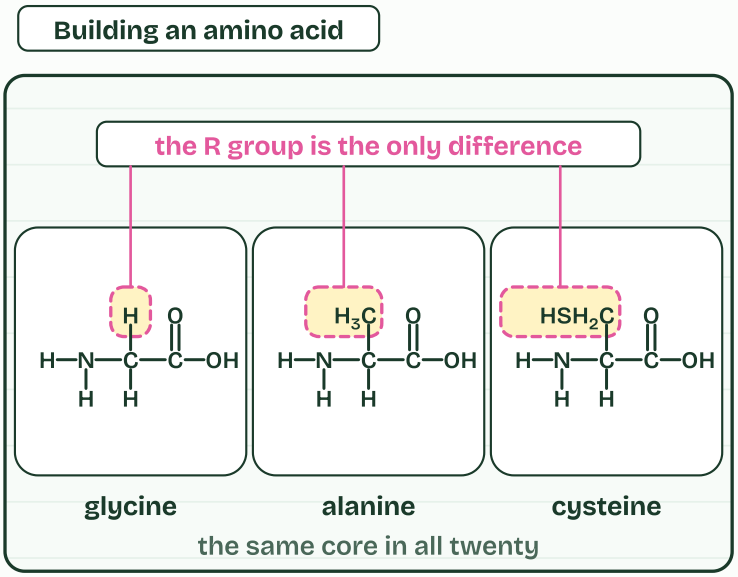
KEY TERMS

amino acids
The monomer of proteins: a central carbon bonded to an amino group, a carboxyl group, a hydrogen and an R group.

amino group
The group NH2 on an amino acid; it can pick up a hydrogen ion and become positively charged.

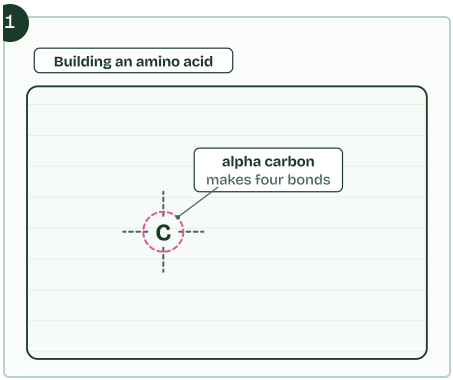
carboxyl group
The group COOH on an amino acid; it can lose a hydrogen ion and become negatively charged.

R group
The side chain on the central carbon of an amino acid, different in each of the twenty kinds. Its chemistry is hydrophobic, hydrophilic or ionic.



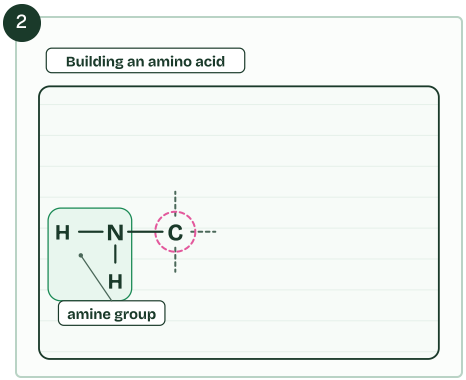
STEP BY STEP
6 STEPS

1



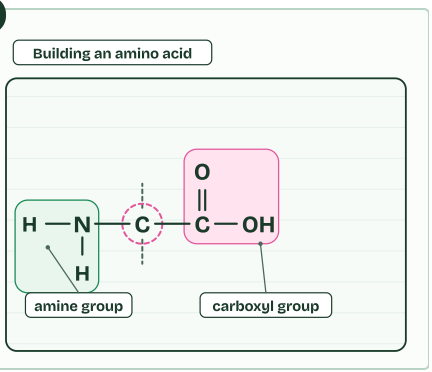
The **alpha carbon** makes four bonds.

2



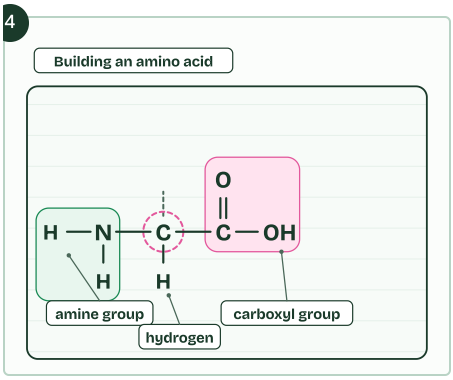
An **amine group** goes on the left bond: a nitrogen with two hydrogens.

3



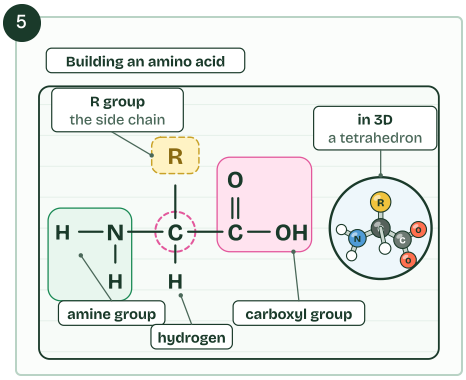
A **carboxyl group** goes on the right bond: a carbon with a double bond to one oxygen and a single bond to an OH.

4



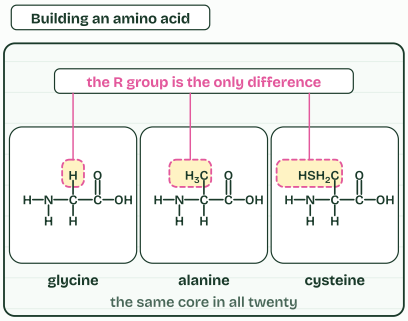
One **hydrogen** atom goes on the bottom bond.

5



The last bond carries the **R group**. It stands for whatever side chain this amino acid has.

6



Three different amino acids: the same core in each, and only the **R group** differs.

WATCH OUT

"Amino acids contain only C, H, O and N." Most do, but two of the twenty carry sulfur in their R groups, and that sulfur can bridge two parts of a protein (chapter 5).

PREDICT

Two amino acids have the same amino group, carboxyl group and hydrogen. What has to be different for them to be two kinds of amino acid?

(A) The central carbon, which is carbon in one amino acid and a nitrogen atom in the other

(B) The R group, the side chain on the central carbon, which differs in every one of the twenty

(C) The number of amino groups, which ranges from one to four in the different kinds of amino acid

Decide before you look. Answer on page 26.

02 A chain with a *beginning* and an end

1.7.A PEPTIDE BONDS AND DIRECTION

Amino acids join by dehydration synthesis. The carboxyl group of one meets the amino group of the next; an OH and an H leave as water, and a covalent **peptide bond** forms between them. Two amino acids make a dipeptide; many make a **polypeptide**.

A polypeptide has direction. Its first amino acid has a free amino group, the **amino (N) terminus**, and its last a free carboxyl group, the **carboxyl (C) terminus**. A cell builds every protein the same way: each new amino acid is added at the carboxyl end, so the chain grows from N to C (Unit 6).

The order of the amino acids along the chain is the protein's sequence. With twenty choices at every position, a chain of just ten can be put together in 20^{10}, about ten million million, ways.

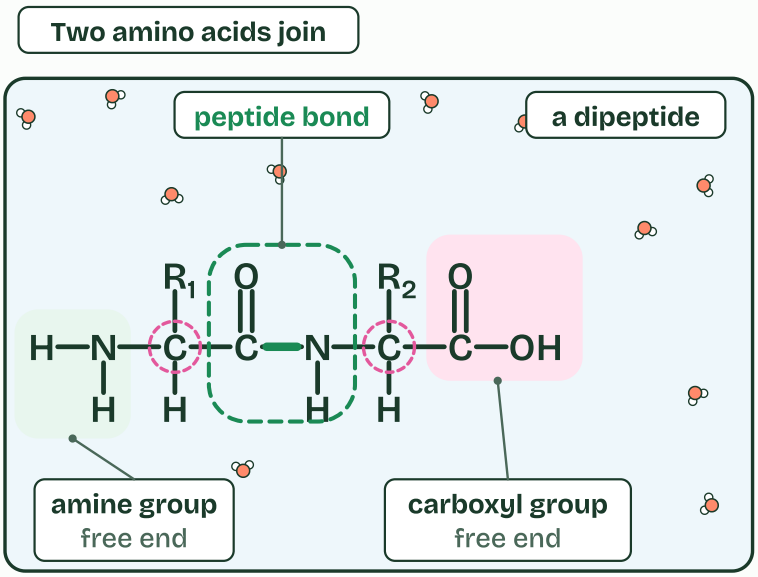
KEY TERMS

peptide bond
The covalent bond between the carboxyl group of one amino acid and the amino group of the next, formed by dehydration synthesis.

polypeptide
A chain of amino acids joined by peptide bonds. A protein is one or more polypeptides, folded.

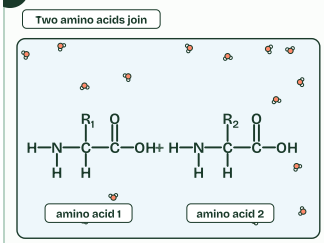
amino (N) terminus
The end of a polypeptide with a free amino group: the N-terminus, where the chain began.

carboxyl (C) terminus
The end of a polypeptide with a free carboxyl group: the C-terminus, where new amino acids are added.



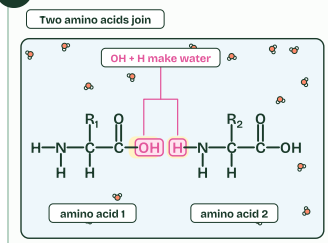
STEP BY STEP
4 STEPS

1



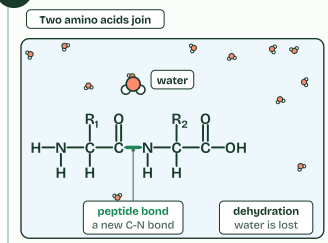
Two amino acids, R_1 and R_2, with the carboxyl group of the first facing the amine group of the second.

2



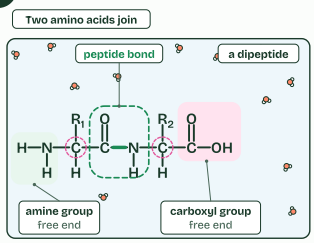
The **OH** from the carboxyl group and one **H** from the amine group are lit: they will leave as **water**.

3



The carbon bonds to the nitrogen and the water drifts away. The new C-N bond is a **peptide bond**.

4

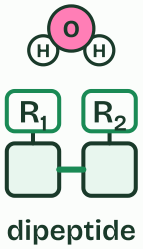


A **dipeptide**, drawn as an examiner wants it. It still has an amine group at one end and a carboxyl group at the other.

amino acid + amino acid ⇌ dipeptide + water

dehydration synthesis

hydrolysis



dipeptide

Join the amino acids, both ways round, then add water to split them again. Count the peptide bonds and the water released.

STEP BY STEP
4 STEPS

1



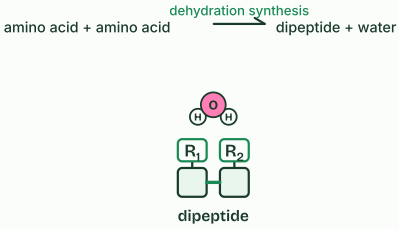
Two **amino acids**.

2



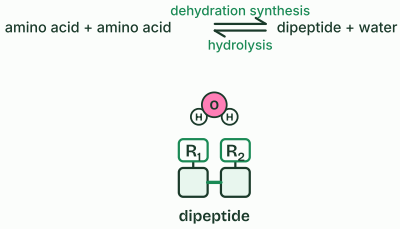
An OH from one and an H from the other face each other.

3



They leave as **water**, and a **peptide bond** joins the carbon to the nitrogen: **dehydration synthesis**, making a **dipeptide**.

4



Add water and the peptide bond splits again, the OH back to the carbon and the H to the nitrogen: **hydrolysis**.

WATCH OUT

Peptide bonds join the backbone, carboxyl to amino. The R groups are not part of the bond: they hang off the chain.

PREDICT

A polypeptide of 120 amino acids is made in a cell. How many peptide bonds does it have, and how many water molecules were released?

(A) 120 bonds and 120 waters

(B) 119 bonds and 119 waters

(C) 119 bonds and 240 waters

(D) 120 bonds and 60 waters

Decide before you look. Answer on page 26.

03 Hydrophobic, hydrophilic, *charged*

1.7.A R GROUPS

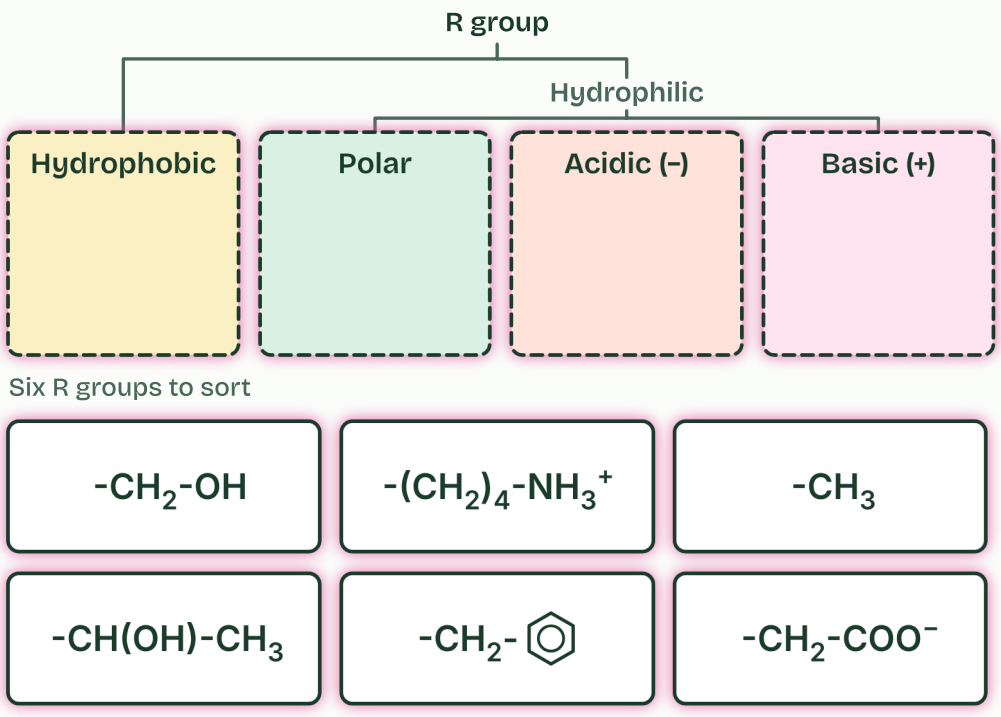
R groups fall into three kinds by their chemistry, and that is what decides how a chain folds.

KEY POINTS

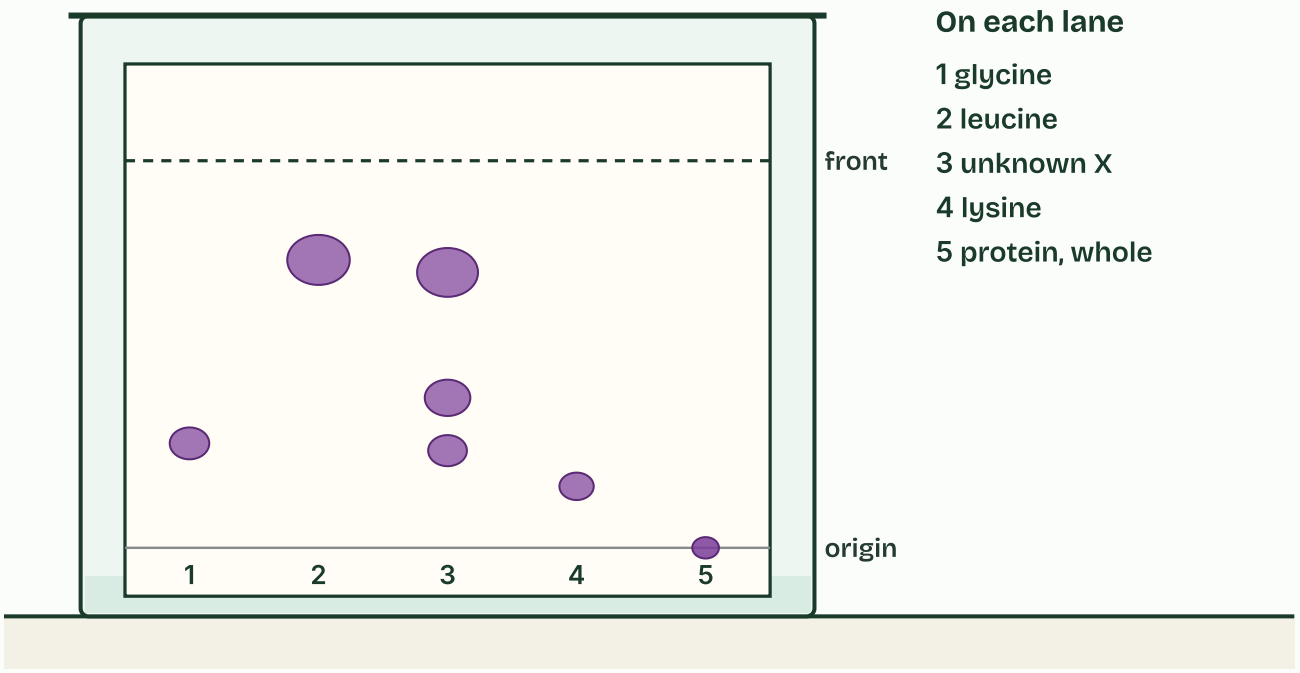
- **Hydrophobic (nonpolar).** Mostly carbon and hydrogen, like a small lipid. In water they cluster together, away from it.
- **Hydrophilic (polar).** They carry OH, or other groups with partial charges, and form hydrogen bonds with water and with each other.
- **Ionic (charged).** Acidic R groups lose a hydrogen ion and become negative; basic ones gain one and become positive. Opposite charges attract.

A protein's surface in water is mostly hydrophilic and charged R groups, and its core mostly hydrophobic ones. A protein that sits in a membrane turns this inside out where it crosses the bilayer: a band of hydrophobic R groups faces the fatty acid tails.

Paper chromatography shows the difference. In the dry lab under this chapter, amino acids with large hydrophobic R groups travel furthest with the solvent, and charged ones cling to the wet paper near where they started.



Six R groups, drawn as condensed formulas, and four bins. Which bin does each belong in, and what tells you?



Spot each lane on the origin line, run the solvent up the paper, dry it, spray with ninhydrin, and measure each spot from the origin. Rf = distance moved by the spot ÷ distance moved by the front.

WATCH OUT

Hydrophilic and hydrophobic describe the R groups. Every amino acid's own amino and carboxyl groups are polar, but in a chain they are tied up in peptide bonds.

PREDICT

A protein dissolves in the cytoplasm. Where in its folded shape would you expect to find most of its hydrophobic R groups?

(A) Spread evenly over its outer surface, where they help the protein to dissolve in the watery cytoplasm

(B) Packed in its core, out of contact with water, while hydrophilic and charged R groups face outward

(C) Only at its two ends, the amino and the carboxyl terminus, where the chain sticks out from the folds

Decide before you look. Answer on page 26.

04 The sequence, then the first *folds*

1.7.A PRIMARY AND SECONDARY STRUCTURE

A protein's structure is described at four levels, each built on the one before.

The **primary structure** is the sequence of amino acids, held by peptide bonds. It decides everything that follows: change one amino acid and the whole protein may fold differently. In sickle cell disease one amino acid in a chain of hemoglobin, a charged one, is swapped for a hydrophobic one; the changed molecules stick together when oxygen is low and distort the red blood cell (Unit 6).

The **secondary structure** is local folding of the backbone into two regular shapes: an **alpha helix**, a coil, and a **beta pleated sheet**, stretches lying side by side. Both are held by hydrogen bonds between the C=O and N–H groups of the backbone itself, not between R groups.

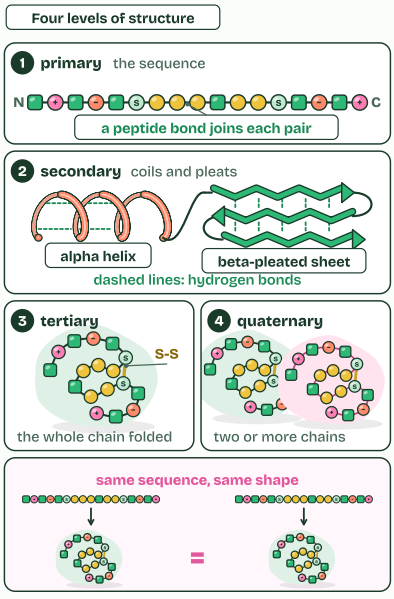
KEY TERMS

primary structure
The sequence of amino acids in a polypeptide, held by peptide bonds. It decides every other level of structure.

secondary structure
Local folding of a polypeptide into alpha helices and beta pleated sheets, held by hydrogen bonds between the backbone's C=O and N–H groups.

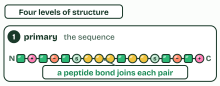
alpha helix
A coil of the backbone held by hydrogen bonds between each C=O and the N–H four amino acids along.

beta pleated sheet
Stretches of the backbone lying side by side, held by hydrogen bonds between them, in a folded sheet.



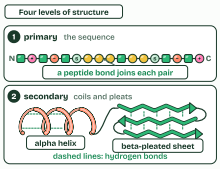
STEP BY STEP
5 STEPS

1



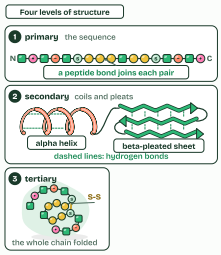
Primary structure: a sequence of amino acids, each joined to the next by a peptide bond.

2



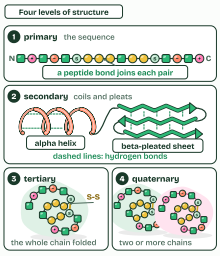
Secondary structure: one stretch coils and another pleats beside itself, held by dashed hydrogen bonds.

3



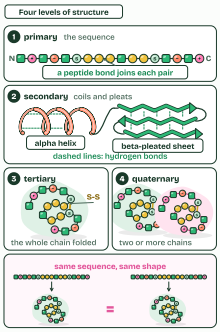
Tertiary structure: the whole chain folded into a compact shape.

4

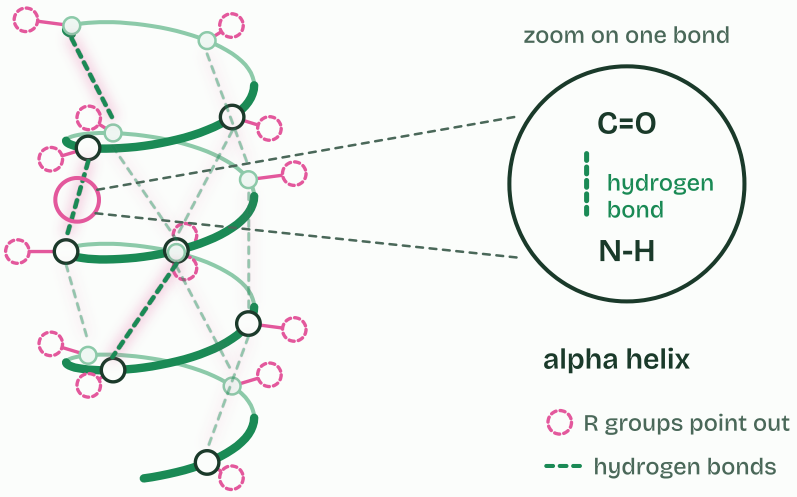


Quaternary structure: two or more folded chains together. Not every protein has one.

5



A second copy of the same sequence folds into the same shape: same sequence, **same shape**, every time.



Hydrogen bond the O of a C=O group in one amino acid and the H of an N-H group four amino acids further along. Both groups are in the backbone.

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Hydrogen bond the O of a C=O group in one strand and the H of an N-H group in the strand beside it. Both groups are in the backbone.

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Beta-pleated sheet stretches of the chain side by side, held by hydrogen bonds between backbone groups.

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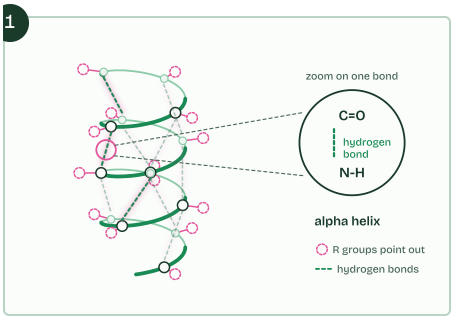
Alpha helix one stretch of the chain coiled, held by hydrogen bonds between backbone groups in regular positions.

Loops the less regular stretches that join the helices and sheets together.

SWITCH IT

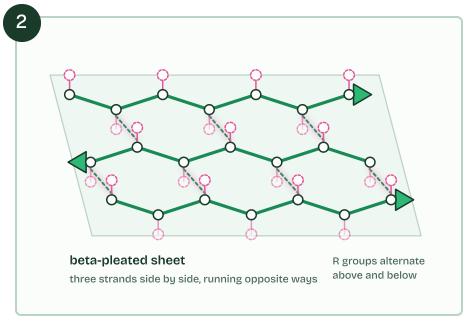
3 SETTINGS

1



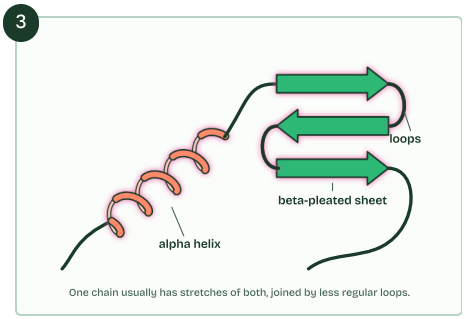
Helix

2

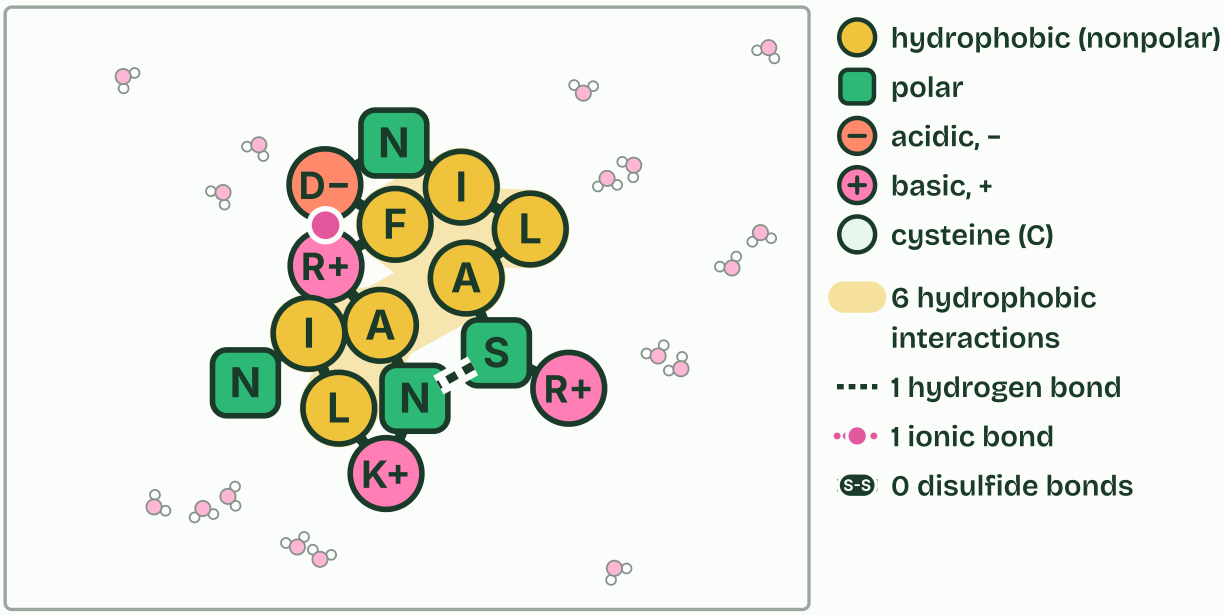


Sheet

3



In a protein

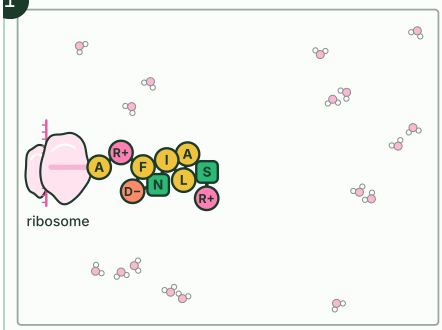


Type your name or pick a gene, press Fold and watch which bonds form and where the nonpolar amino acids end up. Fold the made-up membrane protein across a membrane. Then change one base: try the sickle cell change and make a second copy, then a frameshift.

STEP BY STEP

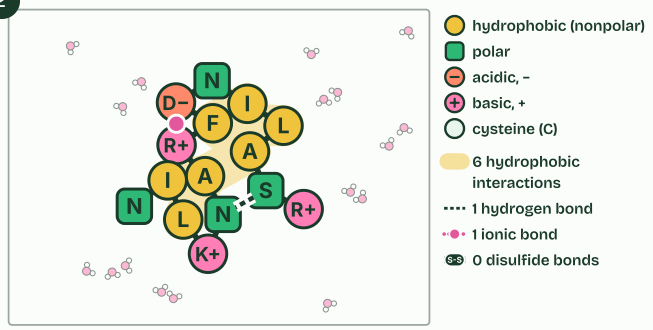
2 STEPS

1



Type **ROSALIND FRANKLIN**: each letter is the code for one amino acid (the O is skipped: no amino acid has that letter). A ribosome makes the chain one amino acid at a time, and it starts to fold as it comes out.

2



In water it folds: the **nonpolar** ones gather inside, away from the water (6 of 7), and the polar ones face outwards. Hydrophobic interactions, hydrogen bonds and ionic bonds hold it.

WATCH OUT

Secondary structure is held by hydrogen bonds in the backbone. The bonds between R groups belong to tertiary structure.

PREDICT

A protein is heated until its folds come undone. Which level of its structure is still there?

(A) The secondary structure, because its hydrogen bonds are the strongest bonds in any protein

(B) The primary structure, because heat breaks the weaker bonds of the folds but not the peptide bonds

(C) None of them, because heating a protein breaks it apart into single amino acids straight away

Decide before you look. Answer on page 26.

05 R groups pull the chain into *shape*

1.7.A TERTIARY AND QUATERNARY STRUCTURE

The **tertiary structure** is the whole chain's three-dimensional shape, and it is set by the R groups. Hydrophobic R groups gather in the core, away from water. Polar R groups form hydrogen bonds, opposite charges form ionic bonds, and the sulfur atoms of two cysteines can join in a covalent **disulfide bridge**. The shape that results is usually the one with the lowest free energy, which is why a chain folds the same way every time.

Some proteins are made of more than one polypeptide, and how the chains fit together is the **quaternary structure**. Hemoglobin is four chains, each holding an iron-containing heme group; collagen is three chains wound into a rope.

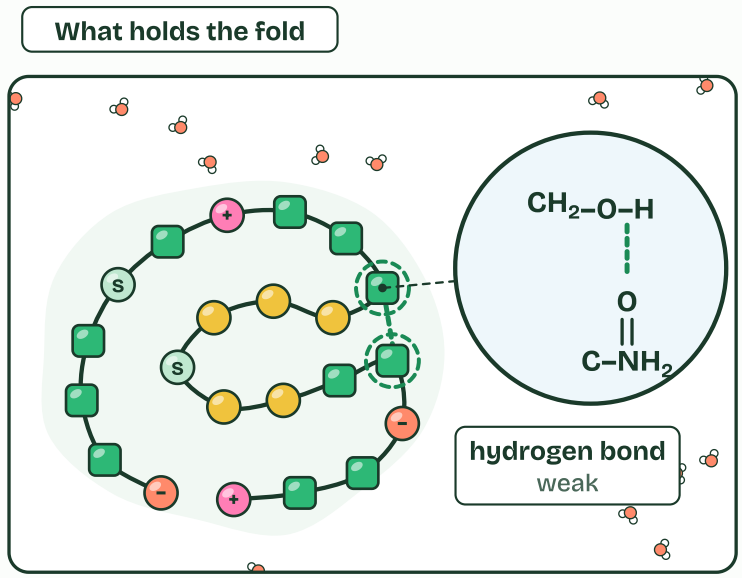
Shape is function. An enzyme's active site, a receptor's binding site and a channel's pore are all pockets made by folding. Change the shape and the function goes with it (chapter 6).

KEY TERMS

tertiary structure
The overall three-dimensional shape of a polypeptide, held by interactions between its R groups.

disulfide bridge
A covalent bond between the sulfur atoms of two cysteine R groups, which locks two parts of a chain together.

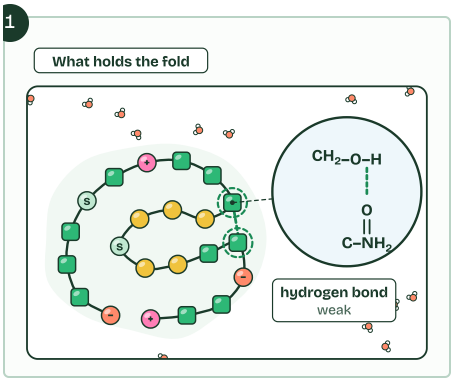
quaternary structure
The arrangement of two or more polypeptides in one protein, held by the same kinds of interaction as tertiary structure.



SWITCH IT

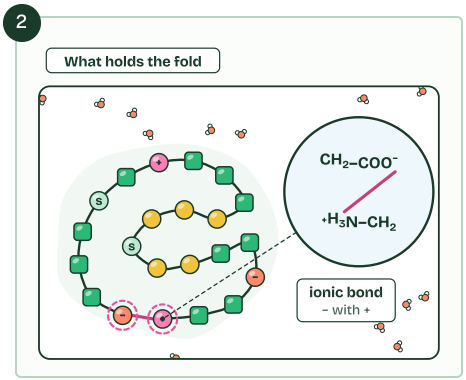
6 SETTINGS

1



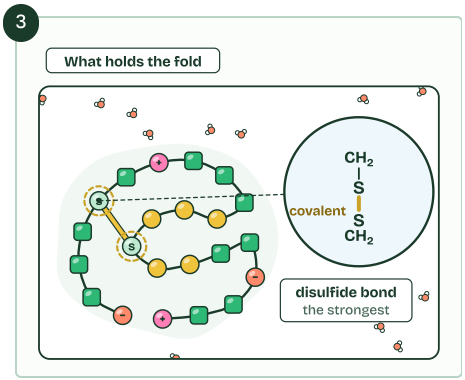
Hydrogen

2



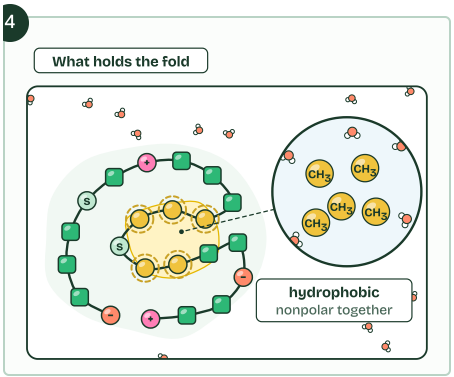
Ionic

3



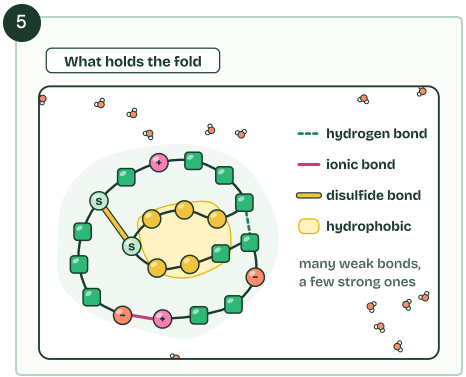
Disulfide

4



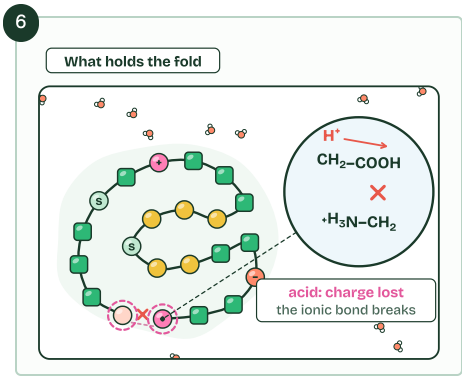
Hydrophobic

5

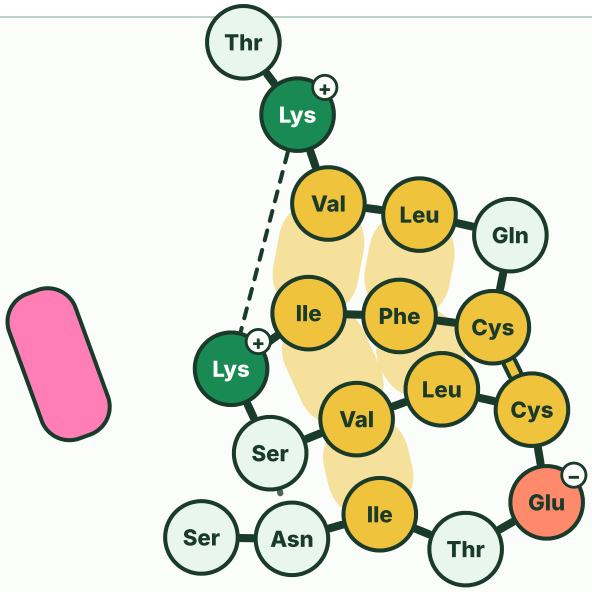


All

6



Lower the pH

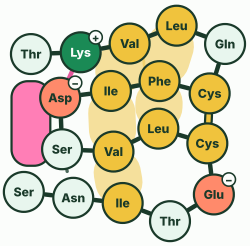


A made-up chain of 18 amino acids with a substrate in its pocket. Tap an amino acid and swap it for another: watch which interactions break, how far the fold moves and whether the substrate still fits. Try swapping a residue for one of the same class, one on the surface and one in the core. It is a toy model, not a real protein.

STEP BY STEP

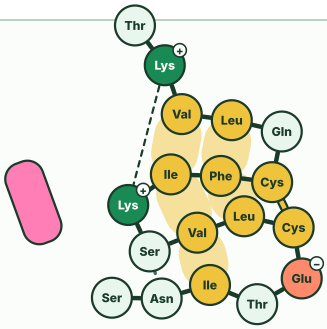
2 STEPS

1

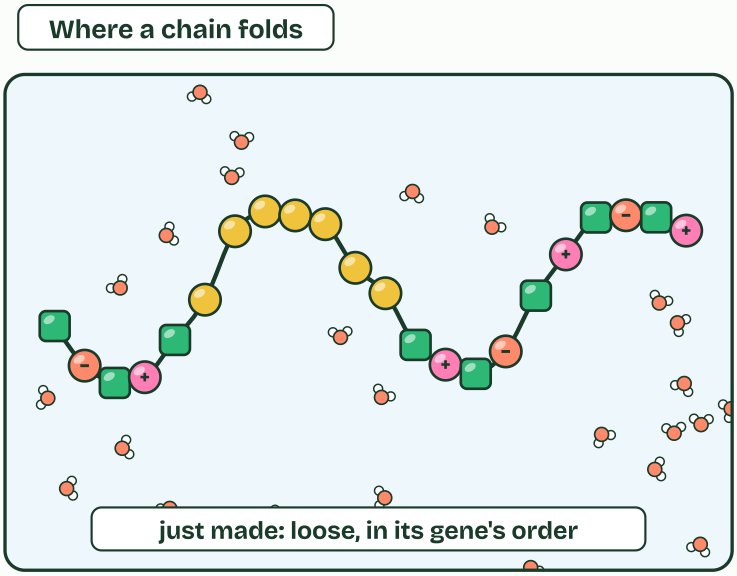


A folded chain of 18 amino acids. The **R groups** hold the fold with hydrophobic interactions, hydrogen bonds, ionic bonds and a disulfide bridge, and a **substrate** sits in the pocket.

2



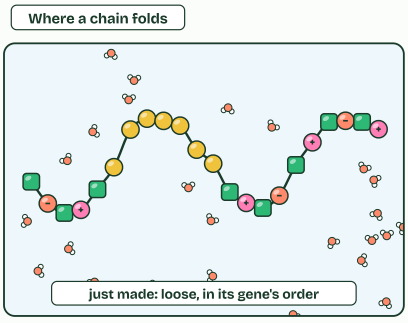
Aspartic acid 9 swapped for lysine: the ionic bond is lost and two like charges repel, so the pocket is **distorted** and the substrate no longer fits.



SWITCH IT

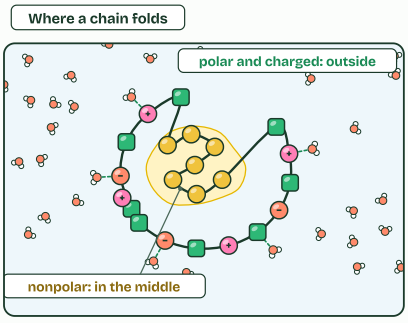
3 SETTINGS

1



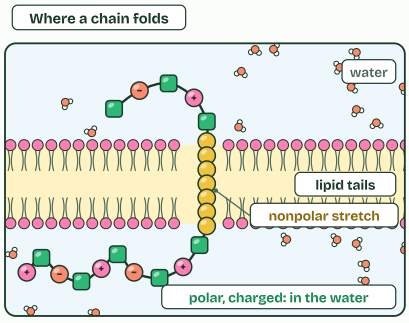
Unfolded

2

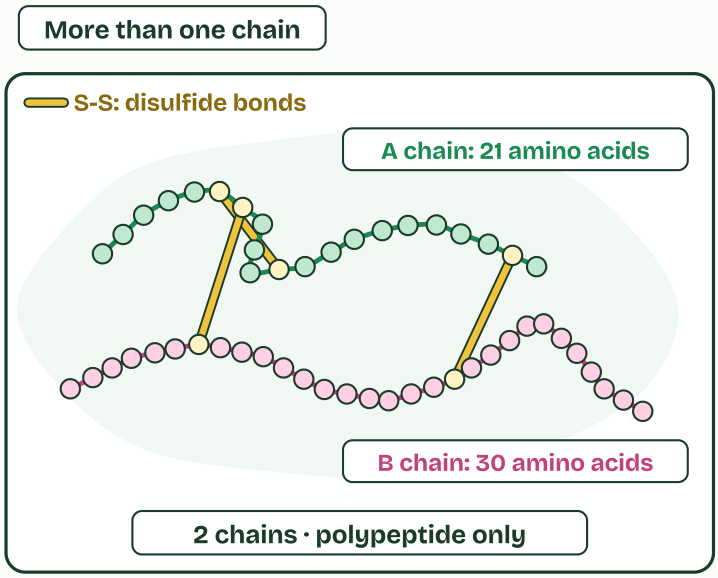


In water

3



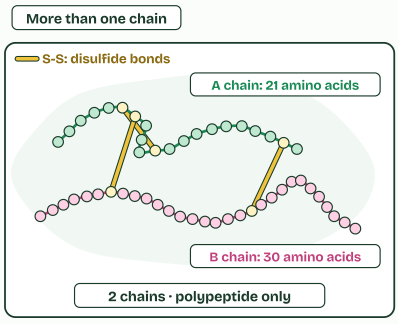
In a membrane



SWITCH IT

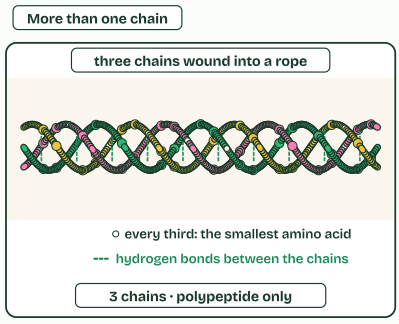
3 SETTINGS

1



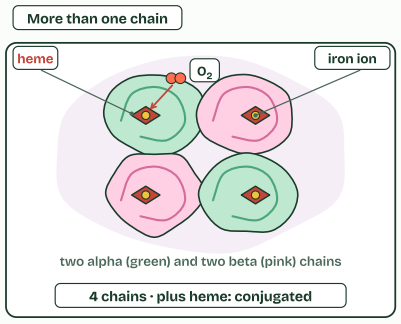
Insulin

2



Collagen

3



Hemoglobin

REMEMBER IT

Four levels of structure

P Pretty	S Super	T Tidy	Q Quilt
Primary the sequence, peptide bonds	**Secondary** helices and sheets, backbone hydrogen bonds	**Tertiary** the whole fold, R group interactions	**Quaternary** more than one chain

WATCH OUT

Not every protein has quaternary structure: only those made of two or more polypeptides.

PREDICT

In one protein, a positively charged R group sits next to a negatively charged one in the folded shape. A mutation swaps the negative one for a hydrophobic R group. What is most likely?

(A) Nothing changes, because one amino acid out of hundreds is far too small a change to affect the shape

(B) The protein breaks into two pieces where the swapped amino acid sits, because its peptide bonds fail

(C) The ionic bond between them is lost, so that part of the chain may fold differently and the function may change

Decide before you look. Answer on page 26.

06 Unfold it and it stops *working*

1.7.A SHAPE, FUNCTION AND DENATURING

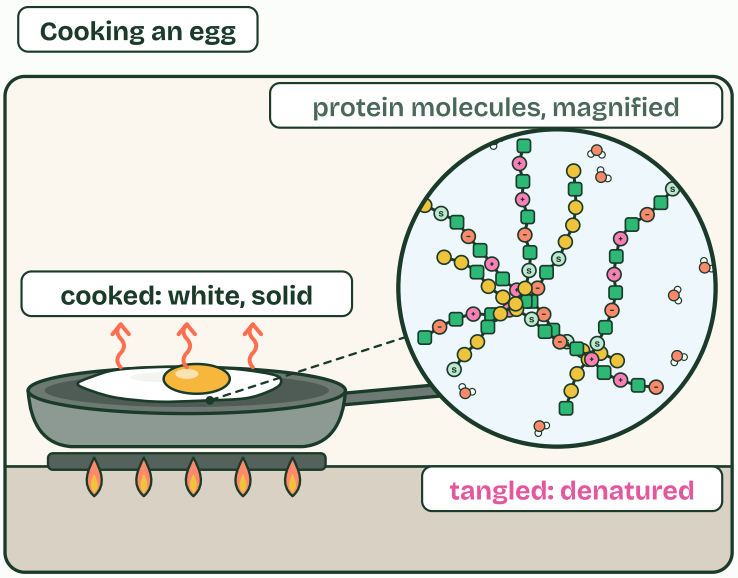
The bonds that hold tertiary structure are weak, and they can be broken. Heat makes the chain vibrate until hydrogen bonds snap. Strong acid or alkali changes the charges on R groups, so ionic bonds and hydrogen bonds fail. Ethanol and other solvents loosen the hydrophobic core. Any of them can unfold a protein: it is **denatured**.

A denatured protein still has its full sequence, but it has lost its shape, and with it its function: an enzyme's active site no longer fits its substrate. Unfolded chains often expose their hydrophobic R groups and stick to each other in clumps, which is what you see when egg white turns white in a pan. Mild unfolding can sometimes be undone, but clumped protein rarely refolds.

Each protein works best in the conditions it evolved in: most human proteins near 37 °C and pH 7, but the enzymes of the stomach near pH 2. How rate depends on temperature and pH, and why, is Unit 3.

KEY TERMS

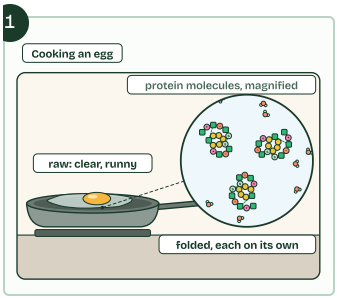
denatured
Changed in shape, by heat, pH or chemicals, so that a protein loses its function. The primary structure is unchanged.



STEP BY STEP

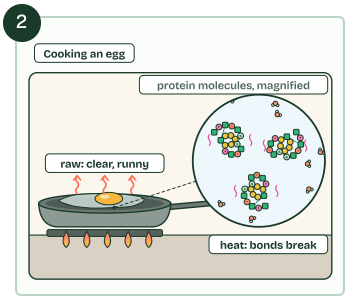
4 STEPS

1



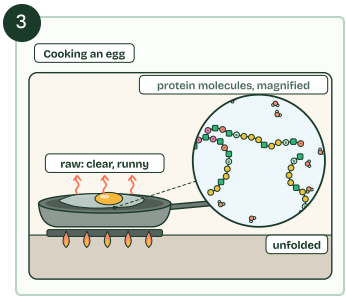
Raw egg white: clear and runny. Magnified, the proteins are **folded**, each on its own among the water molecules.

2



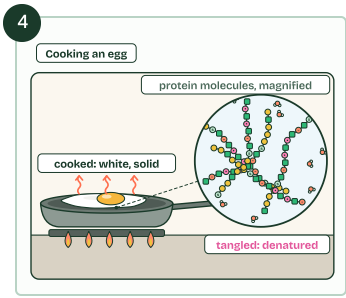
Heat makes the molecules jiggle harder and breaks the bonds that hold the folds.

3



The chains **unfold**: with the bonds gone, their shape is gone.

4

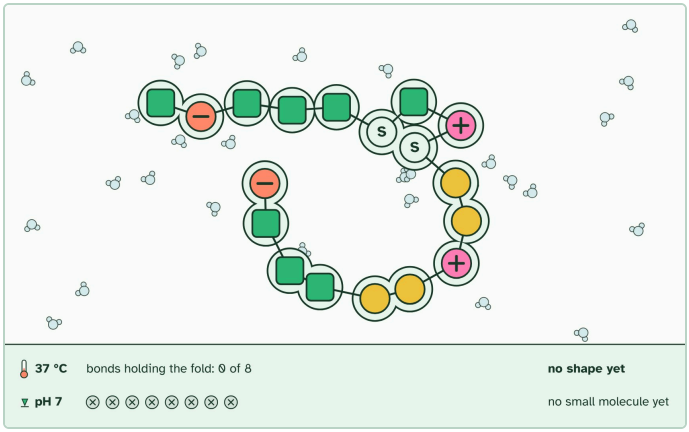


Unfolded chains **tangle** together and the egg white sets, white and solid. The proteins are **denatured**.

ANIMATION · HEAT IT, CHANGE THE PH

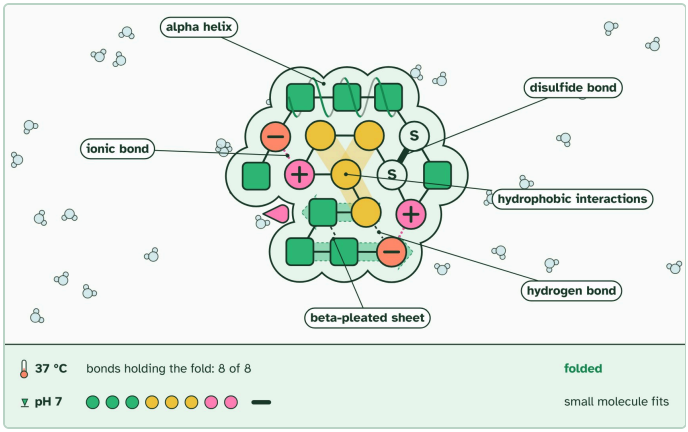
3 MOMENTS

1 — 37 °C, PH 7



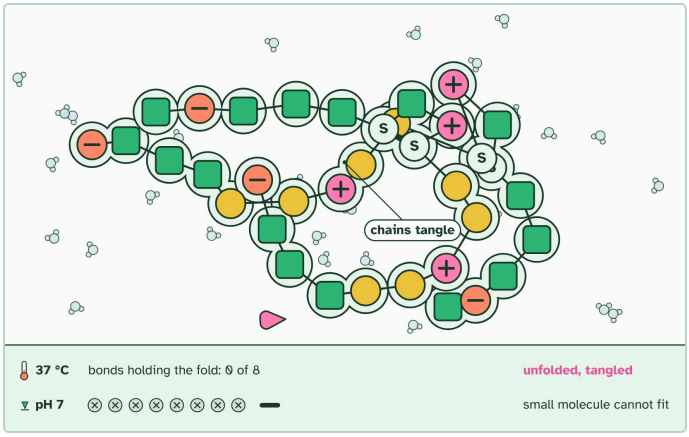
A new chain of amino acids among water molecules: as yet it has **no shape**.

2 — 37 °C, PH 7



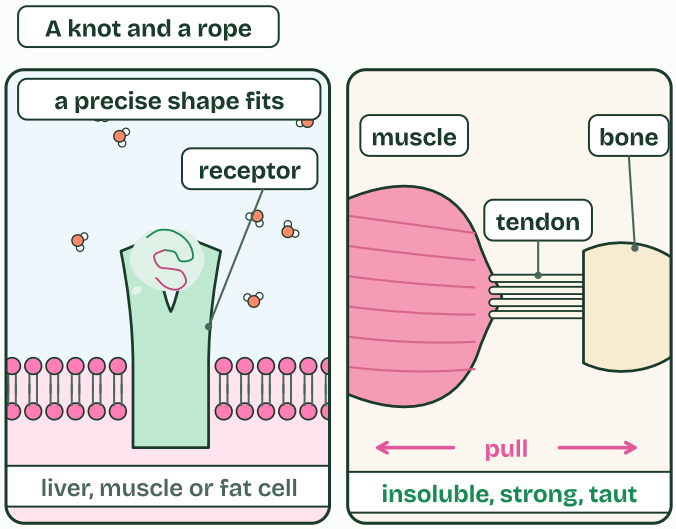
A small molecule **fits** its pocket: one precise shape, one job.

3 — 37 °C, PH 7



Cooled again, it does not refold: the unfolded chains **tangle** together instead.

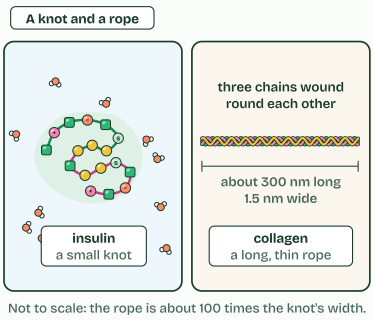
Watch it move, and change it as it runs: biologybybradford.com/guides/ap-biology-unit-1-proteins#denature



STEP BY STEP

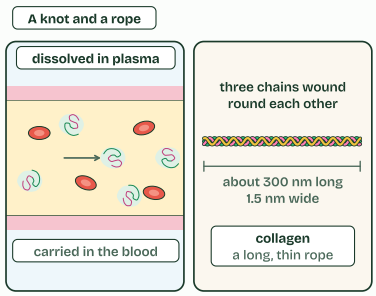
5 STEPS

1



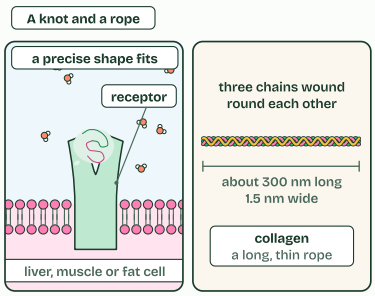
One **insulin** molecule is a small rounded knot among water molecules. One **collagen** molecule is a long, thin rope, about 100 times longer than the knot is wide.

2



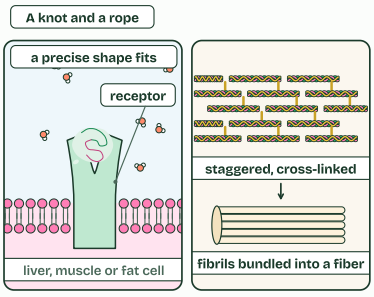
Insulin is **soluble**: dissolved in the plasma, it is carried round the body in the blood.

3



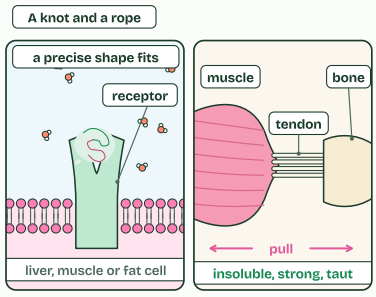
Insulin has a **precise shape** that fits the receptor on its target cells, liver, muscle and fat cells, like a key in a lock.

4



Collagen ropes lie side by side, staggered and **cross-linked**, into fibrils, and fibrils are bundled into fibers.

5



In a tendon, collagen fibers are **insoluble** and strong: they stay taut when muscle pulls on bone.

WATCH OUT

"Denaturing breaks a protein into amino acids." That is hydrolysis. Denaturing breaks only the weaker interactions that hold the shape.

PREDICT

Raw egg white is clear. Cooked, it is white and firm, and it stays white when it cools. Why does it not go back?

(A) Cooking breaks the peptide bonds, so the proteins are now single amino acids, and those are white and solid

(B) The unfolded chains have stuck to each other in clumps, so they cannot find their way back to their folds

(C) Cooking drives all the water out of the egg white, and the dry protein left behind cannot dissolve again

Decide before you look. Answer on page 26.

Key terms

Every term this guide defines, A to Z, with the chapter it is in. Cover the right-hand side and test yourself.

alpha helix 04
A coil of the backbone held by hydrogen bonds between each C=O and the N–H four amino acids along.

amino (N) terminus 02
The end of a polypeptide with a free amino group: the N-terminus, where the chain began.

amino acids 01
The monomer of proteins: a central carbon bonded to an amino group, a carboxyl group, a hydrogen and an R group.

amino group 01
The group NH2 on an amino acid; it can pick up a hydrogen ion and become positively charged.

beta pleated sheet 04
Stretches of the backbone lying side by side, held by hydrogen bonds between them, in a folded sheet.

carboxyl (C) terminus 02
The end of a polypeptide with a free carboxyl group: the C-terminus, where new amino acids are added.

carboxyl group 01
The group COOH on an amino acid; it can lose a hydrogen ion and become negatively charged.

denatured 06
Changed in shape, by heat, pH or chemicals, so that a protein loses its function. The primary structure is unchanged.

disulfide bridge 05
A covalent bond between the sulfur atoms of two cysteine R groups, which locks two parts of a chain together.

peptide bond 02
The covalent bond between the carboxyl group of one amino acid and the amino group of the next, formed by dehydration synthesis.

polypeptide 02
A chain of amino acids joined by peptide bonds. A protein is one or more polypeptides, folded.

primary structure 04
The sequence of amino acids in a polypeptide, held by peptide bonds. It decides every other level of structure.

quaternary structure 05
The arrangement of two or more polypeptides in one protein, held by the same kinds of interaction as tertiary structure.

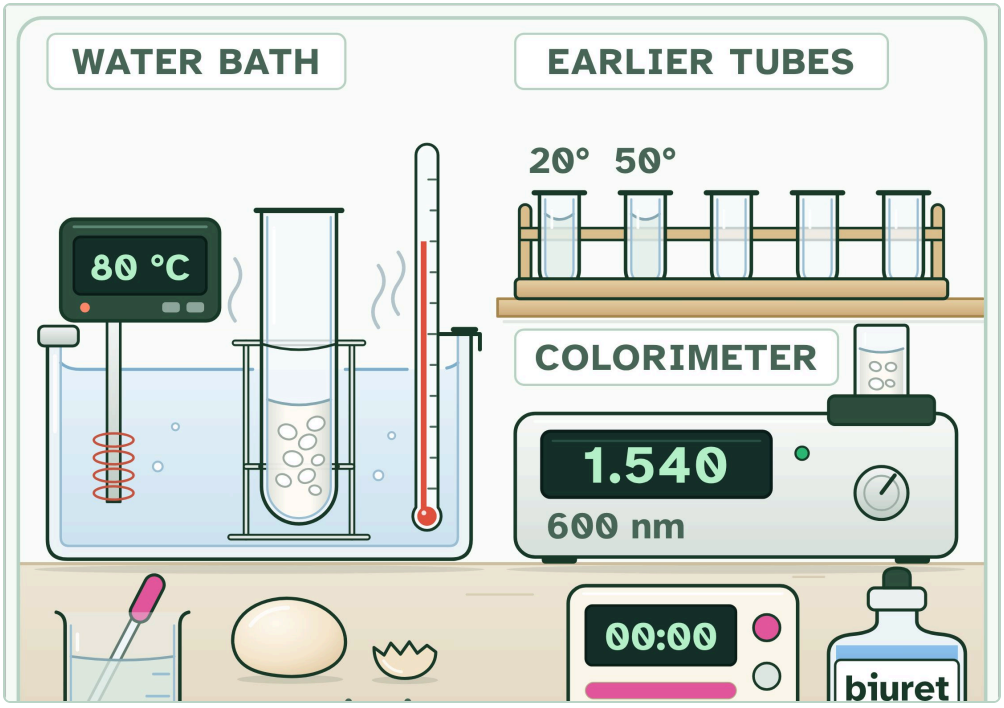
R group 01
The side chain on the central carbon of an amino acid, different in each of the twenty kinds. Its chemistry is hydrophobic, hydrophilic or ionic.

secondary structure 04
Local folding of a polypeptide into alpha helices and beta pleated sheets, held by hydrogen bonds between the backbone's C=O and N–H groups.

tertiary structure 05
The overall three-dimensional shape of a polypeptide, held by interactions between its R groups.

Dry lab: *Unfold a protein*

Heat diluted egg white, change its pH or add ethanol, then read how cloudy it has gone. Find where each treatment starts to unfold the protein, and whether it can fold back.



Run it online: change the variables, run the trials, and the table and graph fill in as you go.
biologybybradford.com/guides/ap-biology-unit-1-proteins#lab

Your question

At what temperature, pH or ethanol concentration does egg white protein unfold, and which of those changes can be undone?

What you can change

The treatment (heat, acid or alkali, ethanol) and its strength. After a treatment you can put the tube back to 25 °C and pH 7 and read it again, or run a biuret test.

What to record

The absorbance at 600 nm of each tube, a measure of how cloudy it is, before and after putting it back. Graph absorbance against the treatment.

Find out

- **Heat first.** Heat a tube at each temperature from 20 to 100 °C and read it. Where does the cloudiness start, and where does it level off?
- **Acid and alkali.** Run the pH series. Compare pH 1, 4.5 and 13: is the cloudiest tube always the one that has unfolded most?
- **Put it back.** After each treatment, bring the tube back to 25 °C and pH 7 and read it again. Which treatments can be undone?
- **Biuret.** Test a clear tube and a white one. What does the result tell you about the peptide bonds?

Record

- Every tube's treatment, its absorbance, and its absorbance after putting it back.
- A graph of absorbance against temperature, pH or ethanol, one treatment at a time.
- One sentence per treatment: which interactions in the protein it disrupts.

Your question At what temperature, pH or ethanol concentration does egg white protein unfold, and which of those changes can be undone?**What you can change**The treatment (heat, acid or alkali, ethanol) and its strength. After a treatment you can put the tube back to 25 °C and pH 7 and read it again, or run a biuret test.**What to record**The absorbance at 600 nm of each tube, a measure of how cloudy it is, before and after putting it back. Graph absorbance against the treatment.

Back to proteins

An enzyme held at 80 °C stops working for good, yet its amino acid sequence is unchanged. Use your heated tube, cooled and then tested with biuret, to explain why.

QUESTIONS ON THE LAB

QUESTION 1

Egg white heated to 80 °C goes white and solid, and cooling it again does not make it clear. Why?

(A) Heat breaks the peptide bonds, so the protein falls apart into its amino acids, and those cannot join up again on cooling

(B) Heat breaks the weak interactions holding the fold, the chains tangle together as they unfold, and they cannot find their shape again

(C) Heat removes the water from the protein, so it dries out into a solid that cannot take the water back up when it cools

Answer on page 27.

QUESTION 2

Egg white at pH 1 is cloudy but not white, though nearly all of it has unfolded. Put back to pH 7, it goes cloudier. Why?

(A) At pH 1 the acid has broken the peptide bonds, and at pH 7 the free amino acids join up again into short chains that clump

(B) At pH 1 every chain carries a positive charge and they repel; at pH 7 those charges go, and exposed hydrophobic R groups clump

(C) At pH 1 the protein is still folded and hides its R groups; it only unfolds at pH 7, once the acid has been neutralized

Answer on page 27.

Check yourself

The check for this guide is online: a fresh paper of past-paper style questions from the exam bank on 1.7 each time, marked as you go, and saved to your Exam practice progress when you are signed in. Scan the code, or type the link.

biologybybradford.com/exam-maker/sit?program=ap&units=U1&ced=1.7&paper=quiz&marks=15&src=ep

Answers

PREDICTIONS IN THE CHAPTERS

01 Two amino acids have the same amino group, carboxyl group and hydrogen. What has to be different for them to be two kinds of amino acid?

B **The R group, the side chain on the central carbon, which differs in every one of the twenty**

The R group. Everything else is the same in all twenty. The R group may be as small as a single hydrogen (glycine) or a large ring, and it may be nonpolar, polar or charged.

02 A polypeptide of 120 amino acids is made in a cell. How many peptide bonds does it have, and how many water molecules were released?

B **119 bonds and 119 waters**

119 of each. A chain of 120 has 119 links, and each link released one water.

03 A protein dissolves in the cytoplasm. Where in its folded shape would you expect to find most of its hydrophobic R groups?

B **Packed in its core, out of contact with water, while hydrophilic and charged R groups face outward**

In the core. As the chain folds, water bonds to the hydrophilic and charged R groups and pushes the hydrophobic ones together inside, much as it pushes phospholipid tails together in a bilayer.

04 A protein is heated until its folds come undone. Which level of its structure is still there?

B **The primary structure, because heat breaks the weaker bonds of the folds but not the peptide bonds**

The primary structure. The folds are held by hydrogen bonds and other weak interactions, which heat breaks; the peptide bonds of the chain are covalent and survive. The denaturing dry lab tests this with biuret.

05 In one protein, a positively charged R group sits next to a negatively charged one in the folded shape. A mutation swaps the negative one for a hydrophobic R group. What is most likely?

C **The ionic bond between them is lost, so that part of the chain may fold differently and the function may change**

The ionic bond is lost. The hydrophobic R group cannot attract the positive one, and it may now pull toward the core instead. One changed R group can change the fold, and with it the function, as in sickle cell hemoglobin. The peptide bonds are unaffected.

06 Raw egg white is clear. Cooked, it is white and firm, and it stays white when it cools. Why does it not go back?

B **The unfolded chains have stuck to each other in clumps, so they cannot find their way back to their folds**

The chains have clumped. Heat broke the bonds holding each protein's shape, the hydrophobic R groups came out, and the chains stuck together into a tangle that scatters light. Cooling does not pull them apart. The peptide bonds are all still there: a cooked egg white still gives a purple biuret test.

QUESTIONS ON THE DRY LAB

Q1 Egg white heated to 80 °C goes white and solid, and cooling it again does not make it clear. Why?

B **Heat breaks the weak interactions holding the fold, the chains tangle together as they unfold, and they cannot find their shape again**

The fold is held by hydrogen bonds, ionic bonds and hydrophobic interactions between R groups, all weak. Heat shakes them apart and the chains unfold, exposing their hydrophobic R groups, which stick to other unfolded chains. The tangle scatters light, so the egg white goes white, and the chains are too knotted together to fold back. The peptide bonds are untouched: the biuret test is still purple.

Q2 Egg white at pH 1 is cloudy but not white, though nearly all of it has unfolded. Put back to pH 7, it goes cloudier. Why?

B **At pH 1 every chain carries a positive charge and they repel; at pH 7 those charges go, and exposed hydrophobic R groups clump**

pH works on the charges. Extra H^+ ions bind to the negatively charged carboxyl groups of R groups and cancel their charge, so ionic bonds and some hydrogen bonds fail and the protein unfolds. But every chain is now positively charged, so the chains push each other apart and stay spread out. Put the pH back and the charges return to normal: some chains fold up again, because the sequence still holds the information for the shape, and others stick together by their exposed hydrophobic R groups and clump. The peptide bonds are untouched throughout.

How this was made. The course structure, the activities and the teaching choices come from my own classroom, my presentations and my years of teaching IB and AP Biology. I use Claude, an AI, to help write and build the interactive guides, lesson plans, slides and practice questions, and to draw the diagrams and code the interactives. I direct the work and review it against the IB and AP specifications before it goes live.

Written and drawn for Biology by Bradford, biologybybradford.com. Free to print and share with a class.