Proteins

B1.2 · SL

Why does cooling not uncook an egg?

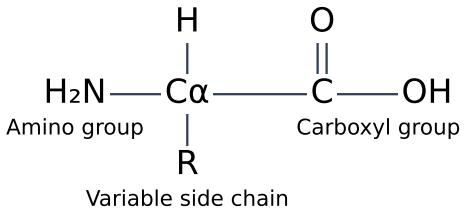
Changing a fold and cutting a chain are different processes

Heating egg white makes an opaque network that ordinary cooling does not reverse. Digestion can still break its proteins into smaller molecules.

Common content: amino acids, peptide formation, dietary requirements, sequence variety and denaturation.

Short letter sequences and numerical datasets are invented teaching examples.

Read the four attachments to the alpha carbon



Neutral representation; charge states depend on pH.

> The R-group varies; amino and carboxyl groups belong to the shared framework.

R is a placeholder, not a new element

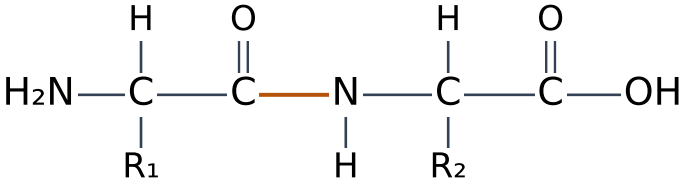
Distinguish the shared backbone from the variable side chain

The alpha carbon attaches to an amino group, carboxyl group, H and R. Glycine has H as its side chain.

The neutral convention shows $-\mathrm{NH_2}$ and $-\mathrm{COOH}$. A common aqueous form has $-\mathrm{NH_3^+}$ and $-\mathrm{COO^-}$; charge depends on pH.

Draw the carbonyl C=O and OH attached to the same carboxyl carbon. Read bonds rather than copying a decorative shape.

Locate the peptide C–N link and retain the carbonyl



Orange C–N link: peptide bond.
Two residues; one peptide bond; one water released in the model.

A **peptide bond** joins a carboxyl carbon to an amino nitrogen; each residue retains its R-group.

Condensation and hydrolysis account for different atoms

The product is a dipeptide plus water in the simple model

OH from a carboxyl group and H from an amino group account for one released water. The new peptide link is a covalent C–N bond.

Hydrolysis uses water to cut peptide bonds. Partial cleavage can produce shorter peptides rather than only free amino acids.

This is molecular accounting. Ribosomal synthesis uses tRNAs, activated amino acids and energy-transfer reactions; free amino acids do not simply assemble spontaneously.

Apply residues minus chains before counting water

1. **One chain.** 35 residues give $35 - 1 = 34$ peptide bonds; 120 residues give 119. Complete peptide hydrolysis uses one water per link.
2. **Two chains.** 12 and 18 residues contain $11 + 17 = 28$ peptide bonds. One new end-to-end peptide link gives 29 in a 30-residue chain.
3. **Limit.** Association through other interactions leaves two chains and 28 peptide bonds. Side-chain cross-links are not peptide bonds.

Essential means dietary supply is needed

Non-essential does not mean unnecessary

Digestion supplies amino acids for synthesis of the body's own proteins. An intact food protein is not simply transferred into a matching body tissue.

Essential amino acids cannot be synthesized in sufficient amounts. Non-essential amino acids can be synthesized, but both types are needed.

Foods differ in amino-acid proportions. Total protein mass alone does not establish every essential amino acid's adequacy. Vegan diets need attention to supply and balance; plant proteins do contain essential amino acids.

A food test detects groups, not a complete structure

Biuret evidence has limits

Add Biuret reagent to the food sample; lilac or purple provides evidence of peptide bonds.

Compare a known protein solution and water as positive and negative controls under the same conditions.

A positive test does not identify the protein, its sequence or its three-dimensional structure.

A limiting amino acid can restrict complete synthesis

1. **Invented model.** Each peptide needs 2 X residues and 3 Y residues. Supplies: 50 X and 60 Y. Other resources are abundant.
2. **Compare.** X permits $50/2 = 25$ copies; Y permits $60/3 = 20$. The maximum is 20 complete copies.
3. **Account.** X remaining $= 50 - 2(20) = 10$. Real synthesis also depends on energy, other amino acids, enzymes and regulation.

The order of residues matters as well as the composition

Primary structure is the sequence in a stated direction

The standard code specifies 20 common amino acids. Chains vary in length and order, producing an enormous range of possible sequences.

Invented A–B–C and A–C–B contain the same types but different orders. They are different primary structures.

Insulin is a hormone, collagen has a structural role, and many enzymes are proteins. Not every protein is an enzyme; some catalysts are RNA.

Count choices at each sequence position

1. **Restricted alphabet.** Three permitted types, repetition allowed, three positions: $3^3 = 27$ possible sequences.
2. **Twenty types.** Four positions give $20^4 = 160000$ possibilities. A fixed length gives a finite count, not literally infinitely many chains.
3. **Interpret.** Having 20 common amino acids does not limit organisms to 20 proteins. Sequence and suitable folding conditions both matter.

Denaturation can destroy function without cutting the backbone

A functional conformation depends on conditions

Heating and pH changes can disrupt interactions that stabilize a fold. Denaturation alters the normal functional conformation, often reducing activity.

Ordinary denaturation need not hydrolyse peptide bonds. Digestion cuts those bonds. Severe chemical conditions can cause additional damage, so identify the process tested.

Some proteins can refold under suitable conditions; others aggregate or fail to recover. Heated egg white forms an altered network that ordinary cooling does not reverse.

Compare activity after every sample returns to the same assay

Invented five-minute treatment	**Activity when assayed at 25°C**
Kept at 25°C	100 units
Heated to 45°C	87 units
Heated to 65°C	20 units
Kept cold at 5°C	98 units

Separate treatment temperature from measurement temperature

1. **Calculate.** 65°C-treated sample retains $20/100 \times 100 = 20\%$ activity; loss $= 80\%$.
2. **Infer.** The assay is always at 25°C, so the difference is not merely an immediate temperature effect during measurement. It supports persistent functional damage.
3. **Limit.** Activity alone does not reveal which interaction changed. Use repeats and an unheated control; check evaporation, concentration and timing.

Test recovery before calling a slow reaction denaturation

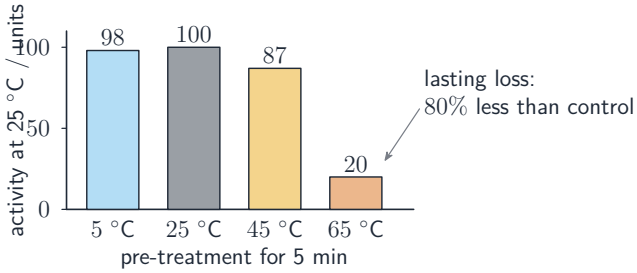
Restore the same conditions and compare with a control

Low activity while an enzyme is cold can reflect reversible slowing. Test activity after the sample returns to the original conditions.

Control enzyme amount, treatment duration, assay temperature, pH, substrate concentration and measurement interval.

Compare repeated measurements rather than one reading. A functional assay supplies evidence of activity, not a complete molecular image.

Is the damage permanent?



Cold slows an enzyme; high heat denatures it

Try chain accounting, sequence counting and recovery reasoning

Pause before the reveal

Two chains contain 12 and 18 residues. Count peptide bonds before and after one new end-to-end peptide link.

With three allowed amino-acid types and four positions, repetition allowed, how many sequences are possible?

A sample has 20 units of activity after treatment and return to the common assay, compared with a 100-unit control. Calculate retention and loss; state the inference limit.

Reveal: count chains and compare controlled measurements

1. **Bonds.** Before: $11 + 17 = 28$. After one new peptide link: 29. Association without that link leaves 28.
2. **Sequences.** $3^4 = 81$. Order and repetition rules must be stated.
3. **Activity.** Retention 20%; loss 80%. This supports persistent functional damage but does not reveal the entire molecular mechanism.

Check yourself

Use bonds, sequence and controlled comparisons

Draw all four alpha-carbon attachments. Identify the carboxyl carbon and amino nitrogen in a peptide link; keep its neighbouring carbonyl oxygen.

State separate chain counts, compare amino-acid supply with demand, and distinguish sequence order from composition.

Explain denaturation as altered functional conformation. Separate pretreatment from assay conditions and test recovery before claiming irreversible loss.