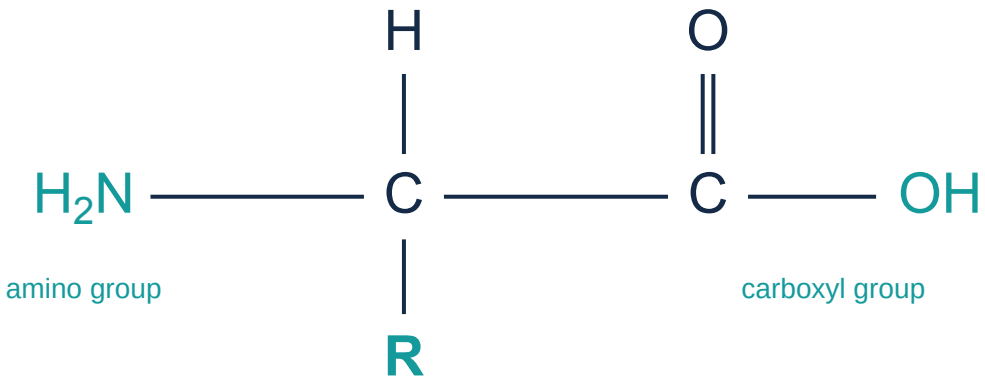
One shared structure, a variable R

Amino acids are the building blocks of proteins. In the general alpha-amino acid structure, the central carbon is attached to four groups: amino, carboxyl, hydrogen and R.

GENERAL STRUCTURE: NON-IONISED DRAWING



R = variable side chain; R is not an element symbol.

1. PUT EVERY GROUP ON THE CENTRAL CARBON

The amino group is -NH_2 and the carboxyl group is -COOH in this convention. The central carbon has four single bonds. The carboxyl carbon is a separate carbon with a C=O double bond and a C-OH bond.

2. CHANGE R TO CHANGE THE AMINO ACID

Glycine	Alanine	Serine
R = H	R = CH_3	R = CH_2OH

These examples are for recognising the variable group, not a list to memorise.

Drawing convention: amino acids in water commonly carry -NH_3^+ and -COO^- groups. The non-ionised forms above make condensation and hydrolysis easier to track; charge depends on pH.

Supporting reading: OpenStax Biology 2e, 3.4 Proteins.

Scope: Cambridge Biology 9700 syllabus, section 2.3, outcome 1, p. 18.

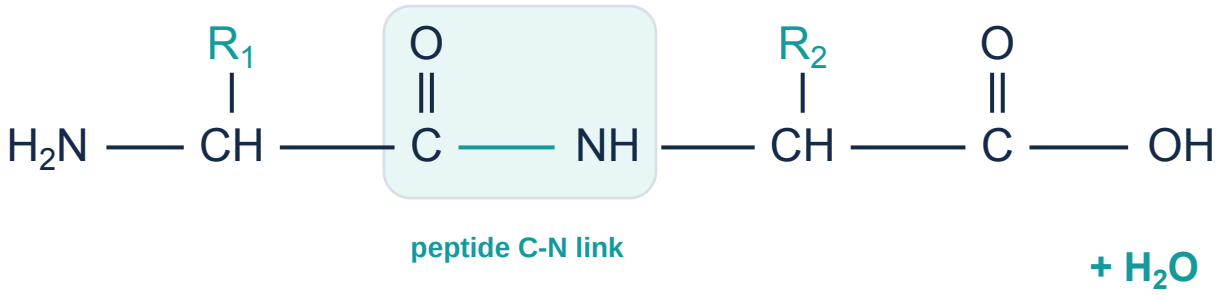
Join two amino acids

A peptide bond is the covalent C-N link between the carboxyl carbon of one amino acid and the amino nitrogen of another. One water molecule is released in the net condensation.

TWO AMINO ACIDS FORM A DIPEPTIDE

$$H_2N\text{-}CH(R_1)\text{-}COOH + H_2N\text{-}CH(R_2)\text{-}COOH$$

condensation



peptide C-N link

+ H_2O

The highlighted -C(=O)-NH- region is the peptide group. The actual peptide bond is its C-N link, not the C=O bond and not a link between the R groups.

1. TRACK THE WATER

Remove OH from the carboxyl group of the first amino acid and H from the amino group of the second. These form H_2O. Join the carbonyl carbon to the nitrogen, keeping the C=O bond and the two R groups unchanged.

2. CHECK THE ENDS AND THE NITROGEN

The dipeptide retains an amino end on the left and a carboxyl end on the right. The internal nitrogen is shown as NH: it still has one H after condensation. Read the sequence from the amino end to the carboxyl end.

This is a net structural reaction. In cells, peptide synthesis is enzyme- and ribosome-mediated and uses activated amino acids; free amino acids do not simply join by mixing.

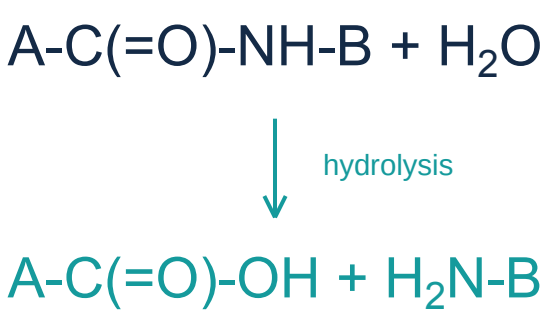
Supporting reading: OpenStax Biology 2e, 3.4 Proteins.

Scope: Cambridge Biology 9700 syllabus, section 2.3, outcome 1, p. 18.

Use water to break the link

Hydrolysis breaks a peptide C-N bond by adding the elements of water across it. The new ends are a carboxyl group and an amino group, shown here in non-ionised form.

THE NET CHANGE AT ONE PEPTIDE LINKAGE



A and B = the remaining fragments, not the amino acid R groups.

1. OH GOES TO THE CARBONYL CARBON; H GOES TO N

Water supplies OH to form the carboxyl end and H to form the amino end. Each peptide bond hydrolysed uses one water molecule in the net reaction. The R groups do not have to be removed or changed.

2. ONE CUT DOES NOT MEAN COMPLETE DIGESTION

Breaking an internal peptide bond splits one chain into two shorter fragments. Complete hydrolysis breaks every peptide link and releases the individual amino acids. Proteases and peptidases catalyse these reactions in organisms.

3. COUNT LINKS IN ONE OPEN, UNBRANCHED CHAIN

n amino acids → n - 1 peptide bonds

Example: four amino acids form three peptide bonds and release three waters. Complete hydrolysis of that chain consumes three waters.

Supporting reading: OpenStax Biology 2e, 3.1 Macromolecule synthesis.

Scope: Cambridge Biology 9700 syllabus, section 2.3, outcome 1, p. 18.