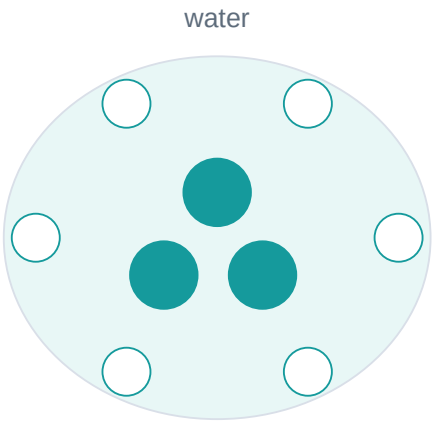
Folding brings groups together

Protein shape is stabilised by many interactions acting together. The syllabus names hydrophobic interactions, hydrogen bonds, ionic bonds and covalent bonds, including disulfide bonds.

1. HYDROPHOBIC INTERACTIONS



Soluble globular protein

Non-polar side chains

Cluster in the interior, reducing their contact with surrounding water.

Polar / charged groups

Often face outward and interact with water. Open circles mark these surface groups.

Schematic cross-section: filled circles are non-polar R groups; the oval is the protein outline, not a membrane. The peptide backbone is omitted.

2. THIS IS NOT A NEW COVALENT BOND

Hydrophobic clustering is driven by the aqueous environment, not by forming a special bond between every pair of non-polar groups. Close packing also allows van der Waals attractions.

3. LOCATION DEPENDS ON THE ENVIRONMENT

The buried-core pattern applies especially to soluble globular proteins. A membrane protein can expose non-polar side chains to the lipid bilayer instead. Not every protein has the same surface pattern.

Connection to sequence: changing an R group can alter its preferred surroundings and the contacts available during folding.

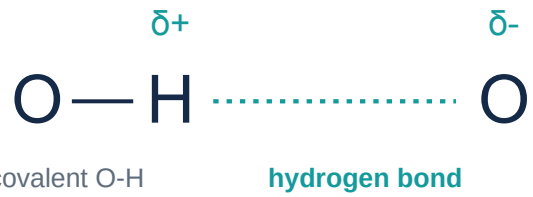
Supporting reading: Alberts et al., Molecular Biology of the Cell, protein structure.

Scope: Cambridge Biology 9700 syllabus, section 2.3, outcome 3, p. 18.

Partial charges or full charges?

Hydrogen bonds and ionic interactions are non-covalent. One is usually weaker than a covalent bond, but many suitable contacts can collectively stabilise a folded protein.

1. HYDROGEN BONDS



A partially positive H attached to O or N is attracted to a suitable O or N atom with a lone pair. The dotted line is the hydrogen bond; the solid O-H line is covalent.

Backbone C=O and N-H groups stabilise helices and sheets. Polar R groups can also hydrogen-bond, helping to stabilise tertiary structure.

2. IONIC INTERACTIONS / SALT BRIDGES



Oppositely charged side chains attract, for example a carboxylate group and a protonated amino group. Unlike a hydrogen bond, this example involves full charges.

A pH change can alter side-chain protonation and charge, weakening or removing a salt bridge. Like charges repel rather than forming an attractive ionic contact.

The drawings isolate interacting groups, not complete amino acids. Nearby regions of one chain, or groups on different subunits, can make stabilising contacts.

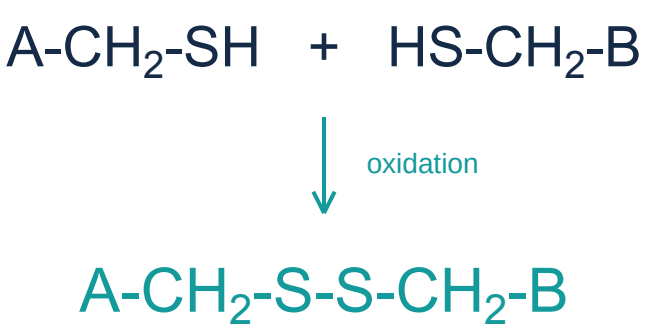
Supporting reading: OpenStax Biology 2e, 3.4 Proteins.

Scope: Cambridge Biology 9700 syllabus, section 2.3, outcome 3, p. 18.

Covalent links and loss of shape

Peptide bonds make the polypeptide backbone. Disulfide bonds are different covalent links: they connect the sulfur atoms of two cysteine side chains.

1. A DISULFIDE BRIDGE JOINS TWO SIDE CHAINS



Covalent S-S link

A/B = rest of protein. Linkage schematic, not a balanced oxidation equation.

2. DISULFIDE IS NOT PEPTIDE

A disulfide bridge can connect distant regions of one chain or link different chains. It is not formed by every sulfur-containing amino acid: cysteine provides the -SH groups. Reduction can break an S-S bridge.

3. DENATURATION IS NOT CHAIN DIGESTION

Changes in temperature, pH or chemical conditions can disrupt stabilising interactions and alter shape and function. Ordinary denaturation generally leaves peptide bonds and the primary sequence intact; hydrolysis breaks the backbone.

KEEP THE TYPES DISTINCT

Non-polar clustering: hydrophobic. Partial-charge attraction involving H: hydrogen bond. Opposite full charges: ionic. Shared electrons in S-S or peptide links: covalent. Heat does not simply break every bond.

Supporting reading: OpenStax Biology 2e, 3.4 Proteins.

Scope: Cambridge Biology 9700 syllabus, section 2.3, outcome 3, p. 18.