

DNA double helix

Photograph 51

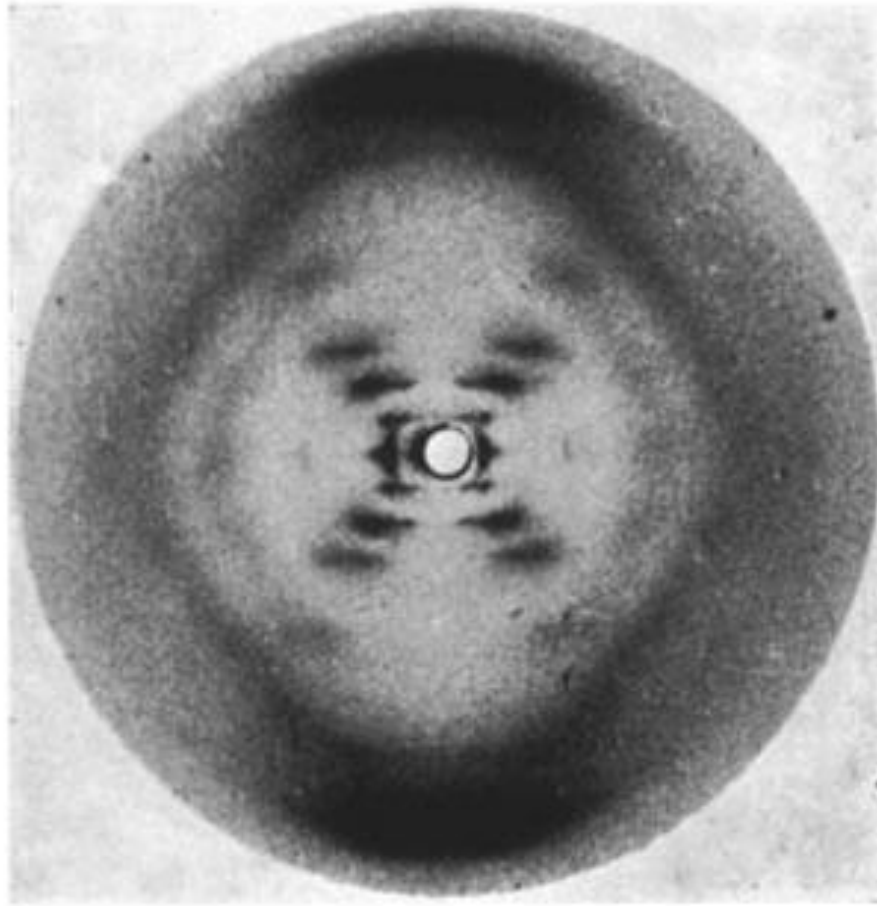
Photograph 51 is the nickname given to an X-ray diffraction image of crystallized DNA taken by Raymond Gosling in May 1952, working as a PhD student under the supervision of Rosalind Franklin, at King's College London in Sir John Randall's group. It was critical evidence in identifying the structure of DNA.

James Watson was shown the photo by his collaborator, Maurice Wilkins, without Rosalind Franklin's approval or knowledge. Wilkins did this, as by this time, Gosling had returned under his supervision, as Franklin was leaving King's and Randall has asked Gosling to share all his data with Wilkins. Along with Francis Crick, Watson used characteristics and features of Photo 51, together with evidence from multiple other sources, to develop the chemical model of the DNA molecule. Their model, and manuscripts by Wilkins and colleagues, and Gosling and Franklin, were first published, together, in 1953, in the same issue of *Nature*. In 1962, the Nobel Prize in Physiology or Medicine was awarded to Watson, Crick and Wilkins. The prize was not awarded to Franklin; she had died four years earlier, and although there was not yet a rule against posthumous awards, the Nobel Committee generally does not make posthumous nominations.

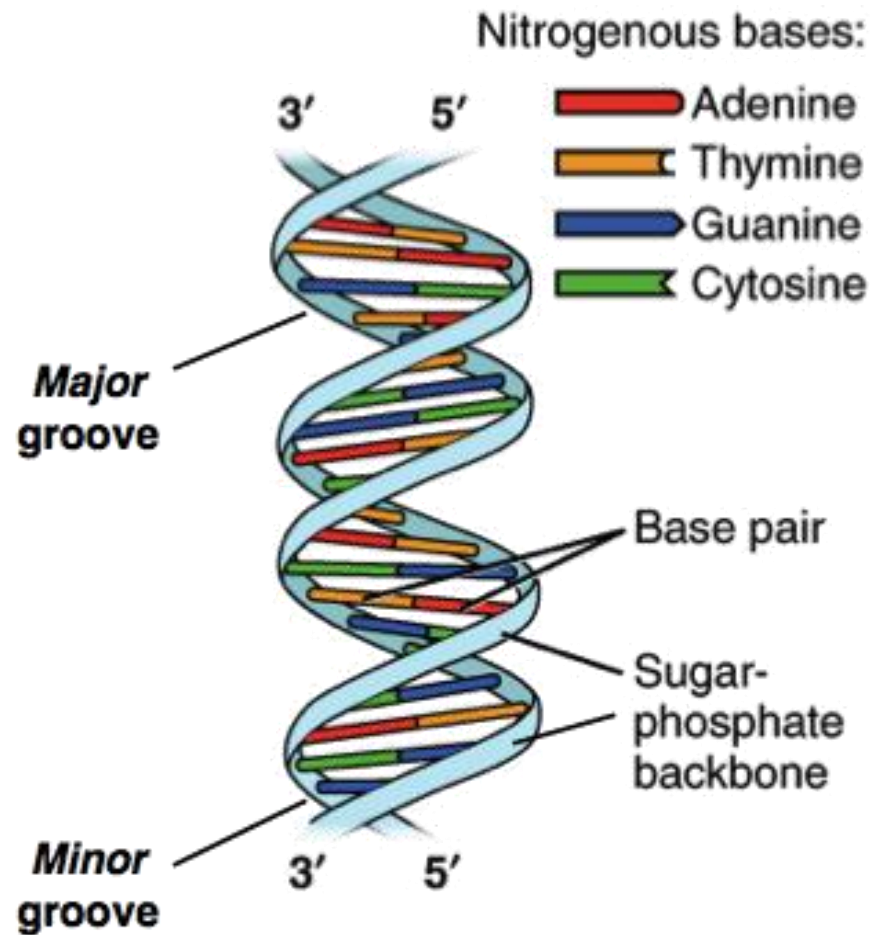
The prior model was triple-stranded DNA.

/Wikipedia/

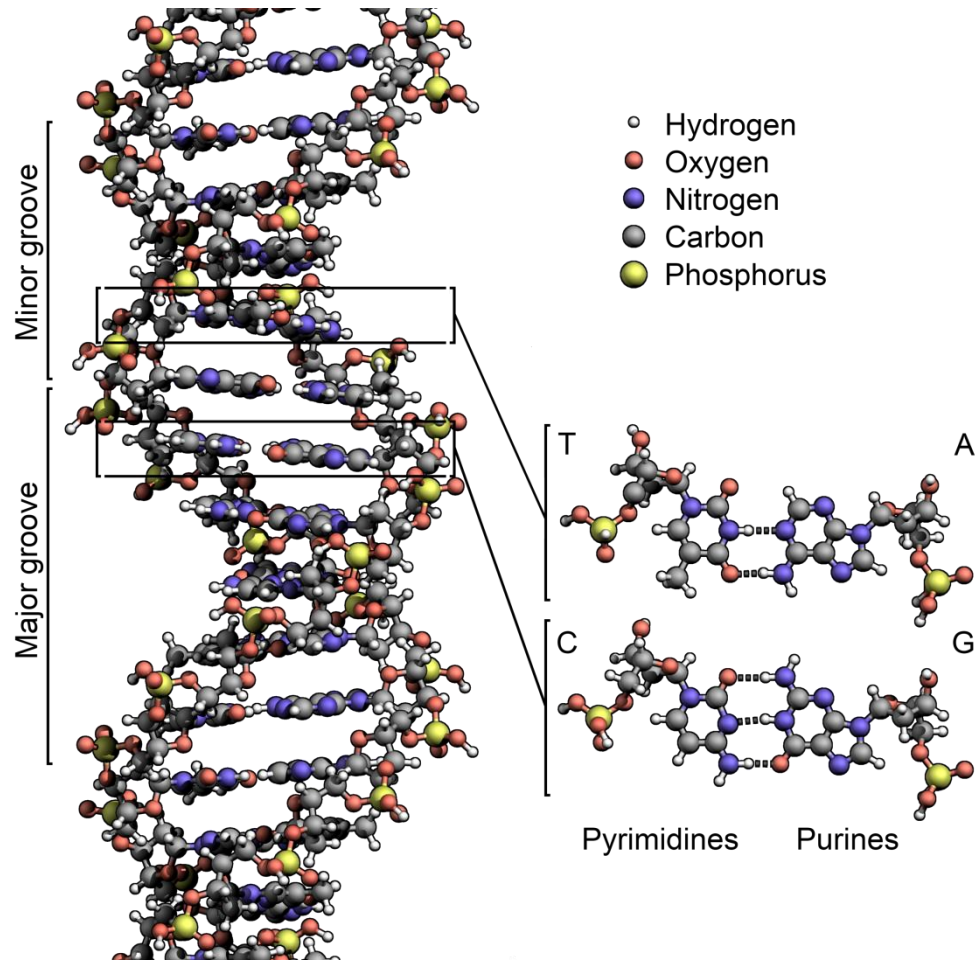
Photograph 51



DNA double helix

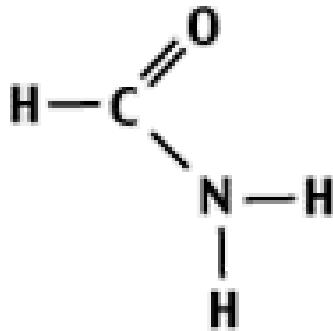


DNA double helix

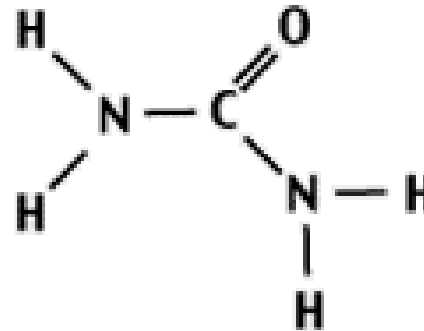


Denaturation of nucleic acids

- Heat
- Chemical agents. Urea or formamide are most commonly used

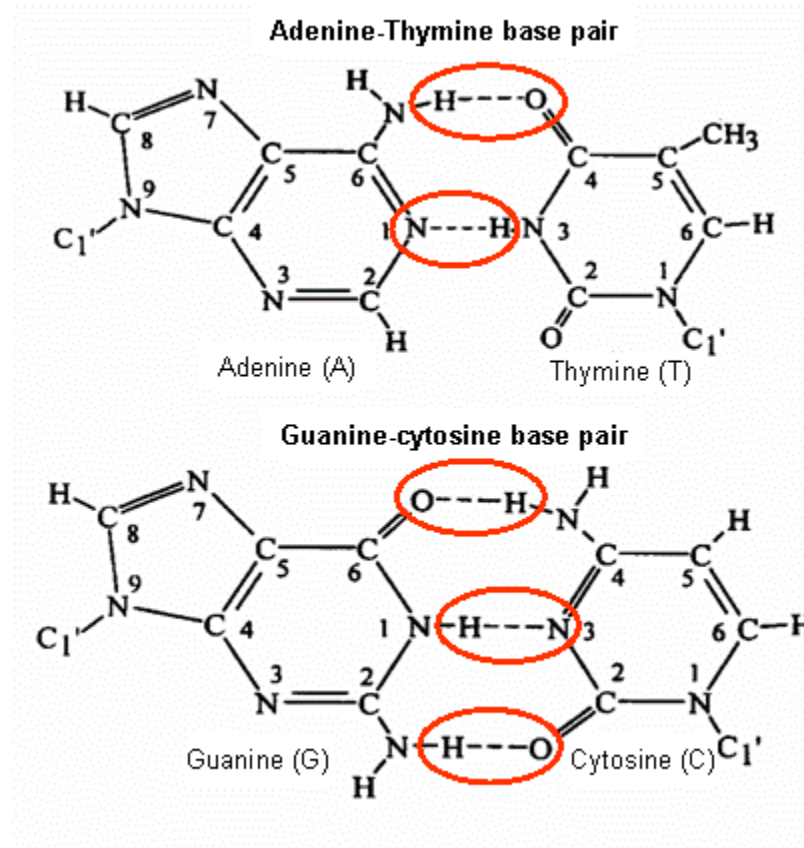


formamide

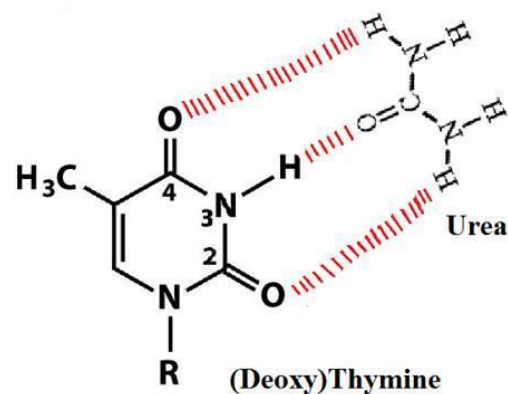
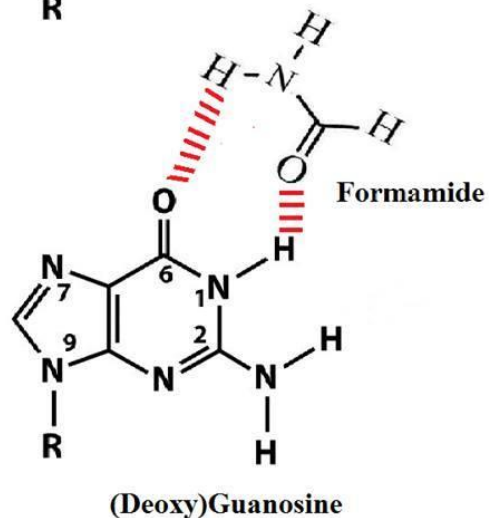
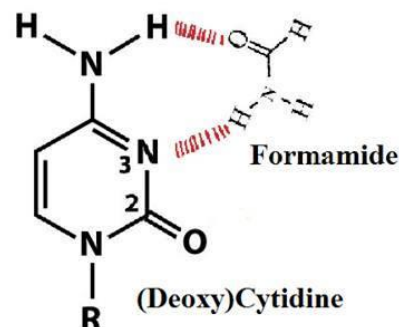
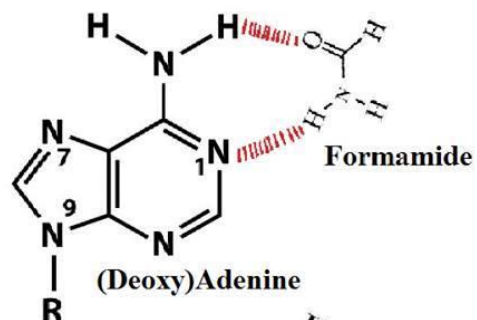


urea

Hydrogen bonds in ds-NA

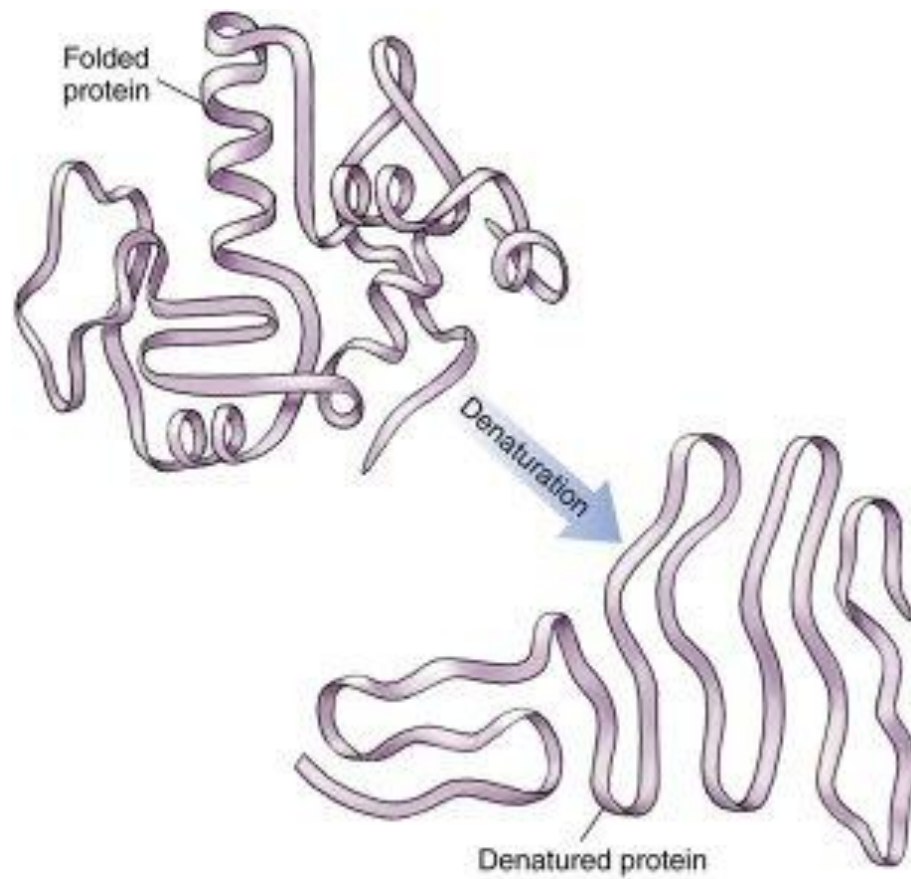


Urea and formamide interaction with NA bases



Denaturation and renaturation of proteins

- Higher levels of protein structure are formed without covalent bonds. Therefore, they are not as stable as peptide covalent bonds which make protein primary structure
- Under external stress like, temperature or action of certain chemical compounds the protein 3-dimensional structure becomes even less stable and can unravel



How denaturation occurs at levels of protein structure

- In **quaternary structure** denaturation, protein sub-units are dissociated and/or the spatial arrangement of protein subunits is disrupted.
- **Tertiary structure** denaturation involves the disruption of:
 - i. Covalent interactions between amino acid side-chains (such as disulfide bridges between cysteine groups)
 - ii. Non-covalent dipole-dipole interactions between polar amino acid side-chains (and the surrounding solvent)
- In **secondary structure** denaturation, proteins lose all regular repeating patterns such as alpha-helices and beta-pleated sheets, and adopt a random coil configuration.
- **Primary structure**, such as the sequence of amino acids held together by covalent peptide bonds, is **not disrupted** by denaturation.

Denaturation usually disrupts the function of a protein.

Heat denaturation

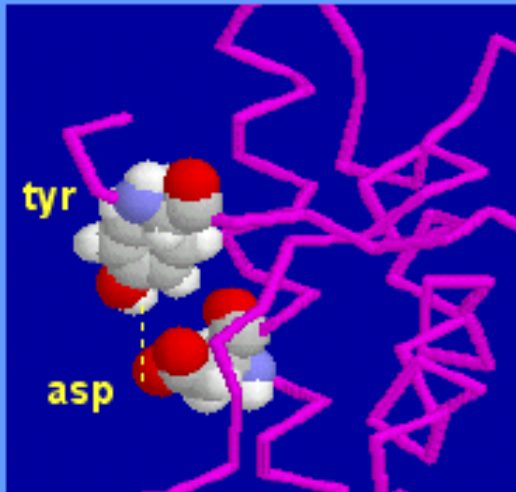
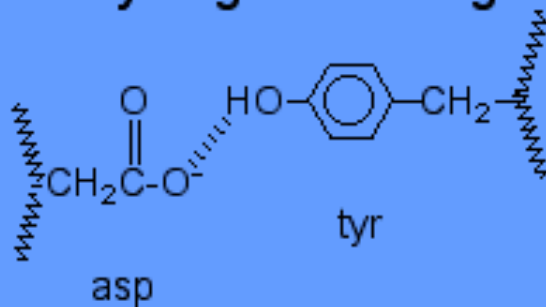
- **Heat** can be used to disrupt hydrogen bonds and non-polar hydrophobic interactions. This occurs because heat increases the kinetic energy and causes the molecules to vibrate so rapidly and violently that the bonds are disrupted. The proteins in eggs denature and coagulate during cooking. Other foods are cooked to denature the proteins to make it easier for enzymes to digest them. Medical supplies and instruments are sterilized by heating to denature proteins in bacteria and thus destroy the bacteria.

Alcohol Disrupts Hydrogen Bonding:

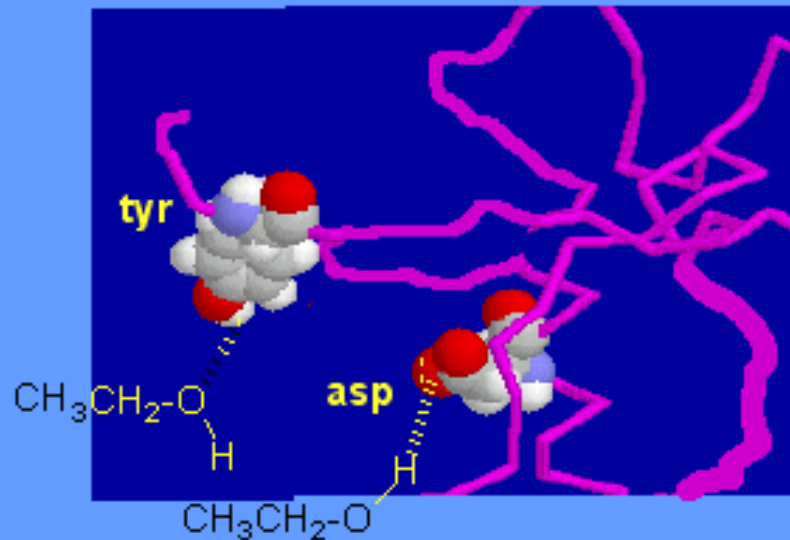
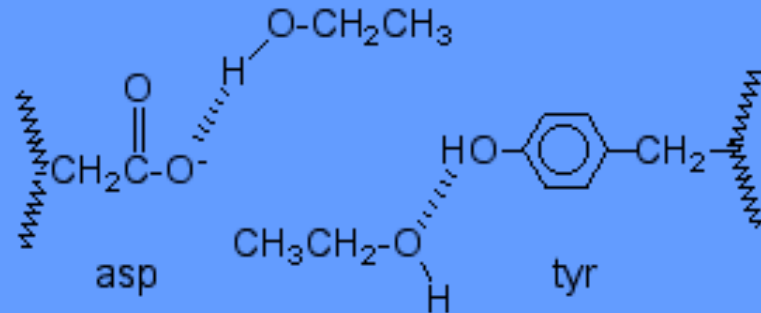
- Hydrogen bonding occurs between amide groups in the secondary protein structure. Hydrogen bonding between "side chains" occurs in tertiary protein structure in a variety of amino acid combinations. All of these are disrupted by the addition of another alcohol.
- A 70% alcohol solution is used as a disinfectant on the skin. This concentration of alcohol is able to penetrate the bacterial cell wall and denature the proteins and enzymes inside of the cell. Alcohol denatures proteins by disrupting the side chain intramolecular hydrogen bonding. New hydrogen bonds are formed instead between the new alcohol molecule and the protein side chains

Alcohol Disrupts Hydrogen Bonding:

Tertiary Structure - Hydrogen Bonding



Denaturation by Alcohol

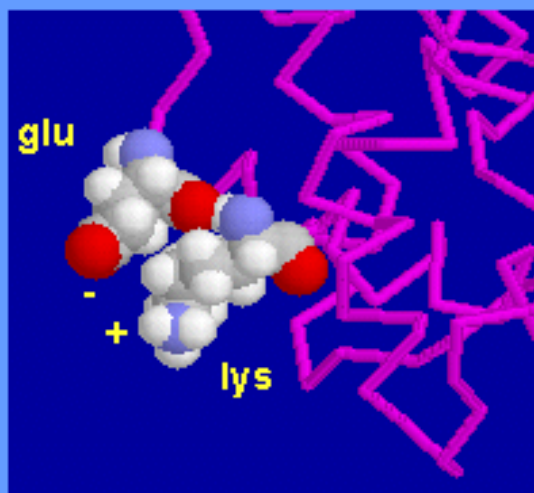
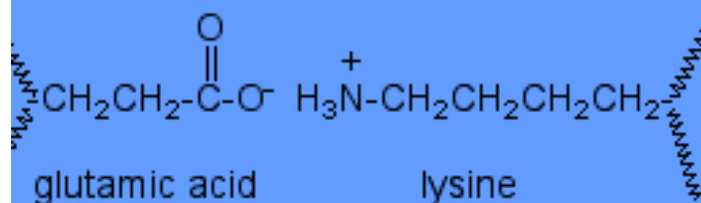


Acids and Bases Disrupt Salt Bridges:

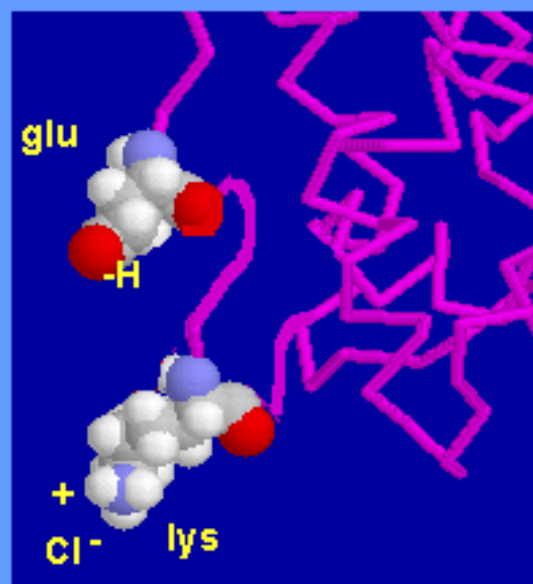
- **Salt bridges** result from the neutralization of an acid and amine on side chains. The final interaction is ionic between the positive ammonium group and the negative acid group.
- As might be expected, **acids and bases disrupt salt bridges** held together by ionic charges. A type of double replacement reaction occurs where the positive and negative ions in the salt change partners with the positive and negative ions in the new acid or base added. This reaction occurs in the digestive system, when the acidic gastric juices cause the curdling (coagulating) of milk.

Acids and Bases Disrupt Salt Bridges:

Tertiary Structure - Salt Bridges

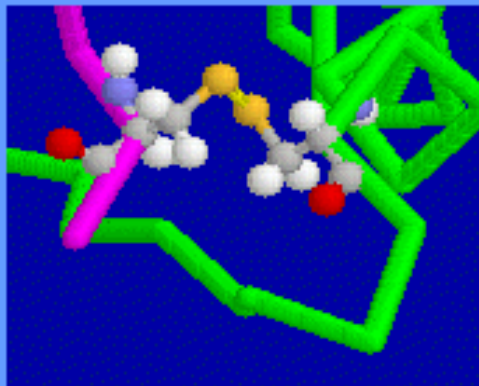
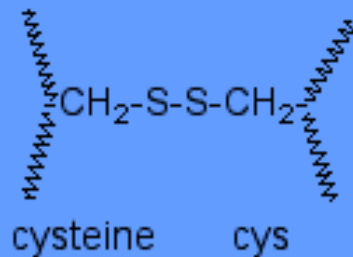


Denaturation by Acid or Base



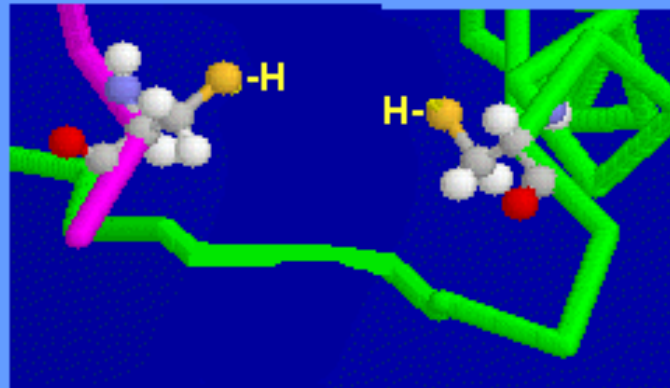
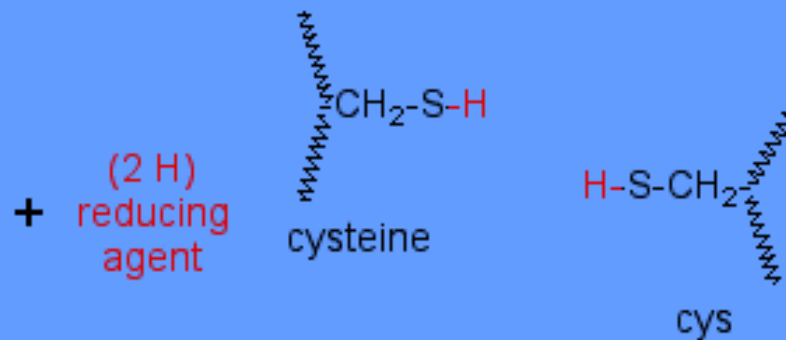
Disruption of disulphide bonds by reducing agents

Tertiary Structure - Disulfide Bonds



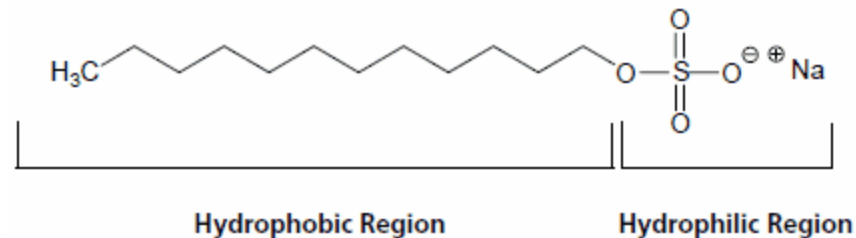
Join two chains

Denaturation by Reducing Agents



Detergents disrupt hydrophobic interactions

- Detergents are used in biomedical laboratories for the disruption of cell membranes (cell lysis) and the release of intracellular materials in a soluble form. Detergents break the protein-protein, protein-lipid and lipid-lipid associations, denature proteins.
- Detergents are molecules that contain both hydrophobic groups (their tails) and hydrophilic groups (their heads)



A detergent – Sodium dodecyl sulphate (SDS)

Detergents

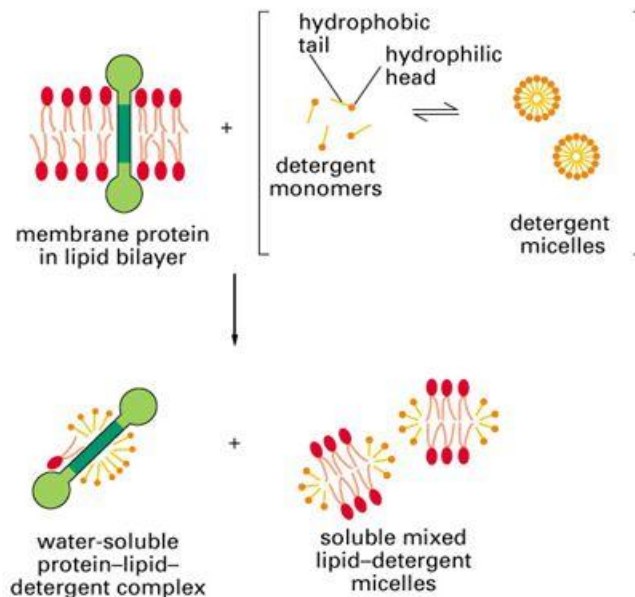


Figure 10-24. Molecular Biology of the Cell, 4th Edition.

Ionic detergent that dissolves membranes and unfolds proteins.

Mild nonionic detergent that dissolves membranes without unfolding proteins.

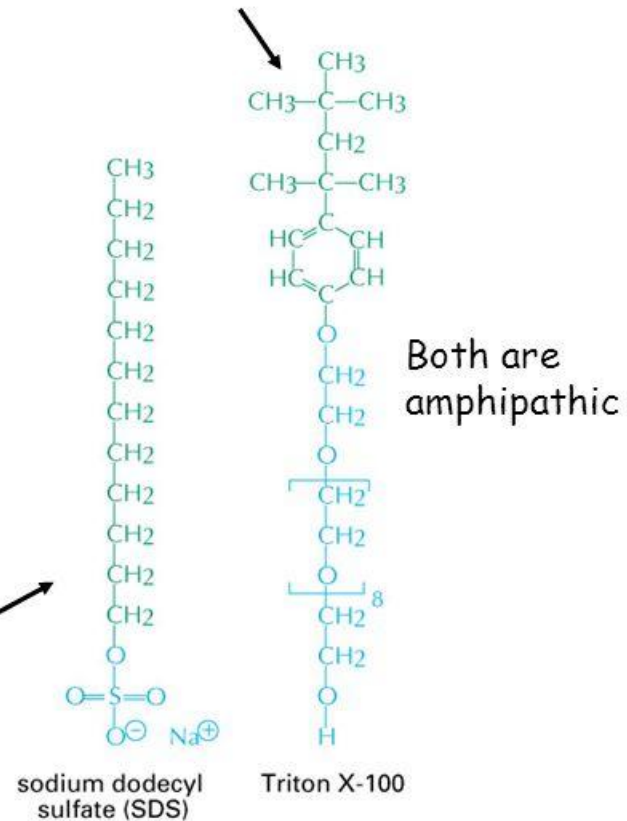
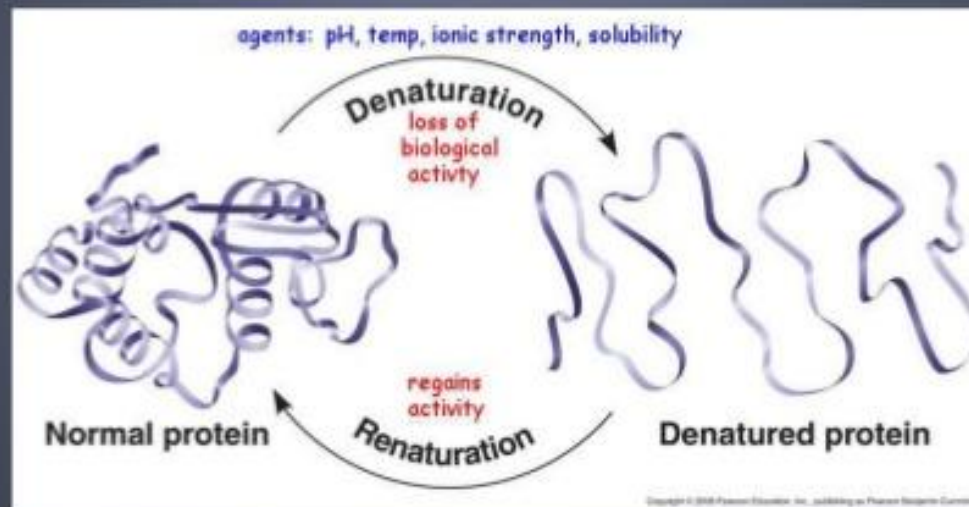


Figure 10-25. Molecular Biology of the Cell, 4th Edition.

Renaturation

- In many cases, denaturation is reversible (the proteins can regain their native state when the denaturing influence is removed). This process is called renaturation. It could be complete or partial.
- Renaturation can completely or partially restore the protein function lost because of denaturation.

- The denatured state does not necessarily equate with complete unfolding of the protein and randomization of conformation.
- Under most conditions, denatured proteins exist in a set of partially folded states that are poorly understood.

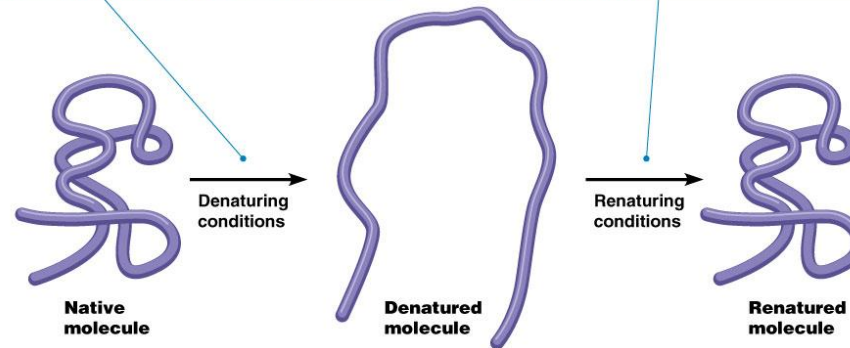


Renaturation is similar to protein folding during protein biosynthesis

(a) Spontaneous refolding of ribonuclease following denaturation. Anfinsen's experiment showed that all the information needed for the proper folding of a ribonuclease polypeptide into its native three-dimensional conformation is present in its amino acid sequence.

1 Denaturation. First, the folded polypeptide was exposed to denaturing conditions (heating) that disrupted noncovalent interactions between its amino acid R groups, resulting in a ribonuclease molecule with no fixed shape and no enzymatic activity.

2 Renaturation. Then, renaturing conditions (cooling) allowed renewed interactions between the amino acid R groups. The polypeptide returned spontaneously to its native conformation, regaining enzymatic activity.



(b) Spontaneous folding of ribonuclease during synthesis. The same interactions between amino acid R groups act on the elongating polypeptide during its synthesis on a ribosome (left to right). This results in the spontaneous folding of the polypeptide into its unique conformation.

