**Name Faisal Khan**

**ID: 15234**

**Course Title Biochemistry-I (Lab)**

**Instructor Sana Khan**

**Disciplne Bs Dt**

**Paper Improvement**

**Q.1 Write a note on that protein whose stabilizing factor is only H-bond.**

**Ans. Introduction**

In 1936 when the structure of globular proteins was beginning to be understood, pauling and mirsky concluded this chain is folded into a uniquely defined configuration in which it is held by hydrogen bonds between the peptide nitrogen and oxygen atoms the importance of the hydrogen bond in protein structure can hardly be overemphasized and they suggested that each hydrogen bond would contribute 5 kcal mol to the stability of the uniquely defined configuration.

 The stability of a protein is not simply the sum of the free energies of formation of the many weak interactions within it however. We have already noted that the stability of proteins is marginal every hydrogen bonding group in a polypeptide chain was hydrogen bonded to water prior to folding. For every hydrogen bond formed in a protein. Hydrogen bonds of similar strength between the same groups and water were broken. The net stability contributed by a given weak interaction, or the difference in free energies of the folded and unfolded state is close to zero. We must therefore explain why the native conformation of a protein is favored. The contribution of weak interaction to protein stability can be understood in terms of the properties of water pure water contains a network of hydrogen bonded water molecules. No other molecule has the hydrogen bonding potential of water, and other molecules present in an aqueous solution will disruptthe hydrogen bonding of water to some extent. Optimizing the hydrogen bonding of water around a hydrophobic molecule results in the formation.

The formation of hydrogen bonds and ionic interactions in a protein is also driven largely by this same entropic effect. Polar groups can generally form hydrogen bonds with water and hence are soluble in water. However, the number of hydrogen bonds per unit mass is generally greater for pure water than for any other liquid or solution and there are limits to the solubility of even themost polar molecules because of the net decrease in hydrogen bonding that occurs when they are present. Therefore a solvation shell of structured water will also solvation shell of structured water will also form to some extent around polar molecules. Even though the energy of formation of an intramolecular hydrogen bond or ionic interaction between two polar groups in a macromolecule is largely canceled out by the elimination of such interactions between the same group and water the release of structured water when the intramolecular interaction is formed provides an entropic driving force for folding. Most of the net change in free energy that occurs when weak interactions are formed within a protein is therefore derived from the increase in entropy in the surrounding aqueous solution. Of the different types of weak interactions hyerophobic interactions are particularly important in stabilizing protein conformation the interior of a protein is generally a densely packed core of hydrophobic amino acid side chains. It is also important that any polar or charged groups in the protein interior have suitable partners for hydrogen bonding or I ionic interactions.

The next major advance occurred in 1951 when pauling’s group used constraints derived from studies of model compounds and their ideas about hydrogen bonds to discover the most important structural elements in globular proteins the alpha helix and the beta sheet in their paper describing the alpha helix they suggested that hydrogen bonds would contribute about 8kcal mol to the stability. But in their next paper describing the beta sheet they had reached a better understanding and suggested that with proteins in an aqueous environment the effective energy of hydrogen bonds in not so great inasmuch as the difference between the energy of the system with N-H O hydrogen bonds surrounded by water and a system with the N-H group and the O atom forming hydrogen bounds with water molecules may be no more than about 2 kcal/mol. This is in line with most current thought.

**Protein secondary structure**

Protein secondary structure is the three dimensional form of local segments of proteins. The two most common secondary structural elements are alpha helices and beta sheets though beta turns and omega loops occur as well. Secondary structure elements typically spontaneously form as an intermediate before the protein folds into its three dimensional tertiary structure. Secondary structure is formally defined by the pattern of hydrogen bonds between the amino hydrogen and carboxyl oxygen atoms in the peptide backbone. Secondary structure may alternatively be defined based on the regular pattern of backbone dihedral angles in a particular region of the remachandran plot regardless of whether it has the correct hydrogen bonds.

**Q.2 Describe the structure of Plasmalema on the basis of Fluid Mosaic Model.**

**Ans. Fluid Mosaic Model**

The fluid mosaic model describes the plasma membrane structure as a mosaic of phospholipids , cholesterol proteins and carbohydrates.

The fluid mosaic model was first proposed by s.j. Singer and Garth L. Nicolson in 1972 to eplain the structure of the plasma membrane. The model has evolved somewhat over time but it still best accounts for the structure and functions of the plasma membrane as we now understand them. The fluid mosaic model describes the structure of the plasma membrane as a mosaic of components including phospholipids cholesterol, proteins and carbohydrate that gives the membrane a fluid character. Plasma membranes range from 5 to 10 nm in thickness. For comparison human red blood cells visible via light microscopy are approximately 8um vide or approximately 1000 times wider than a plasma membrane the proportions of proteins lipids and carbohydrates in the plasma membrane vary with cell type. For example myelin contains 18% protein and 76% lipid. The mitochondrial inner membrane contains 76% protein and 24% lipid.

 **Components of the plasma Membrane**

 **Component Location**

 **Phospholipid** Main fabric of the membrane

 **Cholesterol** Attached between phospholipids and btween the two phospholipid layers

**Integral proteins for example integrins.** Embedded within the phospholipid layers may or may not penetrate through both layers.

**Peripheral proteins.** On the inner or outer surface of the phospholipid bilayer not embedded within the phospholipids

**Carbohydrates components of glycoproteins and glycolipids.**

Generally attached to outside of membrane layer

The principal components of a plasma membrane are lipids phospholipids and cholesterol proteins and carbohydrates attached to some of the lipids and some of the proteins.

**The fluid mosaic model of the plasma membrane.**

The fluid mosaic model of the plasma membrane describes the plasma membrane as a and proteins. Carbohydrates attached to lipids glycolipids and to proteins glycoproteins extend from the outward facing surface of the membrane,

The main fabric of the membrane is composed of amphiphilic or dual loving phospholipid molecules the hydrophilic or water loving areas of these molecules are in contact with the aqueous fluid both inside and outside the cell. Hydrophobic or water hating molecules then to be nonpolar. A phospholipid molecule consists of a three carbon glycerol backbone with two fatty acid molecules attached to carbons 1 and 2 and phosphate containing group attached to the third carbon . This arrangement gives the overall molecule an area described as its head the phosphate containing group which has polar character or negative charge and an area called the tail the fatty acids which has no charge they interact with other nonpolar molecules in chemical reactions but generally do not interact with polar molecules. When placed in water hydrophobic molecules tend to form a ball or cluster. The hydrophilic regions of the phospholipids tend to from hydrogen bond with water and other polar molecules on both the exterior and interior of the cell. Thus the membrane surfaces that face the interior and exterior of the cell are hydrophilic in contrast the middle of the cell membrane is hydrophilic and will not interact with water . Therefore phospholipids form an excellent lipid b ilayer cell membrane that separates fluid within the cell from the fluid outside of the cell.

**Structure of integral membrane proteins.** Integral membrane proteins may have one or more alpha helices that span the membrane examples 1 and 2 or they may have beta sheets that span the membrane example3

**Membrane Fluidity.** There are multiple factors that lead to membrane fluidity. First, the mosaic characteristic of the membrane helps the plasma membrane remain fluid. The integral proteins and lipids exist in the membrane as separate but loosely- attached molecules. The membrane is not like a balloon that can expand and contract rather it is fairly rigid and can burst if penetrated or if a cell takes in to much water. However, because of its mosaic nature, a very fine needle can easily penetrate a plasma membrane without causing it to burst the membrane will flow and self seal when the needle is extracted.

The second factor that leads to fluidity is the nature of the phospholipids themselves. In their saturated form the fatty acids in phospholipid tails are saturated with bound hydrogen atoms. There are no double bonds between adjacent carbon atoms. This results in tails that are relatively straight in contrast, unsaturated fatty acids do not contain a maximal number of hydrogen atoms although they do contain some double bonds between adjacent carbon atoms.