2022

BOTANY HONOURS

Paper : CC-12
(Biochemistry)

Full Marks : 50

The figures in the margin indicate full marks.

Candidates are required to give their answers in their own words as far as practicable.

1. **Answer briefly the following (any five) :**

(a) The Henderson-Hasselbalch equation is used to estimate the pH of a buffer solution when the concentration of the acid and its conjugate base, or the base and the corresponding conjugate acid, are known. It provides a relationship between the pH of acids (in aqueous solutions) and their pKa (acid dissociation constant) [1][2][3].

(b) Chargaff's rule states that in the DNA of any species and any organism, the amount of guanine should be equal to the amount of cytosine and the amount of adenine should be equal to the amount of thymine. A 1:1 stoichiometric ratio of purine and pyrimidine bases (i.e., A+G=T+C) should exist [4][5][6].

© Isozymes are enzymes that differ in amino acid sequence but catalyze the same chemical reaction. They usually have different kinetic parameters or are regulated differently. Isozymes permit the fine-tuning of metabolism to meet the particular needs of a given tissue or developmental stage. Often the only difference among isozymes is the substitution of one to several amino acids. An example of an isozyme is lactate dehydrogenase [7][8][9].

(d) Redox potential, also known as oxidation-reduction potential (ORP), is a measure of the tendency of a chemical species to acquire electrons from or lose electrons to an electrode and thereby be reduced or oxidised respectively[1]. Here are some key points about its significance:

1. **Direction of Reactions**: Redox potential helps determine the direction of an electron transfer reaction[2]. A substance with a higher reduction potential than other species will have a tendency to gain electrons from new species, while one with a lower reduction potential will have a tendency to lose electrons from new species[2].
2. **Oxidation or Reduction**: It helps in representing a substance's tendency to lose electrons to an electrode and to gain electrons from an electrode[2]. It specifies whether the material is oxidized or reduced[2].
3. **Measurement Unit**: Redox potential is calculated in millivolts or volts[2].

4. **Characterization of Reactions**: It allows for quick and easy characterization of the degree of reduction in a chemical reaction, as well as the prediction of compound stability[2]. This is crucial in the regulation of nutrients and metal availability in soils and sediment[2].
5. **Analytical Tool**: Despite

.

(e) A free radical is an atom, molecule, or ion that has at least one unpaired valence electron. With some exceptions, these unpaired electrons make radicals highly chemically reactive. Examples of free radicals include singlet oxygen, hydrogen peroxide, superoxides, and hydroxyl anions [121314].

(f) Methionine is a sulfur-containing amino acid. Its chemical structure is H3C-S-CH2-CH2-CH(NH2)-COOH [1516].

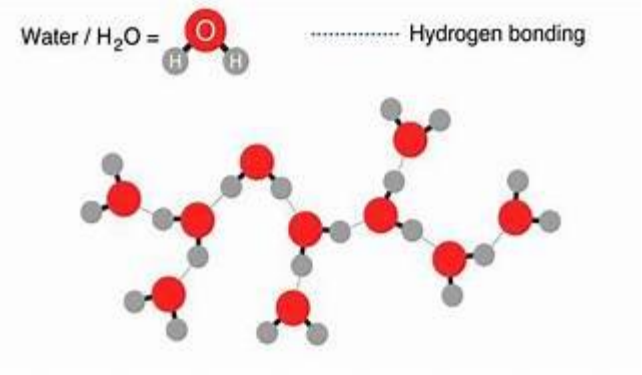
(g) Enantiomers are stereoisomers that are non-superimposable mirror images of each other. They have the same physical and chemical properties except for their ability to rotate plane-polarized light. An example of enantiomers is L-alanine and D-alanine [17].

2. Answer any two of the following :

(a) Competitive and non-competitive enzyme inhibition are two types of enzyme inhibition. Competitive inhibitors are molecules that bind to the active site of an enzyme and compete with the substrate for binding. They are structurally similar to the substrate and can be overcome by increasing the substrate concentration. Non-competitive inhibitors, on the other hand, bind to a site on the enzyme other than the active site and cause a conformational change in the enzyme that reduces its activity. Increasing the substrate concentration cannot overcome non-competitive inhibition [12].
Competitive inhibition is a reversible process, and the degree of inhibition depends on the concentration of the inhibitor and the substrate. The inhibition can be overcome by increasing the concentration of the substrate, which will outcompete the inhibitor for binding to the active site of the enzyme. Non-competitive inhibition, on the other hand, is not affected by the concentration of the substrate. Non-competitive inhibitors bind to the enzyme at a site other than the active site, causing a conformational change in the enzyme that reduces its activity. Non-competitive inhibition can be reversible or irreversible, depending on the nature of the inhibitor [12].

Both competitive and non-competitive inhibition are important in regulating enzyme activity in cells. Competitive inhibitors are often used as drugs to treat diseases caused by enzyme.

(b)



Explore

Hydrogen bonds are many times weaker than covalent bonds, but they are of crucial importance in biomolecules. Hydrogen bonds are responsible for the secondary and tertiary structures of proteins, the double helix structure of DNA, and the structure of water molecules. Hydrogen bonds are also important in the recognition of ligands by enzymes and in the formation of lipid bilayers in cell membranes. Hydrogen bonds are weak individually, but they are strong collectively, and they play a critical role in the stability and function of biomolecules [12].

In proteins, hydrogen bonds are responsible for the formation of alpha helices and beta sheets, which are important secondary structural elements. Hydrogen bonds between amino acid side chains also play a role in stabilizing the tertiary structure of proteins. In DNA, hydrogen bonds between complementary base pairs hold the two strands of the double helix together. In water, hydrogen bonds between water molecules give rise to the unique properties of water, such as its high boiling point and surface tension. In enzymes, hydrogen bonds are involved in the recognition of ligands and in the stabilization of the enzyme-substrate complex. In cell membranes, hydrogen bonds between lipid molecules help to form the lipid bilayer that is essential for the integrity of the membrane [12].

In summary, hydrogen bonds are weak individually, but they are of crucial importance in biomolecules. They play a critical role in the stability and function of proteins, DNA, and cell membranes, and they are responsible for many of the unique properties of water. Hydrogen bonds are an essential component of life, and without them, many of the processes that occur in living organisms would not be possible.

© The secondary structure of a protein refers to the three-dimensional form associated with the local segments of the polypeptide chain[1]. This structure is determined by the dihedral angles of the peptide bonds[2]. The proteins do not exist in just simple chains of polypeptides. These polypeptide chains usually fold due to the interaction between the amine and carboxyl group of the peptide link[3].

The two most common secondary structural elements are:

1. **Alpha helices**: This structure is formed when the polypeptide chains twist into a spiral shape, which is stabilized by hydrogen bonds.
2. **Beta sheets**: This structure is formed when the polypeptide chains align parallel or antiparallel to each other, forming a pleated sheet-like structure, which is also stabilized by hydrogen bonds[4].

These structures are crucial for the overall conformation of the protein, as they provide the necessary framework for the formation of the tertiary structure[5]. Any changes in these structures can significantly affect the function of the protein[3].

Let's go into more detail:

- **Alpha Helices**: In an alpha helix, the polypeptide backbone is twisted into a right-handed coil or spiral. The R groups (side chains) of the amino acids in the helix point outward from the helix's cylinder. The helix is stabilized by hydrogen bonds between the carbonyl oxygen of each peptide bond and the amide hydrogen of the fourth amino acid away in the sequence[2].
- **Beta Sheets**: In a beta sheet, two or more segments of a polypeptide chain line up next to each other, forming a sheet-like structure held together by hydrogen bonds. The segments can be part of the same chain or different chains. The R groups from adjacent amino acids point in opposite directions, making the sheet relatively flat[2].

These secondary structures are held together by hydrogen bonds, which form between the carbonyl oxygen of one amino acid and the amide hydrogen of another[2]. These structures are not static; instead, they can bend and flex in response to other interactions within the protein, as well as interactions with the environment[3].

In conclusion, the secondary structure of proteins is a critical aspect of their overall structure and function. It provides the necessary framework for the formation of the tertiary structure and ultimately determines the protein's function[5].

(d) The fluid mosaic model is a conceptual framework for understanding the structure and behavior of biological membranes. Proposed by S.J. Singer and Garth L. Nicolson, this model describes the plasma membrane of animal cells as a mosaic of components[1].

The main components of the membrane include:

1.Phospholipids: These are amphipathic molecules with a hydrophilic head and a hydrophobic tail. They form a bilayer, with the hydrophilic heads facing the watery environment on either side, and the hydrophobic tails hidden away from the water[1].

2. **Cholesterol**: It helps the plasma membrane to retain fluidity. It is present between the phospholipids and prevents the compaction of hydrophilic tails at low temperatures and their expansion at high temperatures[1].

3. **Proteins**: The plasma membrane has three types of proteins - integral proteins, peripheral proteins, and glycoproteins. These proteins perform various functions, including transporting larger molecules across the membrane and facilitating intercellular communication[1].

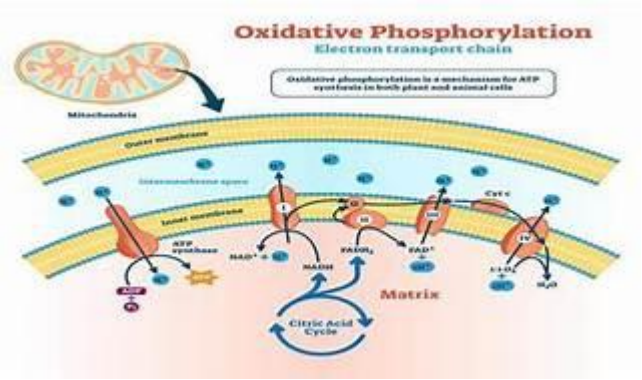
The fluid mosaic model also explains the fluidity of the cell membrane, which is influenced by temperature, cholesterol, and the presence of saturated and unsaturated fatty acids[1]. The cholesterol molecules are randomly distributed along the phospholipid bilayer, preventing it from separating too far or compacting too tightly[1].

In conclusion, the fluid mosaic model provides a comprehensive understanding of the structure and function of the plasma membrane, highlighting its dynamic and complex nature[1].

.. An example of an unsaturated fatty acid present in plants is **linoleic acid**[2]. Linoleic acid is a polyunsaturated omega-6 fatty acid. It is found in many vegetable oils, nuts, and seeds[2].

(3) Answer any three of the following

(a)



Sure, here are the key differences between oxidative phosphorylation and photophosphorylation:

Oxidative Phosphorylation[12]:

1. Occurs during respiration.

2. Takes place inside mitochondria.
3. Pigment systems are not involved.
4. ATP is produced from ADP and inorganic phosphate by utilizing energy released during electron transport.
5. Molecular oxygen is required for terminal oxidation.
6. The ATP molecules produced are released into the cytoplasm and these energy molecules are used to carry out various metabolic reactions of the cell.

Photophosphorylation[12]:

1. Occurs during photosynthesis.
2. Takes place inside chloroplasts.
3. Pigment systems (PS-I and PS-II) are involved.
4. Sunlight is the external energy source for photophosphorylation.
5. Molecular oxygen is not required for photophosphorylation.
6. The ATP molecules produced are used to fix CO2 to carbohydrates in the dark reaction.

In summary, oxidative phosphorylation is a process that uses energy released by the oxidation of nutrients to produce ATP, while photophosphorylation is a process that uses light energy to produce ATP[12].

The chemiosmotic model of ATP synthesis, also known as oxidative phosphorylation, was proposed by Peter Mitchell[1]. This process occurs in the mitochondria and is the major source of ATP in aerobic organisms[1].

Here's a detailed explanation of the process:

1. **Electron Transport Chain (ETC)**: The process begins with the metabolism of energy-rich molecules such as glucose to produce acetyl CoA. The oxidation of acetyl coenzyme A (acetyl-CoA) in the mitochondrial matrix is coupled to the reduction of carrier molecules such as nicotinamide adenine dinucleotide (NAD) and flavin adenine dinucleotide (FAD)[1]. These carriers pass electrons to the ETC in the inner mitochondrial membrane[1]. Each complex in the ETC undergoes a reduction and oxidation reaction to pass the electrons to the subsequent complex[1].
2. **Proton Gradient Formation**: Simultaneously for each electron transfer, protons are transported from the mitochondrial matrix to the intermembrane space[1]. This accumulation of protons in the intermembrane space leads to two things: the first is the generation of a chemical gradient (alkaline in the matrix and acidic in the intermembrane space), and the second is an electrical gradient due to charge separation[1]. The energy from each redox

transfer step in the ETC is used to pump protons (H+) from the matrix into the intermembrane space, creating a transmembrane electrochemical gradient[1].

3. **ATP Synthesis**: The protons move back across the inner membrane through the enzyme ATP synthase[1]. The flow of protons back into the matrix of the mitochondrion via ATP synthase provides enough energy for adenosine diphosphate (ADP) to combine with inorganic phosphate to form ATP[1]. The electrochemical energy built through the difference in proton concentration and separation of charge across the inner mitochondrial membrane translates to the proton motive force (PMF)[2]. The PMF drives the synthesis of ATP as protons flow back into the matrix through the proton-specific channels (F0) component of the ATP synthase[2].

The total energy available for ATP synthesis, called the proton motive force (Δp), is the sum of a proton chemical potential and a transmembrane electric potential, Δp = ΔE − 59(pHi − pHo)[3]. A transmembrane pH difference of 1 pH unit is equivalent to a membrane potential of 59 mV[3].

This chemiosmotic mechanism is also utilized during photosynthesis in chloroplasts[1]. The development of the proton gradient and then the subsequent movement of protons back across the membrane provides the energy required for ATP synthesis[1].

(b) **ssDNA**, or single-stranded DNA, is a DNA molecule that consists of only a single strand[1]. It is created during the replication process of DNA[1].

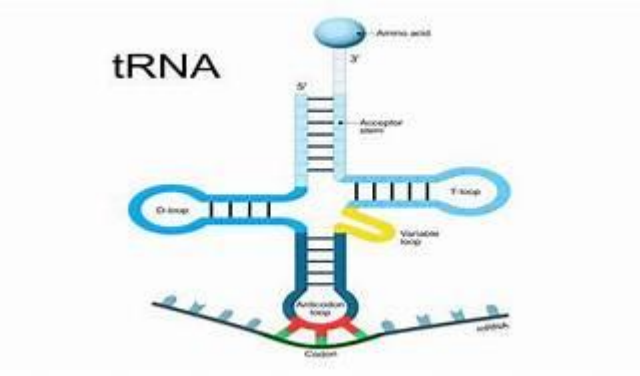
In nature, ssDNA genomes can be found in class II viruses known as the Parvoviridae and bacteriophages called microviridae[1]. Some viruses have ssDNA, and it is found abundantly in viruses of extreme conditions and marine environments[2]. Single-stranded DNA can also be produced artificially by rapidly cooling heat-denatured DNA[1].

mRNA (Messenger RNA)[12345]:

- mRNA is a type of single-stranded RNA involved in protein synthesis.
- It carries genetic information from the DNA in a cell's nucleus to the cell's cytoplasm, where the protein-making machinery reads the mRNA sequence and translates each three-base codon into its corresponding amino acid in a growing protein chain.
- mRNA is made from a DNA template during the process of transcription.

snRNA (Small Nuclear RNA)[6789]:

- snRNA is a class of small RNA molecules that are found within the splicing speckles and Cajal bodies of the cell nucleus in eukaryotic cells.
- The average length of an snRNA is approximately 150 nucleotides.
- They are transcribed by either RNA polymerase II or RNA polymerase III.
- The role of snRNA is to mediate some of these processes, such as intron splicing and other RNA processing.



Transfer RNA (tRNA) is a type of RNA molecule that plays a crucial role in protein synthesis. It acts as an adapter molecule during the translation process, linking amino acids to their corresponding codons on mRNA[1][2]. Here's a detailed description of its structure:

1. **Length**: tRNAs are generally 76-90 nucleotides long[1].
2. **Shape**: The secondary structure of tRNA resembles a clover leaf, while its tertiary structure is like an inverted 'L' shape[1]. This folded structure is formed due to hydrogen bonding between complementary bases[1].
3. **Acceptor Arm**: This is formed by the base pairing of 7-9 nucleotides of the 5' terminal and 3' terminal. The 5' terminal has a phosphate group and the 3' ends with a specific sequence of CCA or CCA tail. The amino acid attaches to the 3' hydroxyl group of the acceptor arm[1].
4. **DHU Loop**: The D arm has a stem of 3-4 base pairs and it ends in a loop called D loop as it generally contains dihydrouridine, a modified nucleotide[1].
5. **Anticodon Loop**: It has a 5 base pair long stem. It has an anticodon loop, which contains the complementary codon (3 nucleotides sequence) present on mRNA for the amino acid it carries[1].
6. **TΨC Loop**: The T arm consists of a stem of 4-5 bp and a loop containing pseudouridine, a modified uridine[1].
7. **Variable Loop**: It is present between the TΨC loop and the anticodon loop. Its size varies from 3-21 bases. It helps in the recognition of the tRNA molecule[1].

Each tRNA is specific to each amino acid and carries them during the translation process in the ribosomal subunits[1]. The tRNA transfers the amino acid to the growing polypeptide chain in the ribosomes, which has three binding sites for tRNA, namely A, P and E, which correspond to aminoacyl, peptidyl and exit, respectively[1]. This decoding of codons of mRNA by specific tRNAs continues until the entire sequence for a polypeptide chain is translated[1].

© Disaccharides are carbohydrates composed of two monosaccharides linked together. They play crucial roles in various biological functions, including energy storage and transport. Here are the major disaccharides present in plants:

1. **Sucrose**[1234]: Sucrose is the most common disaccharide found in plants. It is composed of one molecule of glucose and one of fructose bonded via an α-,β-linkage[1]. Sucrose is formed following photosynthesis in green plants[1]. It is a non-reducing sugar as both the reducing groups of glucose and fructose are involved in the glycosidic bond formation[2]. Many plants, such as sugar cane, are high in sucrose as it is an energy storage source[4].

2. **Maltose**[2]: Maltose is another disaccharide found in plants. It consists of two α-D-glucose units connected by the first carbon of one glucose and linked to the fourth carbon of another glucose unit[2]. Maltose is a reducing sugar as it shows reducing properties[2].

3. **Trehalose**[24]: Trehalose is a disaccharide made up of 2 molecules of glucose linked differently[2]. It can be found in some fungi and plants[4]. Trehalose is used for transport in some algae and fungi[4].

These disaccharides can be found in many common vegetables, including potatoes, onion, garlic, carrots, asparagus, and mushrooms[5]. Other starchy vegetables like corn, peas, string beans, and lentils are also good sources of these sugar molecules[5].

D-Glucose and **L-Glucose** are enantiomers, meaning they are non-superimposable mirror images of each other[1]. They have the same chemical structure but differ in the spatial orientation of their atoms[12].

D-Glucose[123]:

- D-Glucose is a sugar molecule that is abundant in nature[1].
- It can rotate plane polarized light in the clockwise direction[1].

- In the Fischer projection, D-Glucose shows four –OH groups on the sides of the main carbon chain. Three of the –OH groups are on the right side whereas the other –OH group is on the left side[1].

L-Glucose[123]:

- L-Glucose is a sugar molecule that is less abundant in nature[1].
- It can rotate plane polarized light in the anticlockwise direction[1].
- Unlike D-glucose, the oxygen and hydrogen group of atoms in L-glucose points to the left in the Fischer model[4].

In summary, D-Glucose and L-Glucose are isomers of glucose that differ in the orientation of the hydroxyl group on the last asymmetric carbon atom[12354]. D-Glucose is the common sugar that our bodies use for energy[5]. On the other hand, L-Glucose is a reduced sugar that is an excellent option for diabetics[3].

Phospholipids are a type of lipid molecule that is the main component of the cell membrane[1]. They are compound lipids, consisting of phosphoric acids, nitrogen base, alcohol, and fatty acids[2].

Structure of Phospholipids[1234]:

- A phospholipid is made up of two fatty acid tails and a phosphate group head[1].
- Fatty acids are long chains that are mostly made up of hydrogen and carbon, while phosphate groups consist of a phosphorus molecule with four oxygen molecules attached[1].
- These two components of the phospholipid are connected via a third molecule, glycerol[1].
- Phospholipids are able to form cell membranes because the phosphate group head is hydrophilic (water-loving) while the fatty acid tails are hydrophobic (water-hating)[1].
- To form membranes, phospholipids line up next to each other with their heads on the outside of the cell and their tails on the inside[1].
- A second layer of phospholipids also forms with heads facing the inside of the cell and tails facing away[1].
- In this way, a double layer is formed with phosphate group heads on the outside, and fatty acid tails on the inside[1].
- This double layer, called a lipid bilayer, forms the main part of the cell membrane[1].

Biological Functions of Phospholipids[1256]:

- As membrane components, phospholipids are selectively permeable (also called semi-permeable), meaning that only certain molecules can pass through them to enter or exit the cell[1].
- Molecules that dissolve in fat can pass through easily, while molecules that dissolve in water cannot[1].
- Phospholipids can be broken down in the cell and used for energy[1].
- They can also be split into smaller molecules called chemokines, which regulate a variety of activities in the cell such as production of certain proteins and migration of cells to different areas of the body[1].
- Additionally, they are found in areas such as the lung and in joints, where they help lubricate cells[1].
- In pharmaceuticals, phospholipids are used as part of drug delivery systems, which are systems that help transport a drug throughout the body to the area that it is meant to affect[1].
- They regulate the permeability of the membrane[2].
- They are also involved in the absorption of fat from the intestine[2].
- They help in ETC- Electron Transport Chain in the mitochondria[2].
- Phospholipids help by preventing the accumulation of fats in the liver[2].
- They play a major role in the transportation and removal of cholesterol from the cells[2].
- They form the structural components of the cell membrane with the association of proteins[2].
- They act as surfactants in the respiratory system and are also involved in the coagulation of blood cells[2].
- They help in the synthesis of different lipoproteins, prostacyclins, prostaglandins, and thromboxanes[2].