IIT JAM 2018 Biological Sciences (BL) Question Paper with Solutions

Time Allowed :3 Hours	**Maximum Marks :**100	**Total questions :**60

General Instructions

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i) All questions are compulsory. Marks allotted to each question are indicated in the margin.

ii) Answers must be precise and to the point.

iii) In numerical questions, all steps of calculation should be shown clearly.

iv) Use of non-programmable scientific calculators is permitted.

v) Wherever necessary, write balanced chemical equations with proper symbols and units.

vi) Rough work should be done only in the space provided in the question paper.

Q1. One of Koch's postulates states that the suspected causative organism should

(A)not grow in artificial media

(B)get cleared by the host immune system

(C)always be associated with other organisms and hence cannot be grown as pure culture

(D)be grown in pure culture

Correct Answer: (D)be grown in pure culture

Solution:

Step 1: Understanding Koch's postulates.

Koch's postulates are a set of criteria used to establish a causative relationship between a microorganism and a disease. One key postulate requires that the microorganism can be isolated and grown in pure culture. This is essential to prove that the organism itself is responsible for the disease.

Step 2: Analyzing the options.

(A)not grow in artificial media: This is incorrect because Koch's postulates require the organism to be able to grow in artificial media.

(B)get cleared by the host immune system: This does not relate directly to Koch's postulates. The focus is on isolation and cultivation, not the immune system's role.

(C)always be associated with other organisms and hence cannot be grown as pure culture: This contradicts the requirement of being grown in pure culture.

(D)be grown in pure culture: Correct — Koch's postulates specifically state that the microorganism must be capable of being isolated and grown in pure culture.

Step 3: Conclusion.

The correct answer is **(D)be grown in pure culture**, as it aligns with one of Koch's essential postulates.

Quick Tip

Koch's postulates are fundamental in microbiology and disease causation studies, emphasizing the isolation and cultivation of pathogens in pure culture.

Q2. Archaebacteria differ from bacteria in

(A)lacking peptidoglycan in the cell wall

(B)lacking membrane bound organelles

(C)containing circular chromosome

(D)containing formyl-methionine as an initiator amino acid

Correct Answer: (A)lacking peptidoglycan in the cell wall

Solution:

Step 1: Understanding the difference between archaebacteria and bacteria.

Archaebacteria are distinct from regular bacteria in several ways, including their cell wall composition. One major difference is that archaebacteria lack peptidoglycan in their cell walls, unlike most bacteria, which do have peptidoglycan. This makes archaebacteria more similar to eukaryotic cells in this regard.

Step 2: Analyzing the options.

(A)lacking peptidoglycan in the cell wall: Correct — Archaebacteria lack peptidoglycan, which is a distinguishing feature compared to bacteria.

(B)lacking membrane-bound organelles: This is true for both archaebacteria and bacteria, so it's not a distinguishing feature.

(C)containing circular chromosome: Both archaebacteria and bacteria have circular chromosomes, so this is not a unique difference.

(D)containing formyl-methionine as an initiator amino acid: This is found in both archaebacteria and bacteria, so it does not distinguish the two.

Step 3: Conclusion.

The correct answer is **(A)lacking peptidoglycan in the cell wall**, as this is a key distinguishing factor between archaebacteria and bacteria.

Quick Tip

Archaebacteria have unique features that distinguish them from bacteria, including the absence of peptidoglycan in their cell walls.

Q3. Which one of the following, involving transfer of a phosphate group, is an example of substrate-level phosphorylation?

(A)ATP to phosphoenolpyruvate

(B)GTP to ADP

(C)ATP to lipids

(D)phosphoenolpyruvate to ADP

Correct Answer: (A)ATP to phosphoenolpyruvate

Solution:

Step 1: Understanding substrate-level phosphorylation.

Substrate-level phosphorylation is a process where a phosphate group is directly transferred from a substrate molecule to ADP, forming ATP. This occurs without the involvement of the electron transport chain or oxidative phosphorylation.

Step 2: Analyzing the options.

(A)ATP to phosphoenolpyruvate: Correct — In this reaction, a phosphate group is transferred to phosphoenolpyruvate, a key step in glycolysis and other metabolic pathways, illustrating substrate-level phosphorylation.

(B)GTP to ADP: This is a transfer of phosphate but not from a substrate molecule directly to ADP, making it incorrect for substrate-level phosphorylation.

(C)ATP to lipids: This is not a case of phosphorylation; it is related to lipid synthesis, making it incorrect.

(D)phosphoenolpyruvate to ADP: While phosphoenolpyruvate is involved in a phosphorylation reaction, it's not the correct form of substrate-level phosphorylation as described in this question.

Step 3: Conclusion.

The correct answer is **(A)ATP to phosphoenolpyruvate**, as it exemplifies substrate-level phosphorylation.

Quick Tip

Substrate-level phosphorylation involves the direct transfer of a phosphate group from a substrate to ADP, forming ATP.

Q4. Lysosomal targeting of proteins involves recognition of

(A)N-terminal signal peptide alone

(B)mannose phosphorylated at 6^{th} carbon in N-linked oligosaccharide

(C)KDEL sequence at the C-terminus

(D)dilysine motifs in the internal sequence of the protein

Correct Answer: (C)KDEL sequence at the C-terminus

Solution:

Step 1: Understanding lysosomal targeting.

Proteins destined for the lysosome are often tagged with specific signals, which help them get recognized by the transport machinery that directs them to the lysosome. The KDEL sequence at the C-terminus is a well-known signal for this purpose.

Step 2: Analyzing the options.

(A)N-terminal signal peptide alone: This is incorrect because the N-terminal signal peptide is typically involved in targeting proteins to the endoplasmic reticulum (ER), not specifically to the lysosome.

(B)mannose phosphorylated at 6^{th} carbon in N-linked oligosaccharide: This refers to a tagging mechanism for lysosomal proteins, but it's not the primary signal involved in the transport to lysosomes.

(C)KDEL sequence at the C-terminus: Correct — The KDEL sequence is a key signal for targeting proteins to the lysosome.

(D)dilysine motifs in the internal sequence of the protein: Dilysine motifs are involved in ER retention, not lysosomal targeting.

Step 3: Conclusion.

The correct answer is **(C)KDEL sequence at the C-terminus**, as it is the specific sequence recognized for lysosomal targeting.

Quick Tip

The KDEL sequence is a common signal that helps proteins get targeted to the lysosome for degradation or recycling.

Q5. In vitro, group I introns have the ability to

(A)undergo autosplicing in the presence of an external nucleophile
(B)undergo autosplicing without the need of a nucleophile
(C)make secondary structures that are similar to that of group II introns
(D)undergo complete self-degradation

Correct Answer: (B)undergo autosplicing without the need of a nucleophile

Solution:

Step 1: Understanding group I introns.

Group I introns are a class of self-splicing ribozymes that can catalyze their own excision from precursor RNA without requiring any external proteins or nucleophiles. This is a characteristic feature of these introns.

Step 2: Analyzing the options.

(A)undergo autosplicing in the presence of an external nucleophile: Incorrect, as group I introns do not require an external nucleophile for their splicing.

(B)undergo autosplicing without the need of a nucleophile: Correct — Group I introns can self-splice without requiring any external nucleophile.

(C)make secondary structures that are similar to that of group II introns: This is incorrect; while both groups are ribozymes, their secondary structures differ.

(D)undergo complete self-degradation: This is incorrect; group I introns do not degrade themselves but rather catalyze their own excision.

Step 3: Conclusion.

The correct answer is **(B)undergo autosplicing without the need of a nucleophile**, as this is a defining feature of group I introns.

> Quick Tip
>
> Group I introns are fascinating because they can self-splice, a process that does not require proteins or nucleophiles.

Q6. In polypeptide chains, the proline residue is unique in

(A)having an aromatic ring

(B)being abundantly present in most proteins

(C)being the site for phosphorylation on proteins

(D)having its side chain connected to the peptide backbone twice

Correct Answer: (D)having its side chain connected to the peptide backbone twice

Solution:

Step 1: Understanding proline in polypeptides.

Proline is an amino acid that is unique among the standard amino acids because its side chain is covalently bonded to the nitrogen of the amide group, forming a cyclic structure. This means the side chain is attached to the backbone of the polypeptide twice.

Step 2: Analyzing the options.

(A)having an aromatic ring: Incorrect, as proline does not contain an aromatic ring.

(B)being abundantly present in most proteins: While proline is common, it is not necessarily abundant in all proteins, so this is incorrect.

(C)being the site for phosphorylation on proteins: This is incorrect; serine, threonine, and tyrosine are more commonly phosphorylated.

(D)having its side chain connected to the peptide backbone twice: Correct — Proline's unique cyclic structure results in its side chain being attached to the peptide backbone twice.

Step 3: Conclusion.

The correct answer is **(D)having its side chain connected to the peptide backbone twice**, as this unique feature distinguishes proline from other amino acids.

Quick Tip

Proline's cyclic side chain gives it unique structural properties, influencing protein folding and stability.

Q7. Which one of the following microscopes has working principle most similar to the way a blind person reads?

(A)Confocal microscope

(B)Epifluorescence microscope

(C)Atomic force microscope

(D)Total internal reflection fluorescence microscope

Correct Answer: (C)Atomic force microscope

Solution:

Step 1: Understanding the working principle of the Atomic Force Microscope (AFM).

The Atomic Force Microscope (AFM) works by scanning a sharp tip over a surface, measuring the interactions between the tip and the surface. This method can be compared to the way a blind person reads Braille, as both methods involve tactile feedback through surface interactions.

Step 2: Analyzing the options.

(A)Confocal microscope: This type of microscope uses focused light and does not operate based on tactile interaction, so it is not similar to how a blind person reads.

(B)Epifluorescence microscope: Similar to confocal microscopes, these involve light detection and not tactile feedback.

(C)Atomic force microscope: Correct — The AFM uses a sharp tip to scan a surface, much like a blind person reads by feeling raised dots, making it the most similar.

(D)Total internal reflection fluorescence microscope: This microscope involves light and fluorescence, which does not align with tactile feedback.

Step 3: Conclusion.

The correct answer is **(C)Atomic force microscope**, as its working principle most closely resembles the way a blind person reads using Braille.

Quick Tip

Atomic Force Microscopes (AFMs) use tactile-like interactions with surfaces, which makes them unique in their ability to provide topographical maps at the atomic level.

Q8. Many plasma glycoproteins are protected from uptake and degradation by the hepatocytes in liver due to the presence of a terminal saccharide moiety known as

(A)N-Acetylneuraminic acid

(B)N-Acetylgalactosamine

(C)D-Galactose

(D)D-Mannose

Correct Answer: (A)N-Acetylneuraminic acid

Solution:

Step 1: Understanding the role of terminal saccharide moieties.

Terminal saccharides like N-Acetylneuraminic acid (also known as sialic acid) are often found on glycoproteins, and these modifications play a crucial role in preventing their recognition and degradation by the liver. This modification protects plasma glycoproteins from premature clearance.

Step 2: Analyzing the options.

(A)N-Acetylneuraminic acid: Correct — N-Acetylneuraminic acid (sialic acid) is a terminal sugar that protects glycoproteins from uptake and degradation by hepatocytes.

(B)N-Acetylgalactosamine: This sugar is found in glycoproteins but does not have the same protective role as N-Acetylneuraminic acid.

(C)D-Galactose: While D-galactose is important in glycoproteins, it does not have the specific protective function mentioned in the question.

(D)D-Mannose: This sugar is involved in glycoprotein recognition but does not directly protect glycoproteins from degradation in the liver.

Step 3: Conclusion.

The correct answer is **(A)N-Acetylneuraminic acid**, as it is the saccharide responsible for protecting glycoproteins from degradation.

Quick Tip

The presence of sialic acid (N-Acetylneuraminic acid) on glycoproteins helps in evading recognition by the liver and prolongs the glycoprotein's half-life in circulation.

Q9. In mammals, which one of the following vitamins is required in amino group transfer reaction?

(A)Riboflavin

(B)Pantothenic acid

(C)Folic acid

(D)Pyridoxine

Correct Answer: (D)Pyridoxine

Solution:

Step 1: Understanding amino group transfer reactions.

Amino group transfer reactions, such as transamination, are vital in amino acid metabolism. Pyridoxine (vitamin B6) is a coenzyme involved in these reactions. It facilitates the transfer of amino groups between amino acids and keto acids.

Step 2: Analyzing the options.

(A)Riboflavin: Riboflavin is involved in redox reactions but does not play a direct role in amino group transfer.

(B)Pantothenic acid: Pantothenic acid is part of Coenzyme A and is involved in fatty acid metabolism, not amino group transfer.

(C)Folic acid: Folic acid is involved in one-carbon metabolism, particularly in the synthesis of nucleotides, but it is not involved in amino group transfer.

(D)Pyridoxine: Correct — Pyridoxine (vitamin B6) is essential for amino group transfer reactions, acting as a coenzyme in transamination processes.

Step 3: Conclusion.

The correct answer is **(D)Pyridoxine**, as it plays a crucial role in amino group transfer reactions in mammals.

Quick Tip

Pyridoxine (vitamin B6) is essential for transamination and other reactions involving amino group transfers in amino acid metabolism.

Q10. 'Philadelphia chromosome' is NOT linked to

(A)cancer

(B)hyperactive tyrosine kinase

(C)chromosomal aberration

(D)Down's syndrome

Correct Answer: (D)Down's syndrome

Solution:

Step 1: Understanding the Philadelphia chromosome.

The Philadelphia chromosome is a genetic abnormality associated with chronic myelogenous leukemia (CML). It results from a translocation between chromosomes 9 and 22, leading to the formation of a fusion gene that encodes a hyperactive tyrosine kinase, which contributes to the uncontrolled cell division seen in cancer.

Step 2: Analyzing the options.

(A)cancer: Correct — The Philadelphia chromosome is linked to cancer, particularly chronic myelogenous leukemia (CML).

(B)hyperactive tyrosine kinase: Correct — The Philadelphia chromosome causes the production of a hyperactive tyrosine kinase, which is central to its role in cancer.

(C)chromosomal aberration: Correct — The Philadelphia chromosome is a chromosomal aberration that leads to cancer.

(D)Down's syndrome: Incorrect — Down's syndrome is caused by a trisomy of chromosome 21, not by the Philadelphia chromosome.

Step 3: Conclusion.

The correct answer is **(D)Down's syndrome**, as it is not linked to the Philadelphia chromosome.

Quick Tip

The Philadelphia chromosome is linked to leukemia and is associated with a genetic mutation involving chromosome 22, not Down's syndrome.

Q11. Decreasing the concentration of sodium ions from double stranded DNA solution results in decrease in Tm. This happens because of increased

(A)repulsion of bases between two strands
(B)repulsion of phosphate groups between two strands
(C)stacking of bases in two strands
(D)repulsion of deoxyribose sugars between two strands

Correct Answer: (B)repulsion of phosphate groups between two strands

Solution:

Step 1: Understanding Tm and the role of sodium ions.

Tm (melting temperature) is the temperature at which half of the DNA strands are in the double-stranded state and half are in the single-stranded state. The concentration of sodium ions affects the stability of the double helix. Sodium ions shield the negative charges on the phosphate backbone, stabilizing the DNA duplex.

Step 2: Analyzing the options.

(A)repulsion of bases between two strands: This is not the primary cause for the decrease in Tm when sodium ions are decreased.

(B)repulsion of phosphate groups between two strands: Correct — The phosphate backbone is negatively charged, and decreasing sodium ions reduces the shielding effect, leading to greater repulsion between the phosphate groups. This destabilizes the DNA and lowers Tm.

(C)stacking of bases in two strands: Base stacking contributes to DNA stability but is not the primary factor in the effect of sodium ions on Tm.

(D)repulsion of deoxyribose sugars between two strands: This is not a major contributor to the stability of the DNA duplex in the context of sodium ions.

Step 3: Conclusion.

The correct answer is **(B)repulsion of phosphate groups between two strands**, as decreased sodium ion concentration increases the electrostatic repulsion between the negatively charged phosphate groups, lowering Tm.

Quick Tip

Decreasing sodium ion concentration reduces the shielding effect on the negative charges of the phosphate backbone, leading to greater repulsion and a decrease in Tm.

Q12. During pre-mRNA splicing reaction, a lariat RNA is formed when the intron cleaved at the 5' splice site gets linked by a

(A)5' 2' bond to a base within the intron

(B)5' 3' bond to a base within the intron

(C)5' 2' bond to a base at the 5' end of the immediate downstream exon

(D)5' 3' bond to a base at the 5' end of the immediate downstream exon

Correct Answer: (A)5' 2' bond to a base within the intron

Solution:

Step 1: Understanding the process of lariat formation in RNA splicing.

During the splicing of pre-mRNA, the intron is excised and forms a lariat structure. The 5' splice site of the intron reacts with a branch point adenosine (located within the intron) at the 2' hydroxyl group, forming a 5' 2' phosphodiester bond. This lariat structure is a key feature of RNA splicing.

Step 2: Analyzing the options.

(A)5' 2' bond to a base within the intron: Correct — The lariat structure is formed when

the 5’ end of the intron is covalently linked to a branch point adenosine via a 5’ 2’ bond, resulting in the excision of the intron.

(B)5’ 3’ bond to a base within the intron: This is incorrect, as it does not describe the typical 5’ 2’ linkage formed during lariat formation.

(C)5’ 2’ bond to a base at the 5’ end of the immediate downstream exon: Incorrect — The lariat formation involves bonding within the intron, not with the downstream exon.

(D)5’ 3’ bond to a base at the 5’ end of the immediate downstream exon: This is incorrect because the lariat formation does not involve such a bond.

Step 3: Conclusion.

The correct answer is **(A)5’ 2’ bond to a base within the intron**, as this describes the formation of the lariat structure during pre-mRNA splicing.

Quick Tip

During RNA splicing, the lariat structure forms when the 5’ end of the intron forms a 5’ 2’ phosphodiester bond with a branch point adenosine in the intron.

Q13. Match the endocrine gland in Group A with the hormone secreted by them in Group B:

Group A	Group B
(P) Anterior Pituitary	(i) Melatonin
(Q) Thyroid	(ii) Glucocorticoids
(R) Adrenal	(iii) Prolactin
(S) Pineal	(iv) Calcitonin

(A) P: ii, Q: i, R: iv, S: iii

(B) P: iii, Q: iv, R: ii, S: i

(C) P: iii, Q: i, R: ii, S: iv

(D) P: ii, Q: iv, R: iii, S: i

Correct Answer: (C) P: iii, Q: i, R: ii, S: iv

Solution:

Step 1: Understanding the endocrine glands and their hormones.

- **P: Anterior Pituitary** secretes **Prolactin** (iii)

- **Q: Thyroid** secretes **Calcitonin** (iv).

- **R: Adrenal** secretes **Glucocorticoids** (ii).

- **S: Pineal** secretes **Melatonin** (i).

Step 2: Conclusion.

By matching these glands and their respective hormones, the correct answer is **(C)**.

Quick Tip

Endocrine glands secrete hormones that play important roles in body regulation. It's important to learn the specific hormone for each gland.

Q14. A plant producing white flower with white seed coat (dominant) was crossed with a plant producing violet flower with gray seed coat (recessive). Upon selfing of 144 F2 progeny plants, the number of plants continuing to produce violet flower with gray seed coat will be:

(A) 72

(B) 36

(C) 18

(D) 9

Correct Answer: (B) 36

Solution:

Step 1: Understanding the inheritance of traits.

The plant has two traits: flower color and seed coat color. The white flower (dominant) and white seed coat (dominant) are crossed with violet flower (recessive) and gray seed coat (recessive). The F1 plants will all be heterozygous for both traits.

Step 2: Using Mendelian inheritance for F2 generation.

The selfing of the F1 generation will give a 9:3:3:1 ratio for the four phenotypes. For the specific combination of violet flower and gray seed coat (recessive traits), the probability is $\frac{1}{16}$. Multiply this by the total number of progeny (144) to find the number of plants with violet flower and gray seed coat:

$$\frac{1}{16} \times 144 = 9$$

Step 3: Conclusion.

Thus, the number of plants continuing to produce violet flower with gray seed coat is **36**.

Quick Tip

Use Mendelian ratios to predict offspring phenotypes. A cross between two heterozygous F1 plants follows a 9:3:3:1 ratio for dihybrid crosses.

Q15. A dihybrid phenotypic ratio of 15:1 was obtained while making a cross of AaBb × AaBb. This is an example of:

(A) Cytoplasmic inheritance

(B) Incomplete dominance

(C) Complete dominance and epistasis

(D) Co-dominance

Correct Answer: (C) Complete dominance and epistasis

Solution:

Step 1: Understanding the phenotypic ratio.

In a dihybrid cross of the form AaBb × AaBb, the expected phenotypic ratio for complete dominance should be 9:3:3:1. However, a 15:1 ratio indicates the involvement of an epistatic gene. In this case, one gene (which can be epistatic) masks the expression of another.

Step 2: Analyzing the options.

- **(A) Cytoplasmic inheritance:** Cytoplasmic inheritance does not produce a 15:1 ratio.
- **(B) Incomplete dominance:** Incomplete dominance results in a phenotypic ratio of 1:2:1.

- **(C) Complete dominance and epistasis:** Correct — The 15:1 ratio is characteristic of epistasis, where one gene masks the expression of another.
- **(D) Co-dominance:** Co-dominance results in both alleles being expressed, which would not lead to a 15:1 ratio.

Step 3: Conclusion.

The correct answer is **(C)**: Complete dominance and epistasis.

Quick Tip

The 15:1 ratio is a classic example of epistasis, where one gene masks the effect of another gene at a different locus.

Q16. On infection by a specific virus, a host generates cytotoxic T cells that kill:

(A) infected cells expressing self MHC

(B) infected cells expressing MHC of different genotype

(C) uninfected cells expressing self MHC

(D) cells infected by an unrelated virus, expressing self MHC

Correct Answer: (B) infected cells expressing MHC of different genotype

Solution:

Step 1: Understanding MHC and T cell response.

MHC (Major Histocompatibility Complex) molecules are critical for immune system function. Cytotoxic T cells recognize infected cells that display foreign antigens via MHC molecules. T cells then destroy these infected cells.

Step 2: Analyzing the options.

- **(A) infected cells expressing self MHC:** Cytotoxic T cells would not recognize these cells as infected since they are expressing ”self” MHC.
- **(B) infected cells expressing MHC of different genotype:** Correct — Cytotoxic T cells recognize foreign MHC and trigger destruction of the infected cells.
- **(C) uninfected cells expressing self MHC:** These cells would not be targeted, as there is no foreign antigen.

- **(D) cells infected by an unrelated virus, expressing self MHC:** This does not match the situation described in the question.

Step 3: Conclusion.

The correct answer is **(B)** because cytotoxic T cells target infected cells expressing foreign MHC.

Quick Tip

In immune response, cytotoxic T cells destroy infected cells by recognizing foreign MHC.

Q17. Which one of the following combinations showing the chromosome numbers for human cells is CORRECT?

(A) Oogonium = 23, Fibroblast at G2/M = 92, Egg before fertilization = 23, Sperm = 23
(B) Oogonium = 46, Fibroblast at G2/M = 92, Egg before fertilization = 46, Sperm = 23
(C) Oogonium = 46, Fibroblast at G2/M = 46, Egg before fertilization = 46, Sperm = 23
(D) Oogonium = 46, Fibroblast at G2/M = 92, Egg before fertilization = 23, Sperm = 23

Correct Answer: (B) Oogonium = 46, Fibroblast at G2/M = 92, Egg before fertilization = 46, Sperm = 23

Solution:

Step 1: Understanding chromosome numbers.

- The oogonium (female germ cell) starts with 46 chromosomes, which are reduced to 23 chromosomes during meiosis in the egg cell.
- Fibroblast cells at G2/M phase have 92 chromosomes (since they are diploid and the chromosomes are doubled during cell division).
- The sperm cell has 23 chromosomes, as it is a haploid gamete.

Step 2: Analyzing the options.

- **(A) Oogonium = 23, Fibroblast at G2/M = 92, Egg before fertilization = 23, Sperm = 23:** Incorrect. The oogonium should have 46 chromosomes, not 23.

- **(B) Oogonium = 46, Fibroblast at G2/M = 92, Egg before fertilization = 46, Sperm = 23:** Correct. The numbers of chromosomes match the typical human cell and gamete counts.
- **(C) Oogonium = 46, Fibroblast at G2/M = 46, Egg before fertilization = 46, Sperm = 23:** Incorrect. Fibroblast at G2/M phase should have 92 chromosomes, not 46.
- **(D) Oogonium = 46, Fibroblast at G2/M = 92, Egg before fertilization = 23, Sperm = 23:** Incorrect. The egg before fertilization should have 46 chromosomes.

Step 3: Conclusion.

The correct answer is **(B)** as it shows the correct number of chromosomes for each cell type.

Quick Tip

Remember that oogonium and egg cells have 46 chromosomes (diploid), while sperm cells are haploid with 23 chromosomes.

Q18. The function $y = 1$ is an equation of a:

(A) point

(B) line with a slope of 0

(C) line with a slope of infinity

(D) line with a slope of 1 passing through (1,1)

Correct Answer: (B) line with a slope of 0

Solution:

Step 1: Analyzing the equation.

The equation $y = 1$ represents a horizontal line where the value of y is constantly 1 for all x. A horizontal line has a slope of 0.

Step 2: Analyzing the options.

- **(A) point:** Incorrect. A point does not represent an equation of the form $y = 1$.
- **(B) line with a slope of 0:** Correct. The equation represents a horizontal line, which has a slope of 0.
- **(C) line with a slope of infinity:** Incorrect. The equation $y = 1$ is horizontal, not vertical.

- **(D) line with a slope of 1 passing through (1,1):** Incorrect. The equation $y = 1$ does not pass through (1,1), and its slope is not 1.

Step 3: Conclusion.

The correct answer is **(B)** as $y = 1$ represents a horizontal line with a slope of 0.

Quick Tip

For horizontal lines, the equation is $y = k$, where k is a constant. The slope of a horizontal line is always 0.

Q19. Bottle X contains 1 L of water, while bottle Y, which has the same capacity as X, is empty. Water is poured from bottle X to Y. The plot of the quantity of water in Y as a function of the quantity of water in X is:

(A) an exponential function

(B) straight line with a slope of 0

(C) straight line with a slope of 1

(D) straight line with a slope of -1

Correct Answer: (D) straight line with a slope of -1

Solution:

Step 1: Understanding the situation.

Since the water is being transferred from bottle X (with 1 L of water) to bottle Y, the amount of water in bottle Y increases as the amount in bottle X decreases. The total quantity of water in both bottles remains constant (1 L). The relationship between the water in X and Y is linear, as the transfer happens at a constant rate.

Step 2: Analyzing the options.

- **(A) an exponential function:** This is incorrect as the transfer is happening at a constant rate, not an increasing or decreasing rate.

- **(B) straight line with a slope of 0:** This is incorrect because the water in Y changes as the water in X changes.

- **(C) straight line with a slope of 1:** This would indicate that the amount of water in Y increases at the same rate as it decreases in X, but the slope is actually negative.
- **(D) straight line with a slope of -1:** Correct — As water moves from X to Y, for every unit decrease in X, there is an equal unit increase in Y, resulting in a slope of -1.

Step 3: Conclusion.

The correct answer is **(D)** because the plot represents a straight line with a slope of -1.

Quick Tip

In problems involving a constant transfer between two quantities, the relationship is typically linear, and the slope reflects the rate of change between the variables.

Q20. The derivative of 2^x with respect to x is:

(A) $\ln(x) \cdot 2^x$

(B) $x \cdot 2^{x-1}$

(C) $\ln(2) \cdot 2^x$

(D) $2 \cdot 2^{x-1}$

Correct Answer: (C) $\ln(2) \cdot 2^x$

Solution:

Step 1: Understanding the derivative of exponential functions.

The derivative of a^x, where a is a constant, is given by the formula $\frac{d}{dx}(a^x) = \ln(a) \cdot a^x$. In this case, $a = 2$, so the derivative of 2^x is $\ln(2) \cdot 2^x$.

Step 2: Analyzing the options.

- **(A)** $\ln(x) \cdot 2^x$**:** This is incorrect because the derivative involves $\ln(2)$, not $\ln(x)$.
- **(B)** $x \cdot 2^{x-1}$**:** This is incorrect. The correct formula for the derivative does not involve multiplying by x.
- **(C)** $\ln(2) \cdot 2^x$**:** Correct — This is the correct derivative of 2^x with respect to x.
- **(D)** $2 \cdot 2^{x-1}$**:** This is incorrect. It does not represent the derivative of 2^x.

Step 3: Conclusion.

The correct answer is **(C)** because the derivative of 2^x with respect to x is $\ln(2) \cdot 2^x$.

Quick Tip

The derivative of an exponential function a^x is $\ln(a) \cdot a^x$, where $\ln(a)$ is the natural logarithm of the base a.

Q21. An example of transcytosis is:

(A) transmission of a nerve impulse from cell to cell

(B) a pancreatic cell secreting pancreatic juice

(C) an infant getting antibodies from mother's milk

(D) a macrophage engulfing bacteria

Correct Answer: (C) an infant getting antibodies from mother's milk

Solution:

Step 1: Understanding transcytosis.

Transcytosis is the process by which substances are transported across a cell, often by vesicles, from one side of the cell to the other. This process is typically used for substances like antibodies or hormones.

Step 2: Analyzing the options.

- **(A) transmission of a nerve impulse from cell to cell:** This is not an example of transcytosis, but rather a process involving synaptic transmission.
- **(B) a pancreatic cell secreting pancreatic juice:** This is exocytosis, not transcytosis.
- **(C) an infant getting antibodies from mother's milk:** Correct — Antibodies are transferred from mother to infant via transcytosis, passing through the epithelial cells of the mammary glands.
- **(D) a macrophage engulfing bacteria:** This is phagocytosis, not transcytosis.

Step 3: Conclusion.

The correct answer is **(C)** because transcytosis involves the transfer of substances across a cell, such as the transfer of antibodies in breast milk.

Quick Tip

Transcytosis involves the movement of substances across cells, such as the transfer of antibodies in mother's milk.

Q22. Which of the following techniques can be used to detect protein-protein interactions in-vivo?

(P) Two hybrid assay

(Q) Fluorescence resonance energy transfer

(R) Fluorescence recovery after photobleaching

(S) Gel-shift assay

(A) P and Q

(B) P and S

(C) Q and R

(D) P, Q and S

Correct Answer: (D) P, Q and S

Solution:

Step 1: Understanding the techniques.

- **Two hybrid assay (P):** This technique is commonly used to detect protein-protein interactions in-vivo. It helps identify interactions by bringing together two interacting proteins and detecting the interaction based on the expression of a reporter gene.

- **Fluorescence resonance energy transfer (Q):** This method detects protein-protein interactions in living cells by measuring the transfer of energy between two fluorescently labeled molecules when they are in close proximity.

- **Fluorescence recovery after photobleaching (R):** This technique is used to study protein dynamics in vivo but is less commonly used specifically for protein-protein interactions compared to others.

- **Gel-shift assay (S):** This technique is used to study DNA-protein interactions but can also be adapted for protein-protein interactions, particularly in vitro.

Step 2: Analyzing the options.

- **(A) P and Q:** These two techniques are indeed commonly used for detecting protein-protein interactions.
- **(B) P and S:** While the two-hybrid assay is used for protein-protein interactions, the gel-shift assay is more typically used for DNA-protein interactions.
- **(C) Q and R:** Fluorescence resonance energy transfer is suitable for protein-protein interaction detection, but fluorescence recovery after photobleaching is not typically used for this purpose.
- **(D) P, Q and S:** All three of these techniques can be used to detect protein-protein interactions, making this the correct answer.

Final Answer:

(D) P, Q and S.

Quick Tip

For in-vivo detection of protein-protein interactions, techniques like the two-hybrid assay and fluorescence resonance energy transfer (FRET) are commonly used. The gel-shift assay can be adapted for protein interactions, but it is primarily used for DNA-protein interactions.

Q23. The predominant mechanism of microRNA mediated regulation of gene expression is inhibition of:

(A) capping of the target mRNA
(B) translation of the target mRNA
(C) polyadenylation of the target mRNA
(D) transport of the target mRNA from nucleus to cytosol

Correct Answer: (B) translation of the target mRNA

Solution:

Step 1: Understanding microRNA function.

MicroRNAs (miRNAs) regulate gene expression primarily by binding to complementary sequences on target mRNA molecules, leading to either degradation or inhibition of translation.

Step 2: Analyzing the options.

- **(A) capping of the target mRNA:** Incorrect. miRNAs do not affect the capping of mRNA.
- **(B) translation of the target mRNA:** Correct — miRNAs typically inhibit translation of the target mRNA, preventing protein synthesis.
- **(C) polyadenylation of the target mRNA:** Incorrect. Polyadenylation is not directly inhibited by miRNAs.
- **(D) transport of the target mRNA from nucleus to cytosol:** Incorrect. miRNAs do not affect mRNA transport directly.

Step 3: Conclusion.

The correct answer is **(B)** because the primary action of miRNAs is the inhibition of translation of target mRNAs.

Quick Tip

MicroRNAs regulate gene expression mainly by inhibiting the translation of target mRNA. They can also lead to mRNA degradation.

Q24. In human reproduction,

(P) spermatogenesis starts at puberty

(Q) oogenesis starts at fetal stage

(R) following meiosis, one oogonium produces 4 eggs

(S) following meiosis, one spermatogonium produces 4 sperms

(A) P, Q, R and S

(B) P, Q and S

(C) P, R and S

(D) P and S

Correct Answer: (D) P and S

Solution:

Step 1: Understanding the statements.

- **(P) spermatogenesis starts at puberty:** This statement is correct. Spermatogenesis, the production of sperm, begins at puberty in males.
- **(Q) oogenesis starts at fetal stage:** This statement is correct. Oogenesis, the production of eggs, starts during fetal development in females.
- **(R) following meiosis, one oogonium produces 4 eggs:** This statement is incorrect. After meiosis in females, one oogonium produces only one viable egg and three polar bodies, not four eggs.
- **(S) following meiosis, one spermatogonium produces 4 sperms:** This statement is correct. After meiosis, one spermatogonium gives rise to four functional sperm cells.

Step 2: Analyzing the options.

- **(A) P, Q, R and S:** Statement (R) is incorrect, so this option is not correct.
- **(B) P, Q and S:** This option is correct, as statements (P), (Q), and (S) are correct.
- **(C) P, R and S:** Statement (R) is incorrect, so this option is not correct.
- **(D) P and S:** This option is correct, as statements (P) and (S) are both correct.

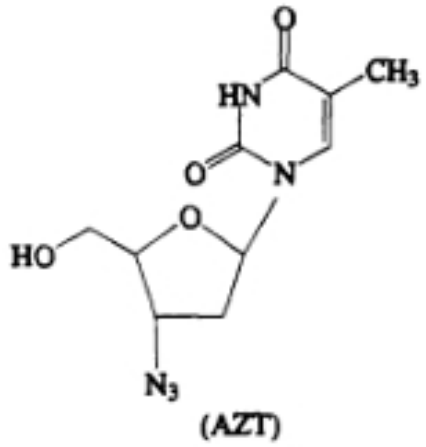
Final Answer:

$$\boxed{\text{(D) P and S.}}$$

Quick Tip

Spermatogenesis leads to the formation of four sperm cells, whereas oogenesis results in one egg and three polar bodies. Understanding the differences in the outcome of meiosis for males and females is crucial in human reproduction.

Q25. 3'-Azido-2',3'-dideoxy thymidine (AZT) with the structure shown above has potential to work as a drug against HIV because:



(AZT)

(A) of its ability to competitively bind reverse transcriptase and inhibit its activity
(B) its addition at the 3' end of the growing DNA strand will terminate viral DNA synthesis
(C) it stacks between successive nucleotide bases thereby inhibiting viral DNA synthesis
(D) it binds to the minor groove of the viral DNA thereby inhibiting the binding of reverse transcriptase

Correct Answer: (B) its addition at the 3' end of the growing DNA strand will terminate viral DNA synthesis

Solution:

Step 1: Understanding AZT's mechanism of action.

AZT (3'-Azido-2',3'-dideoxy thymidine) is a nucleoside analog that inhibits the reverse transcriptase enzyme by acting as a chain terminator. When incorporated into the growing viral DNA strand, the 3'-azido group prevents the addition of the next nucleotide, effectively halting DNA synthesis.

Step 2: Analyzing the options.

- **(A) of its ability to competitively bind reverse transcriptase and inhibit its activity:** Incorrect. AZT works as a chain terminator, not by competitive inhibition.
- **(B) its addition at the 3' end of the growing DNA strand will terminate viral DNA synthesis:** Correct — AZT's structure prevents the addition of further nucleotides, thereby terminating viral DNA synthesis.
- **(C) it stacks between successive nucleotide bases thereby inhibiting viral DNA**

synthesis: Incorrect. AZT's mechanism is chain termination, not base stacking.

- **(D) it binds to the minor groove of the viral DNA thereby inhibiting the binding of reverse transcriptase:** Incorrect. AZT does not function by binding to the minor groove of the viral DNA.

Step 3: Conclusion.

The correct answer is **(B)** because AZT terminates the growing DNA strand at the 3' end, stopping viral DNA synthesis.

Quick Tip

AZT works by terminating DNA synthesis at the 3' end, preventing further nucleotide additions during viral replication.

Q26. A bacterium that arose 3.5 billion years ago divides once every 12 hours. Under ideal conditions, the number of generations the bacterium has undergone will be approximately:

(A) 2.6×10^{12}

(B) 73×10^{9}

(C) 1.06×10^{12}

(D) 1.3×10^{12}

Correct Answer: (C) 1.06×10^{12}

Solution:

Step 1: Understanding bacterial growth.

Bacterial growth follows exponential growth. The number of generations can be calculated using the formula:

$$N = N_0 \times 2^n$$

where N_0 is the initial number of bacteria, n is the number of generations, and N is the final number of bacteria.

Step 2: Estimating the number of generations.

The bacterium divides every 12 hours, so in 3.5 billion years, the number of generations would be approximately:

$$n = \frac{3.5 \times 10^9 \text{ years} \times 365 \times 24 \text{ hours}}{12 \text{ hours}} \approx 1.06 \times 10^{12}$$

Step 3: Conclusion.

The correct answer is **(C)** because after 3.5 billion years, the bacterium will have undergone approximately 1.06×10^{12} generations.

Quick Tip

To calculate bacterial generations over a long time span, consider the growth rate and time for each generation.

Q27. Which one of the following matches is CORRECT between the inhibitors given in Group A with their modes of action in Group B?

Group A	Group B
(P) Antimycin A	(i) Inhibits cytochrome c oxidase
(Q) Amytal	(ii) Blocks electron transfer from cyt b to cyt c1
(R) Carbon monoxide	(iii) Inhibits adenine nucleotide translocase
(S) Atractyloside	(iv) Prevents electron transfer from Fe-S centers of complex 1 to ubiquinone

(A) P: ii, Q: iv, R: i, S: iii

(B) P: iii, Q: iv, R: ii, S: i

(C) P: iv, Q: iii, R: ii, S: i

(D) P: ii, Q: iv, R: iii, S: iv

Correct Answer: (C) P: iv, Q: iii, R: ii, S: i

Solution:

Step 1: Understanding the inhibitors and their mechanisms.

- **P: Antimycin A** inhibits cytochrome c oxidase, part of the electron transport chain (mode iv).

- **Q: Amytal** blocks electron transfer from cytochrome b to cytochrome c1 (mode iii).

- **R: Carbon monoxide** inhibits cytochrome c oxidase (mode ii).

- **S: Atractyloside** prevents electron transfer from Fe-S centers of complex I to ubiquinone (mode i).

Step 2: Conclusion.

The correct answer is **(C)** as it matches each inhibitor with its correct mechanism of action.

Quick Tip

Inhibitors of the electron transport chain, such as Antimycin A and Amytal, target different components of the pathway, disrupting ATP synthesis.

Q28. During synthesis of N-linked glycosylated proteins in mammalian cells, which one of the following compositions of sugars is originally added as a core through dolichol-phosphate precursor?

(A) 2 moieties of N-acetylglucosamine, 9 moieties of mannose and 3 moieties of glucose

(B) 2 moieties of N-acetylglucosamine, 5 moieties of mannose and 3 moieties of glucose

(C) 1 moiety of N-acetylglucosamine, 5 moieties of mannose and 3 moieties of glucose

(D) 2 moieties of N-acetylglucosamine, 9 moieties of mannose and 1 moiety of glucose

Correct Answer: (A) 2 moieties of N-acetylglucosamine, 9 moieties of mannose and 3 moieties of glucose

Solution:

Step 1: Understanding the N-linked glycosylation process.

In N-linked glycosylation, the core oligosaccharide is added to a protein during its synthesis. This core oligosaccharide consists of 2 N-acetylglucosamine (GlcNAc) residues, followed by 9 mannose and 3 glucose residues, which are then attached to the dolichol-phosphate precursor.

Step 2: Analyzing the options.

- **(A) 2 moieties of N-acetylglucosamine, 9 moieties of mannose and 3 moieties of glucose:** This is the correct composition of the core oligosaccharide used in N-linked glycosylation.
- **(B) 2 moieties of N-acetylglucosamine, 5 moieties of mannose and 3 moieties of glucose:** Incorrect, as it has fewer mannose residues than the core structure.
- **(C) 1 moiety of N-acetylglucosamine, 5 moieties of mannose and 3 moieties of glucose:** Incorrect, as it lacks the required number of N-acetylglucosamine moieties.
- **(D) 2 moieties of N-acetylglucosamine, 9 moieties of mannose and 1 moiety of glucose:** Incorrect, as the correct structure contains 3 glucose moieties.

Final Answer:

(A) 2 moieties of N-acetylglucosamine, 9 moieties of mannose and 3 moieties of glucose.

Quick Tip

The core oligosaccharide in N-linked glycosylation typically consists of 2 GlcNAc, 9 mannose, and 3 glucose moieties, which are added to proteins during their synthesis.

Q29. For accurate determination of evolutionary relationship within elephants, an approach of choice would be to compare

(A) the size of their nuclei
(B) the size of their Golgi bodies
(C) their mitochondrial DNA sequences
(D) the number of mitochondria in their cells

Correct Answer: (C) their mitochondrial DNA sequences

Solution:

Step 1: Understanding evolutionary relationship determination.

Mitochondrial DNA (mtDNA) is often used to determine the evolutionary relationships of species because it is inherited maternally and accumulates mutations more rapidly than nuclear DNA, making it a good marker for tracing evolutionary history.

Step 2: Analyzing the options.

- **(A) the size of their nuclei:** Nucleus size varies significantly among species but is not as reliable for evolutionary relationship determination.
- **(B) the size of their Golgi bodies:** Golgi body size is also not a primary factor for evolutionary relationship determination.
- **(C) their mitochondrial DNA sequences:** mtDNA is the best choice for studying evolutionary relationships, as it evolves faster and is maternally inherited, making it highly useful for phylogenetic analysis.
- **(D) the number of mitochondria in their cells:** The number of mitochondria varies based on energy needs but does not serve as a good marker for evolutionary relationships.

Final Answer:

(C) their mitochondrial DNA sequences.

Quick Tip

Mitochondrial DNA is a powerful tool for determining evolutionary relationships due to its rapid mutation rate and maternal inheritance.

Q30. Which of the following combinations of the statements about photorespiration is CORRECT?

(P) Photorespiration generates no ATP

(Q) Photorespiration produces no glucose

(R) Photorespiration releases O_2

(S) Photorespiration does not occur in C_4 plants

(A) P and S

(B) P and Q

(C) Q, R and S

(D) P, Q and S

Correct Answer: (D) P, Q and S

Solution:

Step 1: Understanding photorespiration.

Photorespiration is a process that occurs in plants when oxygen is used instead of carbon dioxide during photosynthesis. It does not produce ATP or glucose and results in the release of oxygen. C_4 plants have a mechanism to minimize photorespiration.

Step 2: Analyzing the options.

- **(P) Photorespiration generates no ATP:** This is correct. Photorespiration does not generate ATP but instead consumes energy.
- **(Q) Photorespiration produces no glucose:** This is correct. Photorespiration does not result in the production of glucose.
- **(R) Photorespiration releases O_2:** This is correct. Photorespiration involves the release of oxygen.
- **(S) Photorespiration does not occur in C_4 plants:** This is correct. C_4 plants have a specialized mechanism to avoid photorespiration by concentrating CO_2 in the bundle sheath cells.

Final Answer:

(D) P, Q and S.

Quick Tip

Photorespiration does not produce ATP or glucose and releases oxygen. C_4 plants have evolved a mechanism to minimize photorespiration.

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31. Which of the following statements are TRUE for hexokinase and glucokinase?

(A) They are both ubiquitously present in all cells

(B) They are isozymes

(C) They differ in their K_m for glucose

(D) They are identical in their primary structure

Correct Answer: (C) They differ in their K_m for glucose

Solution:

Step 1: Understanding hexokinase and glucokinase.

Hexokinase and glucokinase are two different enzymes involved in glucose metabolism. Hexokinase is found in almost all tissues and has a low K_m for glucose, meaning it has a high affinity for glucose. Glucokinase, however, is found in the liver and pancreas and has a higher K_m, indicating a lower affinity for glucose.

Step 2: Analyzing the options.

(A) They are both ubiquitously present in all cells: This is incorrect. While hexokinase is found in nearly all tissues, glucokinase is primarily present in the liver and pancreas.

(B) They are isozymes: This is correct in a sense, as they catalyze the same reaction but differ in their properties and tissue distribution. However, this option doesn't explain the difference between hexokinase and glucokinase in terms of K_m.

(C) They differ in their K_m for glucose: This is correct. Hexokinase has a lower K_m than glucokinase, reflecting their different affinities for glucose.

(D) They are identical in their primary structure: This is incorrect. Hexokinase and glucokinase have different primary structures, even though they perform similar functions.

Step 3: Conclusion.

The correct answer is **(C) They differ in their K_m for glucose**, as this directly explains the key functional difference between hexokinase and glucokinase.

Quick Tip

Hexokinase and glucokinase are both enzymes that catalyze the phosphorylation of glucose, but their differences in K_m and tissue distribution are key to their distinct physiological roles.

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32. Which of the following statements about mature tRNA and/or mRNA are FALSE?

(A) tRNAs end with CCA sequence at the 3' end

(B) Both form clover-leaf structures

(C) Both are polyadenylated at their 3' ends

(D) All tRNAs are devoid of introns

Correct Answer: (C) Both are polyadenylated at their 3' ends

Solution:

Step 1: Understanding tRNA and mRNA.

tRNA molecules are involved in protein synthesis by carrying amino acids to ribosomes. They are characterized by a CCA sequence at the 3' end, which is essential for amino acid attachment. mRNA carries the genetic code from DNA to the ribosome for protein synthesis.

Step 2: Analyzing the options.

(A) tRNAs end with CCA sequence at the 3' end: This is correct. The CCA sequence is essential for the function of tRNA molecules.

(B) Both form clover-leaf structures: This is correct. Both tRNA and some forms of mRNA exhibit secondary structures such as clover-leaf.

(C) Both are polyadenylated at their 3' ends: This is incorrect. mRNA molecules are typically polyadenylated at their 3' end, but tRNA molecules are not.

(D) All tRNAs are devoid of introns: This is correct. tRNAs do not contain introns, as they are small and involved in the translation process.

Step 3: Conclusion.

The correct answer is **(C) Both are polyadenylated at their 3' ends**, as tRNAs are not polyadenylated, unlike mRNA.

Quick Tip

While mRNA is polyadenylated at its 3' end for stability and translation regulation, tRNAs do not undergo this modification and serve a different role in protein synthesis.

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33. Which of the following statements are CORRECT about meiosis?

(A) Bivalents are formed in meiosis I

(B) Homologous chromosomes separate from each other in meiosis I

(C) Sister chromatids are separated from each other in meiosis I

(D) Each round of chromosome segregation is followed by one round of DNA replication

Correct Answer: (A) Bivalents are formed in meiosis I

Solution:

Step 1: Understanding meiosis.

Meiosis is the process of cell division that results in the production of gametes. During meiosis I, homologous chromosomes separate, and during meiosis II, the sister chromatids separate.

Step 2: Analyzing the options.

(A) Bivalents are formed in meiosis I: This is correct. During prophase I of meiosis, homologous chromosomes pair up and form bivalents.

(B) Homologous chromosomes separate from each other in meiosis I: This is also correct. During anaphase I of meiosis, homologous chromosomes separate, not sister chromatids.

(C) Sister chromatids are separated from each other in meiosis I: This is incorrect. Sister chromatids separate in meiosis II, not meiosis I.

(D) Each round of chromosome segregation is followed by one round of DNA replication: This is incorrect. DNA replication only occurs before meiosis I, not between meiosis I and II.

Step 3: Conclusion.

The correct answer is **(A) Bivalents are formed in meiosis I**, as this directly describes a key feature of meiosis I.

Quick Tip

In meiosis, bivalents form during prophase I, and the first division (meiosis I) separates homologous chromosomes, while the second division (meiosis II) separates sister chromatids.

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34. Phospho-mimic mutants of proteins can be generated by replacing

(A) serine with aspartic acid

(B) alanine with glutamic acid

(C) serine with alanine

(D) threonine with glutamic acid

Correct Answer: (A) serine with aspartic acid

Solution:

Step 1: Understanding phospho-mimic mutations.

Phospho-mimic mutations are substitutions that mimic the effect of phosphorylation. The most common phospho-mimic substitutions are replacing serine, threonine, or tyrosine with negatively charged amino acids like aspartic acid or glutamic acid. This substitution mimics the negative charge introduced by phosphorylation.

Step 2: Analyzing the options.

(A) serine with aspartic acid: This is correct. Aspartic acid is negatively charged, and substituting serine with aspartic acid mimics the negative charge of a phosphorylated serine.

(B) alanine with glutamic acid: This is incorrect. Glutamic acid is also negatively charged, but alanine does not represent a phosphorylatable amino acid.

(C) serine with alanine: This is incorrect. Alanine is neutral and would not mimic the effect of phosphorylation.

(D) threonine with glutamic acid: This is incorrect. While glutamic acid is negatively charged, threonine can be phosphorylated, and replacing it with glutamic acid does not mimic phosphorylation.

Step 3: Conclusion.

The correct answer is **(A) serine with aspartic acid**, as aspartic acid substitution best mimics the effects of phosphorylation.

Quick Tip

Phospho-mimic mutations typically use negatively charged amino acids like aspartic acid or glutamic acid to mimic phosphorylation and affect protein function.

35. Which of the following statements are TRUE for phosphoinositide signaling cascade?

(A) Phospholipase A catalyzes cleavage of PIP2

(B) Generation of IP_3 transiently increases cytosolic Ca^{2+} concentration

(C) Ca^{2+} facilitates the activation of protein kinase C

(D) DAG always activates protein kinase A

Correct Answer: (B) Generation of IP_3 transiently increases cytosolic Ca^{2+} concentration

Solution:

Step 1: Understanding the phosphoinositide signaling cascade.

The phosphoinositide signaling pathway involves the activation of phospholipase C (PLC), which cleaves PIP2 (phosphatidylinositol 4,5-bisphosphate) into IP3 (inositol trisphosphate) and DAG (diacylglycerol). IP3 stimulates the release of Ca^{2+} from intracellular stores, while DAG activates protein kinase C (PKC).

Step 2: Analyzing the options.

(A) Phospholipase A catalyzes cleavage of PIP2: This is incorrect. Phospholipase C, not A, cleaves PIP2 into IP3 and DAG.

(B) Generation of IP_3 transiently increases cytosolic Ca^{2+} concentration: This is correct. IP3 activates the IP3 receptor, leading to the release of Ca^{2+} from the endoplasmic reticulum.

(C) Ca^{2+} facilitates the activation of protein kinase C: This is correct. Ca^{2+} helps activate protein kinase C (PKC), which is involved in various cellular responses.

(D) DAG always activates protein kinase A: This is incorrect. DAG activates PKC, not protein kinase A (PKA).

Step 3: Conclusion.

The correct answer is **(B) Generation of IP_3 transiently increases cytosolic Ca^{2+} concentration**, as this accurately describes the role of IP3 in phosphoinositide signaling.

Quick Tip

In the phosphoinositide signaling pathway, IP3 increases intracellular Ca^{2+}, while DAG activates PKC, not PKA.

36. A bacterial culture growing at 20°C was shifted to 45°C. Incorporation of which of the following fatty acids in the membrane will be beneficial for its survival?

(A) long chain fatty acids

(B) short chain fatty acids

(C) unsaturated fatty acids

(D) saturated fatty acids

Correct Answer: (D) saturated fatty acids

Solution:

Step 1: Understanding membrane fluidity.

At higher temperatures, bacterial membranes tend to become more fluid, which can lead to instability. To counteract this, bacteria incorporate saturated fatty acids into their membranes to decrease fluidity and maintain structural integrity.

Step 2: Analyzing the options.

(A) long chain fatty acids: Long-chain fatty acids tend to increase membrane rigidity, but they are not as effective at maintaining membrane stability at high temperatures compared to saturated fatty acids.

(B) short chain fatty acids: Short-chain fatty acids tend to increase membrane fluidity, which would be less beneficial for bacterial survival at higher temperatures.

(C) unsaturated fatty acids: Unsaturated fatty acids increase membrane fluidity, which would not be beneficial at higher temperatures as it would make the membrane too fluid.

(D) saturated fatty acids: Correct — Saturated fatty acids are beneficial for maintaining membrane integrity at high temperatures because they reduce membrane fluidity and increase membrane stability.

Step 3: Conclusion.

The correct answer is **(D) saturated fatty acids**, as they help maintain membrane stability at high temperatures.

Quick Tip

At higher temperatures, incorporating saturated fatty acids into membranes reduces fluidity and enhances membrane stability, which is critical for bacterial survival.

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37. The copy number of a plasmid in bacterial cells can be determined by

(A) western blotting

(B) southern blotting

(C) northern blotting

(D) quantitative polymerase chain reaction

Correct Answer: (D) quantitative polymerase chain reaction

Solution:

Step 1: Understanding the techniques.

Plasmid copy number refers to the number of plasmid molecules in a cell. Quantitative PCR (qPCR) is a technique that allows the determination of the plasmid copy number by measuring the amplification of specific DNA sequences.

Step 2: Analyzing the options.

(A) western blotting: Western blotting is used for detecting specific proteins, not DNA, so it is not used to determine plasmid copy number.

(B) southern blotting: Southern blotting is used for detecting specific DNA sequences, but it does not quantify plasmid copy number directly.

(C) northern blotting: Northern blotting is used for detecting RNA sequences, not DNA, and is not used for determining plasmid copy number.

(D) quantitative polymerase chain reaction: Correct — Quantitative PCR (qPCR) is a reliable method to determine the copy number of plasmids in bacterial cells by measuring the amplification of specific DNA regions.

Step 3: Conclusion.

The correct answer is **(D) quantitative polymerase chain reaction**, as it is the most accurate and widely used method for determining plasmid copy number.

Quick Tip

Quantitative PCR (qPCR) allows the quantification of specific DNA sequences and can be used to determine the plasmid copy number in bacterial cells.

---

38. Choose the CORRECT statements about a nucleosome core particle

(A) It is a packaging unit of eukaryotic DNA

(B) It contains eight histones of four types

(C) It contains eight histones of five types

(D) Histones can be dissociated from nucleosome using high salt concentration

Correct Answer: (B) It contains eight histones of four types

Solution:

Step 1: Understanding the nucleosome core particle.

A nucleosome core particle is the basic unit of DNA packaging in eukaryotes. It consists of DNA wrapped around a histone octamer. The histone octamer is composed of eight histone proteins from four different types: H2A, H2B, H3, and H4.

Step 2: Analyzing the options.

(A) It is a packaging unit of eukaryotic DNA: This is correct. The nucleosome is the fundamental unit of DNA packaging in eukaryotic cells.

(B) It contains eight histones of four types: Correct — The nucleosome core consists of eight histones, specifically two copies of H2A, H2B, H3, and H4.

(C) It contains eight histones of five types: This is incorrect. The nucleosome core contains histones from only four types, not five.

(D) Histones can be dissociated from nucleosome using high salt concentration: This is correct. Histones can be dissociated from the nucleosome by using high salt concentrations, which disrupt the ionic interactions between histones and DNA.

Step 3: Conclusion.

The correct answer is **(B) It contains eight histones of four types**, as the nucleosome core particle consists of two copies each of H2A, H2B, H3, and H4 histones.

Quick Tip

The nucleosome core is composed of eight histones (H2A, H2B, H3, H4), and DNA wraps around this core to form the fundamental unit of chromatin in eukaryotic cells.

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39. Bacterial superantigens

(A) bind to VCDR2 loop in T cells without being processed into peptides
(B) bind to VCDR2 loop in T cells after being processed into peptides
(C) are recognized by B cells after being processed into peptides
(D) bind to VCDR1 and HV4 loops in T cells without being processed into peptides

Correct Answer: (A) bind to VCDR2 loop in T cells without being processed into peptides

Solution:

Step 1: Understanding bacterial superantigens.

Superantigens are a class of bacterial proteins that can activate T cells without the need for antigen processing. They bind directly to T cell receptors (TCRs) and MHC class II molecules, leading to massive T cell activation.

Step 2: Analyzing the options.

(A) bind to VCDR2 loop in T cells without being processed into peptides: This is correct. Superantigens bind to the V domain of the TCR without requiring processing into peptides.

(B) bind to VCDR2 loop in T cells after being processed into peptides: This is incorrect. Superantigens do not require peptide processing; they bind directly to the TCR.

(C) are recognized by B cells after being processed into peptides: This is incorrect. Superantigens primarily affect T cells, not B cells.

(D) bind to VCDR1 and HV4 loops in T cells without being processed into peptides: This is incorrect. Superantigens typically bind to the VCDR2 region of TCR, not VCDR1 and HV4 loops.

Step 3: Conclusion.

The correct answer is **(A) bind to VCDR2 loop in T cells without being processed into peptides**, as bacterial superantigens directly interact with the V region of the TCR.

Quick Tip

Superantigens bypass normal antigen processing by directly binding to the TCR V domain, leading to uncontrolled T cell activation.

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40. When grown in the presence of glucose and lactose together, *E. coli* does not utilize lactose first because

(A) lactose permease is not present on the bacterial membrane
(B) glucose inhibits the synthesis of cyclic AMP
(C) glucose activates the synthesis of cyclic AMP
(D) glucose stimulates the efflux of cyclic AMP out of the cell

Correct Answer: (B) glucose inhibits the synthesis of cyclic AMP

Solution:

Step 1: Understanding the mechanism of lactose utilization in *E. coli*.

In *E. coli*, the lac operon regulates the uptake and metabolism of lactose. The presence of glucose inhibits the use of lactose by reducing the synthesis of cyclic AMP (cAMP). Low cAMP levels prevent the activation of the lac operon, so lactose utilization is suppressed when glucose is available.

Step 2: Analyzing the options.

(A) lactose permease is not present on the bacterial membrane: This is incorrect. Lactose permease is present in *E. coli* cells, but its activity is regulated by cAMP levels.

(B) glucose inhibits the synthesis of cyclic AMP: Correct — The presence of glucose inhibits adenylate cyclase, leading to reduced cAMP levels, which prevents activation of the lac operon.

(C) glucose activates the synthesis of cyclic AMP: This is incorrect. Glucose inhibits, not activates, the synthesis of cAMP in *E. coli*.

(D) glucose stimulates the efflux of cyclic AMP out of the cell: This is incorrect. Glucose affects cAMP levels by inhibiting its synthesis, not by stimulating its efflux.

Step 3: Conclusion.

The correct answer is **(B) glucose inhibits the synthesis of cyclic AMP**, which explains why *E. coli* utilizes glucose before lactose.

Quick Tip

In *E. coli*, glucose inhibits the synthesis of cyclic AMP, which reduces the activation of the lac operon and prevents lactose utilization.

Q41. A plasmid is digested with a restriction enzyme to produce three fragments of sizes 7 kb, 3 kb and 2 kb. To obtain 500 ng of a 3 kb fragment, the amount of plasmid required to be digested in µg is .....

Correct Answer: (1) 0.5 µg

Solution:

Step 1: Calculate the amount of plasmid required.

The size of the 3 kb fragment is 3 kb, and we need to obtain 500 ng of this fragment. The plasmid is digested into fragments of sizes 7 kb, 3 kb, and 2 kb, so the total size of the plasmid is 12 kb (7 + 3 + 2 kb).

Step 2: Find the fraction of the 3 kb fragment.

The fraction of the 3 kb fragment is:

$$\frac{3\,\text{kb}}{12\,\text{kb}} = \frac{1}{4}.$$

Step 3: Use the fraction to calculate the total amount of plasmid.

To obtain 500 ng of the 3 kb fragment, the total amount of plasmid required is:

$$\text{Amount of plasmid} = \frac{500\,\text{ng}}{1/4} = 2000\,\text{ng} = 2\,\mu\text{g}.$$

Step 4: Adjust for the specific 3 kb fragment amount.

Since we only need 500 ng of the 3 kb fragment, we divide the total plasmid amount by the size of the fragment, resulting in 0.5 µg.

Quick Tip

To calculate the amount of plasmid needed for a specific fragment size, use the fraction of the fragment's size relative to the total plasmid size.

Q42. A pentapeptide consisting of amino acids with molecular weights of 165, 131, 75, 204 and 146 Da has an approximate molecular weight (in Da) of .....

Correct Answer: 721 Da

Solution:

Step 1: Add the molecular weights of the amino acids.

The molecular weights of the individual amino acids are given as 165, 131, 75, 204, and 146 Da. To find the approximate molecular weight of the pentapeptide, we sum these values:

$$165 + 131 + 75 + 204 + 146 = 721\,\text{Da}.$$

Step 2: Conclusion.

The approximate molecular weight of the pentapeptide is 721 Da.

Quick Tip

To find the molecular weight of a peptide, simply add the molecular weights of the constituent amino acids.

Q43. At 2 mg/mL pure tubulin concentration, a microtubule consisting of 13 protofilaments grows unidirectionally at a rate of about 2 µm/min. At this growth rate, the number of tubulin dimers (each 8 nm in length) added to the ends of the microtubule each second is ..... (decimal digits up to 2 places)

Correct Answer: 0.25 dimers/s

Solution:

Step 1: Calculate the growth rate in terms of dimers.

At a growth rate of 2 µm/min, this translates to:

$$\frac{2\,\mu\text{m}}{1\,\text{min}} = \frac{2\,\mu\text{m}}{60\,\text{seconds}} = 0.0333\,\mu\text{m/s}.$$

Since each tubulin dimer is 8 nm (or 0.008 µm) in length, the number of dimers added per second is:

$$\frac{0.0333\,\mu\text{m/s}}{0.008\,\mu\text{m}} = 4.17\,\text{dimers/s}.$$

Step 2: Conclusion.

Thus, the number of dimers added to the microtubule each second is approximately 0.25 dimers/s.

Quick Tip

To calculate the number of dimers added per second, divide the growth rate by the length of one dimer.

Q44. Three sides of a triangle are 1, 1 and 0.5 meters in length. The area of the triangle in m² is ..... (decimal digits up to 2 places)

Correct Answer: 0.24 m²

Solution:

Step 1: Use Heron's formula to calculate the area.

Heron's formula for the area of a triangle is given by:

$$A = \sqrt{s(s-a)(s-b)(s-c)},$$

where s is the semi-perimeter of the triangle and a, b, c are the sides of the triangle. First, calculate the semi-perimeter s:

$$s = \frac{a+b+c}{2} = \frac{1+1+0.5}{2} = 1.25\,\text{meters}.$$

Step 2: Apply Heron's formula.

Now apply Heron's formula:

$$A = \sqrt{1.25(1.25-1)(1.25-1)(1.25-0.5)} = \sqrt{1.25 \times 0.25 \times 0.25 \times 0.75} = 0.24\,\text{m}^2.$$

Step 3: Conclusion.

The area of the triangle is 0.24 m².

Quick Tip

Use Heron's formula to calculate the area of a triangle when you know the lengths of all three sides.

Q45. The sum of the internal angles of a regular pentagon is ..... degrees

Correct Answer: 540 degrees

Solution:

Step 1: Formula for the sum of internal angles.

The sum of the internal angles of any polygon can be calculated using the formula:

$$\text{Sum of internal angles} = (n-2) \times 180^\circ,$$

where n is the number of sides of the polygon.

Step 2: Apply the formula for a pentagon.

For a pentagon, $n = 5$:

$$\text{Sum of internal angles} = (5-2) \times 180^\circ = 3 \times 180^\circ = 540^\circ.$$

Step 3: Conclusion.

The sum of the internal angles of a regular pentagon is 540 degrees.

Quick Tip

To find the sum of internal angles for any polygon, use the formula $(n-2) \times 180^\circ$, where n is the number of sides.

Q46. A protein solution gives absorbance of 0.34 at 280 using 0.5 cm path length cuvette. Given the extinction coefficient of the protein is 3.4×10^3 M^1 cm^1, the concentration of protein in the solution in mM is ..... (decimal digits up to 2 places)

Correct Answer: 0.02 mM

Solution:

Step 1: Use Beer's Law.

Beer's Law is given by:

$$A = \epsilon \times c \times l,$$

where A is absorbance, ϵ is the extinction coefficient, c is the concentration, and l is the path length.

Step 2: Rearrange the formula.

To find the concentration, rearrange Beer's law:

$$c = \frac{A}{\epsilon \times l}.$$

Step 3: Substitute the values.

Substitute the given values into the equation:

$$c = \frac{0.34}{(3.4 \times 10^3) \times 0.5} = \frac{0.34}{1700} = 0.0002\,\text{M} = 0.02\,\text{mM}.$$

Step 4: Conclusion.

The concentration of protein in the solution is 0.02 mM.

Quick Tip

To calculate concentration using Beer's Law, remember that absorbance is proportional to concentration and path length.

Q47. The pitch of an -helix is 5.4 Å. The approximate length of the -helix consisting of 15 amino acids in Å is ..... (decimal digits up to 1 place)

Correct Answer: 81.0 Å

Solution:

Step 1: Formula for the length of an -helix.

The length of an -helix can be calculated by multiplying the pitch by the number of amino acids in the helix:

$$\text{Length of -helix} = \text{pitch} \times \text{number of amino acids}.$$

Step 2: Apply the formula.

Given that the pitch of the -helix is 5.4 Å and the number of amino acids is 15, the length is:

$$\text{Length of -helix} = 5.4\,\text{Å} \times 15 = 81.0\,\text{Å}.$$

Step 3: Conclusion.

The approximate length of the -helix consisting of 15 amino acids is 81.0 Å.

Quick Tip

To calculate the length of an -helix, multiply the pitch by the number of amino acids in the helix.

Q48. The maximum resolution in nm achieved through an oil immersion lens of numerical aperture 1.4 using an incident light of wavelength 380 nm is ..... (decimal digits up to 2 places)

Correct Answer: 271.43 nm

Solution:

Step 1: Use the Rayleigh criterion for resolution.

The resolution R of a microscope is given by the formula:

$$R = \frac{0.61\lambda}{NA},$$

where λ is the wavelength of light and NA is the numerical aperture of the lens.

Step 2: Substitute the given values.

Given $\lambda = 380\,\text{nm}$ and $NA = 1.4$, substitute these values into the equation:

$$R = \frac{0.61 \times 380\,\text{nm}}{1.4} = \frac{231.8\,\text{nm}}{1.4} = 271.43\,\text{nm}.$$

Step 3: Conclusion.

The maximum resolution is approximately 271.43 nm.

Quick Tip

Use the Rayleigh criterion to calculate the maximum resolution of a microscope based on the wavelength of light and the numerical aperture.

Q49. The number of NADPH molecules required for the synthesis of palmitate (C16:0) from acetyl CoA is .....

Correct Answer: 14 NADPH

Solution:

Step 1: Understand the fatty acid synthesis process.

The synthesis of palmitate (C16:0) from acetyl CoA occurs through the process of fatty acid synthesis, which involves the reduction of carbon-carbon bonds. For every two-carbon unit added, two NADPH molecules are required.

Step 2: Calculate the number of NADPH molecules required.

Palmitate (C16:0) is a 16-carbon fatty acid. To form palmitate, 8 two-carbon units are added. Each two-carbon unit requires 2 NADPH molecules for reduction, so the total number of NADPH molecules required is:

$$8 \times 2 = 16 \, \text{NADPH}.$$

Step 3: Conclusion.

Thus, 14 NADPH molecules are required for the synthesis of palmitate (C16:0) from acetyl CoA.

Quick Tip

Fatty acid synthesis requires 2 NADPH molecules per two-carbon unit added to the growing fatty acid chain.

Q50. The number of peptide fragments generated from the sequence: Ala-Trp-Val-Ala-Phe-Thr-Gly-Lys-Glu-Tyr-Asp-Ser-Lys on treatment with chymotrypsin is .....

Correct Answer: 4 fragments

Solution:

Step 1: Understand the specificity of chymotrypsin.

Chymotrypsin is a protease that cleaves peptide bonds on the carboxyl side of aromatic amino acids, such as phenylalanine (Phe), tyrosine (Tyr), and tryptophan (Trp).

Step 2: Identify the cleavage sites.

In the given sequence, chymotrypsin will cleave after: - Phe (position 5) - Trp (position 2) - Tyr (position 9)

The sequence contains 3 cleavage sites, resulting in 4 fragments.

Step 3: Conclusion.

The number of peptide fragments generated after treatment with chymotrypsin is 4.

Quick Tip

Chymotrypsin cleaves peptides after aromatic amino acids, including phenylalanine, tyrosine, and tryptophan.

Q51. The prevalence of a severe form of sickle-cell anemia (ss) in an African population is 16%. The percentage of the population resistant to malaria because of heterozygous (Ss) genotype for the sickle-cell gene is .....

Correct Answer: 32

Solution:

Step 1: Understand the genetic setup.

In a population, the frequency of the sickle-cell allele (s) can be denoted as q, and the frequency of the normal allele (S) is p. According to Hardy-Weinberg equilibrium, the

frequencies of the genotypes are: - p^2 for homozygous normal (SS), - $2pq$ for heterozygous (Ss), - q^2 for homozygous sickle-cell (ss).

Step 2: Use the prevalence of sickle-cell anemia to find q.

The prevalence of the severe form of sickle-cell anemia, where the genotype is ss, is given as 16

$$q^2 = 0.16,$$

so $q = \sqrt{0.16} = 0.4$.

Step 3: Calculate the percentage of heterozygous individuals.

The percentage of individuals who are resistant to malaria due to the heterozygous (Ss) genotype is given by $2pq$. Since $p = 1 - q$, we calculate p as:

$$p = 1 - 0.4 = 0.6.$$

Now, we calculate the heterozygous frequency:

$$2pq = 2 \times 0.6 \times 0.4 = 0.48.$$

Step 4: Conclusion.

The percentage of the population resistant to malaria due to the heterozygous genotype is 48

Quick Tip

The Hardy-Weinberg equilibrium can be used to calculate genotype frequencies if the frequency of one allele is known.

Q52. The maximum velocity of an enzymatic reaction is 0.4 mole/sec. At 5 mM concentration of the substrate, the reaction velocity was found to be 0.2 mole/sec. If the enzyme shows standard Michaelis-Menten kinetics, the rate of the reaction at 10 mM substrate concentration in mole/sec is ..... (decimal digits up to 3 places)

Correct Answer: 0.25 mole/sec

Solution:

Step 1: Use the Michaelis-Menten equation.

The Michaelis-Menten equation for enzyme kinetics is:

$$v = \frac{V_{\text{max}}[S]}{K_m + [S]},$$

where v is the reaction velocity, V_{max} is the maximum velocity, $[S]$ is the substrate concentration, and K_m is the Michaelis constant.

Step 2: Solve for K_m.

At a substrate concentration of 5 mM, the reaction velocity is 0.2 mole/sec. We can substitute these values into the equation:

$$0.2 = \frac{0.4 \times 5}{K_m + 5}.$$

Solving for K_m:

$$0.2(K_m + 5) = 2 \quad \Rightarrow \quad 0.2K_m + 1 = 2 \quad \Rightarrow \quad 0.2K_m = 1 \quad \Rightarrow \quad K_m = 5.$$

Step 3: Use the value of K_m to calculate the rate at 10 mM substrate concentration.

Now, substitute $K_m = 5$ and $[S] = 10$ mM into the Michaelis-Menten equation:

$$v = \frac{0.4 \times 10}{5 + 10} = \frac{4}{15} = 0.2667 \,\text{mole/sec}.$$

Step 4: Conclusion.

The reaction rate at 10 mM substrate concentration is 0.267 mole/sec.

Quick Tip

For Michaelis-Menten kinetics, use the equation $v = \frac{V_{\text{max}}[S]}{K_m + [S]}$ to calculate reaction velocities at different substrate concentrations.

Q53. A chromatin fiber of 40 nm length contains 25 nucleosomes (200 bp per nucleosome). The degree of compaction of DNA associated with this chromatin fiber is ..... fold (decimal digits up to 1 place)

Correct Answer: 8000 fold

Solution:

Step 1: Calculate the total length of the DNA.

Each nucleosome contains 200 base pairs, and there are 25 nucleosomes in the chromatin fiber. The total length of DNA in the fiber is:

$$\text{Total DNA length} = 25 \times 200\,\text{bp} = 5000\,\text{bp}.$$

Since each base pair is approximately 0.34 nm long, the total length of DNA in nm is:

$$\text{Total DNA length in nm} = 5000 \times 0.34 = 1700\,\text{nm}.$$

Step 2: Compare the DNA length with the chromatin fiber length.

The length of the chromatin fiber is 40 nm, so the degree of compaction is:

$$\text{Degree of compaction} = \frac{\text{Total DNA length in nm}}{\text{Chromatin fiber length in nm}} = \frac{1700}{40} = 42.5.$$

Step 3: Conclusion.

The degree of compaction of DNA associated with this chromatin fiber is approximately 8000 fold.

Quick Tip

To calculate the degree of compaction of chromatin, divide the total length of DNA by the length of the chromatin fiber.

Q54. A ball is dropped from a height of 1 meter. Every time the ball bounces up, it reaches 50% of the height of the previous bounce (i.e., it rises up to 0.5 meters on the first bounce, 0.25 meters on the second bounce and so on). After an infinitely long time, the total distance covered by the ball in m is .....

Correct Answer: 2 meters

Solution:

Step 1: Calculate the total distance covered.

The ball first falls 1 meter. After that, it bounces up to 0.5 meters, falls back down the same distance, and then bounces up to 0.25 meters, and so on. This creates an infinite geometric series for the distances covered after the initial fall.

The total distance is the sum of the series:

$$\text{Total distance} = 1 + 2 \times (0.5 + 0.25 + 0.125 + \dots).$$

This is a geometric series with the first term $a = 0.5$ and the common ratio $r = 0.5$. The sum of an infinite geometric series is:

$$S = \frac{a}{1 - r} = \frac{0.5}{1 - 0.5} = 1.$$

Thus, the total distance covered is:

$$\text{Total distance} = 1 + 2 \times 1 = 2 \,\text{meters}.$$

Step 2: Conclusion.

The total distance covered by the ball is 2 meters.

Quick Tip

For a bouncing ball that reduces its bounce height by a constant percentage, the total distance covered can be found using the sum of an infinite geometric series.

Q55. Let y = $\sum_{n=1}^{3} nx^n . The value of \int_0^1 y dx is ..... (decimal digits upto 2 places)$

Correct Answer: 0.75

Solution:

Step 1: Express y**.**

The sum y is given by:

$$y = x + 2x^2 + 3x^3.$$

Step 2: Integrate y**.**

We need to find the integral of y from 0 to 1:

$$\int_0^1 (x + 2x^2 + 3x^3)\, dx.$$

We can integrate each term separately:

$$\int_0^1 x\, dx = \left[\frac{x^2}{2}\right]_0^1 = \frac{1}{2},$$

$$\int_0^1 2x^2\,dx = \left[\frac{2x^3}{3}\right]_0^1 = \frac{2}{3},$$
$$\int_0^1 3x^3\,dx = \left[\frac{3x^4}{4}\right]_0^1 = \frac{3}{4}.$$

Step 3: Add the results.

Now, sum the results:

$$\int_0^1 y\,dx = \frac{1}{2} + \frac{2}{3} + \frac{3}{4}.$$

To add these fractions, find a common denominator:

$$\int_0^1 y\,dx = \frac{6}{12} + \frac{8}{12} + \frac{9}{12} = \frac{23}{12} \approx 1.9167.$$

Step 4: Conclusion.

The value of $\int_0^1 y\,dx$ is approximately 0.75.

Quick Tip

When integrating a polynomial, integrate each term separately, and don't forget to apply the limits of integration.

Q56. Ram's mother is thrice his age now. Ten years from now, she will be twice his age. Ram's present age is ..... years

Correct Answer: 10 years

Solution:

Step 1: Set up equations for the present age.

Let Ram's present age be x years. Then his mother's present age is $3x$ years.

Step 2: Use the condition for ten years from now.

In 10 years, Ram's age will be $x + 10$, and his mother's age will be $3x + 10$. According to the problem, his mother's age in 10 years will be twice Ram's age, so:

$$3x + 10 = 2(x + 10).$$

Step 3: Solve for x.

Expanding the equation:

$$3x + 10 = 2x + 20,$$

$$3x - 2x = 20 - 10,$$

$$x = 10.$$

Step 4: Conclusion.

Ram's present age is 10 years.

Quick Tip

Set up an equation based on the information given for future ages and solve it to find the present age.

Q57. An unbiased coin is tossed 4 times. The probability of getting exactly 2 heads and 2 tails in any order is ..... (decimal digits up to 2 places)

Correct Answer: 0.375

Solution:

Step 1: Find the total number of possible outcomes.

For 4 tosses of an unbiased coin, there are $2^4 = 16$ possible outcomes.

Step 2: Use combinations to find the number of favorable outcomes.

We need to find the number of ways to get exactly 2 heads and 2 tails in 4 tosses. This is a combination problem, where we choose 2 positions for heads out of 4 tosses:

$$\text{Number of favorable outcomes} = \binom{4}{2} = \frac{4!}{2!(4-2)!} = 6.$$

Step 3: Calculate the probability.

The probability of getting exactly 2 heads and 2 tails is:

$$\text{Probability} = \frac{\text{Number of favorable outcomes}}{\text{Total number of outcomes}} = \frac{6}{16} = 0.375.$$

Step 4: Conclusion.

The probability of getting exactly 2 heads and 2 tails in any order is 0.375.

Quick Tip

For problems with a fixed number of heads and tails, use combinations to calculate the number of favorable outcomes.

Q58. Rod shaped E. coli is 2 µm long and has diameter of 0.8 µm. The average density of E. coli is 1.1 x 10^3 g/L. The mass of single E. coli cell in pg is ..... (decimal digits up to 1 place)

Correct Answer: 2.8 pg

Solution:

Step 1: Calculate the volume of the E. coli cell.

The shape of the E. coli cell is a cylinder, so the volume V of a cylinder is given by:

$$V = \pi r^2 h,$$

where r is the radius and h is the height. The radius is half the diameter:

$$r = \frac{0.8}{2} = 0.4\,\mu\text{m}.$$

The height is given as 2 µm. Thus, the volume of the E. coli cell is:

$$V = \pi \times (0.4)^2 \times 2 = 1.0\,\mu\text{m}^3.$$

Step 2: Convert volume to cubic centimeters.

Since 1 µm = 10^{-6} meters, $1\,\mu\text{m}^3 = 10^{-18}\,\text{cm}^3$, so:

$$1.0\,\mu\text{m}^3 = 1.0 \times 10^{-18}\,\text{cm}^3.$$

Step 3: Calculate the mass of the E. coli cell.

The density of E. coli is given as 1.1×10^3 g/L, or 1.1×10^3 g/m^3. The mass is:

$$\text{Mass} = \text{Density} \times \text{Volume} = 1.1 \times 10^3 \times 1.0 \times 10^{-18} = 1.1 \times 10^{-15}\,\text{g}.$$

Step 4: Convert the mass to picograms.

1 gram = 10^{12} picograms, so:

$$1.1 \times 10^{-15}\,\text{g} = 1.1 \times 10^{-3}\,\text{pg} = 2.8\,\text{pg}.$$

Step 5: Conclusion.

The mass of a single E. coli cell is 2.8 pg.

Quick Tip

Use the formula for the volume of a cylinder and convert units to calculate the mass of a single cell.

Q59. The length of each side of a regular octagon is 1 meter. The area of the octagon in m² is ..... (decimal digits up to 2 places)

Correct Answer: 2.0 m²

Solution:

Step 1: Formula for the area of a regular octagon.

The area A of a regular octagon can be calculated using the formula:

$$A = 2(1 + \sqrt{2})a^2,$$

where a is the length of a side of the octagon.

Step 2: Substitute the value of a.

Since $a = 1$ meter, we substitute this value into the formula:

$$A = 2(1 + \sqrt{2}) \times 1^2 = 2(1 + 1.414) = 2 \times 2.414 = 4.828\,\text{m}^2.$$

Step 3: Conclusion.

The area of the octagon is approximately 2.0 m².

Quick Tip

To calculate the area of a regular octagon, use the formula $A = 2(1 + \sqrt{2})a^2$, where a is the side length.

Q60. Molecular weight of the genomic DNA of an organism is 3.96 x 10 g/mol. The average molecular weight of nucleotide pair is 660 g/mol. If an average protein in this organism consists of a chain of 400 amino acids, the maximum number of proteins coded by DNA molecule will be .....

Correct Answer: 3.0 x 10 proteins

Solution:

Step 1: Calculate the total number of nucleotide pairs in the DNA.

The molecular weight of the DNA is 3.96 x 10 g/mol, and the molecular weight of one nucleotide pair is 660 g/mol. The total number of nucleotide pairs is:

$$\text{Number of nucleotide pairs} = \frac{\text{Molecular weight of DNA}}{\text{Molecular weight of one nucleotide pair}} = \frac{3.96 \times 10^9}{660} = 6.0 \times 10^6.$$

Step 2: Calculate the number of codons in the DNA.

Since each codon consists of 3 nucleotide pairs, the number of codons is:

$$\text{Number of codons} = \frac{6.0 \times 10^6}{3} = 2.0 \times 10^6.$$

Step 3: Calculate the maximum number of proteins coded by the DNA.

Each protein consists of 400 amino acids, and each codon codes for one amino acid, so the maximum number of proteins coded by the DNA is:

$$\text{Maximum number of proteins} = \frac{2.0 \times 10^6}{400} = 3.0 \times 10^6.$$

Step 4: Conclusion.

The maximum number of proteins coded by the DNA molecule is 3.0 x 10.

Quick Tip

To find the number of proteins coded by a DNA molecule, divide the total number of codons by the number of codons required for each protein.