CSIR NET Life Science Questions Answers With Solutions

Q1. Which one of the following enzymes does NOT catalyze the oxidation of a substrate by reducing the electron acceptor, NAD^+?
(a) Lactate dehydrogenase
(b) Pyruvate dehydrogenase
(c) Succinate dehydrogenase
(d) Isocitrate dehydrogenase

Q2. The pH of endocytic vesicles is 5.2, and the pH of gastric juice is 2.0. The endocytic vesicle has a [H+]that is:
(a) 15.85 times lower than that of gastric juice.
(b) 0.1585 times lower than that of gastric juice.
(c) 158.5 times lower than that of gastric juice.
(d) 1585 times lower than that of gastric juice. .

Q3. One strand of a palindromic dsDNA is composed of 5′-CCGCGGCGG-3′. Which one of the following forms of nucleic acid structures will be adopted in water if sense and antisense strands are mixed in equal proportion followed by annealing?
(a) A-form of double-stranded nucleic acid
(b) B-form of double-stranded nucleic acid
(c) Z-form of double-stranded nucleic acid
(d) Both will remain as single strands

Q4. Which one of the following pairs of metabolic intermediates does NOT provide a backbone carbon skeleton for the synthesis of amino acids?
(a) Succinate and citrate
(b) 3-phosphoglycerate and phosphoenolpyruvate
(c) Ribose 5-phosphate and erythrose 4-phosphate
(d) α-ketoglutarate and oxaloacetate

Q5. Fifteen spontaneous Ara^- mutants of E. coli, unable to utilize arabinose as a sole carbon source at 42°C but able to utilize it at 30°C, were isolated. Based on the above information, which one of the following options represents the most likely type of the mutations?
(a) Deletions
(b) Inversions
(c) Frameshift mutations
(d) Mis-sense mutations

Q6. Which one of the following statements about the distribution of chromosomes within the interphase nucleus of a mammalian cell is correct?
(a) Chromosomes are randomly distributed within the nuclear volume.
(b) The gene-poor chromosomes tend to locate towards the nuclear envelope.
(c) The larger chromosomes tend to locate at the nuclear periphery.
(d) Centromeric regions of all the chromosomes tend to concentrate at the center of the nucleus.

Q7. Which cell cycle phase is typically the shortest in mammalian cells?
(a) G0 phase
(b) G1 phase
(c) G2 phase
(d) Mitosis

Q8. Porins, which are normally present on the outer mitochondrial membrane, reach their destination by:
(a) Direct synthesis of porins on the mitochondrial membrane by the mitochondrial protein synthesis machinery.
(b) Synthesis on the ER and transport via vesicles to the mitochondria.
(c) Synthesis in the cytosol, import by TOM complex, and insertion from the inter-mitochondrial membrane space.
(d) Synthesis in the cytosol, import by TIM complex, and insertion in the membrane.

Q9. During replication, over-winding of DNA is caused by ___ and removed by ___:
(a) Primase, topoisomerase
(b) Primase, single-stranded binding protein
(c) Helicase, gyrase
(d) Helicase, DNA polymerase

Q10. P-bodies are discrete cytoplasmic collections of RNAs and proteins that are involved in:
(a) Deadenylation, decapping, and mRNA degradation
(b) Deadenylation and mRNA degradation only
(c) Deadenylation and decapping only
(d) Decapping and mRNA degradation only

Q11. Which one of the following functions is NOT facilitated by a tmRNA?
(a) Addition of a stop codon at the 3′ end of a defective and/or truncated mRNA.
(b) Addition of a proteolysis-inducing tag at the carboxyl terminus of an unfinished polypeptide.
(c) Release of defective and/or truncated mRNA from the ribosome.
(d) Recycling of the stalled ribosomes.

Q12. RNA polymerase is an enzyme that transcribes DNA sequences into RNA. Which one of the following is NOT a property of RNA polymerase?
(a) RNA polymerases initiate RNA synthesis without primers that provide a free 3′OH group.
(b) RNA polymerases have high fidelity due to the action of proofreading endonuclease activity.
(c) In eukaryotes, RNA that encodes ribosomal proteins is transcribed by RNA polymerase II.
(d) RNA polymerases initiate RNA synthesis from defined regions of DNA.

Q13. Choose the INCORRECT statement:
(a) Tetanospasmin is associated with tetanus.
(b) Tetanospasmin is a neurotoxin.
(c) Tetanospasmin facilitates the release of gamma-aminobutyric acid at synapses.
(d) Immunization with toxoids is used for the prevention of tetanus.

Q14. In a cell signaling event, the enzyme that directly converts $PI(4,5)P_2$ to $PI(3,4,5)P_3$ is:
(a) PI3-Kinase
(b) PLCβ
(c) PTEN
(d) Protein Kinase B

Q15. Which one of the following options is a correct match between terms of Columns X and Y?

Column X		Column Y	
A.	Anchoring junction	i.	Claudins
B.	Occluding junction	ii.	Delta-Notch
C.	Channel-forming junction	iii.	Desmoglein
D.	Signal-relaying junction	iv.	Connexin

(a) A-iii, B-i, C-iv, D-ii
(b) A-iv, B-i, C-iv, D-iii
(c) A-iii, B-i, C-iv, D-i
(d) A-ii, B-iii, C-i, D-iv

Q16. Kaposi's sarcoma is caused by:
(a) Epstein-Barr virus
(b) HIV and HHV-8
(c) HTLV type 1
(d) HPV

Q17. Sperm ___, which helps in penetration of the egg during fertilization in mammals, contains _____:
(a) lysin, hyaluronidase
(b) fertilizin, hyaluronidase
(c) lysin, hyaluronic acid
(d) fertilizin, hyaluronic acid

Q18. Which one of the following statements regarding the developmental potential of cells in the embryo is INCORRECT?
(a) The cells of the 4-cell stage mouse embryo are totipotent.
(b) The cells of the inner cell mass of the mouse blastocyst differentiate into trophectoderm, mesoderm, and endoderm.
(c) Spermatogonial stem cells in testis are unipotent.
(d) Haematopoietic stem cells, which can differentiate into blood cells, are multipotent.

Q19. Which one of the following statements is correct for dosage compensation in humans?
(a) X-chromosome inactivation in females occurs in a zygote immediately after fertilization.
(b) X-chromosome inactivation is non-random; in some individuals, maternal X is inactivated while in others, paternal X-chromosome is inactivated.
(c) Y-chromosome of males is seen as Barr body.
(d) The body of a female is a mosaic of cells, some having paternal X and others having maternal X inactivated.

Q20. Which one of the following floral homeotic genes is transcribed in all four whorls during flower development?

(a) AP1

(b) AP2

(c) AP3/PI

(d) AG

Solutions

S1. Ans. (c) Succinate dehydrogenase

Explanation:

Succinate dehydrogenase is a key enzyme in the citric acid cycle (Krebs cycle), but it does not reduce NAD^+. Instead, it reduces FAD to $FADH_2$ as it oxidizes succinate to fumarate. Other enzymes in the list, such as lactate dehydrogenase, pyruvate dehydrogenase, and isocitrate dehydrogenase, use NAD^+ as the electron acceptor, reducing it to NADH in their respective catalytic reactions.

Information Booster:

1. Lactate dehydrogenase converts pyruvate to lactate, reducing NAD^+ to NADH.
2. Pyruvate dehydrogenase oxidizes pyruvate, reducing NAD^+ to NADH and producing acetyl-CoA.
3. Succinate dehydrogenase reduces FAD to $FADH_2$, bypassing NAD^+ entirely.
4. Isocitrate dehydrogenase reduces NAD^+ to NADH while converting isocitrate to α-ketoglutarate.
5. The distinction between NAD^+ and FAD as electron acceptors is crucial for understanding cellular metabolism. NAD^+ is a common electron acceptor for most dehydrogenases except SDH.
6. SDH reduces FAD, which has a different redox potential than NAD^+.
7. Understanding enzyme specificity helps in identifying metabolic pathways.

Additional Knowledge:

- **Lactate dehydrogenase (LDH):** Catalyzes the interconversion of pyruvate and lactate with simultaneous interconversion of NADH and NAD^+. It plays a vital role in anaerobic glycolysis.
- **Pyruvate dehydrogenase (PDH):** A multi-enzyme complex that converts pyruvate into acetyl-CoA in the mitochondria, producing NADH in the process. It links glycolysis to the citric acid cycle.
- **Succinate dehydrogenase (SDH):** Unique as it functions in both the citric acid cycle and the electron transport chain (Complex II). It reduces FAD to $FADH_2$ and transfers electrons directly to the respiratory chain.
- **Isocitrate dehydrogenase (IDH):** Exists in two forms, one using NAD^+ and the other $NADP^+$. It catalyzes the oxidative decarboxylation of isocitrate to α-ketoglutarate, producing NADH/NADPH.

S2. Ans. (d)

Sol. 1585 times lower than that of gastric juice.

pH of endocytic vesicle = 5.2

$[H^+]$ concentration of endocytic vesicle ⇒

pH = -log $[H^+]$; $[H^+]$ = 10^(-pH)

5.2 = -log $[H^+]$

∴ $[H^+] = 6.31 \times 10^{-6}$ mol/L

pH of gastric juice = 2

$[H^+]$ concentration of gastric juice ⇒

pH = -log $[H^+]$

2 = -log $[H^+]$

∴ $[H^+] = 1 \times 10^{-2}$ mol/L

∴ **$[H^+]$ of gastric juice**

---------- = **1585**

$[H^+]$ of endocytic vesicle

$= (1 \times 10^{-2}) / (6.31 \times 10^{-6})$

$= (1 / 6.31) \times 10^4$

$= 0.1585 \times 10^4$

= **1585**

Information Booster:

1. The pH scale is logarithmic; a one-unit change represents a tenfold difference in [H+].
2. Gastric juice has a highly acidic environment, aiding in digestion.
3. Endocytic vesicles typically maintain a near-neutral to slightly acidic pH.
4. A pH difference significantly impacts enzymatic activity and cellular transport mechanisms.
5. The ratio between [H+] can be calculated using pH = pH2-pH1

Additional Knowledge:

- **pH and Hydrogen Ion Concentration:**
  A decrease in pH represents an increase in [H+]. For example, a pH of 2 corresponds to [H+]=10−2, while a pH of 5.2 corresponds to [H+]=10−5.2.
- **Gastric Juice (pH 2.0):**
  Contains hydrochloric acid (HCl), creating a highly acidic environment essential for protein digestion and killing pathogens. The high [H+] facilitates pepsin activation.
- **Endocytic Vesicles (pH 5.2):**
  Slightly acidic, enabling the vesicles to transport molecules and degrade materials using acid hydrolases.
- **Logarithmic Nature:**
  Each unit on the pH scale corresponds to a tenfold difference in [H+], emphasizing the need for precise pH regulation in biological systems.
- **Calculation Tip:**
  For rapid estimation, subtract the pH values (5.2−2.0=3.2)

S3. Ans. (b)

Sol. B-form of double-stranded nucleic acid

Explanation:

The B-form of DNA is the most stable and predominant form of double-stranded DNA under physiological conditions, such as in water at neutral pH. Palindromic sequences (like 5′-CCGCGGCGG-3′) anneal to form complementary base pairs, resulting in a typical B-form helix. While Z-form DNA can occur in certain conditions with alternating purine-pyrimidine sequences and supercoiling, B-form is favored in aqueous and near-neutral conditions

Information Booster:

B-DNA is the right-handed helical structure adopted by DNA in most biological settings.

Palindromic sequences can lead to self-complementary strands forming stable double-stranded DNA.

A-DNA forms under dehydrated conditions, not in aqueous environments.

Z-DNA forms in high salt or torsional strain conditions but is less stable under standard aqueous environments.

Single strands would not persist after annealing due to complementarity in a palindromic sequence.

B-form DNA is the most common and stable under physiological conditions.

Palindromic sequences form stable complementary double strands.

Z-DNA is rare and occurs under specific conditions, not in aqueous solutions

Additional Knowledge:

A-form DNA: This form of DNA is more compact, right-handed, and occurs under low hydration conditions. RNA-DNA hybrids and double-stranded RNA often adopt this form.

B-form DNA: The canonical form of DNA, characterized by 10.5 base pairs per turn, a diameter of 2 nm, and a right-handed helix. The majority of DNA in cells exists in this form.

Z-form DNA: A left-handed helix formed in sequences with alternating purines and pyrimidines (e.g., CGCG). It is observed under high salt or specific supercoiling conditions but is not common in physiological environments.

Annealing: The process where complementary strands of nucleic acids hybridize to form a double-stranded structure. Palindromic sequences ensure efficient pairing and helix formation.

S4. Ans. (a)

Sol. Succinate and citrate

Explanation:

Succinate and citrate are intermediates of the citric acid cycle but do not directly serve as carbon skeletons for amino acid synthesis. Key intermediates such as **α-ketoglutarate** and **oxaloacetate** provide carbon skeletons for glutamate, aspartate, and other amino acids. Similarly, **3-phosphoglycerate** and **phosphoenolpyruvate** are glycolytic intermediates contributing to amino acid biosynthesis. **Ribose 5-phosphate** and **erythrose 4-phosphate** are part of the pentose phosphate pathway, aiding in synthesizing aromatic amino acids.

Information Booster:

1. **Succinate** and **citrate** are involved in the TCA cycle but do not contribute directly to amino acid synthesis.
2. **3-phosphoglycerate** and **phosphoenolpyruvate** are precursors for serine, glycine, and cysteine.
3. **Ribose 5-phosphate** and **erythrose 4-phosphate** are precursors for aromatic amino acids (phenylalanine, tyrosine, and tryptophan).
4. **α-ketoglutarate** is the precursor for glutamate and proline synthesis.
5. **Oxaloacetate** is the precursor for aspartate, which further gives rise to asparagine, methionine, lysine, and threonine. Amino acid synthesis relies on specific intermediates from glycolysis, the TCA cycle, and the pentose phosphate pathway.
6. The integration of metabolic pathways is essential for biosynthesis and energy regulation.

Additional Knowledge:

- **Succinate and citrate:**
  While crucial for energy metabolism in the citric acid cycle, these intermediates do not directly provide carbon skeletons for amino acid synthesis.
- **3-phosphoglycerate and phosphoenolpyruvate:**
  Derived from glycolysis, these intermediates form amino acids like serine, glycine, and cysteine. Phosphoenolpyruvate (PEP) also contributes to the synthesis of aromatic amino acids via the shikimate pathway in plants and microorganisms.
- **Ribose 5-phosphate and erythrose 4-phosphate:**
  Products of the pentose phosphate pathway, these serve as precursors for aromatic amino acids (phenylalanine, tyrosine, and tryptophan) via the shikimate pathway in plants and some microorganisms.
- **α-ketoglutarate and oxaloacetate:**
  These are primary precursors in the TCA cycle for synthesizing amino acids such as glutamate (from α-ketoglutarate) and aspartate (from oxaloacetate).

S5. Ans. (d) Mis-sense mutations

Explanation:

Mis-sense mutations result in single amino acid changes in proteins. These mutations can lead to temperature-sensitive phenotypes, where the protein is functional at lower temperatures (30°C) but loses functionality at higher temperatures (42°C) due to destabilization. Frameshift mutations, deletions, or inversions are more likely to completely disrupt the gene's function, resulting in a phenotype that is independent of temperature

Information Booster:

1. **Mis-sense mutations** are point mutations causing amino acid substitutions.
2. Temperature sensitivity is often linked to structural instability caused by altered amino acids.
3. **Deletions** typically remove large gene segments, causing loss of function.
4. **Frameshift mutations** result from insertions or deletions that disrupt the reading frame, leading to nonfunctional proteins.
5. **Inversions** rearrange gene segments, often impacting function but not typically creating temperature sensitivity. Temperature-sensitive phenotypes often point to protein instability caused by specific amino acid changes.
6. Mis-sense mutations are the most common cause of such temperature sensitivity.
7. Large-scale changes like deletions, inversions, or frameshifts typically result in nonfunctional proteins, independent of temperature.

Additional Knowledge:

- **Mis-sense mutations:**
  These mutations result from single base pair changes that substitute one amino acid for another. Temperature-sensitive mutations are a hallmark of mis-sense mutations, as the altered protein is only stable and functional under certain conditions.
- **Deletions:**
  Large-scale deletions remove nucleotide sequences, often eliminating functional domains of the protein entirely. Such mutations generally result in a non-functional protein that cannot regain function at different temperatures.

- **Inversions:**
  Inversions involve the reversal of a DNA segment within a chromosome. While they can disrupt gene function or regulation, they are less likely to produce temperature-sensitive phenotypes.
- **Frameshift mutations:**
  These arise due to insertions or deletions that alter the reading frame of the gene, leading to aberrant proteins or premature stop codons. Frameshift mutations usually cause a complete loss of function regardless of temperature.

S6. Ans. (b) The gene-poor chromosomes tend to locate towards the nuclear envelope.
Explanation:
In the interphase nucleus, chromosomes are not randomly distributed but adopt specific spatial arrangements. Gene-poor chromosomes typically localize near the nuclear envelope, while gene-rich chromosomes are found in the interior of the nucleus. This organization facilitates efficient transcription and gene regulation. Larger chromosomes do not necessarily localize at the periphery, and the centromeric regions of all chromosomes do not converge at the nuclear center.
Information Booster:
1. Chromosome territories are distinct regions occupied by individual chromosomes in the nucleus.
2. Gene-poor regions tend to associate with the nuclear periphery, where transcriptional activity is lower.
3. Gene-rich chromosomes are centrally located to optimize transcription.
4. Spatial organization reflects functional compartmentalization of the nucleus.
5. The nuclear organization is dynamic and changes during the cell cycle. Chromosome positioning reflects functional needs, with gene-rich areas active in transcription being centrally located.
6. Gene-poor regions are associated with transcriptionally inactive periphery areas.
7. Chromosome territories enable the compartmentalization of nuclear functions.

Additional Knowledge:
- **Chromosomes are randomly distributed (Option a):**
  This is incorrect. Chromosomes occupy specific territories within the nucleus, a concept called chromosome territoriality.
- **Gene-poor chromosomes locate towards the nuclear envelope (Option b):**
  This is correct. Gene-poor regions are associated with the nuclear periphery, which is generally transcriptionally inactive (heterochromatin).
- **Larger chromosomes at the nuclear periphery (Option c):**
  This is incorrect. Chromosomal positioning depends more on gene density than size, with gene-rich chromosomes typically localizing in the nuclear interior.
- **Centromeric regions concentrate at the nuclear center (Option d):**
  This is incorrect. Centromeres are dispersed within the nucleus, and their positioning depends on the overall organization of the chromosome rather than converging at a single nuclear center.

S7. Ans. (d)
Sol. Mitosis
Explanation:
Mitosis is the shortest phase of the cell cycle, typically lasting around 1–2 hours in mammalian cells. It is a highly regulated process that involves the division of the nucleus and the cytoplasm to produce two daughter cells. In contrast, the G1 phase (gap 1) and G2 phase (gap 2) are longer because they involve growth and preparation for DNA replication or mitosis, while the S phase is dedicated to DNA synthesis.

Information Booster:

1. **Mitosis** consists of prophase, metaphase, anaphase, and telophase.
2. It is shorter than other phases because it primarily focuses on cell division.
3. The G1 phase is the longest in most cells as it involves significant growth and preparation.
4. The G2 phase ensures readiness for mitosis, including checking for DNA damage.
5. The duration of cell cycle phases can vary between different cell types and organisms. The G1 and G2 phases involve extensive cellular activities like growth and checkpoint mechanisms.
6. The G0 phase is not part of the active cycle but is crucial for maintaining non-dividing cells.

Additional Knowledge:

- **G0 phase (Option a):**
  Cells in the G0 phase are in a quiescent state and not actively dividing. This phase can last indefinitely, depending on the cell type and its environmental signals.
- **G1 phase (Option b):**
  This is the first gap phase where the cell grows, synthesizes proteins, and prepares for DNA replication. It is often the longest phase, especially in rapidly dividing cells.
- **G2 phase (Option c):**
  This phase occurs after DNA replication and involves preparation for mitosis. The cell checks for DNA damage and ensures all replication is complete before division.
- **Mitosis (Option d):**
  As the shortest phase, mitosis is highly dynamic and involves chromosomal segregation and cytokinesis. Despite its brevity, it is critical for genetic stability.

S8. Ans.(c)

Sol. Synthesis in the cytosol, import by TOM complex, and insertion from the inter-mitochondrial membrane space.

Explanation:

Porins are β-barrel proteins located in the outer mitochondrial membrane. They are synthesized in the cytosol and transported to the mitochondria. The **TOM (Translocase of the Outer Membrane)** complex facilitates their import into the intermembrane space. From there, they are inserted into the outer mitochondrial membrane via the **SAM (Sorting and Assembly Machinery)** complex. TIM (Translocase of the Inner Membrane) is not involved in their insertion as it primarily transports proteins into or across the inner mitochondrial membrane.

Information Booster:

1. Porins are essential for regulating the exchange of ions and small molecules across the mitochondrial outer membrane.
2. **TOM complex** mediates protein import into the mitochondria.
3. **SAM complex** assists in folding and inserting β-barrel proteins into the outer membrane.
4. Proteins synthesized in the cytosol require mitochondrial targeting sequences for proper import.
5. The inner mitochondrial membrane relies on TIM complexes for protein transport. Porins are synthesized in the cytosol and imported to mitochondria via the TOM and SAM complexes.
6. Mitochondrial protein import depends on specific translocases like TOM (outer membrane) and TIM (inner membrane).
7. β-barrel proteins are uniquely handled by the SAM complex for proper folding and membrane integration.

Additional Knowledge:

- **Option (a): Direct synthesis of porins on mitochondrial membrane:**
  This is incorrect because mitochondria synthesize a small number of their proteins, but porins are not among them. Most mitochondrial proteins are synthesized in the cytosol.
- **Option (b): Synthesis on the ER and transport via vesicles:**
  Incorrect, as porins are not synthesized in the endoplasmic reticulum (ER). Vesicle-based transport is typical for proteins destined for the secretory pathway, not mitochondrial proteins.
- **Option (c): Synthesis in the cytosol, import by TOM complex:**
  Correct. Porins are synthesized in the cytosol, imported through the TOM complex, and inserted into the outer membrane via the SAM complex.
- **Option (d): Synthesis in the cytosol, import by TIM complex:**
  Incorrect, as TIM complexes are specific for the inner membrane and matrix proteins, not β-barrel proteins like porins.

S9. Ans. (c) Helicase, gyrase

Explanation:

During DNA replication, **helicase** unwinds the DNA double helix to create replication forks. This unwinding introduces positive supercoiling (over-winding) ahead of the replication fork. The enzyme **gyrase**, a type of **topoisomerase**, alleviates this supercoiling by introducing negative supercoils, ensuring smooth progression of the replication machinery. Without gyrase (or topoisomerase activity), the replication process would stall due to excessive tension.

Information Booster:

1. Helicase is responsible for unwinding the DNA strands, creating replication forks.
2. Positive supercoils form ahead of the replication fork due to the helicase activity.
3. Gyrase (a type of topoisomerase) relieves these supercoils, maintaining DNA topology.
4. Single-stranded binding proteins stabilize the unwound DNA strands.
5. Proper coordination between helicase and topoisomerase is essential for efficient replication. Supercoiling occurs due to helicase activity during unwinding.
6. Gyrase (topoisomerase) is essential to relieve over-winding and maintain DNA integrity.
7. DNA replication requires the coordination of helicase, primase, topoisomerase, and single-stranded binding proteins.

Additional Knowledge:

- **Helicase:**
  This enzyme separates the two strands of DNA by breaking hydrogen bonds between complementary bases, enabling replication. It moves along the DNA in the 5′ to 3′ direction.
- **Gyrase (Option c):**
  A specialized type II topoisomerase found in prokaryotes, gyrase relieves positive supercoiling by cutting and resealing the DNA strands. It introduces negative supercoils to balance the tension caused by helicase activity.
- **Primase (Option a, b):**
  Primase synthesizes short RNA primers on the lagging strand to provide a starting point for DNA polymerase. It does not directly interact with supercoiling.
- **Single-stranded binding proteins (Option b):**
  These proteins bind to unwound DNA strands to prevent reannealing and protect the strands from nucleases, but they do not manage supercoiling.
- **DNA Polymerase (Option d):**
  This enzyme synthesizes new DNA strands but does not influence supercoiling directly.

S10. Ans.(a)
Sol. Deadenylation, decapping, and mRNA degradation
Explanation:
P-bodies are cytoplasmic granules that play a critical role in mRNA turnover and degradation. They are sites where mRNAs are deadenylated (removal of the poly-A tail) and decapped (removal of the 5′ cap), marking them for degradation by exonucleases. These processes regulate mRNA stability and gene expression. In addition to degradation, P-bodies also serve as temporary storage sites for translationally repressed mRNAs.
Information Booster:
1. **Deadenylation:** Removal of the poly-A tail is the first step in mRNA decay.
2. **Decapping:** The removal of the 5′ cap is necessary for exonucleolytic degradation.
3. **mRNA degradation:** Exonucleases degrade mRNA after decapping.
4. P-bodies also store untranslated mRNAs for possible reactivation or degradation.
5. They are involved in post-transcriptional gene regulation and RNA quality control.

Additional Knowledge:
- **Deadenylation:**
  This is typically mediated by deadenylase enzymes like CCR4-NOT, leading to mRNA destabilization.
- **Decapping:**
  Enzymes like Dcp1 and Dcp2 remove the 5′ cap, rendering mRNA vulnerable to exonucleolytic degradation.
- **mRNA degradation:**
  Once the poly-A tail and 5′ cap are removed, mRNAs are rapidly degraded by exonucleases such as XRN1.
- **Storage Function of P-bodies:**
  In addition to degradation, P-bodies can sequester translationally inactive mRNAs, allowing them to be reactivated later if needed.
- **Exclusion from Translation:**
  mRNAs localized in P-bodies are excluded from translation, ensuring efficient regulation of gene expression.

S11. Ans.(a)
Sol. Addition of a stop codon at the 3′ end of a defective and/or truncated mRNA.
Explanation:
tmRNA does not add a stop codon to defective or truncated mRNAs. Instead, it rescues stalled ribosomes by serving as both tRNA and mRNA. It adds an amino acid tag that signals unfinished polypeptides for degradation and allows the ribosome to terminate translation. tmRNA releases the stalled ribosome and degrades the defective mRNA, but no stop codon is added to the mRNA itself.
Information Booster:
1. tmRNA combines the functions of tRNA and mRNA in bacteria.
2. It rescues stalled ribosomes by replacing defective mRNA.
3. tmRNA adds a proteolysis-inducing peptide tag to unfinished polypeptides.
4. Stalled ribosomes are released and recycled for further translation.
5. tmRNA ensures translation fidelity and prevents the accumulation of defective mRNAs. tmRNA is a bacterial system to rescue ribosomes stalled on defective mRNAs.
6. It acts as both tRNA and mRNA, encoding a degradation signal for incomplete proteins.
7. The defective mRNA is not repaired but is instead targeted for degradation.

Additional Knowledge:

- **Addition of a stop codon (Option a):**
  tmRNA does not alter the defective mRNA or add a stop codon. Instead, it facilitates termination by encoding its own termination sequence.
- **Proteolysis-inducing tag (Option b):**
  tmRNA tags the incomplete polypeptide with a sequence that signals degradation by cellular proteases. This ensures that defective proteins do not accumulate.
- **Release of defective mRNA (Option c):**
  tmRNA enables the release of the defective mRNA by displacing it from the ribosome, allowing degradation of the faulty mRNA.
- **Ribosome recycling (Option d):**
  tmRNA helps disassemble stalled ribosome complexes, making them available for new rounds of translation.

S12. Ans. (b) RNA polymerases have high fidelity due to the action of proofreading endonuclease activity.

Explanation:

RNA polymerases lack proofreading endonuclease activity, unlike DNA polymerases. They exhibit relatively low fidelity compared to DNA polymerases. Errors in transcription are less critical because RNA is not inherited and has a shorter lifespan. RNA polymerases initiate RNA synthesis without primers, transcribe specific DNA regions, and, in eukaryotes, RNA polymerase II transcribes genes encoding ribosomal proteins.

Information Booster:

1. RNA polymerases can initiate RNA synthesis without a primer.
2. They transcribe specific genes or defined DNA regions.
3. RNA polymerase II transcribes mRNA, including ribosomal protein-encoding genes.
4. Errors in transcription are less consequential compared to replication errors.
5. RNA polymerases lack proofreading activity, unlike DNA polymerases.

Additional Knowledge:

- **Primer Independence (Option a):**
  RNA polymerases do not require primers to initiate transcription. They can start de novo synthesis, unlike DNA polymerases, which require a free 3′-OH group provided by a primer.
- **Proofreading Activity (Option b):**
  RNA polymerases lack 3′ to 5′ exonuclease activity for proofreading. Errors are tolerated because transcription is not heritable, and mRNA is short-lived.
- **Transcription by RNA Polymerase II (Option c):**
  In eukaryotes, RNA polymerase II transcribes genes that encode ribosomal proteins, as well as mRNA for other proteins. RNA polymerase I transcribes rRNA (excluding 5S rRNA), and RNA polymerase III transcribes tRNA and 5S rRNA.
- **Defined Regions of DNA (Option d):**
  RNA polymerase initiates transcription at specific promoter regions, ensuring regulated gene expression.

S13. Ans.(c)
Sol. Tetanospasmin facilitates the release of gamma-aminobutyric acid at synapses.
Explanation:
Tetanospasmin, the neurotoxin produced by *Clostridium tetani*, **inhibits** the release of gamma-aminobutyric acid (GABA) and glycine at synapses, causing spastic paralysis. This inhibitory neurotransmitter blockade leads to the characteristic muscle rigidity and spasms seen in tetanus. The other statements are correct: Tetanospasmin is associated with tetanus, it is a neurotoxin, and immunization with tetanus toxoid is a standard preventive measure.
Information Booster:
1. Tetanospasmin blocks GABA and glycine release, causing spastic paralysis.
2. It is one of the most potent neurotoxins known.
3. Tetanus immunization uses an inactivated form of the toxin (toxoid).
4. Tetanospasmin spreads via retrograde axonal transport to the central nervous system.
5. The toxin's effects are irreversible without timely treatment.

Additional Knowledge:
- **Tetanospasmin (Option a, b):**
  Tetanospasmin is a potent neurotoxin produced by *Clostridium tetani*. It enters motor neurons at the site of infection and travels retrogradely to the central nervous system.
- **Inhibition of GABA and Glycine (Option c):**
  Incorrect. Tetanospasmin prevents the release of inhibitory neurotransmitters (GABA and glycine) in the spinal cord and brainstem. This leads to sustained muscle contractions and spasms. It does not facilitate neurotransmitter release.
- **Toxoid Immunization (Option d):**
  Tetanus prevention relies on vaccination with tetanus toxoid, an inactivated toxin. Booster doses are necessary every 10 years to maintain immunity.

S14. Ans. (a)
Sol. PI3-Kinase
Explanation:
PI3-Kinase (phosphoinositide 3-kinase) phosphorylates the inositol ring of $PI(4,5)P_2$ at the 3′ position to generate $PI(3,4,5)P_3$. This conversion is a key step in intracellular signaling pathways, such as those involving growth factor receptors. $PI(3,4,5)P_3$ acts as a second messenger, recruiting proteins with pleckstrin homology (PH) domains, such as Protein Kinase B (PKB/Akt), to the membrane, where they participate in downstream signaling.
Information Booster:
1. **PI3-Kinase** plays a central role in growth, survival, and metabolism signaling pathways.
2. $PI(4,5)P_2$ is a precursor for both $PI(3,4,5)P_3$ and diacylglycerol (DAG).
3. **PTEN** reverses this reaction by dephosphorylating $PI(3,4,5)P_3$ to $PI(4,5)P_2$.
4. **PLCβ** hydrolyzes $PI(4,5)P_2$ to generate DAG and IP_3.
5. $PI(3,4,5)P_3$ facilitates membrane recruitment and activation of signaling proteins.

Additional Knowledge:
- **PI3-Kinase (Option a):**
  This enzyme phosphorylates $PI(4,5)P_2$ at the 3′ position, producing $PI(3,4,5)P_3$. It plays a critical role in pathways activated by receptor tyrosine kinases (RTKs) and G-protein coupled receptors (GPCRs).

- **PLCβ (Option b):**
  Phospholipase C beta (PLCβ) hydrolyzes $PI(4,5)P_2$ into DAG and inositol trisphosphate (IP_3). DAG activates protein kinase C, while IP_3 triggers calcium release from the endoplasmic reticulum.
- **PTEN (Option c):**
  PTEN is a phosphatase that dephosphorylates $PI(3,4,5)P_3$ at the 3′ position, converting it back to $PI(4,5)P_2$. It acts as a tumor suppressor by counteracting PI3-Kinase activity.
- **Protein Kinase B (Option d):**
  Also known as Akt, Protein Kinase B is not an enzyme that acts on PI lipids. Instead, it is activated downstream of PI3-Kinase by binding to $PI(3,4,5)P_3$ at the membrane.

S15. Ans.(a)
Sol. A-iii, B-i, C-iv, D-ii
Explanation:
The correct associations are:
- **Anchoring junction (A) → Desmoglein (iii):** Anchoring junctions include desmosomes and adherens junctions, which use proteins like desmoglein (a cadherin protein) for cell-cell adhesion.
- **Occluding junction (B) → Claudins (i):** Tight junctions, which occlude passage between cells, rely on claudins and occludins for their function.
- **Channel-forming junction (C) → Connexin (iv):** Gap junctions are formed by connexin proteins, enabling intercellular communication via channels.
- **Signal-relaying junction (D) → Delta-Notch (ii):** Signal-relaying junctions involve signaling proteins like Delta and Notch in intercellular communication.

Information Booster:
1. **Anchoring junctions** provide mechanical stability and include desmosomes and adherens junctions.
2. **Occluding junctions** form barriers between cells, regulating paracellular transport.
3. **Channel-forming junctions** allow direct communication between cells via gap junctions.
4. **Signal-relaying junctions** are critical in developmental and intercellular signaling, including Delta-Notch signaling.
5. Junction-specific proteins include desmoglein (anchoring), claudins (tight junctions), connexins (gap junctions), and Delta-Notch (signal-relaying).

Additional Knowledge:
- **Anchoring Junctions (A-iii):**
  Desmoglein is a cadherin family protein found in desmosomes, anchoring adjacent cells together. These junctions are important in tissues subjected to mechanical stress, such as skin and heart.
- **Occluding Junctions (B-i):**
  Tight junctions are formed by claudins and occludins, creating a barrier to prevent the passage of molecules between cells. They are critical in epithelial and endothelial cells.
- **Channel-forming Junctions (C-iv):**
  Connexins assemble to form gap junctions, which create intercellular channels for the exchange of ions, nutrients, and signaling molecules.
- **Signal-relaying Junctions (D-ii):**
  Delta-Notch signaling is crucial in developmental pathways and cell differentiation. These junctions transmit signals between adjacent cells.

S16. Ans.(b)
Sol. HIV and HHV-8
Explanation:
Kaposi's sarcoma is associated with **Human Herpesvirus-8 (HHV-8)**, also known as Kaposi's sarcoma-associated herpesvirus (KSHV). The condition is more prevalent in individuals with compromised immune systems, such as those with **HIV/AIDS**. HIV weakens the immune system, allowing HHV-8 to induce tumorigenesis, resulting in vascular tumors characteristic of Kaposi's sarcoma.
Information Booster:
1. **Kaposi's sarcoma** is a vascular tumor linked to HHV-8 infection.
2. It is common in **HIV-positive** individuals due to immune suppression.
3. HHV-8 infects endothelial cells, leading to abnormal blood vessel formation.
4. The condition presents as purple, reddish-brown skin lesions.
5. Antiretroviral therapy reduces the incidence of Kaposi's sarcoma in HIV patients.

Additional Knowledge:
- **Epstein-Barr Virus (EBV) (Option a):**
  EBV is associated with diseases like Burkitt lymphoma, Hodgkin lymphoma, and nasopharyngeal carcinoma but is not linked to Kaposi's sarcoma.
- **HIV and HHV-8 (Option b):**
  Correct. HHV-8 is the causative agent of Kaposi's sarcoma, and HIV contributes by suppressing the immune system, allowing HHV-8 to trigger tumor formation.
- **HTLV type 1 (Option c):**
  Human T-cell leukemia virus type 1 (HTLV-1) is associated with adult T-cell leukemia/lymphoma but not with Kaposi's sarcoma.
- **HPV (Option d):**
  Human papillomavirus (HPV) is associated with cervical, anal, and oropharyngeal cancers but is unrelated to Kaposi's sarcoma.

S17. Ans.(a)
Sol. lysin, hyaluronidase
Explanation:
During fertilization in mammals, sperm utilize **lysin** and **hyaluronidase** to penetrate the egg's protective layers. Lysin helps digest the zona pellucida, the glycoprotein layer surrounding the egg, while hyaluronidase breaks down the hyaluronic acid in the cumulus oophorus, which surrounds the egg. These enzymes are released from the acrosome, a specialized organelle in the sperm head, during the acrosome reaction.
Information Booster:
1. **Lysin** facilitates the breakdown of the zona pellucida, enabling sperm entry.
2. **Hyaluronidase** digests hyaluronic acid in the cumulus cells surrounding the egg.
3. The acrosome reaction is critical for releasing these enzymes.
4. Fertilization involves both mechanical movement and enzymatic activity.
5. Sperm-egg binding also involves specific recognition proteins on the sperm and egg.

Additional Knowledge:

- **Lysin (Option a):**
  Lysin is a sperm enzyme that dissolves the zona pellucida. It ensures the sperm can access the plasma membrane of the egg.
- **Hyaluronidase (Option a):**
  This enzyme digests hyaluronic acid, a major component of the extracellular matrix of the cumulus oophorus. This step is necessary to clear the path to the zona pellucida.
- **Fertilizin (Options b and d):**
  Fertilizin is not an enzyme; it is a glycoprotein on the egg surface that helps in sperm recognition and binding.
- **Hyaluronic acid (Options c and d):**
  Hyaluronic acid is part of the egg's extracellular matrix, specifically in the cumulus cells. It is not an enzyme but rather a substrate for hyaluronidase.

S18. Ans.(b)

Sol. The cells of the inner cell mass of the mouse blastocyst differentiate into trophectoderm, mesoderm, and endoderm.

Explanation:

The inner cell mass (ICM) of the blastocyst does not differentiate into **trophectoderm**. Instead, it gives rise to the embryonic germ layers: **ectoderm, mesoderm, and endoderm**. The trophectoderm, which forms the placenta and extraembryonic tissues, originates from cells external to the ICM. The ICM is pluripotent and is responsible for forming the embryo proper.

Information Booster:

1. **Totipotent cells** can form all embryonic and extraembryonic structures (e.g., 4-cell stage).
2. **Pluripotent cells** of the ICM form the three germ layers but not extraembryonic tissues.
3. **Unipotent cells** can differentiate into one cell type (e.g., spermatogonial stem cells).
4. **Multipotent cells** can generate multiple related cell types (e.g., hematopoietic stem cells).
5. The trophectoderm forms the outer layer of the blastocyst and contributes to the placenta.

Additional Knowledge:

- **4-cell stage mouse embryo (Option a):**
  These cells are totipotent, meaning they have the potential to form all embryonic and extraembryonic structures, including the placenta.
- **Inner cell mass (Option b):**
  Incorrect. The ICM gives rise to the embryo proper and differentiates into the three germ layers (ectoderm, mesoderm, endoderm). The trophectoderm, which contributes to the placenta, originates from outer blastocyst cells, not the ICM.
- **Spermatogonial stem cells (Option c):**
  These are unipotent cells in the testis, capable of differentiating only into sperm cells.
- **Hematopoietic stem cells (Option d):**
  These are multipotent, meaning they can differentiate into various blood cell types, including red blood cells, white blood cells, and platelets.

S19. Ans.(d)
Sol. The body of a female is a mosaic of cells, some having paternal X and others having maternal X inactivated.
Explanation:
In females, one of the two X chromosomes in each cell is randomly inactivated during early embryonic development, a process called **X-chromosome inactivation**. This ensures dosage compensation between males (XY) and females (XX). The inactivated X-chromosome forms a condensed structure known as the **Barr body**. As X-inactivation is random in each cell, females become mosaics with some cells inactivating the paternal X and others inactivating the maternal X.
Information Booster:
1. X-inactivation occurs in early embryonic development, not immediately after fertilization.
2. It is random, meaning either the maternal or paternal X is inactivated in each cell.
3. The inactivated X forms a Barr body, visible in the nucleus.
4. This process ensures equal expression of X-linked genes between males and females.
5. Females exhibit a mosaic pattern of X-linked gene expression due to random inactivation.

Additional Knowledge:
- **Option (a):**
  Incorrect. X-inactivation does not occur immediately after fertilization but takes place during the blastocyst stage of embryonic development.
- **Option (b):**
  Incorrect. X-inactivation is a random process in each cell, and there is no global preference for maternal or paternal X inactivation.
- **Option (c):**
  Incorrect. The Barr body is a condensed and inactivated X-chromosome, not the Y-chromosome. The Y-chromosome does not undergo inactivation.
- **Option (d):**
  Correct. Female mammals are mosaics for X-linked gene expression, with different cells expressing genes from either the maternal or paternal X-chromosome, depending on which X is inactivated.

S20. Ans. (b)
Sol. AP2
Explanation:
The **AP2 (APETALA2)** gene is a floral homeotic gene transcribed in all four whorls during flower development. It plays a broad role in determining floral organ identity and development. AP2 is not restricted to specific whorls and is involved in regulating genes that control floral meristem development, making it unique among the options provided. Other genes like **AP1**, **AP3/PI**, and **AG** are expressed in specific whorls and are part of the ABC model of floral development.
Information Booster:
1. **AP2** regulates floral meristem identity and organ specification across all whorls.
2. **AP1** is mainly expressed in sepals and petals.
3. **AP3/PI** (APETALA3 and PISTILLATA) control petal and stamen development.
4. **AG** (AGAMOUS) is involved in specifying the reproductive organs, stamens, and carpels.
5. The ABC model explains how combinations of genes specify floral organ identity. AP2 is unique among the floral homeotic genes because of its expression in all four whorls.
6. The ABC model defines the roles of homeotic genes in floral organ specification.
7. AP1, AP3/PI, and AG are expressed in specific whorls, unlike AP2.

Additional Knowledge:

- **AP1:** This gene specifies sepal and petal identity and is active early in floral development. It is not expressed in the reproductive whorls.
- **AP2 (Correct Answer):** AP2 is a member of the AP2/EREBP transcription factor family. It regulates floral organ development across all whorls, including sepals, petals, stamens, and carpels. Unlike AP1, AP3/PI, and AG, it is broadly transcribed.
- **AP3/PI:** These genes are expressed in petals and stamens. They work as part of the B-function genes in the ABC model of floral organ identity.
- **AG:** AGAMOUS is a C-function gene expressed only in the inner two whorls, where it specifies stamen and carpel identity.