# CUET PG 2026 Zoology Question Paper with Solutions Memory Based

| Time Allowed :1 Hours 30 minutes | Maximum Marks :300 | Total Questions :75 |
|---|---|---|

**General Instructions**

1. The exam lasts 90 minutes (1 hour 30 minutes).
2. There are 75 Multiple Choice Questions (MCQs) to be answered.
3. +4 marks for every correct answer. -1 mark (negative marking) for every incorrect answer. 0 marks for unanswered or un-attempted questions.
4. For any discrepancy in questions, the English version is considered final (except for language-specific papers).
5. Click one of the four options to choose an answer.
6. You must click "Save & Next" to confirm your response. Only saved answers are considered for evaluation.
7. Use "Mark for Review & Next" to flag a question for later. You can unselect or change your answer using the "Clear Response" button.
8. All calculations must be done on the Rough Sheets provided at the centre. These must be returned to the invigilator after the exam.

**1. Match the cells in Column I with their primary function in Column II.**

| Column I | Column II |
|---|---|
| A. Plasma cells | 1. Cytotoxic killing |
| B. $CD8^+$ T cells | 2. Antibody secretion |
| C. Dendritic cells | 3. Antigen presentation |
| D. Mast cells | 4. Histamine release |

(A) A-2, B-1, C-3, D-4
(B) A-3, B-2, C-1, D-4
(C) A-2, B-3, C-1, D-4
(D) A-4, B-1, C-3, D-2

**Correct Answer:** (A) A-2, B-1, C-3, D-4

**Solution:**
**Step 1: Understanding the Concept:**
This question tests your knowledge of the primary functions of various cells of the immune system.
**Step 2: Detailed Explanation:**
Let's evaluate each cell type carefully.
- **Plasma cells (A):** These are terminally differentiated B lymphocytes that act as biological factories to produce and secrete large volumes of antibodies.

Thus, A matches with 2 (Antibody secretion).
- **$CD8^+$ T cells (B):** Also known as cytotoxic T lymphocytes (CTLs), their main function is to recognize and directly kill infected cells or tumor cells.
Thus, B matches with 1 (Cytotoxic killing).
- **Dendritic cells (C):** These are professional antigen-presenting cells (APCs) that capture, process, and present antigens to T cells to initiate adaptive immune responses.
Thus, C matches with 3 (Antigen presentation).
- **Mast cells (D):** These cells reside in tissues and contain granules rich in histamine and heparin.
Upon activation (e.g., during allergic reactions), they degranulate and release histamine.
Thus, D matches with 4 (Histamine release).
**Step 3: Final Answer:**
Matching all these gives the sequence: A-2, B-1, C-3, D-4.
This perfectly corresponds to option (A).

Quick Tip

Create a quick reference table for immune cells and their defining functions or markers. Associating "Plasma" with "Antibodies" and "CD8" with "Cytotoxic" will help you quickly solve matching questions.

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**2. Arrange the following events of complement classical pathway in correct order:**
A. Formation of membrane attack complex
B. Binding of C1 to antibody-antigen complex
C. Cleavage of C3
D. Formation of C5 convertase

(A) B → C → D → A
(B) C → B → D → A
(C) B → D → C → A
(D) D → B → C → A

**Correct Answer:** (A) B → C → D → A

**Solution:**
**Step 1: Understanding the Concept:**
The classical complement pathway is an immune mechanism triggered typically by the binding of antibodies to antigens, leading to a cascade of proteolytic cleavage events that ultimately destroy the target cell.
**Step 2: Detailed Explanation:**
The sequential steps of the classical complement pathway occur in a highly regulated order.
1. **Initiation:** The pathway begins when the C1 complex binds to the Fc portion of antibodies (IgM or IgG) that are bound to an antigen.
This is event **B** (Binding of C1 to antibody-antigen complex).
2. **C3 Convertase Formation & Cleavage of C3:** C1 activation leads to the cleavage of

C4 and C2 to form the C3 convertase (C4b2a).
The C3 convertase then cleaves multiple C3 molecules into C3a and C3b.
This corresponds to event **C** (Cleavage of C3).
3. **C5 Convertase Formation:** Some of the generated C3b binds to the existing C3 convertase to form the C5 convertase (C4b2a3b).
This is event **D** (Formation of C5 convertase).
4. **Terminal Pathway (MAC Formation):** The C5 convertase cleaves C5, initiating the recruitment of C6, C7, C8, and C9 to form the membrane attack complex (MAC).
This creates a pore in the target cell membrane, corresponding to event **A** (Formation of membrane attack complex).
**Step 3: Final Answer:**
Therefore, the correct chronological sequence is B → C → D → A.
This matches option (A).

Quick Tip

Remember the general flow of complement pathways: Initiation → C3 convertase → C5 convertase → MAC. The defining starting point for the *classical* pathway is always antibody binding (C1 complex activation).

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**3. Which immunoglobulin is primarily responsible for mucosal immunity?**

(A) IgM
(B) IgG
(C) IgA
(D) IgD

**Correct Answer:** (C) IgA

**Solution:**
**Step 1: Understanding the Concept:**
Immunoglobulins (antibodies) are classified into distinct isotypes (IgM, IgG, IgA, IgE, IgD), each serving unique roles and predominating in different locations within the body.
**Step 2: Detailed Explanation:**
Let's review the primary function of each given isotype.
- **IgA:** Secretory IgA is the most abundant immunoglobulin in mucous secretions such as tears, saliva, colostrum, and secretions of the respiratory and intestinal tracts.
It plays a critical role in mucosal immunity by neutralizing pathogens before they can cross the mucosal barrier.
- **IgM:** This is the first antibody produced in a primary immune response and is mainly found in the blood.
- **IgG:** This is the most abundant antibody in serum, responsible for long-term systemic immunity, and it can cross the placenta.
- **IgD:** This primarily functions as an antigen receptor on the surface of naive B cells.
**Step 3: Final Answer:**

Because IgA is the predominant antibody found in mucosal secretions, it is the correct answer. Therefore, the correct option is (C).

Quick Tip

Use mnemonics for primary antibody functions: **A** for **A**way/secretions (mucosal), **G** for **G**eneral/most abundant (serum), **M** for **M**acro/first responder, **E** for **E**osinophils/All**e**rgy.

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**4. Match the hypersensitivity type with its example.**

| Column I | Column II |
|---|---|
| A. Type I | 1. Myasthenia gravis |
| B. Type II | 2. Serum sickness |
| C. Type III | 3. Allergy |
| D. Type IV | 4. Contact dermatitis |

(A) A-3, B-1, C-2, D-4
(B) A-1, B-3, C-4, D-2
(C) A-3, B-2, C-1, D-4
(D) A-4, B-1, C-2, D-3

**Correct Answer:** (A) A-3, B-1, C-2, D-4

**Solution:**
**Step 1: Understanding the Concept:**
The Gell and Coombs classification system categorizes hypersensitivity reactions into four distinct types based on their underlying immune mechanisms.
**Step 2: Detailed Explanation:**
Let's correctly pair each type with its classic clinical example.
- **Type I Hypersensitivity (A):** This is an immediate, IgE-mediated reaction against an allergen.
Common examples include typical **allergies** (like hay fever or asthma).
Thus, A matches with 3.
- **Type II Hypersensitivity (B):** This is an antibody-mediated (IgG or IgM) cytotoxic reaction targeting cell surface antigens.
In **Myasthenia gravis**, antibodies inappropriately attack acetylcholine receptors at the neuromuscular junction.
Thus, B matches with 1.
- **Type III Hypersensitivity (C):** This is an immune complex-mediated reaction where antigen-antibody complexes deposit in tissues, causing inflammation.
**Serum sickness** is a classic example of a systemic Type III reaction.
Thus, C matches with 2.
- **Type IV Hypersensitivity (D):** This is a cell-mediated (delayed-type) reaction involving

T cells and macrophages.
**Contact dermatitis** (e.g., from poison ivy exposure) is a classic example that takes 48-72 hours to develop.
Thus, D matches with 4.
**Step 3: Final Answer:**
Matching these gives the sequence: A-3, B-1, C-2, D-4.
This corresponds perfectly to option (A).

Quick Tip

Remember the acronym **ACID** for hypersensitivity types: **A**llergic (Type I), **C**ytotoxic (Type II), **I**mmune complex (Type III), **D**elayed (Type IV).

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**5. Which molecule stabilizes the interaction between T cell receptor and MHC class II?**

(A) CD4
(B) CD8
(C) CD28
(D) CD40

**Correct Answer:** (A) CD4

**Solution:**
**Step 1: Understanding the Concept:**
T cells recognize antigens presented by Major Histocompatibility Complex (MHC) molecules using their T cell receptor (TCR).
To ensure specific and highly stable binding, T cells utilize distinct co-receptors that bind to invariant regions of the MHC molecules.
**Step 2: Detailed Explanation:**
Let's examine the role of each given molecule.
- **CD4:** This is a co-receptor expressed primarily on helper T cells.
It specifically binds to the invariant $\beta_2$ domain of **MHC class II** molecules.
This interaction physically stabilizes the TCR-MHC II complex and enhances the intracellular signaling cascade.
- **CD8:** This is a co-receptor expressed on cytotoxic T cells that binds to **MHC class I** molecules.
- **CD28:** This is a costimulatory receptor on T cells that binds to B7 molecules on antigen-presenting cells to provide Signal 2.
- **CD40:** This molecule is found on antigen-presenting cells and interacts with CD40L on T cells to facilitate mutual activation.
**Step 3: Final Answer:**
Because CD4 specifically binds and stabilizes MHC class II interactions, it is the correct answer.
Therefore, the correct option is (A).

Quick Tip

Use the "Rule of 8" to remember TCR-MHC associations: CD**4** × MHC **II** = 8, and CD**8** × MHC **I** = 8.

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**6. Match the enzyme with its function.**

| **Column I** | **Column II** |
|---|---|
| A. DNA ligase | 1. Removes RNA primers |
| B. DNA polymerase I | 2. Joins DNA fragments |
| C. Helicase | 3. Unwinds DNA |
| D. Topoisomerase | 4. Relieves supercoiling |

(A) A-2, B-1, C-3, D-4
(B) A-3, B-2, C-4, D-1
(C) A-2, B-3, C-1, D-4
(D) A-4, B-1, C-2, D-3

**Correct Answer:** (A) A-2, B-1, C-3, D-4

**Solution:**
**Step 1: Understanding the Concept:**
DNA replication is a complex, coordinated process requiring a suite of highly specific enzymes. Each enzyme performs a distinct mechanical or chemical task to ensure the accurate copying of the genome.
**Step 2: Detailed Explanation:**
Let's map each enzyme to its specific functional role during replication.
- **DNA ligase (A):** This enzyme catalyzes the formation of phosphodiester bonds between adjacent nucleotides.
Its primary role is to **join DNA fragments** together, such as sealing the nicks between Okazaki fragments.
Thus, A matches with 2.
- **DNA polymerase I (B):** In prokaryotes, this enzyme possesses a unique 5' to 3' exonuclease activity.
It uses this activity to **remove RNA primers** from the lagging strand and then fills the gaps with DNA.
Thus, B matches with 1.
- **Helicase (C):** This is a motor protein that breaks the hydrogen bonds between complementary base pairs.
Its action serves to **unwind the double-stranded DNA** helix ahead of the replication fork.
Thus, C matches with 3.
- **Topoisomerase (D):** As helicase unwinds the DNA, it creates severe torsional strain ahead of the fork.
Topoisomerase cuts, rotates, and reseals the DNA backbone to **relieve this supercoiling**.
Thus, D matches with 4.
**Step 3: Final Answer:**
Matching these gives the sequence: A-2, B-1, C-3, D-4.

This matches option (A).

Quick Tip

Think of the replication fork as a zipper: Helicase is the slider unzipping it, Topoisomerase untangles the threads ahead, Pol I removes the starting marks, and Ligase glues the final pieces together.

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**7. Arrange the steps of translation initiation in prokaryotes:**
A. Binding of 50S ribosomal subunit
B. Binding of initiator tRNA
C. Binding of mRNA to 30S subunit
D. Formation of complete 70S initiation complex

(A) C $\rightarrow$ B $\rightarrow$ A $\rightarrow$ D
(B) B $\rightarrow$ C $\rightarrow$ A $\rightarrow$ D
(C) C $\rightarrow$ A $\rightarrow$ B $\rightarrow$ D
(D) B $\rightarrow$ A $\rightarrow$ C $\rightarrow$ D

**Correct Answer:** (A) C $\rightarrow$ B $\rightarrow$ A $\rightarrow$ D

**Solution:**
**Step 1: Understanding the Concept:**
Translation initiation in prokaryotes involves the sequential assembly of the ribosomal subunits, mRNA, and initiator tRNA.
This highly ordered process is orchestrated by specific initiation factors (IFs).
**Step 2: Detailed Explanation:**
The sequential events unfold in the following order:
1. **Binding of mRNA to 30S subunit (C):** The small ribosomal subunit (30S), complexed with initiation factors, first binds to the mRNA.
This is facilitated by base-pairing between the Shine-Dalgarno sequence on the mRNA and the 16S rRNA.
2. **Binding of initiator tRNA (B):** Next, the initiator tRNA carrying formylmethionine (fMet-tRNA) binds to the start codon at the P site.
This completes the formation of the 30S initiation complex.
3. **Binding of 50S ribosomal subunit (A):** Once the 30S complex is stable, the large ribosomal subunit (50S) joins the assembly.
This step is accompanied by the hydrolysis of GTP and the release of initiation factors.
4. **Formation of complete 70S initiation complex (D):** The successful joining of the 50S subunit marks the end of the initiation phase.
This results in a fully assembled, translationally active 70S ribosome ready for the elongation phase.
**Step 3: Final Answer:**
The correct temporal sequence is C $\rightarrow$ B $\rightarrow$ A, which culminates in D.

Therefore, the correct option is (A) C → B → A → D.

Quick Tip

Always remember the assembly order: Small subunit first (with mRNA), then the starter tRNA, and finally the large subunit acts as the "lid" to close the complex.

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**8. The Shine–Dalgarno sequence is located in:**

(A) Promoter region
(B) 52 untranslated region of mRNA
(C) Coding sequence
(D) Terminator region

**Correct Answer:** (B) 52 untranslated region of mRNA

**Solution:**
**Step 1: Understanding the Concept:**
The Shine-Dalgarno (SD) sequence is a specific ribosomal binding site found in bacterial and archaeal messenger RNA (mRNA).
It plays a crucial role in recruiting the ribosome to the mRNA to correctly initiate protein synthesis.
**Step 2: Detailed Explanation:**
Let's analyze the correct location for this sequence.
- The SD sequence is typically located a short distance (about 8 bases) upstream of the translation start codon (usually AUG).
- By molecular biology definition, the region of an mRNA molecule that is upstream of the start codon and is not translated into protein is called the **5' untranslated region (5' UTR)**.
- It functions by base-pairing with a complementary anti-Shine-Dalgarno sequence located near the 3' end of the 16S rRNA within the 30S small ribosomal subunit.
- *Note regarding the options:* The text "52 untranslated region" in the image is a typographical error for "5' untranslated region".
- Other options like the Promoter (which is on DNA, not mRNA) and Coding sequence (which is downstream of the start codon) are incorrect.
**Step 3: Final Answer:**
The sequence is located in the 5' untranslated region of the mRNA transcript.
Therefore, option (B) is the correct answer.

Quick Tip

Associate "Shine-Dalgarno" with "Prokaryotic Ribosome Binding" and remember it must be on the mRNA *before* the start codon, hence the 5' UTR. The eukaryotic equivalent is the Kozak consensus sequence.

**9. Match the RNA type with its function.**

| Column I | Column II |
|---|---|
| A. snRNA | 1. RNA splicing |
| B. miRNA | 2. Gene silencing |
| C. rRNA | 3. Ribosome structure |
| D. tRNA | 4. Amino acid transport |

(A) A-1, B-2, C-3, D-4
(B) A-2, B-3, C-4, D-1
(C) A-3, B-1, C-2, D-4
(D) A-1, B-3, C-2, D-4

**Correct Answer:** (A) A-1, B-2, C-3, D-4

**Solution:**
**Step 1: Understanding the Concept:**
Different classes of RNA molecules perform diverse and essential functions within the cell. They act variously as messengers, structural components, adapters, and regulatory molecules.
**Step 2: Detailed Explanation:**
Let's match each RNA type to its primary cellular function.
- **snRNA (Small nuclear RNA) (A):** These molecules are key components of the spliceosome.
They are responsible for removing introns from pre-mRNA during **RNA splicing**.
Thus, A matches with 1.
- **miRNA (MicroRNA) (B):** These are small non-coding RNAs that play a crucial role in post-transcriptional regulation.
They bind to complementary sequences on target mRNAs, leading to **gene silencing** via translational repression or mRNA degradation.
Thus, B matches with 2.
- **rRNA (Ribosomal RNA) (C):** These RNAs associate with proteins to form the bulk of the **ribosome structure**.
They also carry out the catalytic activity (peptidyl transferase) of protein synthesis.
Thus, C matches with 3.
- **tRNA (Transfer RNA) (D):** These molecules function as adapters during translation.
They perform **amino acid transport** by carrying specific amino acids to the ribosome to match the mRNA codon.
Thus, D matches with 4.
**Step 3: Final Answer:**
Matching these pairs gives the sequence: A-1, B-2, C-3, D-4.
This corresponds to option (A).

Quick Tip

Prefixes often give away RNA function: 'sn' = small nuclear (splicing occurs in the nucleus), 'mi' = micro (small regulators/silencers), 'r' = ribosomal, 't' = transfer (transport).

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**10. Which DNA repair mechanism corrects UV-induced thymine dimers?**

(A) Base excision repair
(B) Nucleotide excision repair
(C) Mismatch repair
(D) Photoreactivation only

**Correct Answer:** (B) Nucleotide excision repair

**Solution:**
**Step 1: Understanding the Concept:**
Ultraviolet (UV) radiation causes adjacent pyrimidine bases (often thymines) on a DNA strand to covalently bond, forming bulky lesions known as thymine dimers.
Cells utilize specific repair pathways to identify and remove these structural distortions.
**Step 2: Detailed Explanation:**
Let's evaluate the given repair mechanisms for their relevance to UV damage.
- **Nucleotide Excision Repair (NER):** This is a highly versatile repair pathway specifically designed to recognize bulky, helix-distorting DNA lesions, such as those caused by UV light.
The mechanism involves excising a short, single-stranded patch of DNA containing the dimer and synthesizing a fresh replacement strand.
In placental mammals (including humans), NER is the primary and essential mechanism for repairing thymine dimers.
- **Photoreactivation:** This is another mechanism that uses the enzyme photolyase and visible light to directly break the dimer bonds.
However, the option specifies "only", making it incorrect because NER is widely applicable and humans actually lack the photoreactivation pathway entirely.
- **Base Excision Repair (BER):** This pathway typically repairs small, non-helix-distorting base lesions (like oxidized or deaminated bases), not bulky dimers.
- **Mismatch Repair (MMR):** This pathway corrects errors introduced during DNA replication, such as mispaired bases, not environmental UV-induced damage.
**Step 3: Final Answer:**
Nucleotide excision repair is the correct general and human-relevant mechanism for repairing thymine dimers.
Therefore, option (B) is the correct answer.

Quick Tip

Associate **N**ucleotide **E**xcision **R**epair with bulky, "large scale" damage that distorts the double helix (like UV dimers). Associate **B**ase **E**xcision **R**epair with small, specific base alterations.

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**11. Match the technique with its application.**

| **Column I** | **Column II** |
|---|---|
| A. PCR | 1. DNA amplification |
| B. Western blot | 2. Protein detection |
| C. Northern blot | 3. RNA detection |
| D. Southern blot | 4. DNA detection |

(A) A-1, B-2, C-3, D-4
(B) A-4, B-3, C-2, D-1
(C) A-1, B-3, C-2, D-4
(D) A-2, B-1, C-4, D-3

**Correct Answer:** (A) A-1, B-2, C-3, D-4

**Solution:**
**Step 1: Understanding the Concept:**
These are fundamental laboratory techniques used extensively in molecular biology and biotechnology.
Each technique is uniquely designed to identify, analyze, or quantify specific types of biomolecules.
**Step 2: Detailed Explanation:**
Let's connect each technique to its standard laboratory application.
- **PCR (Polymerase Chain Reaction) (A):** This is an in vitro technique used to rapidly synthesize millions of copies of a specific DNA segment.
Its primary application is **DNA amplification**.
Thus, A matches with 1.
- **Western blot (B):** This is an analytical technique used to detect specific **proteins** in a sample of tissue homogenate or extract.
It relies on the use of target-specific antibodies.
Thus, B matches with 2.
- **Northern blot (C):** This technique is used to detect specific **RNA** sequences in a sample.
It is commonly used to study gene expression by measuring mRNA levels.
Thus, C matches with 3.
- **Southern blot (D):** This is the original blotting method developed by Edwin Southern.
It is used to detect specific **DNA** sequences in a complex DNA sample.
Thus, D matches with 4.
**Step 3: Final Answer:**
Matching these gives the sequence: A-1, B-2, C-3, D-4.
This perfectly aligns with option (A).

Quick Tip

Use the mnemonic **SNOW DROP** to remember blotting targets:
**S**outhern = **D**NA
**N**orthern = **R**NA
**O** = **O** (placeholder)
**W**estern = **P**rotein

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**12. Arrange steps of PCR:**
A. Extension
B. Denaturation
C. Annealing

(A) B → C → A
(B) C → B → A
(C) B → A → C
(D) A → C → B

**Correct Answer:** (A) B → C → A

**Solution:**
**Step 1: Understanding the Concept:**
The Polymerase Chain Reaction (PCR) is an in vitro method used to exponentially amplify a specific DNA sequence.
It relies on thermal cycling, which consists of repeated cycles of heating and cooling to facilitate different temperature-dependent enzymatic reactions.
**Step 2: Detailed Explanation:**
A single cycle of PCR always proceeds through three main temperature steps in a specific order:
1. **Denaturation (B):** The reaction mixture is heated to a high temperature (usually 94-98°C).
This high heat breaks the hydrogen bonds between the two strands of the template DNA, yielding single-stranded DNA required for the next step.
2. **Annealing (C):** The temperature is then lowered (usually to 50-65°C).
This allows short, single-stranded DNA primers to naturally bind (anneal) to their complementary sequences on the single-stranded template DNA.
3. **Extension/Elongation (A):** Finally, the temperature is raised to the optimal working temperature of the thermostable DNA polymerase (typically 72°C for Taq polymerase).
The enzyme binds to the primer-template junction and synthesizes a new DNA strand complementary to the template.
**Step 3: Final Answer:**
The correct chronological sequence is Denaturation → Annealing → Extension.
This translates to the sequence B → C → A, which corresponds to option (A).

Quick Tip

Think of the process logically: you must first separate the strands (Denature), then attach the starting blocks (Anneal primers), and finally build the rest of the wall (Extend).

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**13. Which dye is most commonly used for DNA visualization in agarose gel?**

(A) Ethidium bromide
(B) Crystal violet
(C) Coomassie blue
(D) Safranin

**Correct Answer:** (A) Ethidium bromide

**Solution:**
**Step 1: Understanding the Concept:**
After DNA fragments are separated by size using agarose gel electrophoresis, the DNA must be stained to be visible.
Since DNA is naturally colorless, specific fluorescent dyes are used to label the molecules for visualization under special lighting.
**Step 2: Detailed Explanation:**
Let's review the applications of the given dyes.
- **Ethidium bromide (EtBr):** This is the classic and most commonly used fluorescent dye for visualizing nucleic acids in agarose gels.
It acts as an intercalating agent, meaning its flat molecular structure allows it to slip directly between the stacked base pairs of the DNA double helix.
When exposed to ultraviolet (UV) light, the intercalated EtBr fluoresces with a bright orange-red color, clearly revealing the location of the DNA bands.
- **Crystal violet & Safranin:** These are chemical dyes primarily used in microbiology for the Gram stain technique to differentiate bacterial cell walls, not for routine DNA gel staining.
- **Coomassie blue:** This is a highly common stain used exclusively for visualizing proteins in SDS-PAGE gels, not for DNA.
**Step 3: Final Answer:**
Ethidium bromide is the correct dye for DNA visualization in this context.
Therefore, option (A) is the correct answer.

Quick Tip

Always associate Ethidium Bromide (EtBr) with DNA/RNA agarose gels and UV light visualization. Also, remember that it requires careful handling because its intercalating nature makes it a potential mutagen.

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**14. Match sequencing methods with key feature.**

| Column I | Column II |
|---|---|
| A. Sanger sequencing | 1. Chain termination |
| B. Illumina sequencing | 2. Sequencing by synthesis |
| C. Nanopore sequencing | 3. Electrical signal detection |
| D. Pyrosequencing | 4. Light detection |

(A) A-1, B-2, C-3, D-4
(B) A-2, B-1, C-4, D-3
(C) A-3, B-4, C-1, D-2
(D) A-4, B-3, C-2, D-1

**Correct Answer:** (A) A-1, B-2, C-3, D-4

**Solution:**
**Step 1: Understanding the Concept:**
DNA sequencing technologies have evolved significantly through multiple generations over the decades.
Each distinct platform relies on a unique biochemical or physical principle to accurately read the sequence of nucleotides.
**Step 2: Detailed Explanation:**
Let's pair each sequencing method with its defining technical feature.
- **Sanger sequencing (A):** Also known as the dideoxy method, this first-generation technique relies on the incorporation of dideoxynucleotides (ddNTPs) during DNA replication.
The absence of a 3'-OH group on the ddNTPs causes immediate **chain termination**.
Thus, A matches with 1.
- **Illumina sequencing (B):** This is the currently dominant next-generation sequencing (NGS) platform.
It is characterized as **Sequencing by synthesis** (SBS), where fluorescently labeled, reversibly terminating nucleotides are incorporated and imaged one by one.
Thus, B matches with 2.
- **Nanopore sequencing (C):** This is a third-generation, long-read sequencing method where single-stranded DNA is drawn through a tiny protein pore.
Changes in the **electrical signal** (ionic current) as different specific bases pass through the pore are measured and translated into a sequence.
Thus, C matches with 3.
- **Pyrosequencing (D):** This is an early NGS method that sequences by synthesizing the complementary strand.
It relies on the detection of pyrophosphate release upon nucleotide incorporation, which triggers an enzymatic cascade resulting in a flash of luminescence (**light detection**).
Thus, D matches with 4.
**Step 3: Final Answer:**
Matching these gives the precise sequence: A-1, B-2, C-3, D-4.
This corresponds directly to option (A).

Quick Tip

Key associations for sequencing tech: Sanger = ddNTPs/termination. Illumina = Reversible terminators/fluorescence SBS. Nanopore = Current/electrical changes. Pyrosequencing = Pyrophosphate/Luciferase light flash.

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**15. Which technique separates proteins based on isoelectric point?**

(A) SDS-PAGE
(B) Isoelectric focusing
(C) Gel filtration
(D) Affinity chromatography

**Correct Answer:** (B) Isoelectric focusing

**Solution:**
**Step 1: Understanding the Concept:**
Proteins are complex macromolecules that can be separated using various biochemical techniques.
These techniques exploit distinct physical and chemical properties of the proteins, such as their molecular size, net charge, or specific binding affinities.
**Step 2: Detailed Explanation:**
Let's analyze the primary separation principle of each listed technique.
- **Isoelectric focusing (IEF):** This is an electrophoretic technique where proteins are driven through a gel containing a continuous pH gradient under an electric field.
A protein will migrate through the gel until it reaches the specific pH region that is exactly equal to its isoelectric point (pI).
At this precise pH, the protein's net charge becomes zero, and it stops migrating, meaning it separates purely based on its pI.
- **SDS-PAGE:** This technique uses Sodium Dodecyl Sulfate to denature proteins and coat them with a uniform negative charge.
Consequently, the proteins separate primarily based on their molecular weight (size) as they migrate toward the positive electrode.
- **Gel filtration (Size-exclusion chromatography):** This column chromatography method separates molecules based purely on their physical size and shape as they pass through porous beads.
- **Affinity chromatography:** This method separates proteins based on highly specific biological interactions, such as an enzyme binding to its substrate or an antibody binding to its antigen.
**Step 3: Final Answer:**
Isoelectric focusing is the only technique listed that isolates proteins based on their isoelectric point.
Therefore, option (B) is the correct answer.

Quick Tip

The name of the technique often reveals its exact mechanism. "Isoelectric" directly points to the "isoelectric point" (pI). Remember that 2D gel electrophoresis utilizes IEF as the first dimension (separation by pI) and SDS-PAGE as the second dimension (separation by size).

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