CUET PG 2025 Life Science Question Paper with Solutions

Time Allowed :1 Hour 30 Mins	**Maximum Marks :**300	**Total Questions :**75

General Instructions

Read the following instructions very carefully and strictly follow them:

1. The examination duration is 90 minutes. Manage your time effectively to attempt all questions within this period.
2. The total marks for this examination are 300. Aim to maximize your score by strategically answering each question.
3. There are 75 mandatory questions to be attempted in the Atmospheric Science paper. Ensure that all questions are answered.
4. Questions may appear in a shuffled order. Do not assume a fixed sequence and focus on each question as you proceed.
5. The marking of answers will be displayed as you answer. Use this feature to monitor your performance and adjust your strategy as needed.
6. You may mark questions for review and edit your answers later. Make sure to allocate time for reviewing marked questions before final submission.
7. Be aware of the detailed section and sub-section guidelines provided in the exam. Understanding these will aid in effectively navigating the exam.

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1. To observe the specific part of a tissue section under compound microscope, the contrast can be increased by:

(A) Staining
(B) Changing magnification of the microscope
(C) Changing microscope resolution
(D) Use of fluorescence dyes

Correct Answer: (A) Staining

Solution:

Step 1: The Core Problem of Transparency

The first step explains **why** contrast is needed. Most living cells and thin tissue slices are composed primarily of water and are colorless. When light from a standard microscope passes through them, it is not significantly absorbed or bent differently than when it passes through

the watery background. This results in a faint, almost invisible image. **Contrast** is simply the difference in brightness or color that makes an object stand out from its surroundings.

Step 2: Evaluating the Methods

This step analyzes different ways to create contrast and determines their effectiveness in this context.

- **Staining:** This is the most effective and direct solution. Dyes are colored chemicals that have an affinity for specific biological molecules. For example, a positively charged dye like hematoxylin is attracted to negatively charged DNA in the nucleus, staining the nucleus purple. A negatively charged dye like eosin is attracted to positively charged proteins in the cytoplasm, staining it pink. This process of adding color creates a high-contrast image where different parts of the cell are clearly distinguishable.
- **Adjusting Magnification:** This is a common misconception. Making an image bigger (increasing magnification) does not make it clearer or more visible if there is no underlying contrast. It's like zooming in on a blurry, foggy photograph—you just get a bigger blurry, foggy photograph. This is called **empty magnification**.
- **Modifying Resolution:** Resolution is the ability to see fine details. While crucial for a high-quality image, it is distinct from contrast. You can have a microscope with excellent resolution, but if the specimen is transparent (low contrast), you still won't see anything. Resolution helps you distinguish two small things that are close together, but only if you can see them in the first place.
- **Fluorescence Dyes:** This is a powerful but specialized form of staining. It requires a fluorescence microscope that uses specific wavelengths of light (like UV) to excite the dye and filters to view only the light emitted by the dye. While it produces extremely high contrast, it's not a technique used with a "standard compound (bright-field) microscope."

Step 3: Conclusion

The final answer concludes that for a standard laboratory setting using a compound microscope to view tissue, **staining** is the primary method used to solve the problem of low natural contrast.

Quick Tip

For microscopy questions, remember the key distinctions: **Magnification** makes things bigger, **Resolution** makes things clearer, and **Contrast** makes things stand out from the background. Staining is the classic way to improve contrast.

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2. Which of the following will be the part of the pellet, when tissue cells are homogenized and centrifuged at 1000g for 10 min.?

(A) Microsomes
(B) Mitochondria
(C) Nuclei

(D) Ribosomes

Correct Answer: (C) Nuclei

Solution:

Step 1: The Principle of Separation

The technique works based on a simple principle: when you spin a mixture of particles, the biggest and heaviest ones will settle at the bottom first. In a centrifuge, this "settling" is massively accelerated by high-speed spinning, which generates strong centrifugal forces. The settled material is called the **pellet**, and the remaining liquid is the **supernatant**.

Step 2: The Step-by-Step Process

Differential centrifugation is a process of elimination done in sequential steps, from low speed to high speed.

1. **Low Speed (pellets Nuclei):** The first spin is relatively slow. The largest and densest components in the cell are the nuclei. This initial spin is just fast enough to force the nuclei to the bottom to form the first pellet, leaving smaller organelles suspended in the supernatant.
2. **Medium Speed (pellets Mitochondria, etc.):** The supernatant from the first step is poured into a new tube and spun much faster. The next-heaviest organelles, like mitochondria and lysosomes, are now forced into a pellet.
3. **High Speed (pellets Microsomes):** The process is repeated. The supernatant from the medium-speed spin is spun even faster, pelleting smaller pieces like fragments of the endoplasmic reticulum (called microsomes).
4. **Ultracentrifugation (pellets Ribosomes):** Finally, the remaining supernatant is spun at extremely high speeds (ultracentrifugation) to pellet the very smallest particles, such as ribosomes.

Step 3: Final Answer

The question asks what is pelleted by a low-speed spin (1000 $\times$ g for 10 minutes). Based on the established protocol, this specific step is designed to isolate the largest organelle, the **nucleus**.

Quick Tip

Remember the sedimentation order for differential centrifugation by size: **N**uclei ¿ **M**itochondria ¿ **M**icrosomes ¿ **R**ibosomes. A low speed like 1000g will only bring down the largest component, the nuclei.

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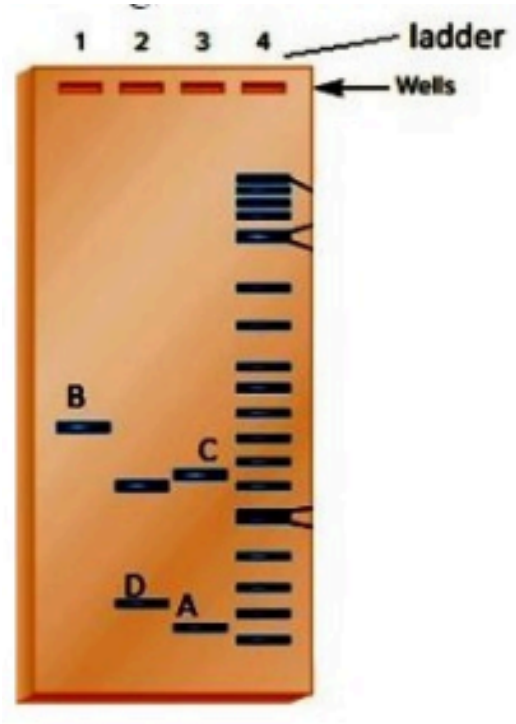
3. Arrange the following DNA fragments A, B, C, D separated after Gel Electrophoresis in increasing order of number of their base pairs



(A) A, B, C, D
(B) A, D, C, B
(C) B, C, D, A
(D) C, B, D, A

Correct Answer: (B) A, D, C, B

Solution:

Step 1: The Fundamentals

The technique relies on two key properties of DNA:

1. **Charge:** DNA has a strong, uniform negative charge because of the phosphate groups in its backbone. This means that when placed in an electric field, it will always move towards the positive pole.
2. **Size:** DNA fragments come in different lengths (measured in base pairs).

The agarose gel is a porous, jelly-like substance that acts as a molecular sieve or obstacle course for the moving DNA.

Step 2: The Migration Process

Imagine a race where all runners are pulled forward with the same force. The race course, however, is a dense forest. The smallest, most agile runners can easily weave through the trees and will travel the farthest in a given amount of time. The largest, bulkiest runners will get tangled frequently and will travel the shortest distance. In this analogy, the DNA fragments

are the runners and the gel matrix is the forest. **Smaller DNA fragments move faster and farther through the gel than larger fragments.**

Step 3: Interpreting the Results

In the given problem:

- Fragment A traveled the farthest, so it must be the **smallest**.
- Fragment B traveled the shortest distance, so it must be the **largest**.
- Fragments D and C are in between, with D having traveled farther than C, meaning D is smaller than C.

The question asks for the order of *increasing* size, which means starting from the smallest and going to the largest.

Step 4: The Final Order

Based on the distance traveled, the order from smallest to largest is **A, D, C, B**.

> Quick Tip
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> In gel electrophoresis, remember the simple rule: "Small runs fast." The fragments at the bottom of the gel are the smallest, and those at the top are the largest. Always check if the question asks for increasing or decreasing order of size.

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4. Which of the following is not true about gel electrophoresis?

(A) Gel electrophoresis can be used to separate nucleic acids or proteins.
(B) Agarose and polyacrylamide are routinely used in gel electrophoresis.
(C) In gel electrophoresis of DNA, the digested DNA fragments move toward the negative electrode of the tank.
(D) In gel electrophoresis of DNA, ethidium bromide, a DNA binding dye, is used to locate the DNA fragments of interest under UV light.

Correct Answer: (C) In gel electrophoresis of DNA, the digested DNA fragments move toward the negative electrode of the tank.

Solution:

Step 1: Foundational Principle

The core idea is that charged molecules move in an electric field. The direction depends on the charge (negative moves to positive, positive moves to negative).

Step 2: Evaluating Each Statement

- **(A) True:** Gel electrophoresis is indeed used for both nucleic acids (DNA/RNA) and proteins. For proteins, the technique is usually modified (SDS-PAGE) to make the proteins negatively charged so they also separate by size, just like DNA.
- **(B) True:** The "mesh size" of the gel is important. Agarose gels have a large mesh size, good for separating large DNA molecules. Polyacrylamide gels (PAGE) have a much finer mesh, providing higher resolution for separating small DNA fragments or proteins.
- **(C) False:** This statement contradicts the fundamental principle. DNA is an acid (Deoxyribo*nucleic Acid*) and is rich in negatively charged phosphate groups. In an electric field, negative charges are repelled by the negative electrode (cathode) and attracted to the **positive electrode (anode)**. Therefore, DNA moves towards the anode, not the cathode.
- **(D) True:** After running the gel, the DNA is invisible. Ethidium bromide is a fluorescent dye that binds to DNA. When you shine UV light on the gel, the dye glows, revealing the location of the DNA bands.

Step 3: Conclusion

Statement **(C)** makes a factually incorrect claim about the direction of DNA movement and is therefore the false statement.

Quick Tip

Remember that DNA is a nucleic **acid**. Acids donate protons, leaving a negative charge. In electrophoresis, opposites attract, so negative DNA migrates to the positive pole (anode).

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5. Which of the following are the types of column chromatography?
A. Paper chromatography
B. Affinity chromatography
C. Size exclusion chromatography
D. Ion-exchange chromatography
Choose the correct answer from the options given below:

(A) A, B and D only
(B) A, B and C only
(C) A, B, C and D
(D) B, C and D only

Correct Answer: (D) B, C and D only

Solution:

Step 1: The Basis for Classification

Chromatography always involves a **stationary phase** (a substance that stays put) and a **mobile phase** (a fluid that moves over or through the stationary phase). A primary way to classify these techniques is by the shape of the stationary phase.

Step 2: The Two Major Classes

- **Column Chromatography:** As the name implies, the stationary material (often resin beads) is packed into a vertical column. The mobile phase (a liquid) flows down through the column, carrying the mixture to be separated with it.
- **Planar Chromatography:** Here, the stationary phase is a flat sheet, such as a piece of paper (paper chromatography) or a glass plate coated with a thin layer of silica (thin-layer chromatography). The mobile phase moves across the flat surface, usually pulled by capillary action.

Step 3: Categorizing the Examples

- **A. Paper Chromatography:** Uses a flat sheet of paper. This is the definition of **planar** chromatography.
- **B, C, and D (Affinity, Size Exclusion, Ion-Exchange):** These are all sophisticated techniques, but they share the same physical setup. In all three, the specialized beads that form the stationary phase are packed into a column. Therefore, they are all types of **column** chromatography.

Step 4: Conclusion

Since three of the options are types of column chromatography, the one that does not belong in that group is paper chromatography, which is a form of planar chromatography.

Quick Tip

To distinguish chromatography types, think about the physical setup. If the stationary phase is inside a tube or column, it's column chromatography. If it's on a flat sheet (like paper or a thin layer on glass), it's planar chromatography.

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6. Tryptophan, tyrosine and phenylalanine, absorb ultraviolet light. Therefore, the protein rich in these amino acids strongly absorbs the light of wavelength _____ due to aromatic side chain of these amino acids.

(A) 90 nm
(B) 420 nm
(C) 550 nm
(D) 280 nm

Correct Answer: (D) 280 nm

Solution:

Step 1: The Principle of Light Absorption

A spectrophotometer measures how much light of a specific color (wavelength) is absorbed by a sample. Molecules absorb light energy at wavelengths that correspond to the energy needed to excite their electrons.

Step 2: The Source of Absorption in Proteins

Most parts of a protein do not absorb light in the UV-Visible range. However, three of the twenty amino acids—**Tryptophan, Tyrosine, and Phenylalanine**—have a special feature: their side chains contain aromatic rings. These ring structures have delocalized π electrons that are very efficient at absorbing UV light.

Step 3: The Specific Wavelength of 280 nm

- Tryptophan and Tyrosine both absorb UV light very strongly, with their peak absorption occurring at or near **280 nanometers (nm)**.
- Phenylalanine absorbs at a lower wavelength ($\sim$260 nm) and less strongly, so its contribution at 280 nm is small.
- Since almost all proteins contain some Tryptophan and Tyrosine, measuring the absorbance of a solution at 280 nm is a quick and convenient way to estimate the total protein concentration. The other wavelengths listed are incorrect because they fall in regions where proteins do not absorb light (e.g., the visible spectrum).

Step 4: Conclusion

The characteristic strong absorption of UV light by proteins is due to the aromatic amino acids and is maximal at a wavelength of **280 nm**.

Quick Tip

Associate aromatic amino acids (Trp, Tyr, Phe) with UV light absorption. The number **280 nm** is a standard wavelength used in biochemistry labs for quick and non-destructive protein quantification (A280).

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7. A scientist wants to separate three protein molecules by ion-exchange chromatography. The pH of the mobile phase of the column is maintained in such a way that the protein molecule (A) has a net charge of -2, protein molecule (B) has a net charge of +2 and protein molecule (C) has a net charge of +1. Which one of the molecule/s will elute first from a cation-exchange resin?

(A) Protein molecule A
(B) Protein molecule B
(C) Protein molecule C

(D) All protein molecules elute simultaneously

Correct Answer: (A) Protein molecule A

Solution:

Step 1: The Principle of Ion Exchange

This technique separates molecules based on their net electrical charge.

- The name refers to the ion that binds to the column. A **cation-exchange** column binds **cations** (positively charged ions).
- For the column to attract and bind positive molecules, the column itself must be made of a **negatively charged** resin. The rule is: opposites attract.

Step 2: Analyzing the Setup

- The column is a **cation-exchange** resin, so the stationary phase is **negative**.
- We have three proteins: A (charge -2), B (charge +2), and C (charge +1).

Step 3: Predicting the Behavior

- **Protein A (-2):** This protein is negatively charged. Since the column resin is also negative, they will repel each other (like trying to push the north poles of two magnets together). Protein A will not stick to the column at all and will wash straight through. It **elutes (emerges) first**.
- **Proteins B (+2) and C (+1):** These proteins are both positively charged and will be attracted to the negative resin. They will "stick" to the column. Protein B has a stronger positive charge (+2) than C (+1), so it will stick more tightly. To get them off, a salt solution is passed through the column. The salt ions compete with the proteins for binding sites on the resin. Protein C, being less tightly bound, will be knocked off and elute before Protein B.

Step 4: Final Answer

The question asks which molecule elutes first. That will be Protein A, because its negative charge causes it to be repelled by the negative column, preventing it from binding.

Quick Tip

Remember: "Cation-exchange" means it *exchanges* (and thus binds) cations. Anions (negatively charged molecules) will not bind at all and will be found in the flow-through, eluting first.

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8. A technique for transferring denatured DNA molecules that have been separated electrophoretically from a gel to a matrix (such as a nitrocellulose or nylon

membrane) on which a hybridization assay can be performed is called

(A) Northern blotting
(B) Southern blotting
(C) Eastern blotting
(D) Western blotting

Correct Answer: (B) Southern blotting

Solution:

Step 1: The Purpose of Blotting

After separating molecules like DNA, RNA, or protein on a gel, it can be difficult to perform further analysis on the flimsy gel. Blotting is the process of transferring these separated molecules from the gel onto a solid, stable membrane (like special paper). This makes the molecules accessible for detection with a specific probe (e.g., a complementary DNA strand or an antibody).

Step 2: The Naming Convention

The names for these techniques are a famous joke in molecular biology.

- **Southern Blotting:** This was the original technique, invented by Edwin Southern to detect **DNA**. It is named after him.
- **Northern Blotting:** Scientists later adapted the technique to detect **RNA**. As a play on words, they called it "Northern" blotting.
- **Western Blotting:** The technique was then further adapted to detect **proteins**. Continuing the joke, this was named "Western" blotting.
- (There are also less common "Eastern" and "Far-Western" blots for detecting other molecular features).

Step 3: Conclusion

The question describes the technique for detecting **DNA**. Based on the established nomenclature, the transfer and detection of DNA is called **Southern blotting**.

Quick Tip

Use the mnemonic **S-N-O-W D-R-O-P**:

- **S**outhern → **D**NA
- **N**orthern → **R**NA
- **O** → **O** (nothing)
- **W**estern → **P**rotein

This helps you remember which blotting technique corresponds to which macromolecule.

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9. The DNA of the bacterial cell is protected from the cell's own restriction enzymes by the addition of methyl group (-CH3) to _____ of cytosine.
A. 4th Carbon
B. 7th Carbon
C. 6th Carbon
D. 5th Carbon
Choose the correct answer from the options given below:

(A) D only
(B) B only
(C) B and D only
(D) B and C only

Correct Answer: (A) D only

Solution:

Step 1: The "Self" vs. "Non-Self" System

Bacteria are under constant attack from viruses that inject foreign DNA. The Restriction-Modification (R-M) system allows a bacterium to distinguish its own DNA from invading DNA. It does this by using a **methyltransferase** enzyme to add a small chemical tag (a methyl group, -CH_3) to its own DNA at specific sequences. A second enzyme, a **restriction enzyme**, patrols the cell and cuts up any DNA that has that same sequence but *lacks* the protective methyl tag.

Step 2: The Sites of Methylation

These methyl tags are added to the DNA bases themselves. In the base cytosine, a very common target for this protective methylation is the carbon atom at the 5th position on the pyrimidine ring structure. This creates a modified base called 5-methylcytosine.

Step 3: Analyzing the Options

The question asks to identify the correct site of this modification on cytosine. While other types of modifications exist, methylation of the **5th carbon (C5)** is a major, well-studied, and crucial mechanism for protecting host DNA in many R-M systems. The other carbon positions listed (4th, 6th, 7th) are not the primary sites for this specific function.

Step 4: Conclusion

The correct statement is that the **5th Carbon** of cytosine is a major site for protective methylation in bacteria.

> Quick Tip
>
> Remember that methylation is like a "do not cut" signal for a bacterium's own restriction enzymes. The most common methylation sites are N6 of Adenine and C5 of Cytosine.

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10. Which of the following statements are correct regarding prokaryotic genomic organization?
A. Most prokaryotes contain a single large circle of double stranded DNA as its genome.
B. The nucleoid is an irregularly shaped region that contains the cell's chromosome and numerous proteins.
C. Nucleoid associated proteins (NAPs) are not particularly important during cell division for the compaction of chromosome.
D. Prokaryotic genomes are much smaller as compared to eukaryotes.
Choose the correct answer from the options given below:

(A) A, B and D only
(B) A, B and C only
(C) A, B, C and D
(D) B, C and D only

Correct Answer: (A) A, B and D only

Solution:

Step 1: The Core Concept of Prokaryotic Organization

Prokaryotes lack a nucleus. Their genetic material is concentrated in a region of the cytoplasm called the nucleoid, but it is not separated by a membrane.

Step 2: Analyzing Each Statement

- **(A) Correct:** Unlike eukaryotes which have multiple linear chromosomes, the typical prokaryote has its entire genome contained in a **single, circular DNA molecule**.

- **(B) Correct:** The **nucleoid** is simply the name for the region where the chromosome is located. It is not an organelle because it is not enclosed by a membrane.
- **(C) Incorrect:** A bacterium's DNA chromosome is extremely long—often 1,000 times the length of the cell itself. To fit inside, it must be intricately folded and compacted. This job is performed by **Nucleoid-Associated Proteins (NAPs)**. These proteins are the functional equivalent of histones in eukaryotes. They are absolutely **critically important** for the physical structure and organization of the chromosome. The statement that they are not is false.
- **(D) Correct:** Prokaryotic genomes are a model of efficiency and are much smaller than eukaryotic genomes. A bacterium might have a few million base pairs, whereas a human has over 3 billion base pairs in their genome.

Step 3: Final Answer

Statements A, B, and D are all correct descriptions. Statement C is incorrect because Nucleoid-Associated Proteins are essential for managing the prokaryotic chromosome.

Quick Tip

When comparing prokaryotes and eukaryotes, remember these key genomic differences: single circular chromosome vs. multiple linear chromosomes, nucleoid vs. nucleus, and significantly smaller genome size in prokaryotes. NAPs are the prokaryotic equivalent of histones for DNA compaction.

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11. In humans, one of the most recognized satellite DNA sequences, found mainly in the centromere region is:

(A) Quinoid family
(B) Deltoid family
(C) Alphoid family
(D) Trepizoid family

Correct Answer: (C) Alphoid family

Solution:

Solution 11: Satellite DNA in Human Centromeres

Step 1: Foundational Concept of Repetitive DNA

The human genome is not just a collection of unique genes. It also contains vast regions of repetitive DNA, where the same sequence of nucleotides is repeated over and over. One major class of this is **satellite DNA**, characterized by large arrays of tandemly (head-to-tail) repeating sequences. These regions are crucial for chromosome structure, particularly at the centromeres.

Step 2: The Role and Structure of the Centromere

The centromere is the constricted region of a chromosome that plays a critical role during cell division. It is the site where the **kinetochore**, a complex protein structure, assembles. The kinetochore acts as the attachment point for spindle fibers, which pull the sister chromatids apart to opposite poles of the cell, ensuring each new daughter cell receives a complete set of chromosomes. The proper formation of the centromere depends on its underlying DNA sequence.

Step 3: In-depth Analysis of Centromeric DNA

- **Alpha-satellite DNA (Alphoid DNA):** The centromeric regions of all human chromosomes are defined by a specific family of satellite DNA known as **alpha-satellite DNA**, or **alphoid DNA**.
- **Hierarchical Structure:** This DNA is not a simple repeat. It consists of a basic monomer unit that is approximately **171 base pairs** long. These monomers are organized into higher-order repeat arrays that extend for millions of base pairs. This complex, repetitive structure is essential for recruiting the specific proteins needed to build the kinetochore.
- **Evaluating the Distractors:** The other names provided (Quinoid, Deltoid, Trepizoid) are fictional distractors. They are designed to sound plausible but have no basis in genetics or molecular biology. Recognizing the correct term, "alphoid DNA," is key.

Step 4: Final Conclusion

The most recognized and essential satellite DNA sequence that defines the structure and function of human centromeres is the **Alphoid family** (alpha-satellite DNA).

Quick Tip

For human genetics, link "alphoid DNA" or "alpha-satellite DNA" directly with the centromere. It's the key repetitive sequence that defines the centromere's identity and function.

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12. Select correct statement about Euchromatin :

(A) Highly condensed
(B) Associated with active transcription
(C) Found outside nucleus only
(D) Does not replicate during S phase

Correct Answer: (B) Associated with active transcription

Solution:

Step 1: Foundational Concept of Chromatin Organization

Inside the nucleus, DNA is not naked; it is tightly packaged by proteins (primarily histones) to form a complex called **chromatin**. This chromatin exists in two main functional states:

- **Euchromatin:** A loosely packed, decondensed form of chromatin.
- **Heterochromatin:** A tightly packed, highly condensed form of chromatin.

This level of packaging directly impacts the accessibility of the DNA for cellular processes like transcription.

Step 2: Systematic Evaluation of Statements about Euchromatin

Let's analyze each statement to determine its accuracy:

- **(A) Highly condensed:** This is incorrect. This statement describes **heterochromatin**. Euchromatin is, by definition, the *less condensed* or "open" form of chromatin. Think of it as an open book, ready to be read.
- **(B) Associated with active transcription:** This is correct. Because euchromatin is in a relaxed, open state, the DNA is physically accessible to the cellular machinery responsible for reading genes. **RNA polymerase** and other transcription factors can bind to the DNA and initiate the process of transcription, actively expressing the genes within these regions.
- **(C) Found outside nucleus only:** This is incorrect. All chromosomal DNA and its associated chromatin (both euchromatin and heterochromatin) are located **inside the nucleus** in eukaryotic cells.
- **(D) Does not replicate during S phase:** This is incorrect. All of the cell's genomic DNA must be duplicated before cell division, and this process occurs during the **S (synthesis) phase** of the cell cycle. In fact, due to its open structure and active nature, euchromatin typically replicates **early** in the S phase, whereas the condensed heterochromatin replicates later.

Step 3: Final Conclusion

The defining and correct statement about euchromatin is that its open structure is **associated with active transcription**.

> Quick Tip
>
> Remember the prefixes: **Eu-** means "true" or "good". Euchromatin is "good" for transcription because it's open and accessible. **Hetero-** means "different". Heterochromatin is different, being condensed and silent (transcriptionally inactive).

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13. Match the LIST-I with LIST-II

LIST-I Types of Chromosome		LIST-II Position of centromere	
A.	Metacentric chromosome	I.	The centromere is located on one side of the central point of the chromosome.
B.	Submetacentric chromosome	II.	The centromere appears to be located at one end of the chromosome.
C.	Acrocentric chromosome	III.	The centromere is located in the center of chromosome.
D.	Telocentric chromosome	IV.	The centromere is located close to one end of the chromosome.

Choose the correct answer from the options given below:

(A) A-I, B - II, C - III, D - IV
(B) A-I, B - III, C - II, D - IV
(C) A-III, B - I, C - IV, D - II
(D) A-III, B - IV, C - I, D - II

Correct Answer: (C) A-III, B - I, C - IV, D - II

Solution:

Step 1: Foundational Concept of Chromosome Morphology

Chromosomes are classified into four main types based on the position of the **centromere**, the primary constriction point. The centromere's location determines the relative lengths of the two chromosome "arms." The short arm is designated as the **'p' arm** (from *petit*), and the long arm is the **'q' arm**.

Step 2: Matching Chromosome Types with Centromere Positions

Let's define each type and match it to its description:

- **A. Metacentric chromosome:** The centromere is located exactly in the middle (*meta*). This creates two arms of equal length (p arm = q arm). This matches with **III. The centromere is located in the center of chromosome.**
- **B. Submetacentric chromosome:** The centromere is located slightly off-center (*sub-meta*). This results in one arm being slightly shorter than the other (p arm ¡ q arm). This matches with **I. The centromere is located on one side of the central point of the chromosome.**
- **C. Acrocentric chromosome:** The centromere is located very close to one end (*acro*). This results in a very short p arm (which often contains non-coding satellite DNA) and a very long q arm. This matches with **IV. The centromere is located close to one end of the chromosome.**

- **D. Telocentric chromosome:** The centromere is located at the very end or tip (*telo*) of the chromosome, within the telomere. This results in there being only one visible arm. This matches with **II. The centromere appears to be located at one end of the chromosome.** (Note: Humans do not have telocentric chromosomes).

Step 3: Final Answer

Based on the definitions, the correct matching is: **A-III, B-I, C-IV, D-II**.

Quick Tip

Remember the prefixes: **Meta-** (middle), **Sub-meta-** (below middle), **Acro-** (peak/tip), and **Telo-** (end). This will help you visualize and remember the centromere positions.

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14. Telomerase acts as a cellular reverse transcriptase that provides the active site for:

(A) RNA-dependent DNA synthesis
(B) DNA-dependent RNA synthesis
(C) RNA-dependent RNA synthesis
(D) DNA-dependent DNA synthesis

Correct Answer: (A) RNA-dependent DNA synthesis

Solution:

Step 1: Foundational Concept: The End Replication Problem

Eukaryotic chromosomes are linear. Standard DNA polymerase enzymes can only synthesize DNA in one direction and require a primer to get started. This leads to the **"end replication problem"**: with each round of cell division, a small portion of the DNA at the very 3' end of the lagging strand cannot be copied, causing the chromosomes to become progressively shorter. To prevent the loss of important genetic information, the ends of chromosomes are protected by caps called **telomeres**, and an enzyme called **telomerase** works to maintain their length.

Step 2: The Unique Mechanism of Telomerase

Telomerase is a special enzyme known as a **ribonucleoprotein**, meaning it is composed of both protein and an RNA component. Its function is to extend the telomeres.

- It contains its own built-in **RNA molecule** that serves as a template.
- The protein component of telomerase is a **reverse transcriptase**, an enzyme that synthesizes a DNA strand using an RNA template.
- Telomerase binds to the end of the chromosome and uses its internal RNA template to add the repetitive telomeric DNA sequence to the 3' end of the DNA strand.

Step 3: Analyzing the Biochemical Terminology

Let's break down the different types of nucleic acid synthesis:

- **DNA-dependent RNA synthesis:** Using a DNA template to make RNA. This is the definition of **transcription**.
- **RNA-dependent RNA synthesis:** Using an RNA template to make more RNA. This is done by enzymes found in some viruses.
- **DNA-dependent DNA synthesis:** Using a DNA template to make a new DNA strand. This is the definition of standard **DNA replication**.
- **RNA-dependent DNA synthesis:** Using an RNA template to make a DNA strand. This is the definition of **reverse transcription**.

Step 4: Final Conclusion

Since telomerase is a reverse transcriptase that uses its own internal RNA molecule as a template to synthesize telomeric DNA, its activity is correctly described as **RNA-dependent DNA synthesis**.

> Quick Tip
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> Remember the enzyme naming convention: The first part describes the template, and the second part describes the product being synthesized. "RNA-dependent DNA synthesis" means "uses RNA as a template to synthesize DNA." This is the definition of reverse transcription, the function of telomerase.

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15. Which of the following molecule/ion is not transported/buffered by hemoglobin?

(A) O_2
(B) CO_2
(C) Na^+
(D) H^+

Correct Answer: (C) Na^+

Solution:

Step 1: Foundational Concept of Hemoglobin's Function

Hemoglobin (Hb) is the iron-containing protein found within red blood cells, giving blood its characteristic red color. Its primary purpose is to transport oxygen from the lungs to the body's tissues, but its complex structure allows it to perform several other critical roles in respiratory gas exchange and in maintaining the delicate pH balance of the blood. This question asks us to identify a substance that hemoglobin does *not* directly interact with as part of its physiological functions.

Step 2: Detailed Examination of Hemoglobin's Interactions

Let's systematically analyze the interaction between hemoglobin and each of the listed molecules or ions:

- **O_2 (Oxygen):** This is the **primary and most well-known function** of hemoglobin. Oxygen from the lungs diffuses into red blood cells and binds reversibly to the iron atom located at the center of the heme group in each of hemoglobin's four subunits. This binding is cooperative, meaning the binding of one oxygen molecule increases the affinity of the other subunits for oxygen. This property allows hemoglobin to efficiently become saturated with oxygen in the lungs and then easily release it in the tissues where oxygen concentration is lower.
- **CO_2 (Carbon Dioxide):** Hemoglobin is a key player in transporting the waste product CO_2 from the tissues back to the lungs. It is responsible for transporting a significant fraction (about 20-25%) of the total CO_2. Unlike oxygen, CO_2 does not bind to the heme iron. Instead, it attaches directly to the amino groups of the globin protein chains, forming a compound called **carbaminohemoglobin**. This binding is also reversible and is favored in the tissues where CO_2 levels are high.
- **H^+ (Protons):** Hemoglobin is a crucial **physiological blood buffer**, helping to prevent drastic changes in pH. In the tissues, high levels of CO_2 lead to the formation of carbonic acid (H_2CO_3), which then dissociates into bicarbonate (HCO_3^-) and H^+ ions, making the blood more acidic. Deoxyhemoglobin (hemoglobin that has released its oxygen) has a higher affinity for H^+ than oxyhemoglobin. It binds these excess protons, effectively removing them from the solution and thus stabilizing the blood's pH. This interaction, where H^+ and CO_2 levels influence oxygen binding, is a key part of the **Bohr effect**.
- **Na^+ (Sodium ions):** Sodium ions are vital electrolytes, essential for maintaining the osmotic balance and the electrical membrane potential of all cells, including red blood cells. However, the concentration and transport of Na^+ across the cell membrane are actively managed by dedicated protein pumps (most notably the **Na^+/K^+-ATPase**) and specific ion channels. Hemoglobin, located within the cytoplasm of the red blood cell, does **not** have a binding site for sodium ions and plays no direct role in their transport or buffering.

Step 3: Final Conclusion

Hemoglobin's physiological roles are centered on respiratory gases and pH balance. It is directly involved in transporting O_2 and CO_2, and in buffering H^+ ions. It is **not involved** in the transport or buffering of **Na^+ ions**, as that function is regulated by membrane-bound proteins.

Quick Tip

Think of hemoglobin's main jobs: gas transport (O_2, CO_2) and pH buffering (H^+). Common electrolytes like Na^+, K^+, and Cl^- are generally handled by membrane pumps and channels, not by hemoglobin.

16. Which of the following pair of class and organism is not correctly matched?

(A) Polyplacophora- Chiton
(B) Gastropoda - Aplysia
(C) Monoplacophora - Chiton
(D) Aplacophora - Chaetoderma

Correct Answer: (C) Monoplacophora - Chiton

Solution:

Step 1: Foundational Concept of Molluscan Classification

The phylum Mollusca is one of the largest and most diverse animal phyla, encompassing a wide range of organisms from snails and clams to squids and octopuses. This vast phylum is organized into several distinct classes based on key characteristics, such as the nature of their shell, the structure of their foot, and the organization of their nervous system. This question tests the ability to correctly associate a representative organism with its proper class.

Step 2: Systematic Evaluation of Each Organism-Class Pair

Let's check the accuracy of each match:

- **(A) Polyplacophora - Chiton:** This is a **correct match**. The class Polyplacophora ("many plate bearers") is defined by the chitons. Their most distinctive feature is a shell composed of eight overlapping dorsal plates, which allows them to be flexible and adhere tightly to rocky intertidal surfaces.
- **(B) Gastropoda - *Aplysia*:** This is a **correct match**. The class Gastropoda ("stomach foot") is the largest and most diverse class of molluscs, including snails, slugs, limpets, and sea slugs. *Aplysia*, commonly known as the sea hare, is a type of marine sea slug and is a well-known member of this class.
- **(C) Monoplacophora - Chiton:** This is an **incorrect match**. As established in (A), the Chiton belongs to the class Polyplacophora due to its eight-plated shell. The class Monoplacophora ("one plate bearer") consists of rare, deep-sea molluscs with a single, cap-like shell. These organisms were once thought to be extinct and are considered "living fossils." The classic example is the genus *Neopilina*. Therefore, placing a chiton in this class is incorrect.
- **(D) Aplacophora - *Chaetoderma*:** This is a **correct match**. The class Aplacophora ("no plate bearers") includes small, worm-like marine molluscs that are distinguished by their complete lack of a shell. They are covered instead by a cuticle embedded with calcareous spicules. *Chaetoderma* is a representative genus of this class.

Step 3: Final Conclusion

By analyzing each pair, it is clear that the pair that is **not correctly matched** is **Monoplacophora - Chiton**. A chiton is a member of the class Polyplacophora.

Quick Tip

Chitons are strongly associated with the class Polyplacophora (poly = many, placo = plates, phora = bearing), which refers to their characteristic eight-plated shell. Seeing Chiton paired with any other class should be an immediate red flag.

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17. Which one of the following statement is incorrect regarding the work of Erwin Chargaff?

(A) The base composition of DNA don't varies from one species to another.
(B) DNA specimens isolated from different tissues of the same species have the same base composition.
(C) The base composition of DNA in a given species does not change with an organism's age, nutritional state, or changing environment.
(D) The sum of the purine residues equals the sum of the pyrimidine residues; that is, A + G = T + C.

Correct Answer: (A) The base composition of DNA don't varies from one species to another.

Solution:

Step 1: Foundational Concept: The Basis of DNA Base Pairing

Before the structure of the double helix was known, biochemist Erwin Chargaff conducted experiments that revealed fundamental rules about the composition of DNA. These rules were a critical piece of evidence that Watson and Crick used to build their model of DNA. The question asks to identify a statement that contradicts Chargaff's findings.

Step 2: In-depth Analysis of Chargaff's Rules and Each Statement

Chargaff established two main rules:

1. **Rule of Base Pairing:** In the DNA of any organism, the amount of adenine (A) is equal to the amount of thymine (T), and the amount of guanine (G) is equal to the amount of cytosine (C). This implies that the total amount of purines (A+G) equals the total amount of pyrimidines (C+T).
2. **Rule of Species Specificity:** The base composition of DNA (the ratio of A+T to G+C) **varies from one species to another**, but is constant in different cells and tissues of the same species.

Let's evaluate the statements:

- **(A) The base composition of DNA don't varies from one species to another:** This statement is grammatically awkward but means "The base composition of DNA does not vary from one species to another." This **directly contradicts** Chargaff's second rule. A key finding was that this composition *is* a unique characteristic that differs between species.

- **(B) DNA specimens isolated from different tissues of the same species have the same base composition:** This is **correct** and is part of Chargaff's second rule. The DNA in your liver is the same as the DNA in your skin.
- **(C) The base composition of DNA... does not change with... age, nutritional state, or changing environment:** This is **correct**. DNA base composition is a stable, inherited trait of a species.
- **(D) The sum of the purine residues equals the sum of the pyrimidine residues; that is, A + G = T + C:** This is **correct** and is a direct consequence of Chargaff's first rule (A=T and G=C).

Step 3: Final Answer

The incorrect statement is **(A)**, as it makes a claim that is the exact opposite of one of Chargaff's most important discoveries.

Quick Tip

Chargaff's rules can be summarized in two main points: 1) A=T and G=C, so Purines=Pyrimidines. 2) The exact percentage of these bases varies between different species. The incorrect statement violates the second point.

---

18. Which of the following amino acids are essential amino acids in humans:
A. Leucine
B. Lysine
C. Isoleucine
D. Serine
Choose the correct answer from the options given below:

(A) A, B, and C Only
(B) B, C, and D Only
(C) A, B, C and D
(D) A, C, and D Only

Correct Answer: (A) A, B, and C Only

Solution:

Step 1: Foundational Concept of Essential vs. Non-Essential Amino Acids

Amino acids are the building blocks of proteins. The human body can synthesize some amino acids from other molecules through various metabolic pathways. These are called **non-essential amino acids**. However, there are other amino acids that the body cannot produce on its own in sufficient quantities. These must be obtained from the diet and are therefore called **essential amino acids**.

Step 2: Listing the Essential Amino Acids

For adult humans, there are nine essential amino acids: Histidine, Isoleucine, Leucine, Lysine, Methionine, Phenylalanine, Threonine, Tryptophan, and Valine.

Step 3: Classifying the Amino Acids in the Question

Let's check each of the given amino acids against the list of essential ones:

- **A. Leucine:** This is an **essential** amino acid.
- **B. Lysine:** This is an **essential** amino acid.
- **C. Isoleucine:** This is an **essential** amino acid.
- **D. Serine:** This is a **non-essential** amino acid. The body can synthesize serine from other molecules, such as the glycolytic intermediate 3-phosphoglycerate.

Step 4: Final Answer

Leucine (A), Lysine (B), and Isoleucine (C) are all essential amino acids that must be supplied by the diet. Serine (D) is non-essential. Therefore, the correct option is the one that includes **A, B, and C only**.

Quick Tip

A useful mnemonic to remember the nine essential amino acids is "PVT TIM HALL": Phenylalanine, Valine, Threonine, Tryptophan, Isoleucine, Methionine, Histidine, Arginine (conditionally essential), Leucine, Lysine.

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19. Match LIST-I with LIST-II

LIST-I Vitamins		LIST-II Major function in the body	
A.	B7 (Biotin)	I.	Used in collagen synthesis
B.	B12 (Cobalamin)	II.	Important in blood clotting
C.	C (Ascorbic acid)	III.	Coenzyme in synthesis of fat, glycogen and amino acids
D.	K (Phylloquinone)	IV.	Production of nucleic acids and red blood cells

Choose the correct answer from the options given below:

(A) A-I, B-III, C - IV, D - II
(B) A - III, B - II, C - IV, D - I
(C) A-I, B-II, C - IV, D - III
(D) A-III, B - IV, C - I, D - II

Correct Answer: (D) A-III, B - IV, C - I, D - II

Solution:

Step 1: Foundational Concept of Vitamins as Coenzymes

Vitamins are essential organic compounds that an organism requires in limited amounts. Many vitamins, particularly those in the B-complex group, function as **coenzymes**—non-protein molecules that are necessary for an enzyme to carry out its catalytic function. This question requires matching several vitamins with their major physiological roles.

Step 2: Detailed Analysis and Matching

Let's determine the primary function for each vitamin:

- **A. B7 (Biotin):** Biotin acts as a crucial coenzyme for a class of enzymes called **carboxylases**, which are responsible for transferring carboxyl (-COOH) groups. These enzymes are vital in several metabolic pathways, including the synthesis of fats (fatty acids), the breakdown of certain amino acids (isoleucine and valine), and the creation of glucose (gluconeogenesis). This broadly fits with **III. Coenzyme in synthesis of fat, glycogen and amino acids.**
- **B. B12 (Cobalamin):** Vitamin B12 is essential for two main types of reactions in the body, one of which is critical for the synthesis of methionine and for folate metabolism. This process is ultimately required for **DNA synthesis**. Cells that divide rapidly, such as red blood cells maturing in the bone marrow, are especially dependent on B12. A deficiency leads to problems with red blood cell production. This matches with **IV. Production of nucleic acids and red blood cells.**
- **C. C (Ascorbic acid):** Vitamin C is a required cofactor for the enzymes that hydroxylate (add -OH groups to) proline and lysine residues during the synthesis of **collagen**. This modification is essential for forming the strong, stable triple-helix structure of collagen, the main structural protein in skin, bones, and other connective tissues. This matches with **I. Used in collagen synthesis.**
- **D. K (Phylloquinone):** Vitamin K is essential for the synthesis of several proteins, known as **clotting factors**, in the liver. It acts as a coenzyme for an enzyme that modifies these proteins, allowing them to bind calcium, which is a necessary step in the blood coagulation cascade. This matches with **II. Important in blood clotting.**

Step 3: Final Answer

The correct matching is: **A-III, B-IV, C-I, D-II**.

> Quick Tip
>
> Associate keywords with each vitamin: Biotin → Coenzyme/Carboxylation, B12 → Red Blood Cells/DNA, C → Collagen/Scurvy, K → Klotting (clotting).

20. The glycosidic bond between the monomers of sucrose is-

(A) Gal($1\beta \rightarrow \beta 4$)Glc
(B) Fru($4\beta \rightarrow \beta 1$)Glc
(C) Fru($4\beta \rightarrow \alpha 2$)Glc
(D) Fru($2\beta \leftrightarrow \alpha 1$)Glc

Correct Answer: (D) Fru($2\beta \leftrightarrow \alpha 1$)Glc

Solution:

Step 1: Foundational Concept of Disaccharides and Glycosidic Bonds

Sucrose (common table sugar) is a **disaccharide**, meaning it is formed from two simpler sugar units (**monosaccharides**). These units are joined together by a **glycosidic bond**. The specific nature of this bond—which monosaccharides are involved and which of their carbons are linked—determines the properties of the disaccharide, including whether it is a "reducing" or "non-reducing" sugar.

Step 2: Deconstructing the Sucrose Molecule

- **The Monomers:** Sucrose is composed of α**-D-glucose** and β**-D-fructose**.
- **Anomeric Carbons:** The anomeric carbon is the central carbon of a hemiacetal or hemiketal group in a cyclic sugar—it's the carbon that was the carbonyl carbon in the open-chain form. For glucose (an aldose), this is C1. For fructose (a ketose), this is C2. These anomeric carbons are typically the most reactive sites and are involved in forming glycosidic bonds.
- **The Linkage:** The glycosidic bond in sucrose is unique because it is formed between the anomeric carbon of glucose (**C1**) and the anomeric carbon of fructose (**C2**).
- **Non-Reducing Property:** Because both anomeric carbons are locked in the glycosidic bond, neither sugar ring can open up to expose a free aldehyde or ketone group. This is why sucrose is a **non-reducing sugar**.

Step 3: Analyzing the Options and Notation

- **(A)** describes the bond in lactose (Galactose β-1,4 Glucose).
- **(B) and (C)** show incorrect linkages or carbon numbers.
- **(D) Fru(2$\beta \leftrightarrow \alpha$1)Glc:** This notation correctly represents the bond.
  - `Glc` = Glucose
  - `Fru` = Fructose
  - α`1` refers to the C1 carbon of glucose in its α-anomeric form.
  - `2`β refers to the C2 carbon of fructose in its β-anomeric form.
  - The double arrow $\leftrightarrow$ is specific shorthand used to indicate a bond formed between two anomeric carbons.

Step 4: Final Answer

The glycosidic bond in sucrose is an **α-1,β-2 linkage** between glucose and fructose. This is correctly and specifically represented by the notation in **option (D)**.

> Quick Tip
>
> Sucrose is unique because its glycosidic bond involves the anomeric carbons of both sugar units. This locks them and makes sucrose a non-reducing sugar. Remember the linkage: α-1 (glucose) to β-2 (fructose).

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21. Match LIST-I with LIST-II

LIST-I Genes involved in *E.coli* DNA replication		LIST-II Product or role	
A.	pol A	I.	Helicase at OriC
B.	pol B	II.	Primase
C.	Dna G	III.	DNA polymerase II
D.	Dna B & C	IV.	DNA polymerase I

Choose the correct answer from the options given below:

(A) A - IV, B - III, C - I, D - II
(B) A - IV, B - III, C - II, D - I
(C) A - I, B - II, C - IV, D - III
(D) A - III, B - IV, C - I, D - II

Correct Answer: (B) A - IV, B - III, C - II, D - I

Solution:

Step 1: Foundational Concept of DNA Replication Machinery

DNA replication is a complex process that requires the coordinated action of numerous enzymes and proteins. In prokaryotes like *E. coli*, specific genes code for these essential components. This question requires matching the genetic nomenclature of key replication genes (the genotype, in LIST-I) with their corresponding protein products or functional roles (the phenotype, in LIST-II).

Step 2: Detailed Analysis and Matching of Each Gene

Let's break down the function of the protein encoded by each gene:

- **A. *polA*:** This gene codes for **DNA Polymerase I**. While DNA Polymerase III is the main workhorse of DNA synthesis, Pol I has a crucial, dual-function cleanup role. Its primary functions are in DNA repair and, most famously, in removing the RNA primers

(used to initiate DNA synthesis) from the Okazaki fragments on the lagging strand and replacing them with DNA. This correctly matches with **IV. DNA polymerase I**.

- **B. *polB*:** This gene codes for **DNA Polymerase II**. This enzyme is not part of the main replication fork machinery. Instead, its primary role is in DNA repair, specifically in restarting replication when it has been stalled by DNA damage. It is a key player in the SOS response to extensive DNA damage. This correctly matches with **III. DNA polymerase II**.
- **C. *DnaG*:** This gene codes for the enzyme **Primase**. DNA polymerases cannot start a new DNA chain from scratch; they can only add nucleotides to an existing 3' end. Primase solves this problem by synthesizing a short RNA primer (about 10-12 nucleotides long) on the template DNA strand. This primer provides the necessary 3' hydroxyl group for DNA Polymerase III to begin synthesis. This correctly matches with **II. Primase**.
- **D. *DnaB* & *C*:** This refers to a crucial protein complex at the start of replication. **DnaB** is the main replicative **Helicase** in *E. coli*, an enzyme that uses ATP to unwind the DNA double helix, creating the replication fork. However, DnaB cannot load onto the DNA by itself. It requires the **DnaC** protein, which is a **helicase loader**. DnaC binds to DnaB and helps escort it to the origin of replication (**OriC**), where it is deposited onto the DNA. Therefore, the DnaB-DnaC complex is responsible for the helicase activity at the origin. This correctly matches with **I. Helicase at OriC**.

Step 3: Final Answer

Based on the functions of these key replication proteins, the correct set of matches is: **A-IV, B-III, C-II, D-I**.

Quick Tip

Remember the key players in E. coli replication: DnaA (initiator), DnaB (Helicase), DnaC (loader), DnaG (Primase), and Pol III (main polymerase). Pol I ('polA') is famous for primer removal, and Pol II ('polB') is for repair.

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22. Arrange the steps of recombinant DNA-cloning procedure in correct sequence of their occurance:
A. Joining the target DNA with cloning vector DNA by ligase enzyme.
B. Targeted DNA from a source organism is cleaved and cloning vector DNA is also cleaved by the same restriction endonuclease.
C. Selection of transformants from non-transformants through antibiotic resistance and color indicators
D. Introduction of recombinant DNA into host cell.
Choose the correct answer from the options given below:

(A) A, B, C, D
(B) A, C, B, D
(C) B, A, D, C

(D) C, B, D, A

Correct Answer: (C) B, A, D, C

Solution:

Step 1: Foundational Concept of Recombinant DNA Technology

Recombinant DNA technology, or gene cloning, is a cornerstone of modern molecular biology. It involves isolating a specific gene or DNA segment and inserting it into a carrier molecule (a vector), which can then be replicated in a host organism. This allows for the production of large quantities of the specific DNA or its protein product. The question asks for the correct chronological order of the essential steps in this process.

Step 2: A Detailed, Step-by-Step Walkthrough of the Cloning Process

Let's arrange the steps in a logical sequence from start to finish:

1. **Step B: Preparation of DNA Fragments (Digestion):** This is the mandatory first step. To join two pieces of DNA, you must first cut them in a compatible way. This involves using a **restriction enzyme** to cut both the source DNA (containing the gene of interest) and the cloning vector (typically a bacterial plasmid). Using the same enzyme on both ensures that the resulting "sticky ends" are complementary, allowing them to anneal (base-pair) with each other.
2. **Step A: Joining DNA Fragments (Ligation):** Once the gene of interest and the vector have been cut, they are mixed together. The complementary sticky ends will anneal. Then, the enzyme **DNA ligase** is added. This enzyme acts as a molecular glue, forming permanent phosphodiester bonds to seal the nicks in the DNA backbone. The result is a single, circular, newly created **recombinant DNA molecule** (the plasmid now containing the gene of interest).
3. **Step D: Introduction into a Host (Transformation):** The newly created recombinant DNA molecule is useless on its own; it must be introduced into a living host cell where it can be replicated. This process of introducing foreign DNA into a bacterium (like *E. coli*) is called **transformation**. This is typically achieved by making the bacterial cell walls temporarily permeable using chemical treatments (e.g., calcium chloride) or an electric shock (electroporation).
4. **Step C: Selection of Transformed Cells:** Transformation is a very inefficient process. Only a tiny fraction of the host bacteria will successfully take up the recombinant plasmid. Therefore, it is essential to identify and isolate these successful "transformants." This is done using a **selectable marker** that is part of the plasmid vector, such as a gene for antibiotic resistance. By growing the bacteria on a medium containing the antibiotic, only the cells that have taken up the plasmid (and are thus resistant) will survive and grow.

Step 3: Final Answer

Following the logical flow of a standard gene cloning experiment, the correct sequence of occurrence is: **B (Digestion) → A (Ligation) → D (Transformation) → C (Selection)**.

> Quick Tip
>
> Think of it like building with LEGOs: 1. Get the right pieces and make sure they fit (Cut with restriction enzyme - B). 2. Stick them together (Ligate - A). 3. Put your creation into a display case (Transform into host cell - D). 4. Find your specific creation among many others (Select - C).

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23. Tetracycline is usually mixed with the culturing medium as selective agents in selecting transformants in gene cloning technique. It acts by:

(A) Inhibiting cell wall formation; inactivated by β-lactamase
(B) Binding to the 30S ribosomal subunit and inhibits the binding of aminoacyl-tRNAs in bacteria
(C) Blocking protein initiation complex formation and causes misreading during translation
(D) Binding to 50S ribosomal subunit and inhibits protein synthesis.

Correct Answer: (B) Binding to the 30S ribosomal subunit and inhibits the binding of aminoacyl-tRNAs in bacteria

Solution:

Step 1: Foundational Concept of Antibiotic Action

Antibiotics are molecules that kill bacteria or inhibit their growth by targeting essential cellular processes that are unique to prokaryotes, thus minimizing harm to the eukaryotic host. A major target is the bacterial ribosome, which is structurally different from eukaryotic ribosomes and is responsible for protein synthesis. Tetracycline is a broad-spectrum antibiotic often used in molecular biology as a selectable marker.

Step 2: Detailed Analysis of Different Antibiotic Mechanisms

Let's evaluate the mechanism described in each option:

- **(A) Inhibiting cell wall formation; inactivated by β-lactamase:** This describes the mechanism of **β-lactam antibiotics** like penicillin and ampicillin. These antibiotics inhibit the enzymes that build the peptidoglycan cell wall, a structure unique to bacteria. Bacterial resistance is often mediated by the enzyme β-lactamase, which breaks down the antibiotic. This is not the mechanism of tetracycline.
- **(B) Binding to the 30S ribosomal subunit and inhibits the binding of aminoacyl-tRNAs in bacteria:** This is the **correct mechanism for tetracycline**. The bacterial ribosome is composed of a small (30S) and a large (50S) subunit. Tetracycline binds

reversibly to the 30S subunit. This binding physically obstructs the A-site (aminoacyl site) of the ribosome. This blockage prevents the incoming charged tRNA molecules (aminoacyl-tRNAs), which carry the next amino acid, from binding. Without the entry of new aminoacyl-tRNAs, protein chain elongation is halted, and protein synthesis stops.

- **(C) Blocking protein initiation complex formation and causes misreading during translation:** This describes the action of **aminoglycoside antibiotics** like streptomycin. Streptomycin also binds to the 30S subunit, but it does so in a way that distorts the A-site, leading to the misreading of the mRNA codon and the incorporation of incorrect amino acids. It also interferes with the formation of the initiation complex.
- **(D) Binding to 50S ribosomal subunit and inhibits protein synthesis:** This describes the mechanism of several other classes of antibiotics, including **macrolides** (like erythromycin) and chloramphenicol, which target the larger 50S ribosomal subunit to inhibit different steps of protein synthesis, such as translocation or peptide bond formation.

Step 3: Final Answer

Tetracycline's specific mode of action is to inhibit bacterial protein synthesis by **binding to the 30S ribosomal subunit and preventing the attachment of aminoacyl-tRNA**.

Quick Tip

For antibiotics used in cloning, remember: Ampicillin/Penicillin → Cell Wall. Tetracycline → 30S ribosome (blocks tRNA binding). Chloramphenicol/Erythromycin → 50S ribosome.

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24. Match LIST-I with LIST-II

	LIST-I Commercial Production		**LIST-II Microorganism**
A.	Citric acid	I.	Corynebacterium glutamicum
B.	Ethanol	II.	Aspergillus niger
C.	Amino acids and nucleotides	III.	Claviceps purpurea
D.	Alkaloids	IV.	Saccharomyces cerevisiae

Choose the correct answer from the options given below:

(A) A - II, B - III, C - IV, D - I
(B) A-I, B-III, C - II, D - IV
(C) A - II, B - IV, C - I, D - III
(D) A-III, B - IV, C - I, D - II

Correct Answer: (C) A - II, B - IV, C - I, D - III

Solution:

Step 1: Foundational Concept of Industrial Microbiology

Industrial microbiology harnesses the metabolic capabilities of microorganisms (bacteria, yeast, fungi) for the large-scale production of valuable commercial products, including chemicals, pharmaceuticals, fuels, and food products. This question requires matching specific products with the primary microorganism used for their industrial fermentation.

Step 2: Detailed Analysis and Matching

Let's identify the correct microorganism for each product:

- **A. Citric acid:** This weak organic acid is widely used as a flavoring agent and preservative in the food and beverage industry. The primary microorganism used for its industrial production is the filamentous fungus (a mold) ***Aspergillus niger***. This fungus is highly efficient at converting sugars into citric acid under specific fermentation conditions. This matches with **II**.
- **B. Ethanol:** Ethanol is produced through the fermentation of sugars and is a key component of alcoholic beverages and an important biofuel. The most famous and widely used microorganism for this process is the yeast ***Saccharomyces cerevisiae*** (also known as brewer's or baker's yeast). This matches with **IV**.
- **C. Amino acids and nucleotides:** The industrial production of amino acids, particularly L-glutamate (used to make MSG) and L-lysine (an essential feed additive), is a massive biotechnological enterprise. The bacterium that is the workhorse for this industry is ***Corynebacterium glutamicum***. Strains of this bacterium have been extensively engineered to overproduce specific amino acids. This matches with **I**.
- **D. Alkaloids:** Ergot alkaloids are a class of biologically active compounds with important pharmaceutical applications (e.g., in treating migraines and controlling postpartum bleeding). These complex molecules are produced by the fungus ***Claviceps purpurea***, which grows on rye and other cereals. This matches with **III**.

Step 3: Final Answer

Based on the key players in industrial microbiology, the correct set of matches is: **A-II, B-IV, C-I, D-III**.

Quick Tip

Associate key products with their microbes: Ethanol → Yeast (Saccharomyces), Citric Acid → Aspergillus niger, Amino Acids (especially Glutamate) → Corynebacterium. These are classic examples in industrial microbiology.

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25. For sterilization, the culture media and glasswares must be generally autoclaved at:

(A) 121°C and 19 psi
(B) 121°C and 15 psi

(C) 112°C and 15 psi
(D) 120°C and 20 psi

Correct Answer: (B) 121°C and 15 psi

Solution:

Step 1: Foundational Concept of Sterilization by Autoclaving

Autoclaving is the "gold standard" for sterilization in laboratory and medical settings. It is a physical method that uses high-pressure saturated steam to eliminate all forms of microbial life, including vegetative cells, viruses, fungi, and, most importantly, highly resistant **bacterial endospores**. The effectiveness of autoclaving depends on achieving specific conditions of temperature, pressure, and time.

Step 2: Detailed Explanation of the Conditions

- **The Target Organism:** The standard operating conditions are designed to be lethal to the most heat-resistant life forms known: bacterial endospores (e.g., from *Geobacillus stearothermophilus*). If conditions are sufficient to kill these spores, it is assumed that all other less-resistant microbes have also been eliminated.
- **The Role of Pressure:** At normal atmospheric pressure (sea level), water boils at 100°C. This temperature is not high enough to reliably kill bacterial endospores in a reasonable amount of time. To increase the boiling point of water, the pressure must be increased. This is the fundamental principle of a pressure cooker or an autoclave.
- **The Standard Temperature and Pressure:** By increasing the pressure inside the sealed autoclave chamber to approximately **15 psi (pounds per square inch)** above atmospheric pressure, the temperature at which water boils and turns into saturated steam is raised to **121°C (250°F)**. Saturated steam is a highly efficient agent for transferring thermal energy, rapidly denaturing the essential proteins and enzymes of microorganisms.
- **The Time Component:** These conditions of 121°C and 15 psi are typically maintained for a minimum exposure time of **15-20 minutes**. The exact time required can be longer depending on the size and nature of the load. For example, a large volume of liquid will take longer to reach the target temperature at its core than the surface of a surgical instrument.

Step 3: Final Answer

The generally accepted standard conditions for achieving sterilization in a laboratory autoclave are a temperature of **121°C** and a pressure of **15 psi** above atmospheric pressure.

Quick Tip

The combination of **121°C** and **15 psi** is the universal standard for autoclaving in microbiology labs. Memorize this pair of values as they are fundamental to sterilization protocols.

26. Benzoic acid or benzoates are used to preserve food from
A. Insects
B. Yeast
C. Clostridia
D. Molds
Choose the correct answer from the options given below:

(A) A and B only
(B) B and C only
(C) A, C and D only
(D) B and D only

Correct Answer: (D) B and D only

Solution:

Step 1: Foundational Concept of Chemical Food Preservation

Benzoic acid and its more soluble salt, sodium benzoate, are common chemical preservatives used to prevent food spoilage. Their effectiveness is not universal; they are targeted against specific types of spoilage microorganisms and work best under particular chemical conditions, most notably an acidic pH.

Step 2: Detailed Evaluation of Benzoic Acid's Targets

Let's evaluate the effectiveness of benzoates against each group of organisms:

- **A. Insects:** Benzoic acid is an **antimicrobial agent**, meaning it acts against microscopic organisms. It is not an insecticide and has no effect on insects.
- **B. Yeast:** Yeasts are a **primary target** for benzoates. These preservatives are particularly effective at inhibiting the growth of acid-tolerant fermentative yeasts that are common spoilage agents in acidic foods like fruit juices, jams, jellies, and carbonated soft drinks. In an acidic environment, benzoic acid is in its undissociated form, which can easily pass through the yeast cell membrane and disrupt its metabolism.
- **C. *Clostridia*:** *Clostridia* are bacteria, many of which can form highly resistant spores. Benzoates generally have weak antibacterial activity and are particularly ineffective against spore-forming bacteria. For controlling bacteria like *Clostridium botulinum*, especially in cured meats, preservatives like **nitrites** are much more commonly and effectively used.
- **D. Molds:** Like yeasts, molds are fungi and are also **primary targets** for benzoates. The preservative is effective in preventing the growth of molds on the surface of acidic foods such as cheese, bread, and pickles.

Step 3: Final Answer

Benzoic acid and benzoates are primarily used as antifungal agents in acidic foods to preserve them from spoilage by **yeasts (B)** and **molds (D)**.

> Quick Tip
>
> Remember that benzoic acid and sorbic acid are classic anti-fungal preservatives used in acidic foods. Think of them as targeting the "fungal foes" of acidic products: yeasts and molds.

---

27. The Bdellovibrios bacteria is a _____ bacteria:
A. Gram negative
B. Predator of gram negative bacteria
C. It has a single polar flagellum
D. Reproduce by producing spores called myxospore during nutrient deficit conditions
Choose the correct answer from the options given below:

(A) A, B and D only
(B) A, B and C only
(C) A, B, C and D
(D) B, C and D only

Correct Answer: (B) A, B and C only

Solution:

Step 1: Foundational Concept of Predatory Bacteria

Bdellovibrio is a fascinating and unique genus of bacteria known for its predatory lifestyle. Unlike most bacteria that obtain nutrients from their non-living environment, *Bdellovibrio* actively hunts and kills other bacteria for its food. This question asks to identify the correct set of characteristics for this organism.

Step 2: Detailed Analysis of Each Statement

Let's analyze the accuracy of each characteristic:

- **A. Gram negative:** This is **correct**. *Bdellovibrio* is a Gram-negative bacterium, which is relevant to its predatory behavior.
- **B. Predator of gram negative bacteria:** This is **correct** and is the most distinctive feature of *Bdellovibrio*. It is a predator that specifically targets other Gram-negative bacteria (like *E. coli* or *Pseudomonas*). It invades the periplasmic space (the space between the inner and outer membranes of its prey), consumes the host's cellular contents, and replicates within the now-dead host cell, called a bdelloplast.

- **C. It has a single polar flagellum:** This is **correct**. The free-living, "attack phase" of the *Bdellovibrio* life cycle is characterized by a very small, highly motile cell. This motility is powered by a single, thick, sheathed flagellum located at one pole of the cell, which propels it at high speed in search of prey.
- **D. Reproduce by producing spores called myxospore during nutrient deficit conditions:** This is **incorrect**. This statement describes the life cycle of a completely different group of bacteria, the **Myxobacteria**. Myxobacteria are known for their social behavior and their ability to form multicellular fruiting bodies that produce resting spores called myxospores when nutrients are scarce. *Bdellovibrio* does not form any type of spore. Its reproductive cycle involves growing into a long filament inside its host and then fragmenting into multiple new progeny cells, which then lyse the host cell to escape.

Step 3: Final Answer

The correct statements describing *Bdellovibrio* are A, B, and C. Statement D is incorrect as it confuses the reproductive strategy of *Bdellovibrio* with that of Myxobacteria.

> Quick Tip
>
> Associate Bdellovibrio with "predator." It's a Gram-negative predator of other Gram-negative bacteria. Its predatory lifestyle requires it to be fast, hence the powerful single polar flagellum. Don't confuse its complex life cycle with spore formation in other bacteria like Myxobacteria or Bacillus.

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28. Organisms belongs to the genus bacteroides are:

(A) Chemoautotrophs, aerobic and gram positive.
(B) Causative agents of Lyme diseases.
(C) Anaerobic, gram-negative, nonspore-forming rods and usually nonmotile.
(D) Not able to degrade cellulose, pectins, and other complex carbohydrates.

Correct Answer: (C) Anaerobic, gram-negative, nonspore-forming rods and usually nonmotile.

Solution:

Step 1: Foundational Concept of Gut Microbiota

The genus *Bacteroides* comprises a major group of bacteria that are dominant inhabitants of the mammalian gastrointestinal tract, particularly the large intestine. They play a crucial role in human health by helping to digest complex molecules that humans cannot break down on their own. The question asks for the most accurate description of these important bacteria.

Step 2: Detailed Evaluation of Each Description

Let's evaluate the accuracy of each statement:

- **(A) Chemoautotrophs, aerobic and gram positive:** This is incorrect on all three counts. *Bacteroides* are **chemoheterotrophs** (they get energy from organic chemicals), **obligate anaerobes** (oxygen is toxic to them), and are **Gram-negative**.
- **(B) Causative agents of Lyme diseases:** This is incorrect. Lyme disease is a tick-borne illness caused by the spirochete bacterium *Borrelia burgdorferi*. *Bacteroides* are gut commensals, although they can be opportunistic pathogens if they escape the gut.
- **(C) Anaerobic, gram-negative, nonspore-forming rods and usually nonmotile:** This is the **correct textbook description** of the genus *Bacteroides*. They are rod-shaped bacteria that are perfectly adapted to the oxygen-free (anaerobic) environment of the large intestine. They do not form spores and are typically nonmotile.
- **(D) Not able to degrade cellulose, pectins, and other complex carbohydrates:** This is incorrect; in fact, **the exact opposite is true**. The key ecological role of *Bacteroides* in the gut is their remarkable ability to degrade complex plant polysaccharides (dietary fiber) that are indigestible by human enzymes. Their genomes contain an extensive array of enzymes specifically for this purpose.

Step 3: Final Answer

The most accurate and comprehensive description of organisms from the genus *Bacteroides* is given in option **(C)**.

Quick Tip

When you see Bacteroides, immediately think "gut anaerobe." They are the dominant Gram-negative anaerobes in the human colon, and their claim to fame is digesting the complex carbs (fiber) in our diet.

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29. A method for culturing anaerobes is the GasPak System, which uses hydrogen and a _____ catalyst to remove O_2.

(A) Rubidium
(B) Lead
(C) Iridium
(D) Palladium

Correct Answer: (D) Palladium

Solution:

Step 1: Foundational Concept of Culturing Anaerobes

Obligate anaerobes are microorganisms that cannot grow in the presence of oxygen; in fact, oxygen is often toxic to them. To culture these organisms in a laboratory, a special oxygen-free atmosphere must be created. The **GasPak system** is a self-contained method for generating an anaerobic environment within a sealed jar, commonly used in clinical microbiology. It relies on a chemical reaction to remove all the free oxygen.

Step 2: Detailed Explanation of the GasPak System

- **The Gas-Generating Sachet:** The system uses a disposable envelope or sachet containing chemicals (often sodium borohydride and sodium bicarbonate). When a small amount of water is added, the sachet is activated and begins to produce two gases: **hydrogen ($\mathbf{H_2}$)** and carbon dioxide (CO_2). The CO_2 is beneficial for the growth of some anaerobic bacteria.
- **The Chemical Reaction for Oxygen Removal:** The hydrogen gas (H_2) is the key ingredient for removing oxygen. It reacts with the free oxygen (O_2) present in the air inside the sealed jar to produce water (H_2O). The balanced chemical reaction is:

$$2H_2 + O_2 \rightarrow 2H_2O$$

- **The Need for a Catalyst:** This reaction, while thermodynamically favorable, does not occur spontaneously at room temperature. It has a high activation energy and requires a **catalyst** to proceed at a useful rate.
- **The Palladium Catalyst:** The catalyst is contained within a wire mesh basket, which is typically attached to the inside of the jar's lid. This catalyst consists of **palladium** pellets. Palladium is a metal that is highly effective at catalyzing the reaction between hydrogen and oxygen. As the sachet releases hydrogen, the palladium facilitates its rapid combination with all the oxygen in the jar, effectively scrubbing the atmosphere of O_2 and creating the required anaerobic conditions for the bacteria to grow.

Step 3: Final Answer

The catalyst used in the GasPak system to facilitate the chemical removal of oxygen from the atmosphere is **Palladium**.

Quick Tip

For anaerobic culture methods, associate the GasPak system with its two key components: a hydrogen-generating sachet and a **palladium** catalyst. Palladium is a well-known catalyst for hydrogenation reactions, which is essentially what happens when H_2 removes O_2.

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30. The antimicrobial agent mercuric chloride functions by

(A) Interfering with cellular oxidation process.
(B) Inhibiting the enzymes which contain the sulfhydryl group.

(C) Alkylation reactions with organic compounds such as enzymes and other proteins.
(D) Denaturation of proteins, interference with glycolysis and membrane damage.

Correct Answer: (B) Inhibiting the enzymes which contain the sulfhydryl group.

Solution:

Step 1: Foundational Concept of Heavy Metal Toxicity

Heavy metal compounds, such as those containing mercury, silver, or copper, are potent antimicrobial agents. Their toxicity (to both microbes and humans) stems from their ability to bind to and inactivate key cellular proteins, particularly enzymes. This disrupts essential metabolic pathways, leading to cell death.

Step 2: Detailed Explanation of Mercury's Mode of Action

- **The Target: Sulfhydryl Groups:** The mode of action of heavy metal ions like mercury (Hg^{2+}) is primarily due to their very high affinity for **sulfhydryl (-SH) groups**. These functional groups are found on the side chain of the amino acid **cysteine**.
- **Formation of Mercaptides:** When the Hg^{2+} ion encounters one or more sulfhydryl groups within a protein, it binds to them very strongly, displacing the hydrogen atom and forming a stable covalent bond. This structure is known as a **mercaptide** (e.g., Protein-S-Hg-S-Protein).
- **Enzyme Inactivation:** Cysteine residues and their sulfhydryl groups are often located in the **active site** of enzymes, where they are crucial for binding substrates or for the catalytic reaction itself. By binding to these critical sulfhydryl groups, the mercury ion disrupts the protein's correct three-dimensional (tertiary) structure and blocks the active site. This process, known as **sulfhydryl group inhibition**, effectively inactivates the enzyme.
- **Comparing Other Options:** While high concentrations of heavy metals can cause general protein denaturation (Option D), their primary, most specific mechanism at biocidal concentrations is the targeted inhibition of sulfhydryl-containing enzymes. Other mechanisms like alkylation (Option C) are characteristic of different agents (e.g., ethylene oxide).

Step 3: Final Answer

The primary antimicrobial function of mercuric chloride is the **inhibition of enzymes by binding to their essential sulfhydryl groups**.

Quick Tip

Remember that heavy metals like mercury, silver, and arsenic are "sulfhydryl seekers." They poison cells by attacking the -SH groups in proteins, effectively shutting down vital enzymes.

31. Match LIST-I with LIST-II

LIST-I Antimicrobial agent		LIST-II Mode of action	
A.	Cephalosporins	I.	Act by inhibition of biosynthesis of the peptidoglycan cell-wall structure.
B.	Nalidixic acid	II.	Inhibition of DNA synthesis in gram-negative bacteria.
C.	Isoniazid	III.	Inhibits protein synthesis as a result of binding on the 50S subunit ribosome.
D.	Erythromycin	IV.	Blocking pyridoxin and nicotinamide-catalyzed reactions in the microbial cell.

Choose the correct answer from the options given below:

(A) A-I, B-II, C-III, D-IV
(B) A-I, B-III, C-II, D-IV
(C) A-I, B-II, C-IV, D-III
(D) A-III, B-IV, C-I, D-II

Correct Answer: (C) A-I, B-II, C-IV, D-III

Solution:

Step 1: Foundational Concept of Antimicrobial Action

Antimicrobial agents are a diverse group of compounds that kill or inhibit the growth of microorganisms. Their effectiveness stems from their ability to target specific, vital structures or metabolic pathways within the microbe that are often absent in the host. This question requires matching several key antimicrobial drugs with their precise molecular mechanism of action.

Step 2: Detailed Analysis and Matching of Each Agent

Let's break down the function of each antimicrobial drug:

- **A. Cephalosporins:** Cephalosporins belong to the **β-lactam** class of antibiotics, which also includes penicillins. Their molecular structure features a β-lactam ring that is crucial for their activity. They work by targeting the bacterial cell wall, a structure essential for bacterial survival but absent in human cells. Specifically, they inhibit the transpeptidase enzymes (also known as penicillin-binding proteins) that are responsible for the final cross-linking step of peptidoglycan synthesis. Without these cross-links, the cell wall is weakened, leading to cell lysis and death. This matches with **I. Act by inhibition of biosynthesis of the peptidoglycan cell-wall structure.**
- **B. Nalidixic acid:** This is the parent compound of the **quinolone** class of antibiotics. Quinolones target DNA replication by inhibiting a crucial bacterial enzyme called **DNA**

gyrase (a type II topoisomerase). DNA gyrase is responsible for introducing negative supercoils into the bacterial chromosome, a process that is essential to relieve the torsional stress that builds up during DNA unwinding at the replication fork. By inhibiting this enzyme, quinolones block DNA replication and repair, leading to cell death, particularly in gram-negative bacteria. This matches with **II. Inhibition of DNA synthesis in gram-negative bacteria.**

- **C. Isoniazid:** This is a front-line antituberculosis drug, highly specific for bacteria in the genus *Mycobacterium*. Its effectiveness comes from its ability to inhibit the synthesis of **mycolic acids**, which are unique, long-chain fatty acids that are the primary component of the waxy, impermeable cell wall of mycobacteria. The synthesis of mycolic acids requires enzymatic reactions that depend on cofactors derived from pyridoxine (Vitamin B6) and nicotinamide (a form of Niacin/Vitamin B3). Isoniazid, once activated, blocks these specific enzymatic steps. This matches with **IV. Blocking pyridoxin and nicotinamide - catalyzed reactions in the microbial cell.**
- **D. Erythromycin:** This is a member of the **macrolide** class of antibiotics. Macrolides target protein synthesis by binding to the large **50S subunit** of the bacterial ribosome. Specifically, erythromycin binds near the entrance of the polypeptide exit tunnel. This binding physically blocks the growing polypeptide chain from exiting the ribosome, which in turn inhibits the translocation step (the movement of the ribosome along the mRNA). This causes premature dissociation of the nascent peptide chain and halts protein synthesis. This matches with **III. Inhibits protein synthesis as a result of binding on the 50S subunit ribosome.**

Step 3: Final Answer

Based on the specific molecular targets of these antimicrobial agents, the correct set of matches is: **A-I, B-II, C-IV, D-III**.

Quick Tip

Categorize antibiotics by target: Cell Wall (β-lactams like Cephalosporins), DNA Synthesis (Quinolones like Nalidixic acid), Protein Synthesis (Macrolides like Erythromycin target 50S), and Metabolic Pathways (Isoniazid targets mycolic acid synthesis).

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32. The Ti plasmid and its T-DNA have been genetically modified for use as a vector for the insertion of recombinant DNA into plant chromosomes to prevent dicots from tumor diseases. The source of Ti plasmid is:

(A) Asparagus sp.
(B) Arthrobacter luteus
(C) Aspergillus niger
(D) Agrobacterium tumefaciens

Correct Answer: (D) Agrobacterium tumefaciens

Solution:

Step 1: Foundational Concept of Natural Genetic Engineering

The Ti (Tumor-inducing) plasmid is a remarkable natural tool that has become a cornerstone of plant genetic engineering. It is a large plasmid found in a specific type of bacterium that allows the bacterium to act as a "natural genetic engineer," transferring its own genes into a plant's genome. The question asks to identify the specific bacterium that is the natural source of this plasmid.

Step 2: Detailed Explanation of the Ti Plasmid and its Source

- **The Source Organism:** The Ti plasmid is naturally found in the soil-dwelling bacterium ***Agrobacterium tumefaciens***.
- **Crown Gall Disease:** This bacterium is a plant pathogen responsible for causing a disease known as **crown gall disease**. The disease is characterized by the formation of tumor-like growths (galls) at the site of infection on plants, primarily affecting dicotyledonous species.
- **The T-DNA Transfer Mechanism:** *Agrobacterium* causes this disease by transferring a specific segment of its Ti plasmid, known as the **T-DNA (transfer DNA)**, directly into the plant cell's nucleus, where it becomes integrated into the plant's own chromosomes. The T-DNA carries genes that code for the synthesis of plant growth hormones (auxins and cytokinins), which cause uncontrolled cell division (the tumor), and for the production of unusual amino acids called opines, which the bacterium uses as a food source.
- **Harnessing the System for Genetic Engineering:** Scientists have brilliantly exploited this natural gene transfer system. They have created "disarmed" Ti plasmids by removing the tumor-causing hormone genes from the T-DNA region. A gene of interest (e.g., for herbicide resistance or insect resistance) can then be inserted into this modified T-DNA region. The engineered *Agrobacterium* can then be used as a highly efficient vector to deliver this desired gene into plant cells, creating a transgenic plant.
- **Evaluating Other Options:** The other options are incorrect. Asparagus is a plant. *Arthrobacter* is another common genus of soil bacteria, but it is not associated with the Ti plasmid or crown gall disease. *Aspergillus* is a genus of fungus (a mold).

Step 3: Final Answer

The natural source of the tumor-inducing (Ti) plasmid is the soil bacterium ***Agrobacterium tumefaciens***.

Quick Tip

Think of Agrobacterium tumefaciens as "nature's genetic engineer." The name itself gives a clue: *tumefaciens* means "tumor-making," which refers to the crown gall disease caused by its **Ti** (Tumor-inducing) plasmid.

33. The ability of a molecule to function as an antigen depends on its:
A. Size
B. Structural complexity
C. Chemical nature
D. Degree of foreign nature to the host
Choose the correct answer from the options given below:

(A) A, B and D only
(B) A, B and C only
(C) A, B, C and D
(D) B, C and D only

Correct Answer: (C) A, B, C and D

Solution:

Step 1: Foundational Concept of Antigenicity

An **antigen** is any molecule, typically a protein or polysaccharide, that can bind to specific receptors on lymphocytes (B cells or T cells) and trigger an adaptive immune response. The ability of a molecule to act as a potent antigen, a property known as **immunogenicity**, is not inherent to all molecules but depends on a combination of several key physical and chemical characteristics.

Step 2: Detailed Analysis of Each Factor Determining Immunogenicity

Let's analyze the contribution of each property:

- **A. Size (Molecular Weight):** This is a critical factor. In general, **larger molecules are better antigens**. Molecules with a molecular weight below 5,000-10,000 Daltons (Da) are typically poor immunogens. Very small molecules, known as **haptens**, are not immunogenic on their own but can become antigenic if they are chemically attached to a larger carrier protein.
- **B. Structural complexity:** Simple, repeating polymers (homopolymers) are poor antigens because they lack the structural diversity needed for effective B and T cell recognition. **Greater structural complexity leads to greater immunogenicity**. Proteins, with their complex primary, secondary, tertiary, and quaternary structures, are the most potent antigens because they present a wide variety of three-dimensional shapes, called **epitopes** (or antigenic determinants), for the immune system to recognize.
- **C. Chemical nature:** The chemical class of a molecule is very important. Due to their complexity and variety, **proteins are the most potent antigens**. Large polysaccharides are also good antigens. In contrast, lipids and nucleic acids are generally poor antigens unless they are complexed with a protein or polysaccharide carrier molecule.
- **D. Degree of foreign nature to the host:** The adaptive immune system is trained from an early stage to recognize and tolerate the body's own molecules, a process called

self-tolerance. To elicit an immune response, a molecule must be recognized as **"non-self" or foreign**. The more phylogenetically (evolutionarily) distant the source of the antigen is from the host, the more foreign it will appear, and the more potent the immune response it will elicit. For example, bovine serum albumin will cause a much stronger immune response in a chicken than it will in a goat.

Step 3: Final Answer

All four properties described—**size, structural complexity, chemical nature, and foreignness**—are crucial and interdependent determinants of a molecule's ability to function as a potent antigen. Therefore, all statements A, B, C, and D are correct.

Quick Tip

To remember the properties of a good antigen, think of a "big, complex, foreign protein." **Big** (size), **complex** (structure), **foreign** (foreignness), and usually a **protein** (chemical nature). All these factors contribute to strong antigenicity.

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34. Match LIST-I with LIST-II

LIST-I Immunoglobin class		**LIST-II Characterstics**	
A.	IgG	I.	Serves as part of B-cell receptor complex
B.	IgA	II.	Anaphylactic mediating antibody
C.	IgD	III.	Most abundant in body fluid, neutralize toxins, opsonizes bacteria
D.	IgE	IV.	Secretary antibody and protect mucous membrane.

Choose the correct answer from the options given below:

(A) A-I, B-II, C - III, D - IV
(B) A-I, B - III, C - II, D - IV
(C) A-I, BII, C - IV, D - III
(D) A-III, B - IV, C - I, D - II

Correct Answer: (D) A-III, B - IV, C - I, D - II

Solution:

Step 1: Foundational Concept of Immunoglobulin Classes

Immunoglobulins, or antibodies, are key proteins of the humoral adaptive immune system. In humans, they are divided into five major classes, or **isotypes** (IgG, IgA, IgM, IgD, IgE), based on the type of heavy chain they possess. Each isotype has a distinct structure and is specialized for a particular set of functions and locations within the body.

Step 2: Detailed Analysis and Matching of Each Isotype

Let's match each immunoglobulin class with its primary characteristic:

- **A. IgG:** This is the **most abundant** immunoglobulin in the blood serum and body fluids, making up about 75-80% of the total antibody pool. It is the workhorse of the secondary immune response. As a versatile monomer, IgG is capable of **neutralizing toxins** and viruses, **opsonizing** (tagging) pathogens for enhanced phagocytosis, and activating the complement system. This matches with **III. Most abundant in body fluid, neutralize toxins, opsonizes bacteria.**
- **B. IgA:** This is the main antibody found in mucosal secretions, including mucus, saliva, tears, and breast milk. While it is the second most abundant antibody in serum (as a monomer), its primary role is at mucosal surfaces where it exists as a dimer, linked by a J-chain and protected by a "secretory component." It plays a crucial frontline role in neutralizing pathogens before they can enter the body. This matches with **IV. Secretory antibody and protect mucous membrane.**
- **C. IgD:** This immunoglobulin is found in very low concentrations in the serum, and its soluble form has a limited role. Its primary and most important function is as a surface-bound antigen receptor on mature, naive B-lymphocytes. Along with IgM, it forms the **B-cell receptor (BCR) complex**, which is responsible for recognizing antigens and activating the B cell. This matches with **I. Serves as part of B-cell receptor complex.**
- **D. IgE:** Even though it is present in the lowest concentration in the serum, IgE is famous for its central role in **allergic reactions** (Type I hypersensitivity) and in defense against parasitic worms. It binds to high-affinity receptors on the surface of mast cells and basophils. When an allergen (like pollen) cross-links these surface-bound IgE molecules, it triggers the cells to degranulate, releasing a flood of inflammatory mediators like histamine, which cause the symptoms of allergy and anaphylaxis. This matches with **II. Anaphylactic mediating antibody.**

Step 3: Final Answer

Based on the distinct roles of each antibody isotype, the correct matching is: **A-III, B-IV, C-I, D-II**.

> Quick Tip
>
> Use the mnemonic "GAME-D" to remember the isotypes. **G** is the most abundant and goes everywhere. **A** is in secretions ("secretory"). **M** is the first responder (not in this list). **E** is for allergy ("Eeeek! a bee!"). **D** is a receptor on B-cells.

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35. The cationic antimicrobial peptide, histatin is found in human's_____.

(A) Synovial fluid
(B) Cerebrospinal fluid
(C) Bile juice

(D) Saliva

Correct Answer: (D) Saliva

Solution:

Step 1: Foundational Concept of Antimicrobial Peptides (AMPs)

Antimicrobial peptides (AMPs) are an ancient and evolutionarily conserved component of the innate immune system. They are small, typically cationic peptides that provide a rapid, non-specific first line of defense against a broad range of pathogens, including bacteria, fungi, and viruses. **Histatins** are one such specific family of AMPs. The question asks for their primary location in the human body.

Step 2: Detailed Explanation of Histatins

- **Chemical Nature:** Histatins are a family of small, positively charged (cationic) peptides that are uniquely rich in the amino acid **histidine**.
- **Source of Secretion:** They are produced and secreted almost exclusively by the major **salivary glands** in the oral cavity—specifically, the parotid and submandibular glands.
- **Primary Location:** Consequently, histatins are a major protein component of human **saliva**.
- **Functions in the Oral Cavity:** Their presence in saliva allows them to perform several crucial protective functions in the mouth. They are best known for their potent **antifungal activity**, especially against the opportunistic yeast *Candida albicans* (the cause of oral thrush). They also possess antibacterial activity and are believed to play a role in promoting oral wound healing.
- **Other Body Fluids:** Histatins are not characteristically found in other major body fluids like synovial fluid (in joints), cerebrospinal fluid (surrounding the brain and spinal cord), or bile (produced by the liver). Their production is highly localized to the salivary glands.

Step 3: Final Answer

The antimicrobial peptide histatin is found as a primary component of human **saliva**.

Quick Tip

Associate histatins with the oral cavity. The name itself contains "hist-" for histidine-rich and "-statin" suggesting a stopping/inhibiting action, which in this case is microbial growth in the mouth.

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36. Convalescent sera belongs to

(A) Sera from healthy individual
(B) Sera of patients chronically infected with bacterial disease
(C) Sera of patients recovering from infectious disease
(D) Sera of patients in the latent phase of infection

Correct Answer: (C) Sera of patients recovering from infectious disease

Solution:

Step 1: Foundational Concept of Convalescence and Serum

To understand the term "convalescent sera," we must first define its components. "Convalescent" refers to the period of gradual recovery from an illness. "Sera" is the plural of serum, which is the fluid component of blood that remains after the blood cells and clotting factors have been removed. Therefore, convalescent serum is blood serum collected from an individual during a specific phase of their interaction with a disease.

Step 2: Detailed Explanation

- **The Convalescent Phase:** Convalescence is the phase of recovery that follows an infection. During this time, the patient's adaptive immune system has successfully fought off and cleared the pathogen.
- **High Titer of Specific Antibodies:** A key result of a successful immune response is the production of a large quantity of high-affinity antibodies that are specific to the invading pathogen. These antibodies circulate in the blood.
- **Composition of Convalescent Serum:** Consequently, the blood serum of a convalescing patient is rich in these specific, protective antibodies. Therefore, convalescent serum is defined as the serum obtained from patients who are **recovering from an infectious disease**.
- **Therapeutic Use (Passive Immunotherapy):** This antibody-rich serum can be collected and used as a form of therapy. When administered to another individual who is actively sick with the same disease, it provides them with a direct infusion of pre-formed, pathogen-fighting antibodies. This is a form of **passive immunotherapy**, known as convalescent plasma therapy, which can help the recipient's immune system control the infection.

Step 3: Final Answer

Convalescent sera refers to the serum collected from **patients recovering from an infectious disease**, which is valuable due to its high concentration of specific antibodies.

Quick Tip

Break down the term: "Convalescent" = Recovering. "Sera" = blood serum. So, "Convalescent sera" = serum from a recovering patient, which is valuable because it's full of disease-specific antibodies.

37. Typhoid Vi antigen type of vaccine is:

(A) Bacterial products
(B) Killed products
(C) Live products
(D) Subunit

Correct Answer: (D) Subunit

Solution:

Step 1: Foundational Concept of Vaccine Classification

Vaccines are biological preparations that provide active acquired immunity to a particular infectious disease. They are classified into several types based on the nature of the antigen they contain—that is, the part of the pathogen that is presented to the immune system. The question asks to classify the typhoid vaccine that is based on the Vi antigen.

Step 2: Detailed Analysis of Vaccine Types

Let's analyze the main classes of vaccines:

- **Live Attenuated Vaccines:** These use a live, but weakened (attenuated), form of the pathogen that can still replicate but does not cause disease. They typically provide a very strong and long-lasting immune response. The oral typhoid vaccine (Ty21a) is an example.
- **Killed (Inactivated) Vaccines:** These use the whole pathogen that has been killed by heat or chemicals. The pathogen cannot replicate, so these vaccines are very safe but may require booster shots. The older, injectable whole-cell typhoid vaccine was of this type.
- **Subunit Vaccines:** These vaccines do not use the whole pathogen at all. Instead, they use only specific, purified components (subunits) of the pathogen that are known to be antigenic, such as a surface protein, a sugar capsule, or a toxin. This makes them extremely safe as they cannot cause disease.
- **The Typhoid Vi Vaccine:** The bacterium that causes typhoid fever, *Salmonella* Typhi, protects itself with a surface capsule made of a specific polysaccharide called the **Vi antigen**. The typhoid Vi vaccine is composed of this **purified Vi capsular polysaccharide**.
- **Conclusion on Classification:** Since this vaccine uses only a specific molecular component (the polysaccharide capsule) of the bacterium rather than the entire organism (either live or killed), it is classified as a **subunit vaccine**. More specifically, it is a polysaccharide subunit vaccine. (There are also conjugate versions where the polysaccharide is linked to a protein to create a stronger immune response, especially in young children, but this is still a type of subunit vaccine).

Step 3: Final Answer

The typhoid vaccine based on the Vi antigen is a type of **subunit vaccine**.

> Quick Tip
>
> If a vaccine is named after a specific part of a pathogen (like the "Vi antigen" or "Spike protein"), it is almost always a **subunit** or **recombinant** vaccine. These vaccines isolate a key antigenic component to induce a targeted immune response.

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38. Which one of the given statement is not correct about plant viruses ?

(A) In viruses, the envelope proteins may even project from the envelope surface as spikes are also called as protomers
(B) In viruses, the envelope proteins may even project from the envelope surface as spikes are also called as concatemers
(C) In viruses, the envelope proteins may even project from the envelope surface as spikes are also called as peplomers.
(D) In viruses, the envelope proteins may even project from the envelope surface as spikes are also called as capsomers

Correct Answer: (B) In viruses, the envelope proteins may even project from the envelope surface as spikes are also called as concatemers

Solution:

Step 1: Foundational Concept of Viral Terminology

Virology uses a precise set of terms to describe the components that make up a virus particle (virion). This question asks to identify an incorrect term used to describe the glycoprotein spikes found on the surface of an enveloped virus. While the question mentions "plant viruses," the terminology is general to the field of virology.

Step 2: Detailed Explanation and Definition of Terms

Let's define each term and evaluate its relevance to envelope spikes:

- **Protomers:** This is a general biochemical term for any individual protein subunit that assembles to form a larger, oligomeric protein complex. The protein shell (capsid) of a virus is made of protomers. While the glycoprotein spikes are also made of protein subunits, "protomer" refers to the building block, not the final spike structure itself.
- **Peplomers:** This is the **correct and specific technical term** for the glycoprotein spike-like projections found on the outer surface of a viral envelope. The word is derived from the Greek *peplos*, meaning "robe" or "envelope." These structures are responsible for viral attachment to host cells.

- **Capsomers:** These are the morphological subunits that make up the viral **capsid** (the protein shell that encloses the viral genome). They are visible in electron micrographs as repeating structural units. They are part of the capsid, not the envelope.
- **Concatemers:** This term is completely unrelated to viral structural proteins. A concatemer is a long DNA molecule composed of multiple copies of a genome linked end-to-end in series. This structure is an intermediate in the replication of the genome of some viruses (notably certain bacteriophages and herpesviruses), a process known as rolling-circle replication. It has **nothing to do with protein spikes**.

Step 3: Final Answer

The statement that is definitively incorrect is that envelope spikes are called concatemers. **Concatemers** are structures related to viral DNA replication, not the protein spikes on the viral envelope.

Quick Tip

Remember these key viral structure terms: **Capsid** is the protein coat, made of **capsomers**. The optional outer membrane is the **envelope**, which has spikes called **peplomers**. A **concatemer** is a long string of replicated genomes.

---

39. Hepatitis C virus can cause liver cancer. It has:

(A) ds DNA genome
(B) ssDNA genome
(C) ss RNA genome
(D) ds RNA genome

Correct Answer: (C) ss RNA genome

Solution:

Step 1: Foundational Concept of Viral Genome Classification

Viruses are classified based on the nature of their genetic material. The Baltimore classification system, for example, categorizes viruses based on their type of genome (DNA or RNA, single-stranded or double-stranded) and their method of replication. This question asks to identify the specific type of genome found in the Hepatitis C virus (HCV).

Step 2: Detailed Explanation of the HCV Genome

- **Viral Family:** Hepatitis C virus (HCV) is a member of the **Flaviviridae** family of viruses.
- **Genome Type:** The genome of HCV is a **single-stranded, positive-sense RNA molecule**. This is often abbreviated as **ss(+)RNA**.

- **Positive-Sense RNA:** The term "positive-sense" (or "plus-strand") means that the viral RNA genome has the same sequence as the messenger RNA (mRNA) that is translated into proteins. This has a significant consequence: upon entering a host cell, the ss(+)RNA genome can be immediately recognized and translated by the host cell's ribosomes to produce viral proteins. This allows for a very rapid start to the infection cycle.
- **Dual Role of the Genome:** The HCV genomic RNA serves two essential functions: it acts as the mRNA for protein translation, and it serves as the template for the replication of new viral genomes.
- **Comparison with Other Hepatitis Viruses:** It is important to note that different viruses that cause hepatitis have different types of genomes. For example, Hepatitis B virus (HBV) is a hepadnavirus with a partially double-stranded DNA (dsDNA) genome. Hepatitis A virus (HAV) is a picornavirus, which, like HCV, has an ss(+)RNA genome.

Step 3: Final Answer

The Hepatitis C virus (HCV) has a **single-stranded RNA (ssRNA)** genome.

Quick Tip

Remember the hepatitis virus genomes: Hep **B** has DNA (**B** is the only DNA one). Hep **A** and **C** have RNA. Most RNA viruses that cause chronic infections (like HCV, HIV) are single-stranded.

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40. The role of slow sand filters in water treatment facilities is:

(A) To remove water borne microbes upto a set standard.
(B) To remove excess ammonia present in the polluted water
(C) To evaluate the microbiological characteristics of water.
(D) To neutralize the increased pH of the water.

Correct Answer: (A) To remove water borne microbes upto a set standard.

Solution:

Step 1: Foundational Concept of Water Purification

Slow sand filtration is a reliable and widely used method for purifying water, particularly in centralized water treatment systems. It is an ecological purification method that relies on both physical and biological processes to produce safe, potable water. The question asks for the primary function of this process.

Step 2: Detailed Explanation of the Slow Sand Filter Mechanism

- **The Process:** A slow sand filter operates by passing raw water slowly (by gravity) through a bed of fine sand.

- **The Schmutzdecke:** The primary mechanism of purification is not simple physical straining by the sand. Over time, a complex, gelatinous biological layer, known by the German term ***schmutzdecke*** ("dirty layer"), develops on the surface of the sand.
- **The Biological Heart of the Filter:** This *schmutzdecke* is a living ecosystem, a matrix composed of a community of beneficial bacteria, fungi, protozoa, rotifers, and algae. It is this biological layer that is responsible for the majority of the water purification.
- **Mechanisms of Purification:** The microorganisms within the *schmutzdecke* actively purify the water in several ways: they trap suspended particles, they prey upon and consume pathogenic microbes (like bacteria, viruses, and protozoan cysts), and they outcompete them for nutrients.
- **The Primary Role:** As a result of this highly effective biological action, the primary and most important role of slow sand filters is the **removal of waterborne pathogenic microbes**. These filters are extremely effective, often reducing microbial counts and turbidity by over 99%, thereby rendering the water safe for human consumption.
- **Evaluating Other Roles:** While some secondary chemical changes can occur (e.g., some ammonia removal via nitrification), these are not the primary purpose of the filter. It is a treatment method, not an evaluation method, and it does not significantly alter the pH.

Step 3: Final Answer

The main role of slow sand filters in water treatment is to **remove waterborne microbes** to produce a standard of water that is safe for consumption.

Quick Tip

The key to understanding slow sand filters is the "schmutzdecke" – the "dirty layer" on top. This biological layer is what "eats" the bad microbes. So, the main job of the filter is biological purification, i.e., removing microbes.

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41. Match LIST-I with LIST-II

	LIST-I Gene interaction		**LIST-II Modified F2 ratio**
A.	Complementary gene action	I.	12:3:1
B.	Supplementary gene action	II.	13:3
C.	Inhibitory gene action	III.	9:3:4
D.	Masking gene action	IV.	9:7

Choose the correct answer from the options given below:

(A) A-I, B-II, C - III, D - IV
(B) A-II, B-I, C - IV, D - III
(C) A-IV, B - III, C - II, D-I
(D) A-III, B - IV, C - I, D - II

Correct Answer: (C) A-IV, B - III, C - II, D-I

Solution:

Step 1: Foundational Concept of Epistasis and Modified Ratios

In genetics, **epistasis** is a form of gene interaction where the phenotypic expression of one gene is affected (masked, inhibited, or modified) by one or more other genes at different loci. These interactions cause the classic 9:3:3:1 Mendelian F2 dihybrid ratio to be modified into other characteristic ratios. This question requires matching different types of epistasis with their resulting F2 phenotypic ratios.

Step 2: Detailed Analysis and Matching of Each Interaction

Let's analyze how each gene interaction modifies the standard 9 (A_B_) : 3 (A_bb) : 3 (aaB_) : 1 (aabb) ratio:

- **A. Complementary gene action:** In this case, the dominant alleles of *two different genes* are required to produce a single phenotype. If either dominant allele is absent, a different phenotype is produced.
  - Genotype A_B_ (9 parts) → Phenotype 1 (e.g., purple)
  - Genotypes A_bb (3 parts), aaB_ (3 parts), and aabb (1 part) all lack at least one of the required dominant alleles → Phenotype 2 (e.g., white)
  - This combines the 3, 3, and 1 classes, resulting in a phenotypic ratio of **9:7**. This matches with **IV**.
- **B. Supplementary gene action (Recessive Epistasis):** Here, a recessive allele pair at one locus (e.g., aa) masks the expression of alleles at another locus (the B/b locus).
  - Genotype A_B_ (9 parts) → Phenotype 1 (e.g., agouti)
  - Genotype A_bb (3 parts) → Phenotype 2 (e.g., black)
  - Genotypes aaB_ (3 parts) and aabb (1 part) → The 'aa' is epistatic, so they both produce Phenotype 3 (e.g., albino).
  - This combines the 3 and 1 classes, resulting in a phenotypic ratio of **9:3:4**. This matches with **III**.
- **C. Inhibitory gene action (Dominant and Recessive Epistasis):** A dominant allele at one locus (e.g., I, the inhibitor gene) prevents the expression of a dominant allele at another locus (e.g., C, for color).
  - Genotypes I_C_ (9 parts) and I_cc (3 parts) → The dominant 'I' inhibits color expression, resulting in Phenotype 1 (e.g., white).
  - Genotype iiC_ (3 parts) → The inhibitor is absent, so color is expressed, resulting in Phenotype 2 (e.g., colored).
  - Genotype iicc (1 part) → No inhibitor, but also no color gene, resulting in Phenotype 1 (e.g., white).
  - This combines the 9, 3, and 1 classes, resulting in a phenotypic ratio of **13:3**. This matches with **II**.

- **D. Masking gene action (Dominant Epistasis):** A dominant allele at one locus (e.g., A) masks the expression of alleles at another locus (the B/b locus).
  - Genotypes A_B_ (9 parts) and A_bb (3 parts) → The dominant 'A' is epistatic, so they both produce Phenotype 1.
  - Genotype aaB_ (3 parts) → Phenotype 2.
  - Genotype aabb (1 part) → Phenotype 3.
  - This combines the 9 and 3 classes, resulting in a phenotypic ratio of **12:3:1**. This matches with **I**.

Step 3: Final Answer

The correct matching of gene interactions to their characteristic F2 ratios is: **A-IV, B-III, C-II, D-I**.

Quick Tip

To quickly recall these ratios, remember the totals. Complementary (9+7=16), Recessive Epistasis (9+3+4=16), Dominant Epistasis (12+3+1=16), and Inhibitory (13+3=16). Associate Complementary with 9:7 and Dominant Epistasis with 12:3:1 as the most common examples.

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42. The F_1 hybrid (Rr Ii) is crossed with a variety double recessive for both the traits. How many types of zygotes will be produced in the cross?

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

Correct Answer: (D) 4

Solution:

Step 1: Foundational Concept of the Test Cross

A **test cross** is a genetic cross performed to determine the unknown genotype of an individual that displays a dominant phenotype. This is done by crossing the individual in question with another individual that is homozygous recessive for the trait(s) of interest. In a **dihybrid** test cross, we are examining two different genes simultaneously. The types of offspring (zygotes) produced reveal the types of gametes produced by the parent with the unknown genotype.

Step 2: Key Formula for Gamete Production

The number of different types of gametes an individual can produce through meiosis is determined by the number of heterozygous gene pairs it has. The formula is $\mathbf{2}^n$, where n is the

number of heterozygous gene pairs. The different combinations are a result of Mendel's Law of Independent Assortment.

Step 3: Detailed Explanation of the Cross

The specified cross is: **RrIi** $\times$ **rrii**

- **Gametes from the F_1 hybrid (RrIi):**
  - This individual is heterozygous for two gene pairs (R/r and I/i), so n = 2.
  - The number of different gamete types it can produce is $2^n = 2^2 = \mathbf{4}$.
  - According to the Law of Independent Assortment, the alleles for the two genes will segregate into gametes independently of one another. The four possible combinations, produced in equal proportions (1:1:1:1), are: **RI, Ri, rI, and ri**.
- **Gametes from the double recessive parent (rrii):**
  - This individual is homozygous for both gene pairs (n = 0 heterozygous pairs).
  - The number of different gamete types it can produce is $2^0 = \mathbf{1}$.
  - The only possible gamete it can produce is **ri**.
- **Formation of Zygotes:** The number of different zygote genotypes will be equal to the number of different gamete types produced by the heterozygous parent, as the recessive parent contributes the same gamete ('ri') to every fertilization.
  - Gamete RI + Gamete ri $\rightarrow$ Zygote RrIi
  - Gamete Ri + Gamete ri $\rightarrow$ Zygote Rrii
  - Gamete rI + Gamete ri $\rightarrow$ Zygote rrIi
  - Gamete ri + Gamete ri $\rightarrow$ Zygote rrii

  There are **4** distinct types of zygotes produced.

Step 4: Final Answer

In a dihybrid test cross between RrIi and rrii, the heterozygous parent produces 4 types of gametes, leading to the formation of **4** different types of zygotes.

Quick Tip

In a test cross, the number of resulting phenotypes and genotypes is determined solely by the number of different gametes the heterozygous parent can produce. For a dihybrid cross (2 heterozygous pairs), it's always 4. For a trihybrid, it would be $2^3 = 8$.

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43. Which of the following statement is wrong about C_4 plants

(A) Kranz anatomy is present
(B) Initial CO_2 acceptor is Phosphoenol-pyruvate (PEP)
(C) First stable product is 3-phosphoglycerate

(D) Calvin cycle operates along with the Hatch and Slack cycle.

Correct Answer: (C) First stable product is 3-phosphoglycerate

Solution:

Step 1: Foundational Concept of C_4 Photosynthesis

C_4 photosynthesis (also known as the Hatch-Slack pathway) is a specialized adaptation found in certain plants (like corn, sugarcane, and sorghum) that live in hot, dry climates. It serves as a highly efficient **CO_2-concentrating mechanism** designed to reduce **photorespiration**, a wasteful process that occurs when the enzyme RuBisCO fixes O_2 instead of CO_2.

Step 2: Detailed Analysis of Each Statement

Let's analyze the key features of the C_4 pathway:

- **(A) Kranz anatomy is present:** This is **correct**. C_4 plants exhibit a unique leaf structure called **Kranz anatomy** (from the German word for "wreath"). This consists of two distinct types of photosynthetic cells: an outer layer of mesophyll cells surrounding an inner layer of bundle sheath cells, which in turn surround the vascular bundles. This spatial separation is crucial for the C_4 pathway.
- **(B) Initial CO_2 acceptor is Phosphoenol-pyruvate (PEP):** This is **correct**. In the mesophyll cells of a C_4 plant, CO_2 is first fixed by the enzyme **PEP carboxylase**. This enzyme has a very high affinity for CO_2 and is not inhibited by O_2. It uses the 3-carbon molecule **phosphoenol-pyruvate (PEP)** as the substrate to which it attaches the CO_2.
- **(C) First stable product is 3-phosphoglycerate:** This is **wrong**. When PEP carboxylase fixes CO_2 to the 3-carbon PEP molecule, the first stable product formed is **oxaloacetate**, which is a **4-carbon acid**. This is why the pathway is called C_4 photosynthesis. Oxaloacetate is then quickly converted to other 4-carbon acids (like malate or aspartate) for transport. In contrast, **3-phosphoglycerate** (a 3-carbon compound) is the first stable product of the standard Calvin cycle (the C_3 pathway), formed when RuBisCO fixes CO_2 to RuBP.
- **(D) Calvin cycle operates along with the Hatch and Slack cycle:** This is **correct**. The C_4 cycle does not replace the Calvin cycle; it precedes it. The entire purpose of the C_4 pathway is to act as a CO_2 pump. It captures CO_2 in the mesophyll cells, transports it as a 4-carbon acid to the bundle sheath cells, and then releases the CO_2 in high concentrations right next to the RuBisCO enzymes. This highly concentrated CO_2 then enters the standard **Calvin cycle** to be converted into sugars.

Step 3: Final Answer

The statement that is incorrect is (C). The first stable product of C_4 photosynthesis is the 4-carbon acid oxaloacetate, not the 3-carbon compound 3-phosphoglycerate.

Quick Tip

The names C3 and C4 come directly from the number of carbons in the first stable product of CO2 fixation. For C3 plants, it's a 3-carbon compound (3-PGA). For C4 plants, it's a 4-carbon compound (oxaloacetate).

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44. The plants bloom when the light duration is less than 12 hours per day are know as.

(A) Short day plants
(B) Long day plants
(C) Mid day plants
(D) Day neutral plants

Correct Answer: (A) Short day plants

Solution:

Step 1: Foundational Concept of Photoperiodism

Photoperiodism is the physiological and developmental response of an organism, particularly plants, to the relative lengths of the light (photoperiod) and dark periods. This ability to measure day length allows plants to time seasonal activities, the most critical of which is flowering, to ensure reproductive success under favorable conditions. This timing mechanism is controlled by photoreceptor proteins, primarily phytochromes, which can detect the presence or absence of light. Plants are broadly categorized based on their specific photoperiodic requirements for flowering.

Step 2: Detailed Explanation of Photoperiodic Categories

Let's define each category in detail:

- **Short-day plants (SDPs):** These plants initiate flowering only when the day length is shorter than a certain critical duration. However, extensive research has shown that it is actually the length of the *uninterrupted dark period* that is the true determining factor. Therefore, it is more accurate to call them **"long-night" plants**. They require a continuous period of darkness that is *longer* than a critical length to induce flowering. If this long night is interrupted even by a brief flash of light, flowering is inhibited. The description "blooming when the light duration is less than 12 hours" implies a night longer than 12 hours, which perfectly fits this category. Examples include chrysanthemums, poinsettias, and soybeans, which typically flower in the late summer or autumn.
- **Long-day plants (LDPs):** These plants initiate flowering when the day length is longer than a critical duration. Correspondingly, they are more accurately described as **"short-night" plants**, as they flower when the uninterrupted dark period is *shorter* than a critical length. In fact, interrupting the night with a flash of light can artificially induce flowering

in LDPs. Examples include spinach, lettuce, and iris, which typically flower in the spring and early summer.

- **Day-neutral plants (DNPs):** The flowering in these plants is not controlled by the photoperiod. Instead, flowering is initiated based on other cues, such as reaching a certain developmental stage or age (maturation), or in response to environmental factors like a period of cold temperatures (vernalization). Their flowering is independent of day length. Examples include tomatoes, cucumbers, corn, and roses.
- **Mid-day plants:** This is **not a standard scientific classification** for photoperiodism. The critical mechanism in plants is based on measuring the duration of a continuous dark period, leading to the long-night and short-night classifications, along with the day-neutral category.

Step 3: Final Answer

Based on the established definitions of photoperiodism, plants that bloom when the light duration is short (implying a critically long, uninterrupted night) are known as **short-day plants**.

> Quick Tip
>
> It's a common misconception that day length is the trigger. The critical factor is actually the length of the uninterrupted dark period. Short-day plants are really long-night plants, and long-day plants are really short-night plants.

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45. A rock body through which ground water flows is called

(A) Lake
(B) Artesian well
(C) Springs
(D) Aquifer

Correct Answer: (D) Aquifer

Solution:

Step 1: Foundational Concept of Hydrogeology

Hydrogeology is the area of geology that deals with the distribution and movement of groundwater in the soil and rocks of the Earth's crust. It uses specific terminology to describe formations based on their ability to hold and transmit water. The key properties are **porosity** (the amount of void space in a rock that can hold water) and **permeability** (the ability of the rock to allow water to flow through it). This question asks for the term that describes a rock formation with both high porosity and high permeability.

Step 2: Detailed Explanation of Hydrogeological Terms

Let's define the given terms:

- **Lake:** A lake is a large body of fresh water on the Earth's surface. It is a form of **surface water** and is not contained within a rock body in the way that groundwater is. Therefore, this term is incorrect.
- **Artesian well:** An artesian well is not a rock formation itself, but a **man-made structure** used to extract water from a specific type of aquifer known as a confined aquifer. In a confined aquifer, water is held under pressure between two impermeable layers. A well drilled into this formation allows the pressurized water to flow upward without pumping. It is a way to access an aquifer, not the aquifer itself.
- **Springs:** A spring is a **natural feature**, not a rock body. It is a location on the Earth's surface where groundwater naturally emerges, typically because the water table intersects the ground surface. A spring is a point of discharge *from* an aquifer.
- **Aquifer:** This is the correct term. An aquifer is defined as a body of porous and permeable rock, sand, or gravel that can both store and transmit a significant quantity of groundwater. Materials like sand, gravel, and fractured sandstone are excellent aquifers because they have both the storage capacity (porosity) and the interconnectedness of pores (permeability) to allow water to flow. Aquifers are the essential sources of groundwater for wells and springs. This definition directly matches the description in the question.

Step 3: Final Answer

A rock body that has the capacity to store and transmit groundwater, allowing it to flow, is correctly termed an **aquifer**.

Quick Tip

Think of an aquifer as an underground "river" or "sponge" made of rock and sand. It's the container and conduit for groundwater. Wells and springs are just ways for that water to be accessed or to escape.

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46. Match LIST-I with LIST-II

LIST-I **Bacterial DNA replication proteins**		**LIST-II** **Functions**	
A.	Helicase	I.	Removes RNA nucleotides of primer...
B.	DNA pol I	II.	Unwinds parental double helix at replication forks.
C.	DNA pol III	III.	Relieves overwinding strain ahead of replication forks...
D.	Topoisomerase	IV.	Using parental DNA as a template, synthesizes new DNA strand...

Choose the correct answer from the options given below:

(A) A-I, B- II, C - III, D - IV
(B) A-I, B- III, C - II, D - IV
(C) A-II, B-I, C - IV, D - III
(D) A-III, B - IV, C - I, D - II

Correct Answer: (C) A-II, B-I, C - IV, D - III

Solution:

Step 1: Foundational Concept of the Bacterial Replisome

Bacterial DNA replication is a highly coordinated process carried out by a complex assembly of enzymes and proteins known as the replisome. Each component has a specific and essential role in ensuring the accurate and efficient duplication of the chromosome. This question requires matching key replication enzymes with their precise functions.

Step 2: Detailed Analysis and Matching of Each Enzyme

Let's match each protein from LIST-I with its function from LIST-II:

- **A. Helicase:** This enzyme is the "unzipper" of the DNA. It is situated at the very front of the replication fork and uses the energy from ATP hydrolysis to break the hydrogen bonds between the base pairs, thereby separating the two parental strands of the DNA double helix. This unwinding process creates the single-stranded templates needed for replication. This matches with **II. Unwinds parental double helix at replication forks.**
- **B. DNA pol I:** While DNA polymerase III is the main replicative enzyme, DNA Polymerase I performs a crucial "clean-up" and repair function. On the lagging strand, DNA synthesis is discontinuous and initiated by multiple RNA primers. DNA Pol I uses its **5' to 3' exonuclease** activity to remove these RNA primers one nucleotide at a time. Simultaneously, it uses its **5' to 3' polymerase** activity to fill the resulting gap with the correct DNA nucleotides. This matches with **I. Removes RNA nucleotides of primer...and replaces them with DNA nucleotides...**
- **C. DNA pol III:** This is the main "workhorse" enzyme of bacterial DNA replication. It is a highly processive enzyme, meaning it can add thousands of nucleotides without dissociating from the template. It is responsible for the rapid and continuous synthesis of the leading strand and the discontinuous synthesis of Okazaki fragments on the lagging strand, always adding nucleotides to the 3' end of a pre-existing primer. This matches with **IV. Using parental DNA as a template, synthesis new DNA strand by adding nucleotides...**
- **D. Topoisomerase:** As helicase unwinds the DNA, it induces torsional strain and overwinding (positive supercoils) in the double helix ahead of the replication fork. If not relieved, this strain would halt replication. **Topoisomerases** are enzymes that relieve this strain. In bacteria, the specific topoisomerase involved is called **DNA gyrase**. It works by making a transient double-strand break in the DNA, allowing the helix to unswivel, and

then resealing the break. This matches with **III. Relieves overwinding strain ahead of replication forks...**

Step 3: Final Answer

The correct matching of each enzyme to its specific function in bacterial DNA replication is: **A-II, B-I, C-IV, D-III**.

Quick Tip

Think of replication as road construction. **Helicase** is the bulldozer that separates the lanes. **Topoisomerase** is the crew that manages traffic jams (supercoils) up ahead. **DNA Pol III** is the paver laying down the new road (DNA). **DNA Pol I** is the repair crew that replaces the temporary starting cones (RNA primers) with permanent pavement (DNA).

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47. The left-handed helix, Z-DNA is 18 Å (1.8 nm) in diameter which contains _____.

(A) 10 bp per turn
(B) 11 bp per turn
(C) 10.4 bp per turn
(D) 12 bp per turn

Correct Answer: (D) 12 bp per turn

Solution:

Step 1: Foundational Concept of DNA Polymorphism

The DNA double helix is not a rigid, static structure. It is a dynamic molecule that can adopt several different three-dimensional conformations, a property known as polymorphism. The most common form found in cells is the right-handed B-DNA described by Watson and Crick. However, under specific conditions of hydration, ion concentration, or DNA sequence, it can adopt other forms, such as A-DNA and Z-DNA. These forms are distinguished by key structural parameters, including the helical direction (handedness) and the number of base pairs per helical turn.

Step 2: Detailed Comparison of Major DNA Forms

Let's compare the key features of the major DNA conformations:

- **B-DNA:** This is the classic, physiologically predominant form of DNA. It is a **right-handed** helix with approximately **10.5 base pairs per turn**. The base pairs are nearly perpendicular to the helix axis, and it has a distinct major and minor groove. Its diameter is about 20 Å.

- **A-DNA:** This form is observed under dehydrating (low water) conditions. It is also a **right-handed** helix, but it is wider and more compact than B-DNA. It features **11 base pairs per turn**. The base pairs are significantly tilted relative to the helix axis. DNA-RNA hybrids and double-stranded RNA adopt a similar A-form conformation.
- **Z-DNA:** This is a radically different conformation. It is a **left-handed** helix, the opposite of A- and B-DNA. Its sugar-phosphate backbone follows a distinct **zigzag** path, which gives it its name. It is thinner and more elongated than B-DNA and is known to form in sequences with alternating purines and pyrimidines (e.g., poly(GC)). Structurally, Z-DNA contains **12 base pairs per turn**.

Step 3: Final Answer

Based on its unique structural properties, the left-handed Z-DNA helix contains **12 base pairs per helical turn**.

Quick Tip

Memorize the key stats for the three main DNA forms. **B-DNA** is the 'normal' one (10.5 bp/turn). **A-DNA** is short and fat (11 bp/turn). **Z-DNA** is the 'weird' one: **Z**igzag, **Z**any (left-handed), and has the most base pairs per turn (12).

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48. Choose the correct sequence of events as they occur during a bacterial transcription
A. RNA polymerase sigma (σ) subunits recognizes promoters
B. DNA double helix unwind
C. Sigma (σ) subunit dissociates from the holoenzyme
D. Formation of hairpin secondary structure
Choose the correct answer from the options given below:

(A) A, B, C, D
(B) A, C, B, D
(C) B, A, D, C
(D) C, B, D, A

Correct Answer: (A) A, B, C, D

Solution:

Step 1: Foundational Concept of Bacterial Transcription

Transcription is the process of synthesizing an RNA molecule from a DNA template. In bacteria, it is carried out by the enzyme RNA polymerase and proceeds through three main stages: initiation (recognizing the start of a gene), elongation (synthesizing the RNA chain), and termination (recognizing the end of the gene). This question asks to arrange the key events within these stages into their correct chronological order.

Step 2: Detailed Analysis of the Sequence of Events

Let's analyze the logical progression of transcription:

1. **Initiation (Step A): Promoter Recognition and Binding.** The process must begin with the RNA polymerase enzyme finding the correct starting point of a gene. The complete **RNA polymerase holoenzyme** (core enzyme + sigma factor) accomplishes this. Specifically, the **sigma (σ) subunit** is responsible for recognizing and binding to the specific DNA sequences of the **promoter** (e.g., the -10 and -35 boxes), forming a stable but "closed" complex.

2. **Initiation (Step B): Open Complex Formation.** After binding to the promoter, the RNA polymerase must gain access to the nucleotide information on the template strand. To do this, it unwinds a short segment of the DNA double helix (about 10-17 base pairs) at the promoter region. This unwound structure is called the transcription bubble or the **"open complex."**

3. **Elongation (Step C): Sigma Factor Dissociation.** Once transcription has successfully begun and the polymerase has synthesized a short RNA transcript (about 10 nucleotides), the enzyme undergoes a conformational change to transition from initiation to the highly processive elongation phase. This transition involves the release of the **sigma (σ) subunit**, which is no longer needed. The remaining **core enzyme** continues to move along the DNA, elongating the RNA chain.

4. **Termination (Step D): Hairpin Formation and Dissociation.** The process ends when the polymerase transcribes a **terminator sequence**. In Rho-independent termination (the most common type in bacteria), this sequence in the newly synthesized RNA folds back on itself to form a very stable, GC-rich **hairpin secondary structure**. This hairpin, followed by a stretch of U residues in the RNA, destabilizes the DNA-RNA hybrid, causing the RNA polymerase to pause and dissociate from the DNA template, releasing the completed RNA transcript.

Step 3: Final Answer

The logical and chronological sequence of events in bacterial transcription is: **A (Promoter Binding) → B (Open Complex Formation) → C (Sigma Dissociation) → D (Termination)**.

Quick Tip

Think of transcription like a train journey. **A**: The conductor (σ-factor) finds the station (promoter). **B**: The doors open (DNA unwinds). **C**: The train leaves the station and the conductor gets off (σ-factor dissociates). **D**: The train reaches its destination and the brakes are applied (hairpin forms for termination).

---

49. Choose the correct answer regarding the translation of mRNA to proteins when AUG is the start codon and codes for methionine.

(A) All proteins have methionine as the first amino acids.
(B) Methionine never added at the beginning of protein synthesis.
(C) An enzyme can cleave the methionine amino acid from the polypeptide after synthesis.
(D) Methionine fall off automatically from the polypeptide just after termination step of the protein synthesis.

Correct Answer: (C) An enzyme can cleave the methionine amino acid from the polypeptide after synthesis.

Solution:

Step 1: Foundational Concept of Translation Initiation

The process of translation, or protein synthesis, is universally initiated at the start codon **AUG** on the messenger RNA (mRNA). This codon specifies the amino acid **methionine** (or a modified form, N-formylmethionine (fMet), in bacteria). Therefore, every polypeptide chain is initially synthesized with methionine as its first, N-terminal amino acid. The question asks what happens to this initial methionine in the final, mature protein.

Step 2: Detailed Evaluation of Each Statement

Let's analyze the fate of the N-terminal methionine:

- **(A) All proteins have methionine as the first amino acid.** This is incorrect. While protein synthesis *begins* with methionine, analysis of mature proteins reveals that a large proportion (often more than 50%) do not have methionine at their N-terminus. This implies that it is frequently removed.
- **(B) Methionine is never added at the beginning of protein synthesis.** This is incorrect. This statement contradicts the fundamental rule of the genetic code, where the AUG start codon explicitly directs the incorporation of methionine by the initiator tRNA to begin translation.
- **(C) An enzyme can cleave the methionine amino acid from the polypeptide after synthesis.** This is **correct**. The removal of the initial methionine is a very common type of **post-translational modification** (a change made to a protein after it has been synthesized). This specific process is called **N-terminal methionine excision (NME)**. It is carried out by a dedicated class of enzymes called **methionine aminopeptidases (MAPs)**. Whether the methionine is cleaved or not is not random; it is determined by the identity of the second amino acid in the chain. If the second amino acid has a small side chain (e.g., Alanine, Glycine, Serine), the methionine is usually removed.
- **(D) Methionine falls off automatically from the polypeptide.** This is incorrect. The peptide bond linking the first methionine to the second amino acid is a stable covalent bond. Its removal requires energy and the specific catalytic action of an enzyme (a MAP). It does not happen spontaneously or automatically.

Step 3: Final Answer

The correct statement is that the initial methionine residue can be, and often is, **enzymatically cleaved** from the polypeptide chain after synthesis in a process known as N-terminal methionine excision.

> Quick Tip
>
> Think of the initial methionine as a temporary "start signal" tag. Just like you might remove a price tag from new clothes before wearing them, the cell often removes the starting methionine with a specific enzyme after the protein is made.

---

50. Choose the correct sequence of different regions on a typical eukaryotic DNA segment when we go from the upstream to the downstream of a transcription start point.
A. Initiation site
B. CAAT box
C. Enhancer
D. TATA box
Choose the correct answer from the options given below:

(A) B, D, A, C
(B) A, C, B, D
(C) B, A, D, C
(D) C, B, D, A

Correct Answer: (D) C, B, D, A

Solution:

Step 1: Foundational Concept of Eukaryotic Gene Regulation

Eukaryotic gene transcription is regulated by a complex interplay of proteins (transcription factors) and DNA sequence elements. These elements are organized in a modular fashion relative to the **transcription start point (designated as +1)**. Sequences located before the start site are termed **upstream** (given negative numbers), while those after are **downstream**. This question asks for the typical spatial arrangement of these elements, moving from the most upstream to the most downstream.

Step 2: Detailed Explanation of Element Locations

Let's locate each element relative to the +1 start site:

- **C. Enhancer:** These are **distal control elements**, meaning they are located far from the gene they regulate. They can be tens of thousands of base pairs **upstream** or even located downstream or within an intron. Due to their position-independent nature and ability to

function over long distances (by causing the DNA to loop), enhancers are generally the farthest regulatory elements from the start site.

- **B. CAAT box:** This is a **proximal control element**, meaning it is located relatively close to the promoter. Its consensus sequence (GGCAATCT) is typically found around position **-80 to -70** upstream of the start site. It binds transcription factors and significantly increases the rate of transcription.
- **D. TATA box:** This is a **core promoter element**, located very close to the start site. Its consensus sequence (TATAAA) is typically found at position **-35 to -25** upstream. It is the binding site for the TATA-binding protein (TBP), which is a component of the TFIID complex that initiates the assembly of the entire transcription preinitiation complex.
- **A. Initiation site (INR):** This is the most downstream element in the list. It is not a regulatory element in the same sense as the others, but the specific DNA sequence that encompasses the **+1 position**, where the first RNA nucleotide is synthesized.

Step 3: Final Answer

Arranging these elements in order from most upstream (most distant, largest negative number) to most downstream (the +1 site itself), the correct sequence is: **Enhancer** → **CAAT box** → **TATA box** → **Initiation site**. This corresponds to the order **C, B, D, A**.

> Quick Tip
>
> Think of approaching a gene like landing a plane. The **Enhancer** is the distant airport beacon. The **CAAT box** is the outer marker. The **TATA box** is the runway threshold. The **Initiation site** is the touchdown point. The sequence is always from far to near: Enhancer → Proximal Elements (CAAT) → Core Promoter (TATA) → Start Site.

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51. Which one of the following acid is hydrophobic with non polar side chain?

(A) Tyrosine
(B) Proline
(C) Glutamine
(D) Serine

Correct Answer: (B) Proline

Solution:

Step 1: Foundational Concept of Amino Acid Properties

The 20 common amino acids that make up proteins are classified based on the chemical properties of their unique side chains (R-groups). A **hydrophobic** (or nonpolar) amino acid has a side chain that is primarily composed of hydrocarbons and is repelled by water. In an aqueous

environment, these side chains tend to get buried in the interior core of a folded protein, away from the surrounding water.

Step 2: Detailed Analysis of Each Amino Acid's Side Chain

Let's analyze the R-group of each amino acid:

- **Tyrosine:** The side chain of tyrosine contains a large aromatic ring, which is a nonpolar, hydrophobic component. However, it is terminated by a **hydroxyl (-OH) group**. This -OH group is polar and capable of forming hydrogen bonds. Due to the presence of this highly polar group, tyrosine is classified as a **polar amino acid**.
- **Proline:** Proline is unique because its side chain is an aliphatic hydrocarbon group that loops back and forms a covalent bond with the main-chain nitrogen atom, creating a rigid five-membered ring. This side chain consists only of carbon and hydrogen atoms, making it entirely nonpolar. Therefore, proline is a **hydrophobic amino acid**.
- **Glutamine:** The side chain of glutamine contains an **amide group (-$CONH_2$)**. This group is highly polar due to the electronegativity of the oxygen and nitrogen atoms and their ability to participate in hydrogen bonding. Glutamine is a **polar amino acid**.
- **Serine:** The side chain of serine contains a **hydroxyl (-OH) group**, similar to tyrosine but on a smaller aliphatic backbone. This -OH group makes the side chain polar and hydrophilic. Serine is a **polar amino acid**.

Step 3: Final Answer

Among the given options, only **proline** has a side chain that is entirely nonpolar and aliphatic, classifying it as a hydrophobic amino acid.

Quick Tip

To identify hydrophobic amino acids, look for side chains made mostly of carbon and hydrogen (aliphatic or aromatic). To identify polar amino acids, look for electronegative atoms like oxygen or nitrogen in groups like -OH (hydroxyl), -$CONH_2$ (amide), or -SH (thiol). Proline's hydrocarbon ring is a classic nonpolar structure.

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52. Choose the correct order of steps involved in nucleotide excision repair of damaged bases as their occur.
A. A fresh burst of DNA synthesis
B. Cuts are made on both the 3' side and the 5' side of the damaged area
C. The DNA is unwound producing a "bubble".
D. A DNA ligase covalent binds the fresh piece into the backbone.
Choose the correct answer from the options given below:

(A) A, B, C, D
(B) B, C, A, D
(C) C, B, A, D

(D) A, B, D, C

Correct Answer: (C) C, B, A, D

Solution:

Step 1: Foundational Concept of Nucleotide Excision Repair (NER)

Nucleotide Excision Repair (NER) is a versatile and critically important DNA repair pathway found in nearly all organisms. Its primary function is to remove bulky, helix-distorting DNA lesions. A classic example of such a lesion is a pyrimidine dimer (e.g., a thymine dimer) formed as a result of exposure to ultraviolet (UV) light. The process involves removing a short stretch of the damaged strand and resynthesizing it.

Step 2: Detailed Explanation of the Steps of NER in Logical Order

The steps of NER occur in a specific and logical sequence:

1. **Step C: Damage Recognition and Unwinding.** The process must begin with the cell identifying that damage has occurred. Specialized NER proteins do not recognize the specific damaged base but rather the **distortion** it creates in the DNA double helix. Once the lesion is recognized, a DNA helicase (part of the TFIIH complex in humans) is recruited to unwind the DNA in the vicinity of the damage, creating a bubble of single-stranded DNA and making the lesion accessible to other enzymes.
2. **Step B: Excision.** Once the DNA is unwound, a specialized endonuclease complex called an **excinuclease** makes two cuts in the damaged DNA strand, one on the 5' side of the lesion and another on the 3' side. This dual incision excises a short single-stranded DNA segment (oligonucleotide) that contains the bulky lesion.
3. **Step A: Synthesis.** The excision step leaves a single-stranded gap in the DNA. A **DNA polymerase** then uses the intact, complementary strand as a template to synthesize a new stretch of DNA, accurately filling the gap with the correct nucleotides.
4. **Step D: Ligation.** The synthesis step fills the gap, but leaves a final "nick" (a break in the sugar-phosphate backbone) between the 3' end of the newly synthesized DNA and the 5' end of the original, pre-existing strand. The enzyme **DNA ligase** catalyzes the formation of a phosphodiester bond, sealing this nick and completing the repair process, fully restoring the integrity of the DNA strand.

Step 3: Final Answer

The correct chronological sequence of steps in Nucleotide Excision Repair is: **C (Recognition) → B (Excision) → A (Synthesis) → D (Ligation)**.

Quick Tip

Think of NER as "Find, Cut, Fill, Seal." **Find** and open up the damage (unwind, C). **Cut** out the bad section (excision, B). **Fill** in the gap with new DNA (synthesis, A). **Seal** the final connection (ligation, D).

53. Match LIST-I with LIST-II

LIST-I Types of DNA Repair Systems in E. coli		LIST-II Enzymes/proteins	
A.	Mismatch repair	I.	Dam methylase
B.	Base-excision repair	II.	ABC excinuclease
C.	Nucleotide-excision repair	III.	AP endonucleases
D.	Direct repair	IV.	DNA photolyases

Choose the correct answer from the options given below:

(A) A-I, B-II, C - III, D- IV
(B) A-I, B - III, C - II, D - IV
(C) A-I, B-II, C - IV, D - III
(D) A-III, B - IV, C - I, D - II

Correct Answer: (B) A-I, B - III, C - II, D - IV

Solution:

Step 1: Foundational Concept of DNA Repair Diversity

Cells have evolved a sophisticated and diverse toolkit of DNA repair pathways to deal with the various types of damage that DNA can sustain. Each pathway is specialized for a particular type of lesion and relies on a unique set of key enzymes or proteins that define its mechanism. This question requires matching major DNA repair pathways with their characteristic enzymes.

Step 2: Detailed Analysis and Matching of Each Pathway

Let's match each repair system with its key enzymatic component:

- **A. Mismatch repair (MMR):** This system's job is to correct errors (mismatched bases) that are mistakenly incorporated during DNA replication. A critical challenge for MMR is to distinguish the newly synthesized strand (containing the error) from the original template strand (which is correct). In *E. coli*, this is achieved through DNA methylation. The **Dam methylase** enzyme methylates the adenine base within GATC sequences. For a short period after replication, the new strand is unmethylated. The MMR machinery recognizes this hemimethylated state and directs the repair to the unmethylated (new) strand. Thus, Dam methylase is key to the system's specificity. This matches with **I**.
- **B. Base-excision repair (BER):** This pathway deals with damage to single bases, such as deamination or oxidation. The process starts with a specific DNA glycosylase enzyme that recognizes and removes the damaged base, leaving behind an "AP site" (apurinic/apyrimidinic site) - a sugar with no base attached. The next crucial step is performed by an **AP endonuclease**, which recognizes the AP site and cuts the phosphodiester backbone next to it, creating a nick that allows a DNA polymerase to remove and replace the sugar and a few adjacent nucleotides. This matches with **III**.

- **C. Nucleotide-excision repair (NER):** As previously discussed, this pathway removes bulky, helix-distorting lesions. The key enzyme complex in *E. coli* that performs the recognition and excision steps is composed of the UvrA, UvrB, and UvrC proteins. This complex is collectively known as the **ABC excinuclease**. It recognizes the lesion, unwinds the DNA, and makes two incisions on either side of the damage to remove an oligonucleotide. This matches with **II**.
- **D. Direct repair:** This is the simplest repair mechanism, where the lesion is chemically reversed in a single enzymatic step without excising any part of the DNA. The classic example is the repair of pyrimidine dimers caused by UV light. The enzyme **DNA photolyase** contains a light-absorbing cofactor. When activated by visible light, it uses that energy to directly break the aberrant covalent bonds between the adjacent pyrimidines, restoring the original bases. This matches with **IV**.

Step 3: Final Answer

The correct matching of each DNA repair pathway to its characteristic enzyme or protein is: **A-I, B-III, C-II, D-IV**.

> Quick Tip
>
> Associate keywords: **Mismatch** → Methylation (**Dam methylase**). **Base** Excision → AP site (**AP endonuclease**). **Nucleotide** Excision → Bulky lesion (**ABC excinuclease**). **Direct** Repair → Light/UV (**Photolyase**).

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54. Frequency of recombination between linked genes in Drosophila is affected by
A. Distance between genes
B. Sex of heterozygotes for linked genes
C. Age of female
D. Temperature
Choose the correct answer from the options given below:

(A) A, B and D only
(B) A, B and C only
(C) A, B, C and D
(D) B, C and D only

Correct Answer: (C) A, B, C and D

Solution:

Step 1: Foundational Concept of Genetic Recombination

Genetic recombination, which occurs via **crossing over** during meiosis, is the process by which homologous chromosomes exchange segments of DNA. This process creates new combinations of alleles on the chromosomes, generating genetic diversity. The frequency of recombination

between two genes located on the same chromosome (linked genes) is not a fixed constant but can be influenced by a variety of genetic and environmental factors.

Step 2: Detailed Analysis of Each Factor

Let's analyze the effect of each listed factor on recombination frequency:

- **A. Distance between genes:** This is the most fundamental factor governing recombination frequency. According to Alfred Sturtevant's principle of gene mapping, the probability of a crossover event occurring between two genes is **directly proportional to the physical distance** separating them on the chromosome. Genes that are far apart have a higher recombination frequency, while genes that are very close together have a low recombination frequency.
- **B. Sex of heterozygotes for linked genes:** This is a well-documented genetic phenomenon, particularly famous in the model organism ***Drosophila melanogaster*** (the fruit fly). In *Drosophila*, crossing over and recombination are **completely absent in males**. Recombination only occurs in females. Therefore, the sex of the heterozygous parent from which gametes are being formed has a dramatic, all-or-nothing effect on the outcome.
- **C. Age of female:** The rate of recombination is not necessarily constant throughout an organism's reproductive lifespan. Studies, again notably in *Drosophila*, have clearly shown that the frequency of recombination can be influenced by the **maternal age**, with the rate generally decreasing as the female fly gets older.
- **D. Temperature:** Recombination is an enzymatic process, and the activity of the enzymes involved can be influenced by environmental factors. **Temperature** is a key environmental factor that has been shown to affect recombination rates. Exposing *Drosophila* to temperatures that are outside their optimal physiological range (either significantly higher or lower) can alter the frequency of crossing over.

Step 3: Final Answer

All four listed factors—**distance between genes, sex, age, and temperature**—are well-documented variables known to influence the frequency of genetic recombination, particularly in the extensively studied model organism *Drosophila*.

Quick Tip

While distance is the primary determinant of recombination frequency, remember that it's a biological process, not a fixed physical constant. Therefore, other factors like genetics (sex), physiology (age), and environment (temperature) can modulate the rate of crossing over. The lack of recombination in male Drosophila is a classic exam topic.

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55. Match the LIST-I with LIST-II

LIST-I Term		LIST-II Type of change	
A.	Nullisomic	I.	One chromosome missing
B.	Monosomic	II.	One chromosome pair missing
C.	Allotetraploid	III.	Four copies of the same genome present
D.	Autotetraploid	IV.	Two distinct genomes; each has two copies

Choose the correct answer from the options given below:

(A) A-I, B - II, C - III, D - IV
(B) A-II, B-I, C - III, D - IV
(C) A-I, B-II, C - IV, D - III
(D) A-II, B-I, C - IV, D - III

Correct Answer: (D) A-II, B-I, C - IV, D - III

Solution:

Step 1: Foundational Concept of Chromosomal Aberrations

An organism's chromosome number is typically constant for a given species. Variations from this standard number are known as chromosomal aberrations. These are broadly divided into two main categories: **aneuploidy**, which involves the gain or loss of one or more individual chromosomes, and **polyploidy**, which involves the presence of extra entire sets of chromosomes. This question tests the precise terminology used to describe these different conditions.

Step 2: Detailed Explanation and Matching of Each Term

Let's match each term with its correct definition:

- **A. Nullisomic:** This is a form of aneuploidy. The term "nulli-" means none. A nullisomic individual has lost a complete homologous pair of chromosomes. The chromosomal composition is therefore represented as **(2n - 2)**, where 'n' is the haploid number of chromosomes. This matches with **II. One chromosome pair missing.**
- **B. Monosomic:** This is another form of aneuploidy. The term "mono-" means one. A monosomic individual has lost a single chromosome from one of its homologous pairs, leaving only one copy. The chromosomal composition is represented as **(2n - 1)**. A well-known human example is Turner Syndrome (XO). This matches with **I. One chromosome missing.**
- **C. Allotetraploid:** This is a form of polyploidy. The prefix "allo-" means "different," and "tetra-" means "four." An allotetraploid is an organism that contains four sets of chromosomes in its somatic cells, with these sets being derived from **two or more different species**. For example, if species 1 has the genome AA and species 2 has the genome BB, a hybrid could be formed, and following chromosome doubling, an allotetraploid with the genome **AABB** would be created. This matches with **IV. Two distinct genomes; each has two copies.**

- **D. Autotetraploid:** This is another form of polyploidy. The prefix "auto-" means "self." An autotetraploid is an organism that has four sets of chromosomes, all of which are derived from a **single ancestral species**. This can occur, for example, through a failure of cell division after chromosome replication. If the basic genome of a diploid species is AA, an autotetraploid would have the genome **AAAA**. This matches with **III. Four copies of the same genome present.**

Step 3: Final Answer

The correct matching of each term for chromosomal number variation with its definition is: **A-II, B-I, C-IV, D-III**.

Quick Tip

Break down the prefixes: **Nulli-** (none, zero) → a whole pair is gone. **Mono-** (one) → one chromosome is gone. **Auto-** (self) → multiple genomes from the same species. **Allo-** (other) → multiple genomes from different species.

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56. In general F_2, F_3 and the subsequent generations do not show segregation for a cytoplasmically inherited trait. This is because

(A) The F_1 individuals generally receive plasmagenes from one parent only.
(B) The F_1 individuals generally receive nuclear genes from one parent only.
(C) The F_1 individuals generally receive plasmagenes from both parents.
(D) The F_1 individuals generally receive nuclear genes from both parents.

Correct Answer: (A) The F_1 individuals generally receive plasmagenes from one parent only.

Solution:

Step 1: Understanding the Concept

This question explores the principles of **cytoplasmic inheritance**, also known as extranuclear or maternal inheritance. This mode of inheritance pertains to traits that are controlled by genes located in the cytoplasm, specifically within organelles like **mitochondria** and **chloroplasts**. These genes are collectively referred to as **plasmagenes**. The central query is to understand why these traits do not follow the classic Mendelian patterns of segregation, such as the 3:1 ratio, in the F2 and subsequent generations.

Step 2: Detailed Explanation

- **Mendelian Segregation:** The foundation of Mendelian genetics lies in the segregation of alleles for nuclear genes. During sexual reproduction, both parents contribute their nuclear genes to the offspring. In the F1 generation, these alleles are combined, and when the F1 individuals produce gametes through meiosis, the alleles segregate. This segregation is

what leads to the predictable phenotypic ratios (e.g., 3:1 for a monohybrid cross) observed in the F2 generation.

- **The Role of Gametes in Cytoplasmic Inheritance:** In the majority of sexually reproducing organisms, including most animals and plants, the contribution of cytoplasm from the male and female gametes is highly unequal. The female gamete (the egg or ovum) is large and contains a substantial amount of cytoplasm, which includes organelles like mitochondria and, in plants, chloroplasts. In contrast, the male gamete (sperm or pollen) is typically much smaller and contributes primarily its nucleus, with a negligible amount of cytoplasm.
- **Uniparental (Maternal) Inheritance:** As a consequence of this unequal cytoplasmic contribution, the zygote, and therefore the resulting F1 individual, inherits almost all of its plasmagenes from the female parent. This is the cornerstone of maternal inheritance. The traits determined by these mitochondrial or chloroplast genes are passed down from the mother to all her offspring.
- **Absence of Segregation:** Since the F1 individuals receive their plasmagenes from a single source (the mother), there is only one type of cytoplasmic genotype present. Unlike nuclear genes where an individual can be heterozygous (e.g., Aa), there are no alternative alleles from a second parent to segregate during meiosis.
- **Phenotypic Uniformity in Subsequent Generations:** Because there is no segregation of plasmagenes, all offspring in the F2, F3, and later generations will have the same cytoplasmic genotype as the original maternal parent. This results in a lack of phenotypic variation for these traits, and the characteristic Mendelian ratios are not observed.

Step 3: Final Answer

The absence of segregation for traits determined by cytoplasmic inheritance is a direct result of the F1 generation inheriting its plasmagenes from a single parent, which is typically the mother. Therefore, Option (A) provides the correct explanation. Options (B) and (D) are incorrect because they refer to nuclear genes, which are inherited from both parents. Option (C) is incorrect because plasmagenes are characteristically inherited from only one parent, not both.

Quick Tip

Remember the rule for cytoplasmic inheritance: "Mom gives the mitochondria." Since the F1 generation gets all its cytoplasmic genes from one parent, there's no mix of alleles to segregate in later generations, unlike with nuclear genes which follow Mendelian rules.

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57. Which of the given factors can affect frequency in Mendelian population?
A. Migration
B. Mutation
C. Selection
D. Random shift

Choose the correct answer from the options given below:

(A) A, B and D only
(B) A, B and C only
(C) A, B, C and D
(D) B, C and D only

Correct Answer: (C) A, B, C and D

Solution:

Step 1: Understanding the Concept

This question delves into the field of **population genetics**, focusing on the factors that can cause a change in allele and genotype frequencies within a Mendelian population. These factors are the driving forces of evolution and are the reasons why populations deviate from the state of **Hardy-Weinberg equilibrium**, which describes a hypothetical, non-evolving population.

Step 2: Detailed Explanation

The Hardy-Weinberg principle serves as a null hypothesis in population genetics, stating that allele and genotype frequencies will remain constant from generation to generation in the absence of specific evolutionary influences. The factors that disrupt this equilibrium are:

- **A. Migration (Gene Flow):** This refers to the movement of individuals, and consequently their alleles, into (immigration) or out of (emigration) a population. Gene flow can introduce new alleles into a population's gene pool or alter the frequencies of existing alleles. The extent of its effect is proportional to the rate of migration.
- **B. Mutation:** Mutation is the ultimate source of all new genetic variation. It is the process by which new alleles are created through changes in the DNA sequence. While the rate of mutation for any single gene is typically very low, over evolutionary time, it is the fundamental raw material upon which other evolutionary forces act.
- **C. Selection (Natural Selection):** Natural selection occurs when individuals with certain genotypes have a higher fitness, meaning they have a greater rate of survival and reproduction than individuals with other genotypes. This differential success leads to an increase in the frequency of the alleles associated with higher fitness in subsequent generations.
- **D. Random Shift (Genetic Drift):** Genetic drift refers to random, chance fluctuations in allele frequencies from one generation to the next. Its effects are most pronounced in small populations. Events such as the random sampling of gametes during fertilization can lead to the loss of alleles or the fixation (frequency of 100%) of others, purely by chance and not due to any selective advantage.

Step 3: Final Answer

All four of these factors—Migration (Gene Flow), Mutation, Selection (Natural Selection), and Genetic Drift (Random Shift)—are recognized as the primary evolutionary forces that can alter allele and genotype frequencies in a population.

Quick Tip

The five conditions for a population to be in Hardy-Weinberg equilibrium (i.e., not evolving) are: No mutation, No migration, No selection, Large population size (to avoid genetic drift), and Random mating. Any factor that violates these conditions will affect allele frequencies.

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58. In 1963, several varieties such as Sonalika and Kalyan Sona were introduced all over the wheat-growing belt in India. They were

(A) High yielding and disease susceptible
(B) Low yielding and disease susceptible
(C) High yielding and disease resistant
(D) Low yielding and disease resistant

Correct Answer: (C) High yielding and disease resistant

Solution:

Step 1: Understanding the Concept

This question pertains to a significant period in agricultural history known as the **Green Revolution in India**. A key aspect of this period was the development and introduction of new, improved crop varieties. The question specifically asks about the key characteristics of the wheat varieties **Sonalika** and **Kalyan Sona**.

Step 2: Detailed Explanation

- **Origins and Development:** Sonalika and Kalyan Sona were semi-dwarf wheat varieties that were developed from Mexican wheat strains. This pioneering work was led by the Nobel laureate Dr. Norman Borlaug, who is often hailed as the "Father of the Green Revolution."
- **Introduction in India:** These varieties were introduced in India during the mid-1960s as a response to pressing food shortages and to increase agricultural productivity.
- **Key Advantages:**
    1. **High-Yielding:** The semi-dwarf nature of these plants was a crucial innovation. It meant that the plants allocated more of their energy to producing grains rather than growing tall stalks (straw). Furthermore, their shorter and sturdier stems made them

less susceptible to *lodging* (bending over) when heavily fertilized, which allowed for more intensive farming practices and resulted in a significant increase in grain yield per unit area.

2. **Disease Resistant:** A major challenge to wheat production was the prevalence of diseases, particularly rust fungi, which could devastate crops. Sonalika and Kalyan Sona were specifically bred to be resistant to these common wheat pathogens, thereby ensuring more stable and reliable harvests.

- **Impact:** The combined traits of being high-yielding and disease-resistant led to a dramatic increase in wheat production across India. This agricultural transformation was instrumental in making the country self-sufficient in food grains and ensuring food security for its growing population.

Step 3: Final Answer

The wheat varieties Sonalika and Kalyan Sona were instrumental in the Green Revolution in India due to their dual characteristics of being both high-yielding and disease resistant.

Quick Tip

Sonalika and Kalyan Sona are the star players of India's Green Revolution. The entire purpose of the Green Revolution was to increase food production, which was achieved by developing varieties that were both high-yielding and resilient (disease-resistant).

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59. Among the following species of bryophytes, which is not an example of mosses?

(A) Funaria
(B) Marchantia
(C) Polytrichum
(D) Sphagnum

Correct Answer: (B) Marchantia

Solution:

Step 1: Understanding the Concept

This question focuses on the classification within the division **Bryophyta**. This division is typically subdivided into three classes: **Hepaticae** (Liverworts), **Anthocerotae** (Hornworts), and **Musci** (Mosses). The task is to identify which of the given organisms does not belong to the class Musci.

Step 2: Detailed Explanation

Let's examine the classification of each of the provided bryophytes:

- **Funaria:** This is a widely distributed and commonly studied genus of moss. As such, it is a member of the class **Musci**.
- **Marchantia:** This is a classic textbook example of a thalloid liverwort. It belongs to the class **Hepaticae**. Its distinct features include a flattened, dichotomously branched thallus and specialized reproductive structures known as antheridiophores and archegoniophores.
- **Polytrichum:** Commonly referred to as hair-cap moss, this is another well-known genus of moss and is classified under the class **Musci**.
- **Sphagnum:** Widely known as peat moss, *Sphagnum* is an economically and ecologically significant genus of moss. It is also a member of the class **Musci**.

Step 3: Final Answer

Based on the classification, *Funaria*, *Polytrichum*, and *Sphagnum* are all examples of mosses and belong to the class Musci. In contrast, *Marchantia* is a liverwort, and therefore, it is the organism that does not belong to the class Musci.

Quick Tip

Remember the three main groups of bryophytes: Liverworts, Hornworts, and Mosses. Marchantia and Riccia are the most common examples of liverworts you'll encounter in textbooks. If you see them, think "liverwort," not "moss."

---

60. Who among the following is known as the father of Indian paleobotany?

(A) Prof. Bhishma Sahni
(B) Prof. Balraj Sahni
(C) Prof. Birbal Sahni
(D) Prof. Birpal Sahni

Correct Answer: (C) Prof. Birbal Sahni

Solution:

Step 1: Understanding the Concept

This is a factual question that asks for the identification of the scientist who is widely recognized as the pioneer and "father" of **paleobotany** (the study of fossil plants) in India.

Step 2: Detailed Explanation

- **Professor Birbal Sahni (1891–1949):** He was a distinguished Indian paleobotanist who made profound contributions to the field.

- **Scientific Contributions:** His research on the fossil flora of the Indian subcontinent was groundbreaking. It provided crucial insights into the paleogeography, geology, and evolutionary history of the region.
- **Institutional Founder:** In 1946, he founded the Institute of Palaeobotany in Lucknow. In recognition of his immense contributions, this institute was later renamed the **Birbal Sahni Institute of Palaeosciences** in his honor.
- **Legacy:** Due to his pioneering efforts and the vast body of his research, Professor Birbal Sahni is universally acclaimed as the "Father of Indian Paleobotany."
- **Other Individuals Mentioned:** The other names provided are incorrect in this context. Bhishma Sahni was a celebrated Hindi writer, and Balraj Sahni was a renowned film actor. They were both the brothers of Birbal Sahni.

Step 3: Final Answer

Professor Birbal Sahni is known as the father of Indian paleobotany.

Quick Tip

The name **Birbal Sahni** is synonymous with Indian paleobotany. The existence of the Birbal Sahni Institute of Palaeosciences in Lucknow is a strong clue to his foundational role in this field in India.

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61. The symmetry in which a flower can be divided into two equal and similar halves by only one vertical division is

(A) Actinomorphic
(B) Polymorphic
(C) Metamorphic
(D) Zygomorphic

Correct Answer: (D) Zygomorphic

Solution:

Step 1: Understanding the Concept

The question is about **floral symmetry**, which describes the arrangement of the parts of a flower around its central axis. This is a significant characteristic used in the classification of plants. The specific term being sought is the one that describes bilateral symmetry in flowers.

Step 2: Detailed Explanation

Let's define the relevant terms associated with floral symmetry:

- **Actinomorphic:** This term describes **radial symmetry**. A flower is considered actinomorphic if it can be divided into two equal halves by any vertical plane that passes through its center. Examples of plants with actinomorphic flowers include mustard, datura, and chilli.
- **Zygomorphic:** This term describes **bilateral symmetry**. A flower is zygomorphic if it can be divided into two similar halves by only one specific vertical plane. This is the term that perfectly matches the description in the question. Examples of plants with zygomorphic flowers include pea, gulmohar, bean, and cassia.
- **Polymorphic and Metamorphic:** These are not standard botanical terms used to describe floral symmetry.

Step 3: Final Answer

The type of symmetry in which a flower can be divided into two equal halves by only one vertical plane is known as **zygomorphic symmetry**.

Quick Tip

Associate **Actino**morphic with "acting" like a star or a wheel (radial symmetry) and **Zygo**morphic with "zygote" or pairing (bilateral symmetry). Zygomorphic flowers have a distinct top and bottom, or left and right, like a human face.

---

62. In homosporous pteridophyte species, the development of gametophyte is

(A) Hemisporic
(B) Episporic
(C) Endosporic
(D) Exosporic

Correct Answer: (D) Exosporic

Solution:

Step 1: Understanding the Concept

This question addresses the mode of gametophyte development in **homosporous pteridophytes**. The core of the question is whether the gametophyte develops inside (endosporic) or outside (exosporic) the original spore wall.

Step 2: Detailed Explanation

- **Homosporous Pteridophytes:** These plants, which include most ferns and lycophytes, produce only one type of spore, which is typically small in size. These spores are released from the parent sporophyte plant.

- **Exosporic Development:** When a spore from a homosporous pteridophyte lands in a suitable environment (e.g., moist soil), it germinates. During germination, the spore wall ruptures, and the gametophyte develops **outside** the spore wall. This mode of development is termed **exosporic**. The resulting gametophyte is free-living, independent of the parent sporophyte, and is usually photosynthetic, producing its own food.
- **Heterosporous Pteridophytes:** In contrast, heterosporous pteridophytes (such as *Selaginella* and *Salvinia*) produce two distinct types of spores: small microspores (which develop into male gametophytes) and large megaspores (which develop into female gametophytes).
- **Endosporic Development:** In these plants, the gametophytes are highly reduced in size and develop either mostly or entirely **inside** the protective wall of the spore. This is known as **endosporic** development.
- **Other Terms:** "Hemisporic" and "Episporic" are not standard terms used in this context of classification.

Step 3: Final Answer

The development of the gametophyte in homosporous pteridophytes is **exosporic**.

Quick Tip

Remember the prefixes: **Exo-** means "outside," and **Endo-** means "inside." Homosporous species release their spores, which then grow into a gametophyte outside the spore wall (exosporic). Heterosporous species keep the developing gametophyte protected inside the spore wall (endosporic), a key step in the evolution towards the seed habit.

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63. More recently discovered plant hormone, Jasmonates, play an important role both in plant defense and development, is derived from which fatty acid?

(A) Palmitic acid
(B) Oleic acid
(C) Linoleic acid
(D) Linolenic acid

Correct Answer: (D) Linolenic acid

Solution:

Step 1: Understanding the Concept

This question focuses on the biosynthesis of **jasmonates** (like jasmonic acid), which are a class of plant hormones. These hormones play crucial roles in a wide array of plant processes, most

notably in regulating responses to various stresses, including insect and pathogen attacks. The question asks to identify the precursor molecule from which jasmonates are synthesized.

Step 2: Detailed Explanation

- **The Octadecanoid Pathway:** The biosynthesis of jasmonic acid (JA) occurs through a series of enzymatic reactions known as the octadecanoid pathway.
- **Starting Material:** This pathway is initiated with a polyunsaturated fatty acid that is released from the plant cell membrane.
- **The Specific Precursor:** The specific precursor fatty acid for jasmonate synthesis is **α-linolenic acid**. This is an 18-carbon fatty acid that contains three double bonds (C18:3).
- **Biosynthetic Steps:** Following its release from the membrane, linolenic acid is converted into jasmonic acid through a sequence of enzymatic steps. Key enzymes involved in this pathway include lipoxygenase and allene oxide synthase.
- **Other Fatty Acids:** Palmitic acid is a saturated fatty acid. Oleic and linoleic acids are unsaturated fatty acids, but they have fewer double bonds than linolenic acid and are not the direct precursors for jasmonate synthesis.

Step 3: Final Answer

Jasmonates are derived from the fatty acid **linolenic acid**.

Quick Tip

Associate Jasmonates with plant defense (like responding to being wounded or eaten). Their synthesis starts with the highly unsaturated fatty acid, α-linolenic acid, being released from the cell membrane.

---

64. Plants can assimilate only two inorganic forms of nitrogen. These are:
A. Nitrite (NO_2^-)
B. Ammonium (NH_4^+)
C. Nitric acid (HNO_3)
D. Nitrate (NO_3^-)
Choose the correct answer from the options given below:

(A) A and D only
(B) B and D only
(C) B, C and D only
(D) A, B and D only

Correct Answer: (B) B and D only

Solution:

Step 1: Understanding the Concept

This question addresses the topic of plant nutrition, specifically focusing on **nitrogen**, an essential macronutrient. Although the Earth's atmosphere is rich in nitrogen gas (N2), plants are unable to use it in this form directly. They must absorb nitrogen from the soil in specific inorganic forms. The question asks to identify these forms.

Step 2: Detailed Explanation

- **Nitrogen Absorption:** Plants primarily absorb nitrogen from the soil through their root systems.
- **Major Inorganic Forms:** The two principal inorganic forms of nitrogen that can be taken up and assimilated by plant roots are **nitrate (NO3-)** and **ammonium (NH4+)**.
- **Nitrate (D):** In well-aerated soils, nitrate is typically the most abundant form of available nitrogen. It is highly mobile in the soil solution. Once absorbed by the plant, nitrate must be reduced back to ammonium before it can be incorporated into organic molecules like amino acids. This reduction process requires energy from the plant.
- **Ammonium (B):** Ammonium can be taken up directly by plants and used to synthesize amino acids without the need for reduction. This makes it energetically more efficient for the plant to use. However, ammonium is less mobile in the soil as it can bind to negatively charged soil particles, and it can be toxic to plants at high concentrations.
- **Other Nitrogen Forms:**
  - **Nitrite (A):** Nitrite (NO2-) is an intermediate compound in the nitrogen cycle, specifically in the processes of nitrification (the conversion of ammonium to nitrate) and denitrification (the conversion of nitrate back to nitrogen gas). It is generally not a major form of nitrogen taken up by plants and can also be toxic.
  - **Nitric Acid (C):** Nitric acid is not a form of nitrogen that is assimilated by plants from the soil.

Step 3: Final Answer

The two inorganic forms of nitrogen that plants can assimilate from the soil are **ammonium (B)** and **nitrate (D)**.

Quick Tip

Remember that plants "eat" nitrogen in two main forms from the soil: nitrate (NO_3^-) and ammonium (NH_4^+). All other forms of nitrogen in the soil are generally converted to one of these two forms before the plant can use them.

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65. Lenticels permit the:

(A) Exchange of water between the outer atmosphere and internal tissue of the stem in most woody trees.

(B) Exchange of gases between the outer atmosphere and internal tissue of the stem in most woody trees.
(C) Exchange of heat between the outer atmosphere and internal tissue of the stem in most woody trees.
(D) Exchange of radiation between the outer atmosphere and internal tissue of the stem in most woody trees.

Correct Answer: (B) Exchange of gases between the outer atmosphere and internal tissue of the stem in most woody trees.

Solution:

Step 1: Understanding the Concept

This question is about the function of **lenticels**, which are specialized structures found on the bark of woody stems and roots. The question asks for their primary function.

Step 2: Detailed Explanation

- **Gas Exchange in Young Stems:** In young, non-woody stems, gas exchange with the atmosphere occurs through small pores called stomata, which are typically found in the epidermis.
- **Secondary Growth and the Periderm:** As a stem undergoes secondary growth (i.e., it becomes woody), the original epidermis is replaced by a new protective layer called the periderm, which is the main component of bark. This periderm, particularly its outer layer of cork (phellem), is largely impermeable to gases and water.
- **The Need for Gas Exchange in Woody Stems:** Despite the impermeable nature of the bark, the living cells within the woody stem (such as those in the phloem and cambium) still need to respire. This requires a supply of oxygen and the removal of carbon dioxide.
- **The Role of Lenticels:** To facilitate this gas exchange, specialized porous tissues called lenticels are formed. A lenticel consists of cells with large intercellular spaces. These pores breach the otherwise impermeable cork layer of the bark.
- **Primary Function:** The primary function of lenticels is to create a pathway for the direct exchange of gases—primarily oxygen, carbon dioxide, and water vapor—between the internal living tissues of the stem and the external atmosphere.
- **Other Possibilities:** Lenticels are not primarily designed for the bulk exchange of liquid water (A), heat (C), or radiation (D). While some water vapor is lost through lenticels in a process called lenticular transpiration, their main and most crucial role is to facilitate the gas exchange necessary for respiration.

Step 3: Final Answer

Lenticels permit the exchange of gases between the outer atmosphere and the internal tissues of the stem.

Quick Tip

Think of lenticels as the "stomata of the bark." Just as stomata allow leaves to breathe, lenticels allow the woody stem to breathe. Their function is gas exchange.

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66. The membrane potential of a resting neuron is:

(A) -20 and -60 millivolts
(B) -30 and -80 millivolts
(C) -20 and -80 millivolts
(D) -60 and -80 millivolts

Correct Answer: (D) -60 and -80 millivolts

Solution:

Step 1: Understanding the Concept

The question asks about the **resting membrane potential**, which is a foundational concept in neurobiology. It refers to the stable electrical charge difference, or voltage, across the plasma membrane of a neuron (or any cell) when it is in a non-excited state. This electrical potential is crucial because it represents stored energy that the neuron can use to generate and transmit nerve impulses (action potentials).

Step 2: Detailed Explanation

The establishment and maintenance of the resting membrane potential is a dynamic process governed by two main factors:

- **Ion Concentration Gradients and the Na+/K+ Pump:** The **sodium-potassium (Na+/K+) pump** is an active transport protein that continuously pumps three sodium ions (Na+) out of the cell for every two potassium ions (K+) it pumps into the cell. This action consumes ATP and establishes steep concentration gradients: a high concentration of K+ inside the cell and a high concentration of Na+ outside the cell. It also contributes slightly to the negative charge inside the cell due to the unequal movement of positive ions.
- **Differential Permeability due to Ion Channels:** The cell membrane is not equally permeable to all ions. In a resting state, the neuron's membrane has many open K+ channels, often called **"leak" channels**, which allow K+ to move freely across the membrane. In contrast, there are very few open Na+ channels.
- **Establishment of the Potential:** Because the concentration of K+ is high inside the cell, K+ ions will diffuse out of the cell down their concentration gradient through the open leak channels. As these positively charged potassium ions leave the cell, they leave behind large, negatively charged molecules (like proteins and organic anions) that are too big to cross the membrane.

- **Resulting Negative Charge:** This exodus of positive charge (K+) without a corresponding exit of negative charge makes the inside of the plasma membrane negative relative to the outside. This separation of charge is the resting membrane potential.
- **Typical Value:** For most neurons, this electrochemical equilibrium is reached at a voltage of approximately **-60 to -80 millivolts (mV)**. A commonly cited average value is -70 mV. The negative sign indicates that the inside of the cell is negative with respect to the outside.
- **Incorrect Ranges:** Other voltage ranges, especially positive ones, would represent a state of excitation (depolarization), not rest.

Step 3: Final Answer

The membrane potential of a resting neuron is typically maintained within the range of **-60 to -80 millivolts**.

Quick Tip

For a resting neuron, remember the number **-70 mV** as the classic textbook value. This will help you quickly identify the correct range, which is -60 to -80 mV. The negative sign is crucial; it means the inside of the cell is negative compared to the outside.

---

67. Which one of the following amino acids is involved in synthesis of hormone epinephrine in humans?

(A) Threonine
(B) Tryptophan
(C) Tyrosine
(D) Phenylalanine

Correct Answer: (C) Tyrosine

Solution:

Step 1: Understanding the Concept

This question asks to identify the amino acid precursor for the synthesis of **epinephrine** (also known as adrenaline). Epinephrine is a crucial hormone and neurotransmitter belonging to a class of molecules called **catecholamines**. Like many complex biological molecules, it is synthesized through a multi-step enzymatic pathway starting from a simpler building block.

Step 2: Detailed Explanation

The biosynthetic pathway for all catecholamines (dopamine, norepinephrine, and epinephrine) is a sequential process that begins with a specific amino acid.
The pathway is as follows:

Tyrosine
↓ *(Tyrosine hydroxylase)*
L-DOPA
↓
Dopamine
↓
Norepinephrine (Noradrenaline)
↓
Epinephrine (Adrenaline)

- **Step 1: Tyrosine to L-DOPA:** The pathway begins with the amino acid **Tyrosine**. The enzyme tyrosine hydroxylase adds a hydroxyl group to tyrosine, converting it to L-DOPA. This is the rate-limiting step of the pathway.
- **Subsequent Steps:** L-DOPA is then converted to dopamine, dopamine to norepinephrine, and finally, norepinephrine is converted to epinephrine.
- **Direct Precursor:** Therefore, **Tyrosine** is the direct amino acid precursor that initiates the catecholamine synthesis pathway.
- **Other Amino Acids:**
  - **Phenylalanine (D):** While it is true that the body can synthesize tyrosine from phenylalanine using the enzyme phenylalanine hydroxylase, phenylalanine does not directly enter the catecholamine pathway. Tyrosine is the immediate precursor.
  - **Tryptophan (B):** Tryptophan is the precursor for the synthesis of the neurotransmitter serotonin and the hormone melatonin. It is not involved in catecholamine synthesis.
  - **Threonine:** Threonine is an essential amino acid but is not the precursor for these specific hormones.

Step 3: Final Answer

Tyrosine is the amino acid that is directly involved in the synthesis of epinephrine.

Quick Tip

Remember the precursors for key neurotransmitters/hormones: **T**yrosine → **D**opamine, **N**orepinephrine, **E**pinephrine (Adrenaline). **T**ryptophan → **S**erotonin.

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68. Match LIST-I with LIST-II

LIST-I Diseases		**LIST-II Causative agents**	
A.	Wool sorter's disease	I.	E.coli
B.	Gas gangrene	II.	Human papilloma virus
C.	Urinary tract infection	III.	Bacillus anthracis
D.	Cervical cancer	IV.	Clostridium perfringens

Choose the correct answer from the options given below:

(A) A - I, B - II, C - III, D - IV
(B) A - I, B - III, C - II, D - IV
(C) A - I, B - II, C - IV, D - III
(D) A - III, B - IV, C - I, D - II

Correct Answer: (D) A - III, B - IV, C - I, D - II

Solution:

Step 1: Understanding the Concept

This question requires matching four different infectious diseases with their specific causative agents (pathogens). This tests knowledge of common pathogens and the diseases they cause.

Step 2: Detailed Explanation

Let's analyze each disease and identify its corresponding pathogen:

- **A. Wool sorter's disease:** This is the historical name for the inhalational form of **anthrax**. It is a severe lung infection that results from inhaling the spores of the bacterium ***Bacillus anthracis*** (III). The name originates from its occupational association with workers who handled and sorted wool from infected animals like sheep.
- **B. Gas gangrene:** This is a life-threatening infection of muscle tissue, known as myonecrosis, which is characterized by the production of gas bubbles in the infected tissue. The primary causative agent is the anaerobic, spore-forming bacterium ***Clostridium perfringens*** (IV).
- **C. Urinary tract infection (UTI):** While various microbes can cause UTIs, the overwhelming majority (approximately 80-90%) of community-acquired cases are caused by the bacterium ***Escherichia coli*** (I), which is a common resident of the gut.
- **D. Cervical cancer:** The vast majority of cervical cancer cases are caused by persistent infection with certain high-risk strains of the **Human papillomavirus (HPV)** (II). This virus can integrate its DNA into the host cell's genome and produce oncoproteins (like E6 and E7) that disrupt normal cell cycle control, leading to malignant transformation.

Step 3: Final Answer

The correct matching is as follows:

- A (Wool sorter's disease) $\rightarrow$ III (*Bacillus anthracis*)
- B (Gas gangrene) $\rightarrow$ IV (*Clostridium perfringens*)
- C (Urinary tract infection) $\rightarrow$ I (*Escherichia coli*)
- D (Cervical cancer) $\rightarrow$ II (Human papillomavirus)

Quick Tip

Associate keywords: Anthrax → Wool sorters. Gas gangrene → Clostridium. UTI → E. coli. Cervical Cancer → HPV. These are classic pairings in medical microbiology.

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69. Which one of the following granulocyte has following features?
Highly phagocytic; nucleus with three to five lobes; primary and secondary granules; limited life span:

(A) Eosinophil
(B) Mast cells
(C) Neutrophil
(D) Basophil

Correct Answer: (C) Neutrophil

Solution:

Step 1: Understanding the Concept

The question asks to identify a specific type of **granulocyte** based on a set of descriptive features. Granulocytes are a category of white blood cells distinguished by the presence of granules in their cytoplasm and include neutrophils, eosinophils, and basophils.

Step 2: Detailed Explanation

Let's evaluate the given features to pinpoint the correct cell type:

- **Highly phagocytic:** This is a major clue pointing towards **neutrophils**. Neutrophils are professional phagocytes, meaning their primary function is to engulf and destroy pathogens, especially bacteria. They are the most abundant type of phagocyte in the bloodstream and are the first responders to sites of acute inflammation. Eosinophils are only weakly phagocytic, and basophils are not considered phagocytic.
- **Nucleus with three to five lobes:** This describes the characteristic multi-lobed, or **polymorphonuclear**, appearance of a mature neutrophil's nucleus. This unique nuclear shape is a hallmark feature used to identify them. In contrast, eosinophils typically have a bi-lobed (two-lobed) nucleus, and basophils have a bi-lobed or S-shaped nucleus that is often difficult to see because it is obscured by their large, dark granules.
- **Primary and secondary granules:** Neutrophils possess different types of cytoplasmic granules that contain enzymes and antimicrobial substances. Primary (azurophilic) granules contain enzymes like myeloperoxidase and defensins. Secondary (specific) granules contain substances like lactoferrin. This dual granule system is characteristic of neutrophils.

- **Limited life span:** Neutrophils are very short-lived cells. They circulate in the blood for only a few hours before migrating into tissues, where they survive for just a few days before undergoing apoptosis.

Step 3: Final Answer

All the provided features—being highly phagocytic, having a multi-lobed nucleus, containing primary and secondary granules, and having a short lifespan—are definitive characteristics of the **neutrophil**.

Quick Tip

When you see "multi-lobed nucleus" and "highly phagocytic," your first thought should always be **neutrophil**. They are the professional phagocytes of the innate immune system.

---

70. Which of the following are autosomal recessive genetic disorder?
A. Huntington disease
B. Sickle cell anemia
C. Lesch-Nyhan syndrome
D. Tay-Sachs disease
Choose the correct answer from the options given below:

(A) B and D only
(B) A, B and C only
(C) A, B, C and D
(D) B, C and D only

Correct Answer: (A) B and D only

Solution:

Step 1: Understanding the Concept

This question requires identifying which of the listed genetic disorders follow an **autosomal recessive** pattern of inheritance.

- **Autosomal** means the gene responsible for the disorder is located on one of the non-sex chromosomes (autosomes).
- **Recessive** means that an individual must inherit two copies of the mutated gene (one from each parent) to express the disease phenotype. An individual with only one copy is a carrier but is typically unaffected.

Step 2: Detailed Explanation

Let's analyze the inheritance pattern of each listed disorder:

- **A. Huntington disease:** This is a classic example of an **autosomal dominant** disorder. An individual only needs to inherit one copy of the mutated huntingtin gene to develop the disease. It does not fit the recessive pattern.
- **B. Sickle cell anemia:** This is a textbook example of an **autosomal recessive** disorder. The gene for hemoglobin is on an autosome. Individuals must be homozygous for the recessive sickle cell allele (HbS/HbS) to have the full-blown disease. Heterozygotes (HbA/HbS) have the "sickle cell trait" and are generally healthy carriers.
- **C. Lesch-Nyhan syndrome:** This is an **X-linked recessive** disorder. The gene responsible is located on the X chromosome. Because males (XY) have only one X chromosome, a single copy of the mutated gene will cause the disorder. It is not an autosomal disorder.
- **D. Tay-Sachs disease:** This is a fatal lysosomal storage disorder that follows an **autosomal recessive** inheritance pattern. An individual must inherit two copies of the defective gene for the HEXA enzyme (one from each parent) to be afflicted with the disease. Carriers have one defective copy but are phenotypically normal.

Step 3: Final Answer

Based on the analysis, the two disorders on the list that follow an autosomal recessive inheritance pattern are **Sickle cell anemia (B)** and **Tay-Sachs disease (D)**.

Quick Tip

For genetics questions, it's crucial to memorize the inheritance patterns of benchmark diseases. **Huntington's = Autosomal Dominant**. **Cystic Fibrosis, PKU, Sickle Cell, Tay-Sachs = Autosomal Recessive**. **Duchenne Muscular Dystrophy, Hemophilia, Lesch-Nyhan = X-linked Recessive**.

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71. Which one of the following proteins is often referred to as "the guardian of the genome"?

(A) PFU
(B) Rb
(C) Myc
(D) p53

Correct Answer: (D) p53

Solution:

Step 1: Understanding the Concept

The question asks to identify the protein that has earned the well-known epithet **"guardian of the genome."** This title is given to a specific tumor suppressor protein due to its central role in protecting the cell from genetic damage and preventing cancer.

Step 2: Detailed Explanation

- **The Protein p53:** The protein known as **p53** is a transcription factor that is often called the "guardian of the genome." Its critical function is to monitor the integrity of the cell's DNA.
- **Response to Cellular Stress:** p53 is activated in response to various forms of cellular stress, most notably DNA damage (e.g., from UV radiation or chemical mutagens).
- **p53's Two Main Functions:** Once activated, p53 can initiate two major cellular responses:
  1. **Cell Cycle Arrest:** p53 can halt the cell cycle, typically at the G1/S checkpoint. This provides the cell with time to repair the damaged DNA before it proceeds to DNA replication (S phase).
  2. **Apoptosis (Programmed Cell Death):** If the DNA damage is too extensive or severe to be repaired, p53 will trigger apoptosis. This process eliminates the potentially cancerous cell, preventing it from proliferating and forming a tumor.
- **Tumor Suppression:** By preventing cells with damaged DNA from dividing, p53 maintains genomic stability and acts as a powerful tumor suppressor. Mutations in the p53 gene are found in over 50% of all human cancers.
- **Other Options:**
  - **Rb (Retinoblastoma protein):** Another important tumor suppressor that also controls the G1/S checkpoint, but p53 is the one known as the "guardian."
  - **Myc:** A proto-oncogene that promotes cell proliferation. Its uncontrolled activation contributes to cancer formation.
  - **PFU (Plaque-Forming Unit):** This is a term used in virology to quantify the number of infectious virus particles in a sample. It is not a protein.

Step 3: Final Answer

The protein **p53** is referred to as "the guardian of the genome."

Quick Tip

The link between **p53** and "guardian of the genome" is one of the most famous in molecular cancer biology. Mutations in the TP53 gene (which codes for p53) are found in over 50% of all human cancers, highlighting its critical role.

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72. Colibactin is a DNA-damaging compound and when taken up by human intestinal cells, colibactin result in double stranded DNA break and can cause human

colorectal cancers. It is synthesized by:

(A) Certain strain of E. coli
(B) Helicobacter pylori
(C) Bacteroides fragilis
(D) Bifidobacterium spp.

Correct Answer: (A) Certain strain of E. coli

Solution:

Step 1: Understanding the Concept

The question asks to identify the bacterial source of **colibactin**. Colibactin is a **genotoxin**, which is a toxin that causes damage to DNA. This particular genotoxin has been implicated in the development of colorectal cancer.

Step 2: Detailed Explanation

- **Production of Colibactin:** Colibactin is a secondary metabolite, meaning it is not essential for the bacterium's basic growth but provides some other advantage. Its production is directed by a specific cluster of genes located on a genomic island known as the **polyketide synthase (pks) island**.
- **Bacterial Source:** This pks island is found in **certain strains of *Escherichia coli*** (E. coli), particularly those belonging to the B2 phylogroup. It can also be found in some other related bacteria like *Klebsiella pneumoniae*.
- **Role in Gut Microbiota:** These pks-positive E. coli strains can be part of the normal gut microbiota in some individuals without causing immediate illness.
- **Mechanism of Action:** The colibactin produced by these bacteria acts as a DNA alkylating agent. It can cause double-strand breaks in the DNA of the host's intestinal epithelial cells. This DNA damage, if not properly repaired, can lead to chromosomal instability and mutations that promote the development of colorectal cancer over time.
- **Other Bacteria:**
  - ***Helicobacter pylori*:** Famously associated with stomach ulcers and stomach cancer, but not with colibactin.
  - ***Bacteroides fragilis*:** Certain strains can produce a different toxin (BFT - *B. fragilis* toxin) that is also linked to colon cancer, but it is not colibactin.
  - ***Bifidobacterium*:** This genus of bacteria is generally considered probiotic and beneficial to gut health.

Step 3: Final Answer

Colibactin is synthesized by certain strains of ***Escherichia coli*** (E. coli).

Quick Tip

Remember the link: **Coli**bactin is produced by E. **coli**. The name of the toxin itself points to its bacterial origin.

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73. Agar is used for preparing solid media for culture. Which of the following is not true about agar media?

(A) Agar is obtain from a sea weed
(B) It has virtually no nutritive value.
(C) It melts at 98°C and usually sets on 42°C depending on agar concentration.
(D) For solid media 0.2% to 0.5% agar concentration is employed.

Correct Answer: (D) For solid media 0.2% to 0.5% agar concentration is employed.

Solution:

Step 1: Understanding the Concept

The question asks to identify an incorrect statement about the properties of **agar**, which is the most widely used solidifying agent for preparing microbiological culture media.

Step 2: Detailed Explanation

Let's evaluate the correctness of each statement:

- **(A) Agar is obtained from a seaweed:** This statement is **true**. Agar is a complex polysaccharide that is extracted from the cell walls of various species of red algae, primarily from the genera *Gelidium* and *Gracilaria*.
- **(B) It has virtually no nutritive value:** This statement is **true**. A key advantage of agar is that it is a complex carbohydrate that the vast majority of microorganisms cannot metabolize or degrade. This ensures that it serves purely as an inert solidifying matrix and does not interfere with the nutritional composition of the medium.
- **(C) It melts at 98°C and usually sets on 42°C...:** This statement is **true**. Agar exhibits a property called **hysteresis**, meaning its melting temperature is much higher than its solidifying temperature. It melts at around 95-100°C but does not solidify until it cools to around 40-45°C. This is extremely useful because it allows heat-sensitive supplements (like blood, vitamins, or antibiotics) to be added to the molten agar at a lower temperature before it solidifies.

- **(D) For solid media 0.2% to 0.5% agar concentration is employed:** This statement is **false**. This concentration range (0.2% to 0.5%) is used to prepare **semi-solid media**, which have a consistency similar to jelly and are primarily used for motility testing (to observe if bacteria can swim through the medium). To create a standard **solid medium** (e.g., an agar plate or a slant), a higher concentration of **1.5% to 2.0%** agar is required to produce a firm gel that can support colony growth on its surface.

Step 3: Final Answer

The incorrect statement is (D). The concentration of 0.2% to 0.5% agar is used for semi-solid media, not solid media.

Quick Tip

Remember the standard concentrations for agar media: **Solid** media (plates, slants) $\rightarrow$ **1.5%**. **Semi-solid** media (motility) $\rightarrow$ **0.4-0.5%**. **Broth** (liquid) $\rightarrow$ **0%**.

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74. Which one of the following groups of animal is devoid of gill slits?

(A) Osteichthyes
(B) Cyclostomata and Chondrichthyes
(C) Echinodermata
(D) Adult Amphibians

Correct Answer: (C) Echinodermata

Solution:

Step 1: Understanding the Concept

The question is based on a key characteristic of the phylum **Chordata**. One of the defining features of all chordates is the presence of **pharyngeal gill slits** at some stage of their life cycle. The task is to identify the animal group listed that does not possess this feature.

Step 2: Detailed Explanation

Let's analyze each group in the context of being a chordate:

- **Osteichthyes (Bony fish):** These are chordates. They possess gills that are covered by a protective flap called an operculum. These gills are used for respiration throughout their entire lives.
- **Cyclostomata (Jawless fish) and Chondrichthyes (Cartilaginous fish):** These are also chordates. They possess exposed gill slits (not covered by an operculum) which they use for respiration throughout their lives.

- **Adult Amphibians:** Amphibians are chordates. While the adult forms, such as frogs, typically lose their gills and develop lungs for breathing air, their larval stage (the tadpole) is aquatic and possesses gills for respiration. The presence of pharyngeal gill slits at any point in the life cycle (even if only in the larval stage) is a chordate characteristic.
- **Echinodermata (e.g., starfish, sea urchins):** This group belongs to a completely different phylum of marine **invertebrates**. They are not chordates and therefore completely lack pharyngeal gill slits at all stages of their life. Their methods of gas exchange include dermal branchiae (skin gills) or tube feet, which are structurally and developmentally different from chordate gill slits.

Step 3: Final Answer

Echinodermata is the only group listed that is not part of the phylum Chordata and, as a result, is completely devoid of pharyngeal gill slits.

Quick Tip

Pharyngeal gill slits are a hallmark of Chordates. To answer this question, you simply need to identify which group is not a chordate. Echinoderms (starfish, etc.) are a distinct invertebrate phylum.

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75. Which one of the following is not a tetrapods character?

(A) Dermal scales
(B) Neck and ribs
(C) Pelvic girdle
(D) Flat skull

Correct Answer: (A) Dermal scales

Solution:

Step 1: Understanding the Concept

The question asks to identify a feature that is not a typical characteristic of the superclass **Tetrapoda**. Tetrapods are the four-limbed vertebrates (amphibians, reptiles, birds, and mammals) that evolved from lobe-finned fishes and adapted to a terrestrial lifestyle.

Step 2: Detailed Explanation

Let's evaluate each feature as it relates to the evolution and characteristics of tetrapods:

- **Neck and ribs:** The evolution of a distinct neck, separating the head from the pectoral girdle, was a crucial adaptation for life on land, allowing for independent movement of the head for feeding and scanning the environment. Well-developed ribs provide structural

support for the body cavity and protect internal organs against gravity, which is a much greater force on land than in the supportive environment of water. This is a **key tetrapod character**.

- **Pelvic girdle:** A strong pelvic girdle that is firmly attached to the vertebral column is essential for supporting the body's weight on the hind limbs and enabling terrestrial locomotion. This is a **key tetrapod character**.
- **Flat skull:** Early, transitional tetrapods like *Acanthostega* and *Ichthyostega* are characterized by having broad, flat skulls. While skull shape has diversified greatly since then, this feature is considered a classic characteristic of the **ancestral tetrapod body plan**.
- **Dermal scales:** Dermal scales, which are bony plates embedded in the dermis, are a characteristic feature of **fish**. A major evolutionary trend in the transition from lobe-finned fish to the first tetrapods (amphibians) was the **loss** of these scales. Early amphibians developed smooth, moist skin that was capable of cutaneous respiration (breathing through the skin). While some later tetrapods, like reptiles, re-evolved scale-like structures, these are epidermal scales (made of keratin) and are structurally different. The presence of fish-like dermal scales is therefore a fish character, and their loss is a defining trend in the origin of tetrapods. Thus, their presence is **not a general tetrapod character**.

Step 3: Final Answer

Dermal scales are a characteristic of fish that were generally lost during the evolution of tetrapods. Therefore, they are not considered a characteristic feature of the tetrapod group as a whole.

Quick Tip

Think about the adaptations needed to move from water to land. You need stronger support (pelvic girdle, ribs), a way to look around (neck), but you would typically lose features adapted for water, such as fins and fish scales.
