TS PGECET 2026 Bio Technology (BT)

Question Paper with Solutions

Conducted by JNTU, Hyderabad

General Instructions

(i) The test is of 2 hours duration.

(ii) This test paper consists of 120 questions. The maximum marks are 120.

(iii) Each question carries +1 marks for correct answer and there is no negative marking for wrong answer.

1. The matrix

$$A = \begin{bmatrix} 1 & 1+i & 2i \\ 1-i & 3 & 4 \\ -2i & 4 & 5 \end{bmatrix}$$

has

(A) only real eigen values

(B) eigen values of the form $a+ib,\ a \neq 0,\ b \neq 0$

(C) eigen values of the form $x+iy,\ x=0$

(D) no inverse

Correct Answer: (A) only real eigen values

Solution:

Step 1: Check whether the matrix is Hermitian.

A matrix is Hermitian if

$$A = A^H,$$

where A^H denotes the conjugate transpose.

For the given matrix,

$$\overline{(1+i)} = 1-i, \qquad \overline{(2i)} = -2i,$$

and the corresponding symmetric entries satisfy

$$a_{12} = \overline{a_{21}}, \qquad a_{13} = \overline{a_{31}}, \qquad a_{23} = \overline{a_{32}}.$$

Hence,

$$\boxed{A = A^H.}$$

Step 2: Use the property of Hermitian matrices.

A Hermitian matrix always has

$$\boxed{\text{all eigen values real.}}$$

Therefore,

$$\boxed{\text{only real eigen values}}$$

is the correct answer.

Thus,

$$\boxed{(A)}$$

is the correct answer.

Quick Tip: For complex matrices,

$$\boxed{A = A^H \implies \text{All eigen values are real.}}$$

This is one of the most important properties of Hermitian matrices.

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2. An eigen vector of the matrix

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$$A = \begin{bmatrix} 3 & 2 \\ 1 & 2 \end{bmatrix}$$

is

(A) $\begin{bmatrix} 7 \\ 2 \end{bmatrix}$

(B) $\begin{bmatrix} -2 \\ 1 \end{bmatrix}$

(C) $\begin{bmatrix} -1 \\ 2 \end{bmatrix}$

(D) $\begin{bmatrix} 5 \\ -5 \end{bmatrix}$

Correct Answer: (D)

$$\begin{bmatrix} 5 \\ -5 \end{bmatrix}$$

Solution:

Step 1: Use the eigenvector definition.

A vector X is an eigenvector if

$$AX = \lambda X$$

for some scalar λ.

Step 2: Check option (D).

Let

$$X = \begin{bmatrix} 5 \\ -5 \end{bmatrix}.$$

Then,

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$$AX = \begin{bmatrix} 3 & 2 \\ 1 & 2 \end{bmatrix} \begin{bmatrix} 5 \\ -5 \end{bmatrix} = \begin{bmatrix} 15-10 \\ 5-10 \end{bmatrix} = \begin{bmatrix} 5 \\ -5 \end{bmatrix}.$$

Thus,

$$AX = 1 \cdot X.$$

Hence,

$$\boxed{\begin{bmatrix} 5 \\ -5 \end{bmatrix}}$$

is an eigenvector corresponding to the eigenvalue

$$\lambda = 1.$$

Therefore,

$$\boxed{(D)}$$

is the correct answer.

Quick Tip: To verify an eigenvector, simply check

$$\boxed{AX = \lambda X.}$$

If the resulting vector is a scalar multiple of the original vector, then it is an eigenvector.

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3. A convergent series from the given series is

(A)

$$\sum_{n=1}^{\infty} \frac{1}{\sqrt{n}}$$

(B)

$$\sum_{n=1}^{\infty} \frac{(-1)^n}{\sqrt{n+1}}$$

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(C)

$$\sum_{n=1}^{\infty} \frac{3n^4+5}{n^2(n^2+4n+5)}$$

(D)

$$\sum_{n=3}^{\infty} \frac{\log n}{n}$$

Correct Answer: (B)

$$\sum_{n=1}^{\infty} \frac{(-1)^n}{\sqrt{n+1}}$$

Solution:

Step 1: Test each series for convergence.

For option (A),

$$\sum \frac{1}{\sqrt{n}} = \sum \frac{1}{n^{1/2}}$$

is a p-series with

$$p = \frac{1}{2} < 1,$$

so it diverges.

For option (B),

$$\sum_{n=1}^{\infty} \frac{(-1)^n}{\sqrt{n+1}}$$

is an alternating series.

Since

$$\frac{1}{\sqrt{n+1}}$$

is positive, decreasing and

$$\lim_{n\to\infty} \frac{1}{\sqrt{n+1}} = 0,$$

the series converges by the Leibniz Alternating Series Test.

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For option (C),

$$\frac{3n^4+5}{n^2(n^2+4n+5)} \sim 3,$$

which does not approach zero.

Hence the series diverges.

For option (D),

$$\sum \frac{\log n}{n}$$

diverges by the Integral Test.

Step 2: Choose the convergent series.

Only option (B) satisfies the convergence criterion.

Therefore,

$$\boxed{\sum_{n=1}^{\infty} \frac{(-1)^n}{\sqrt{n+1}}}$$

is the convergent series.

Thus,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Remember:

$$\boxed{\begin{aligned} \sum \frac{1}{n^p} &\text{ converges if } p > 1, \\ \sum (-1)^n a_n &\text{ converges if } a_n \downarrow 0. \end{aligned}}$$

---

4. Fourier series of x^2, $0 < x < 2$ is

$$f(x) = \frac{a_0}{2} + \sum_{n=1}^{\infty} a_n \cos(n\pi x) + \sum_{n=1}^{\infty} b_n \sin(n\pi x),$$

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then $b_2 =$

(A) Zero since x^2 is an even function

(B)

$$\int_0^2 x^2 \sin 2x \, dx$$

(C)

$$\int_0^2 x^2 \cos 2\pi x \, dx = -\frac{2}{\pi}$$

(D)

$$\int_0^2 x^2 \sin 2\pi x \, dx = -\frac{2}{\pi}$$

Correct Answer: (D)

$$\int_0^2 x^2 \sin 2\pi x \, dx = -\frac{2}{\pi}$$

Solution:

Step 1: Recall the Fourier coefficient.

For the interval

$$0 < x < 2,$$

the sine coefficient is

$$\boxed{b_n = \int_0^2 f(x) \sin(n\pi x) \, dx.}$$

Since

$$f(x) = x^2,$$

we obtain

$$b_2 = \int_0^2 x^2 \sin(2\pi x) \, dx.$$

Step 2: Evaluate the integral.

Using integration by parts,

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$$\int_0^2 x^2 \sin(2\pi x)\,dx = -\frac{2}{\pi}.$$

Hence,

$$\boxed{b_2 = -\frac{2}{\pi}.}$$

Therefore,

$$\boxed{(D)}$$

is the correct answer.

Quick Tip: For Fourier series on

$$0 < x < 2L,$$

$$\boxed{b_n = \frac{1}{L}\int_0^{2L} f(x)\sin\left(\frac{n\pi x}{L}\right)dx.}$$

Here,

$$L = 1,$$

so

$$b_n = \int_0^2 f(x)\sin(n\pi x)\,dx.$$

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5. If y_1, y_2 are two dependent solutions of a second order linear homogeneous differential equation then $y_1y_2' - y_2y_1'$ is

(A) Positive

(B) Negative

(C) Non-zero

(D) Zero

Correct Answer: (D) Zero

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Solution:

Step 1: Recall the Wronskian.

The Wronskian of two functions y_1 and y_2 is

$$\boxed{W(y_1, y_2) = y_1 y_2' - y_2 y_1'.}$$

Step 2: Use the property of linearly dependent solutions.

If y_1 and y_2 are linearly dependent, then

$$y_2 = C y_1,$$

where C is a constant.

Differentiating,

$$y_2' = C y_1'.$$

Substituting into the Wronskian,

$$W = y_1(C y_1') - (C y_1) y_1' = 0.$$

Hence,

$$\boxed{y_1 y_2' - y_2 y_1' = 0.}$$

Therefore,

$$\boxed{(D)}$$

is the correct answer.

Quick Tip: For two solutions of a linear differential equation,

$$\boxed{\begin{aligned} W \neq 0 &\Longrightarrow \text{Linearly Independent} \\ W = 0 &\Longrightarrow \text{Linearly Dependent} \end{aligned}}$$

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6. The general solution of one dimensional wave equation

$$\frac{\partial^2 v}{\partial t^2} = c^2 \frac{\partial^2 v}{\partial x^2}$$

is $u(x,t) =$

(A) $f(x+ct)\,g(x-ct)$

(B) $f(x+ct)+g(x-ct)$

(C) $f(x-ct)+g(x-ct)$

(D) $f(x+ct)+g(x+ct)$

Correct Answer: (B)

$$u(x,t) = f(x+ct)+g(x-ct)$$

Solution:

Step 1: Recall D'Alembert's solution of the wave equation.

The one-dimensional wave equation

$$\frac{\partial^2 u}{\partial t^2} = c^2 \frac{\partial^2 u}{\partial x^2}$$

has the general solution

$$\boxed{u(x,t) = f(x-ct)+g(x+ct),}$$

where f and g are arbitrary functions.

Step 2: Compare with the given options.

Since the names of arbitrary functions can be interchanged,

$$f(x-ct)+g(x+ct)$$

is equivalent to

$$f(x+ct)+g(x-ct).$$

Hence,

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$$\boxed{u(x,t) = f(x+ct) + g(x-ct).}$$

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: D'Alembert's solution is

$$\boxed{u(x,t) = f(x-ct) + g(x+ct),}$$

representing two waves travelling in opposite directions with speed c.

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7. If

$$F(x) = \begin{cases} 0, & x < -7, \\ \left(\frac{x+7}{a}\right), & -7 < x < 7, \\ 1, & x > 7, \end{cases}$$

represents the probability distribution function of a continuous random variable, then $a =$

(A) -7

(B) 21

(C) 7

(D) 14

Correct Answer: (D) 14

Solution:

Step 1: Use the property of a distribution function.

For a cumulative distribution function,

$$\boxed{F(\infty) = 1.}$$

Also, the function must be continuous.

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Step 2: Apply continuity at $x = 7$.

For

$$-7 < x < 7,$$

$$F(x) = \frac{x+7}{a}.$$

At

$$x = 7,$$

$$\frac{7+7}{a} = 1.$$

Hence,

$$\frac{14}{a} = 1.$$

Therefore,

$$a = 14.$$

Thus,

$$\boxed{14}$$

is the correct answer.

Hence,

$$\boxed{(D)}$$

is the correct answer.

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Quick Tip: For a cumulative distribution function,

$$\boxed{F(-\infty)=0, \qquad F(\infty)=1.}$$

Use continuity at the boundary points to determine unknown constants.

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8. Mean and variance pair is given below. A pair representing the data of a binomial distribution is

(A) $(7,4)$

(B) $(12,5)$

(C) $(15,6)$

(D) $(18,10)$

Correct Answer: (C) $(15,6)$

Solution:

Step 1: Recall the formulas for a binomial distribution.

For a binomial distribution,

$$\boxed{\mu = np,}$$

and

$$\boxed{\sigma^2 = npq,}$$

where

$$q = 1-p.$$

Hence,

$$\sigma^2 = \mu q.$$

Since

$$0 < q < 1,$$

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it follows that

$$\boxed{\sigma^2 < \mu.}$$

Step 2: Check the given pairs.

For option (A),

$$4 < 7,$$

but

$$p = \frac{3}{7},$$

giving

$$n = \frac{7}{3/7} = \frac{49}{3},$$

which is not an integer.

Hence, not possible.

For option (B),

$$5 < 12,$$

$$p = \frac{7}{12},$$

so

$$n = \frac{12}{7/12} = \frac{144}{7},$$

not an integer.

Hence, not possible.

For option (C),

$$6 < 15,$$

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$$q = \frac{6}{15} = \frac{2}{5}, \qquad p = \frac{3}{5}.$$

Thus,

$$n = \frac{15}{3/5} = 25,$$

which is an integer.

Hence, this pair is valid.

For option (D),

$$10 < 18,$$

$$p = \frac{4}{9},$$

giving

$$n = \frac{18}{4/9} = 40.5,$$

not an integer.

Hence, not possible.

Therefore,

$$\boxed{(15, 6)}$$

is the correct pair.

Thus,

$$\boxed{(C)}$$

is the correct answer.

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Quick Tip: For a binomial distribution,

$$\boxed{\mu = np, \qquad \sigma^2 = npq.}$$

To verify a given mean-variance pair,

$$\boxed{p = 1 - \frac{\sigma^2}{\mu}, \qquad n = \frac{\mu}{p}.}$$

A valid binomial distribution requires

$$\boxed{n}$$

to be a positive integer.

---

9. If $x_0 = 1.2$ is the initial guess of the solution of $x^3 + 2x - 1 = 0$, then the 1^{st} iteration solution $x_1 =$

(A) 0.705

(B) 0.675

(C) 0.815

(D) 0.795

Correct Answer: (A) 0.705

Solution:

Step 1: Use the Newton-Raphson formula.

For

$$f(x) = x^3 + 2x - 1,$$

Newton-Raphson iteration is

$$\boxed{x_{n+1} = x_n - \frac{f(x_n)}{f'(x_n)}.}$$

Differentiate:

$$f'(x) = 3x^2 + 2.$$

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Step 2: Evaluate $f(x_0)$ and $f'(x_0)$.

Given,

$$x_0 = 1.2.$$

Then,

$$f(1.2) = (1.2)^3 + 2(1.2) - 1 = 1.728 + 2.4 - 1 = 3.128.$$

Also,

$$f'(1.2) = 3(1.2)^2 + 2 = 3(1.44) + 2 = 6.32.$$

Step 3: Compute the first iteration.

$$x_1 = 1.2 - \frac{3.128}{6.32} = 1.2 - 0.4949 \approx 0.705.$$

Hence,

$$\boxed{x_1 \approx 0.705.}$$

Therefore,

$$\boxed{(A)}$$

is the correct answer.

Quick Tip: Newton-Raphson iteration is

$$\boxed{x_{n+1} = x_n - \frac{f(x_n)}{f'(x_n)}.}$$

It provides quadratic convergence when the initial guess is sufficiently close to the root.

---

10. A multistep method used to solve differential equations is

(A) Runge-Kutta 4^{th} order differential method

(B) Euler's modified method

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(C) Adams-Bashforth method

(D) Successive approximation method

Correct Answer: (C) Adams-Bashforth method

Solution:

Step 1: Recall the classification of numerical methods.

Numerical methods for ordinary differential equations are classified as

- Single-step methods,
- Multi-step methods.

Single-step methods compute the next value using only the current point.

Multi-step methods use values from several previous points.

Step 2: Identify the multistep method.

Among the given options,

$$\boxed{\text{Adams-Bashforth method}}$$

uses information from previous steps to predict the next solution.

Hence, it is a multistep method.

Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Examples of numerical methods:

$$\boxed{\begin{array}{l}\text{Single-step : Euler, Modified Euler, Runge-Kutta}\\ \text{Multi-step : Adams-Bashforth, Adams-Moulton}\end{array}}$$

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11. Origin of replication usually contains

(A) GC Rich Sequences

(B) GCG-Rich Sequences

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(C) No particular stretch of Sequences

(D) AT-Rich Sequences

Correct Answer: (D) AT-Rich Sequences

Solution:

Step 1: Recall the origin of replication.

The origin of replication (*Ori*) is the specific DNA sequence where DNA replication begins.

Step 2: Identify its characteristic feature.

Origin of replication generally contains

$$\boxed{\text{AT-rich sequences.}}$$

Since adenine-thymine (A–T) base pairs are connected by only two hydrogen bonds, they separate more easily than G–C base pairs during DNA replication.

Hence,

$$\boxed{\text{AT-Rich Sequences}}$$

is the correct answer.

Therefore,

$$\boxed{(D)}$$

is the correct answer.

Quick Tip: AT-rich regions are preferred at the origin of replication because

$$\boxed{\text{A–T pairs have only two hydrogen bonds,}}$$

making DNA unwinding easier.

---

12. Which of the following cellular components is present in eukaryotic cells but absent in prokaryotic cells?

(A) Plasma membrane

(B) Ribosomes

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(C) Mitochondria

(D) Cell wall

Correct Answer: (C) Mitochondria

Solution:

Step 1: Compare prokaryotic and eukaryotic cells.

Both prokaryotic and eukaryotic cells possess

- Plasma membrane,
- Ribosomes.

Many prokaryotes and some eukaryotes also possess a cell wall.

Step 2: Identify the membrane-bound organelle.

Membrane-bound organelles such as mitochondria are found only in eukaryotic cells.

Prokaryotic cells lack membrane-bound organelles.

Hence,

$$\boxed{\text{Mitochondria}}$$

is the correct answer.

Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Prokaryotes lack membrane-bound organelles such as

$$\boxed{\text{Mitochondria, Chloroplasts, Endoplasmic Reticulum and Golgi Apparatus.}}$$

---

13. A bacterium has a generation time of 30 minutes. Starting with 1×10^4 (10000) cells, how many cells will be present after 2 hours?

(A) 4×10^4

(B) 8×10^4

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(C) 1.6×10^5

(D) 6.4×10^5

Correct Answer: (C) 1.6×10^5

Solution:

Step 1: Determine the number of generations.

Given,

$$\text{Generation time} = 30 \text{ min.}$$

Total time,

$$2 \text{ hours} = 120 \text{ min.}$$

Hence,

$$n = \frac{120}{30} = 4.$$

Step 2: Use the bacterial growth formula.

The number of cells after n generations is

$$\boxed{N = N_0\, 2^n,}$$

where

- $N_0 = 10^4$,
- $n = 4$.

Therefore,

$$N = 10^4 \times 2^4 = 10^4 \times 16 = 1.6 \times 10^5.$$

Hence,

$$\boxed{1.6 \times 10^5}$$

is the correct answer.

Therefore,

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$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Bacterial population growth follows

$$\boxed{N = N_0\, 2^n,}$$

where

$$n = \frac{\text{Total Time}}{\text{Generation Time}}.$$

---

14. Which of the following correctly matches a virus with its type of nucleic acid?

(A) Poliovirus – double-stranded DNA

(B) Influenza virus – negative-sense single-stranded RNA

(C) Adenovirus – single-stranded RNA

(D) HIV – single-stranded DNA

Correct Answer: (B) Influenza virus – negative-sense single-stranded RNA

Solution:

Step 1: Recall the nucleic acid present in common viruses.

Some important viral genomes are

$$\begin{aligned} \text{Poliovirus} &\rightarrow \text{Positive-sense single-stranded RNA,} \\ \text{Influenza virus} &\rightarrow \text{Negative-sense single-stranded RNA,} \\ \text{Adenovirus} &\rightarrow \text{Double-stranded DNA,} \\ \text{HIV} &\rightarrow \text{Positive-sense single-stranded RNA (Retrovirus).} \end{aligned}$$

Step 2: Identify the correct match.

Among the given options,

$$\boxed{\text{Influenza virus – negative-sense single-stranded RNA}}$$

is the correct combination.

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Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Remember the important viral genomes:

Poliovirus	$\rightarrow$ (+)ssRNA
Influenza virus	$\rightarrow$ (−)ssRNA
Adenovirus	$\rightarrow$ dsDNA
HIV	$\rightarrow$ (+)ssRNA (Retrovirus)

---

15. Viruses are considered as living organisms because they perform

(A) Metabolism

(B) Respiration

(C) Replication

(D) Multiply outside the host cell

Correct Answer: (C) Replication

Solution:

Step 1: Recall the characteristics of viruses.

Viruses are acellular particles that do not possess their own metabolic machinery.

They cannot carry out respiration or independent metabolism.

Step 2: Identify the property associated with life.

Inside a suitable host cell, viruses reproduce by making copies of themselves.

Thus,

$$\boxed{\text{Viruses perform replication inside living host cells.}}$$

Therefore,

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Replication

is the correct answer.

Hence,

(C)

is the correct answer.

Quick Tip: Viruses are

Outside host → Non-living

Inside host → Living (replicate only)

They do not perform independent metabolism or respiration.

---

16. Match the following

	Genetic element/process		Characteristic
A	F plasmid	*I*	Uptake of naked DNA
B	Transformation	*II*	Sex pilus formation
C	Generalized transduction	*III*	Random bacterial DNA transfer
D	Hfr strain	*IV*	High-frequency chromosomal gene transfer

The correct answer is

(A) A – II, B – I, C – III, D – IV

(B) A – I, B – II, C – IV, D – III

(C) A – III, B – IV, C – I, D – II

(D) A – II, B – III, C – I, D – IV

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

Solution:

Step 1: Match each genetic process with its characteristic.

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F plasmid → Sex pilus formation (II)

Transformation → Uptake of naked DNA (I)

Generalized transduction → Random bacterial DNA transfer (III)

Hfr strain → High-frequency chromosomal gene transfer (IV)

Step 2: Write the correct matching.

Thus,

$$\boxed{A-\text{II},\ B-\text{I},\ C-\text{III},\ D-\text{IV}}$$

Therefore,

$$\boxed{(A)}$$

is the correct answer.

Quick Tip: Remember the bacterial gene transfer methods:

Transformation → Naked DNA

Transduction → Bacteriophage-mediated transfer

Conjugation → Sex pilus (F plasmid)

Hfr strain → Chromosomal gene transfer

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17. The site of light reactions of photosynthesis occurs on

(A) Stroma

(B) Cytosol

(C) Thylakoid membrane

(D) Inner mitochondrial membrane

Correct Answer: (C) Thylakoid membrane

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Solution:

Step 1: Recall the two stages of photosynthesis.

Photosynthesis consists of

- Light reactions,
- Dark reactions (Calvin cycle).

Step 2: Identify the site of light reactions.

The light-dependent reactions occur on the

$$\boxed{\text{Thylakoid membrane}}$$

of chloroplasts, where chlorophyll, Photosystem I, Photosystem II and the electron transport chain are located.

The Calvin cycle occurs in the stroma.

Therefore,

$$\boxed{\text{Thylakoid membrane}}$$

is the correct answer.

Hence,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Photosynthesis occurs at two locations:

$$\boxed{\begin{array}{l}\text{Light reaction} \rightarrow \text{Thylakoid membrane} \\ \text{Calvin cycle} \rightarrow \text{Stroma}\end{array}}$$

---

18. Which of the following yields the maximum ATP?

(A) Glycolysis

(B) Fermentation

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(C) Aerobic respiration

(D) Anaerobic respiration

Correct Answer: (C) Aerobic respiration

Solution:

Step 1: Recall the ATP yield of different processes.

$$\text{Glycolysis} \rightarrow 2 \text{ ATP}$$

$$\text{Fermentation} \rightarrow 2 \text{ ATP}$$

$$\text{Anaerobic respiration} \rightarrow \text{Less ATP than aerobic respiration}$$

$$\text{Aerobic respiration} \rightarrow 36\text{–}38 \text{ ATP}$$

Step 2: Identify the process producing maximum ATP.

Since aerobic respiration completely oxidizes one glucose molecule in the presence of oxygen, it produces the maximum amount of ATP.

Hence,

$$\boxed{\text{Aerobic respiration}}$$

is the correct answer.

Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: ATP yield per glucose:

$$\boxed{\begin{array}{c}\text{Glycolysis} \rightarrow 2 \text{ ATP} \\ \text{Aerobic respiration} \rightarrow 36\text{–}38 \text{ ATP}\end{array}}$$

Aerobic respiration gives the highest energy yield.

---

19. Consider the following and choose the correct answer

Assertion [A]: Aerobic respiration is more efficient than anaerobic respiration.

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Reason [R]: Oxygen allows complete oxidation of glucose.

The correct answer is

(A) Both [A] and [R] are true and [R] is the correct explanation of [A]

(B) Both [A] and [R] are true and [R] is not correct explanation of [A]

(C) [A] is true, but [R] is false

(D) [A] is false, but [R] is true

Correct Answer: (A) Both [A] and [R] are true and [R] is the correct explanation of [A]

Solution:

Step 1: Examine the assertion.

Aerobic respiration produces much more ATP than anaerobic respiration.

Therefore,

$$\boxed{\text{Assertion [A] is true.}}$$

Step 2: Examine the reason.

In aerobic respiration, oxygen acts as the final electron acceptor, allowing complete oxidation of glucose into carbon dioxide and water.

Hence,

$$\boxed{\text{Reason [R] is true.}}$$

Step 3: Establish the relationship.

Complete oxidation of glucose releases maximum energy, which explains why aerobic respiration is more efficient.

Thus,

$$\boxed{\text{Both [A] and [R] are true and [R] correctly explains [A].}}$$

Therefore,

$$\boxed{(A)}$$

is the correct answer.

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Quick Tip: Aerobic respiration is more efficient because

Oxygen enables complete oxidation of glucose.

Complete oxidation produces the maximum ATP.

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20. What are the products of the light reaction utilized during the Calvin cycle?

(A) Oxygen

(B) NADH

(C) ATP and NADPH

(D) CO_2

Correct Answer: (C) ATP and NADPH

Solution:

Step 1: Recall the products of the light reaction.

The light-dependent reactions of photosynthesis produce

ATP,

NADPH,

Oxygen.

Step 2: Identify the products used in the Calvin cycle.

The Calvin cycle requires

ATP

as the energy source and

NADPH

as the reducing power to convert carbon dioxide into carbohydrates.

Therefore,

ATP and NADPH

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are utilized during the Calvin cycle.

Hence,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Photosynthesis summary:

$$\boxed{\begin{array}{l}\text{Light Reaction} \rightarrow \text{ATP, NADPH, } O_2 \\ \text{Calvin Cycle} \rightarrow \text{Uses ATP and NADPH}\end{array}}$$

---

21. Identify the following organism which is a symbiotic nitrogen fixer?

(A) Azotobacter

(B) Rhizobium

(C) Clostridium

(D) Nitrosomonas

Correct Answer: (B) Rhizobium

Solution:

Step 1: Recall the types of nitrogen-fixing organisms.

Nitrogen-fixing bacteria are classified as

- Free-living nitrogen fixers,
- Symbiotic nitrogen fixers.

Step 2: Identify the symbiotic nitrogen fixer.

Azotobacter → Free-living aerobic nitrogen fixer,

Clostridium → Free-living anaerobic nitrogen fixer,

Nitrosomonas → Nitrifying bacterium,

Rhizobium → Symbiotic nitrogen fixer.

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Rhizobium lives in the root nodules of leguminous plants and fixes atmospheric nitrogen.

Hence,

$$\boxed{\textit{Rhizobium}}$$

is the correct answer.

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Remember the important nitrogen-fixing bacteria:

Rhizobium → Symbiotic
Azotobacter → Free-living aerobic
Clostridium → Free-living anaerobic

---

22. Match the following

	List-I		List-II
A	*Azotobacter*	*I*	Anaerobic nitrogen fixer
B	*Clostridium*	*II*	Symbiotic nitrogen fixer
C	*Rhizobium*	*III*	Free-living aerobic fixer
D	Leghemoglobin	*IV*	Oxygen buffering protein

The correct answer is

(A) A – III, B – I, C – II, D – IV

(B) A – I, B – III, C – IV, D – II

(C) A – I, B – IV, C – II, D – III

(D) A – IV, B – II, C – III, D – I

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

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Solution:

Step 1: Match each organism with its characteristic.

Azotobacter	→ Free-living aerobic nitrogen fixer (III)
Clostridium	→ Anaerobic nitrogen fixer (I)
Rhizobium	→ Symbiotic nitrogen fixer (II)
Leghemoglobin	→ Oxygen buffering protein (IV)

Step 2: Write the correct matching.

Thus,

$$\boxed{A-\text{III},\ B-\text{I},\ C-\text{II},\ D-\text{IV}}$$

Therefore,

$$\boxed{(A)}$$

is the correct answer.

Quick Tip: Important associations:

Azotobacter	→ Aerobic nitrogen fixer
Clostridium	→ Anaerobic nitrogen fixer
Rhizobium	→ Symbiotic nitrogen fixer
Leghemoglobin	→ Maintains low oxygen concentration in root nodules

---

23. Select the enzyme complex responsible for biological nitrogen fixation?

(A) Nitrate reductase

(B) Nitrogenase

(C) Nitrite reductase

(D) Glutamine synthetase

Correct Answer: (B) Nitrogenase

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Solution:

Step 1: Recall the enzyme involved in nitrogen fixation.

Biological nitrogen fixation is the conversion of atmospheric nitrogen

$$N_2$$

into ammonia

$$NH_3.$$

This reaction is catalyzed by the enzyme complex

$$\boxed{\text{Nitrogenase.}}$$

Step 2: Identify the correct enzyme.

Nitrogenase consists of

- Fe-protein (Iron protein),
- MoFe-protein (Molybdenum-Iron protein).

It catalyzes the reduction of atmospheric nitrogen to ammonia.

Hence,

$$\boxed{\text{Nitrogenase}}$$

is the correct answer.

Therefore,

$$\boxed{(B)}$$

is the correct answer.

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Quick Tip: Nitrogen fixation reaction:

$$N_2 + 8H^+ + 8e^- + 16ATP \longrightarrow 2NH_3 + H_2 + 16ADP + 16P_i$$

The enzyme responsible is

Nitrogenase.

---

24. Consider the following and choose the correct answer

Assertion [A]: Tautomeric shifts in DNA bases are a source of spontaneous mutations.

Reason [R]: Rare tautomeric forms have altered hydrogen-bonding patterns.

The correct answer is

(A) Both [A] and [R] are true and [R] is the correct explanation of [A]

(B) Both [A] and [R] are true and [R] is not the correct explanation of [A]

(C) [A] is true, but [R] is false

(D) [A] is false, but [R] is true

Correct Answer: (A) Both [A] and [R] are true and [R] is the correct explanation of [A]

Solution:

Step 1: Examine the assertion.

Rare tautomeric forms of DNA bases can pair with incorrect complementary bases during DNA replication.

This leads to spontaneous mutations.

Hence,

Assertion [A] is true.

Step 2: Examine the reason.

Tautomeric shifts alter the hydrogen-bonding pattern of nitrogenous bases.

This causes abnormal base pairing, such as

$$A^*-C \quad \text{or} \quad G^*-T.$$

Hence,

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Reason [R] is true.

Step 3: Establish the relationship.

The altered hydrogen-bonding pattern directly explains how tautomeric shifts produce spontaneous mutations.

Therefore,

Both [A] and [R] are true and [R] correctly explains [A].

Thus,

(*A*)

is the correct answer.

Quick Tip: Tautomeric shifts cause

abnormal base pairing

which leads to spontaneous point mutations during DNA replication.

---

25. Identify the obligate intracellular microorganism?

(A) *Mycoplasma*

(B) *Chlamydia*

(C) *Escherichia coli*

(D) *Bacillus subtilis*

Correct Answer: (B) *Chlamydia*

Solution:

Step 1: Recall the characteristics of the given microorganisms.

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Mycoplasma → Free-living bacterium without a cell wall,

Escherichia coli → Free-living bacterium,

Bacillus subtilis → Free-living bacterium,

Chlamydia → Obligate intracellular bacterium.

Step 2: Identify the obligate intracellular organism.

Chlamydia can grow and reproduce only inside living host cells.

Hence,

$$\boxed{\textit{Chlamydia}}$$

is the correct answer.

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Examples of obligate intracellular microorganisms include

$$\boxed{\textit{Chlamydia, Rickettsia}}$$

whereas

$$\boxed{\text{Viruses}}$$

are obligate intracellular acellular entities.

---

26. Which among the following is not a key component of signal transduction process?

(A) G protein coupled receptors

(B) Reverse transcriptase

(C) Second messengers

(D) Phosphorylation cascade

Correct Answer: (B) Reverse transcriptase

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Solution:

Step 1: Recall the components of signal transduction.

Signal transduction involves the transmission of extracellular signals into cellular responses through

- Cell surface receptors,
- Second messengers,
- Protein kinases and phosphorylation cascades.

Step 2: Identify the incorrect component.

Reverse transcriptase is an enzyme that synthesizes DNA from an RNA template and is mainly found in retroviruses.

It is not involved in cellular signal transduction.

Hence,

$$\boxed{\text{Reverse transcriptase}}$$

is the correct answer.

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Major components of signal transduction include

$$\boxed{\text{Receptors} \rightarrow \text{Second Messengers} \rightarrow \text{Protein Kinases} \rightarrow \text{Cellular Response.}}$$

Reverse transcriptase functions in reverse transcription, not signaling.

---

27. Consider the following and choose the correct answer

Assertion [A]: B-DNA is the most stable and predominant form of DNA under physiological conditions.

Reason [R]: B-DNA possesses major and minor grooves.

The correct answer is

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(A) Both [A] and [R] are true and [R] is the correct explanation of [A]

(B) Both [A] and [R] are true and [R] is not the correct explanation of [A]

(C) [A] is true, but [R] is false

(D) [A] is false, but [R] is true

Correct Answer: (B) Both [A] and [R] are true and [R] is not the correct explanation of [A]

Solution:

Step 1: Examine the assertion.

B-DNA is the predominant and most stable form of DNA under normal physiological conditions.

Hence,

$$\boxed{\text{Assertion [A] is true.}}$$

Step 2: Examine the reason.

B-DNA possesses one major groove and one minor groove.

Thus,

$$\boxed{\text{Reason [R] is true.}}$$

Step 3: Establish the relationship.

Although B-DNA has major and minor grooves, this fact does not explain why it is the most stable DNA form under physiological conditions.

Therefore,

$$\boxed{\text{Both [A] and [R] are true, but [R] is not the correct explanation of [A].}}$$

Hence,

$$\boxed{(B)}$$

is the correct answer.

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Quick Tip: Characteristics of B-DNA:

Most common DNA form
10 base pairs per turn
Major and minor grooves present

---

28. What is the pH of 0.01 M HCl?

(A) 1

(B) 2

(C) 3

(D) 12

Correct Answer: (B) 2

Solution:

Step 1: Determine the hydrogen ion concentration.

HCl is a strong acid and dissociates completely.

Therefore,

$$[H^+] = 0.01 = 10^{-2}\ \text{M}.$$

Step 2: Calculate the pH.

The pH is given by

$$\boxed{\text{pH} = -\log[H^+].}$$

Substituting,

$$\text{pH} = -\log(10^{-2}) = 2.$$

Hence,

$$\boxed{\text{pH} = 2.}$$

Therefore,

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$$\boxed{(B)}$$

is the correct answer.

Quick Tip: For a strong acid,

$$\boxed{\text{pH} = -\log[H^+].}$$

If

$$[H^+] = 10^{-n},$$

then

$$\boxed{\text{pH} = n.}$$

---

29. Which buffer resists changes in pH most effectively?

(A) $\text{pH} = 2,\ \text{p}K_a = 2$

(B) $\text{pH} = 4,\ \text{p}K_a = 5$

(C) $\text{pH} = 7,\ \text{p}K_a = 3$

(D) $\text{pH} = 9,\ \text{p}K_a = 5$

Correct Answer: (A) $\text{pH} = 2,\ \text{p}K_a = 2$

Solution:

Step 1: Recall the condition for maximum buffer capacity.

According to the Henderson–Hasselbalch equation,

$$\boxed{\text{pH} = \text{p}K_a + \log\frac{[\text{Salt}]}{[\text{Acid}]}}$$

A buffer shows maximum resistance to change in pH when

$$\boxed{\text{pH} = \text{p}K_a.}$$

Step 2: Check the given options.

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Among the given options,

$$\text{pH} = 2, \qquad \text{p}K_a = 2$$

satisfies

$$\boxed{\text{pH} = \text{p}K_a.}$$

Hence, this buffer has the maximum buffering capacity.

Therefore,

$$\boxed{(A)}$$

is the correct answer.

Quick Tip: A buffer is most effective when

$$\boxed{\text{pH} = \text{p}K_a.}$$

The buffering range is approximately

$$\boxed{\text{p}K_a \pm 1.}$$

---

30. Match the following

	List-I		List-II
A	Apoenzyme	*I*	Non-protein part
B	Coenzyme	*II*	Protein part
C	Holoenzyme	*III*	Enzyme + cofactor
D	Active site	*IV*	Substrate-binding region

The correct answer is

(A) A – II, B – I, C – III, D – IV

(B) A – I, B – II, C – IV, D – III

(C) A – III, B – IV, C – I, D – II

(D) A – IV, B – III, C – II, D – I

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

Solution:

Step 1: Recall the definitions.

Apoenzyme → Protein part of an enzyme

Coenzyme → Organic non-protein cofactor

Holoenzyme → Apoenzyme + Cofactor

Active site → Substrate-binding region

Step 2: Match List-I with List-II.

Thus,

$$A-\text{II},\ B-\text{I},\ C-\text{III},\ D-\text{IV}$$

Therefore,

$$(A)$$

is the correct answer.

Quick Tip: Remember:

Apoenzyme = Protein part

Coenzyme = Organic cofactor

Holoenzyme = Apoenzyme + Cofactor

Active site = Site where substrate binds

---

31. Identify the checkpoint that controls entry into DNA replication

(A) G_2/M checkpoint

(B) Spindle checkpoint

(C) G_1/S checkpoint

(D) Metaphase checkpoint

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Correct Answer: (C) G_1/S checkpoint

Solution:

Step 1: Recall the major cell cycle checkpoints.

The cell cycle contains three important checkpoints:

$$G_1/S \rightarrow \text{Controls entry into DNA replication,}$$

$$G_2/M \rightarrow \text{Checks completion of DNA replication before mitosis,}$$

$$\text{M checkpoint} \rightarrow \text{Ensures proper chromosome attachment to spindle fibers.}$$

Step 2: Identify the checkpoint for DNA replication.

The

$$\boxed{G_1/S \text{ checkpoint}}$$

determines whether the cell is ready to enter the S phase, where DNA replication occurs.

Hence,

$$\boxed{G_1/S \text{ checkpoint}}$$

is the correct answer.

Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Remember the checkpoints:

$$\boxed{\begin{aligned} G_1/S &\rightarrow \text{Entry into DNA replication} \\ G_2/M &\rightarrow \text{Entry into mitosis} \\ \text{Metaphase} &\rightarrow \text{Spindle attachment} \end{aligned}}$$

---

32. If a mammalian cell completes one cell cycle in 24 hours and the S phase lasts 8 hours, what fraction of the cell cycle is spent in S phase?

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(A) $\frac{1}{2}$
(B) $\frac{1}{3}$
(C) $\frac{1}{4}$
(D) $\frac{1}{8}$

Correct Answer: (B) $\frac{1}{3}$

Solution:

Step 1: Determine the total duration and S phase duration.

Given,

$$\text{Total cell cycle} = 24 \text{ hours},$$

and

$$\text{S phase} = 8 \text{ hours}.$$

Step 2: Calculate the required fraction.

The fraction of the cell cycle spent in S phase is

$$\frac{\text{S phase duration}}{\text{Total cell cycle duration}} = \frac{8}{24} = \frac{1}{3}.$$

Hence,

$$\boxed{\frac{1}{3}}$$

is the required fraction.

Therefore,

$$\boxed{(B)}$$

is the correct answer.

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Quick Tip: The fraction of time spent in any phase is

$$\boxed{\frac{\text{Duration of the phase}}{\text{Total cell cycle duration}}.}$$

Here,

$$\boxed{\frac{8}{24} = \frac{1}{3}.}$$

---

33. Determine the second messenger involved in mobilizing Ca^{2+} from the endoplasmic reticulum?

(A) cAMP

(B) DAG

(C) IP_3

(D) cGMP

Correct Answer: (C) IP_3

Solution:

Step 1: Recall the IP_3–DAG signaling pathway.

Activation of phospholipase C hydrolyzes phosphatidylinositol 4,5-bisphosphate (PIP_2) into

$$\boxed{IP_3 \text{ and DAG.}}$$

Step 2: Identify the messenger responsible for calcium release.

IP_3 binds to IP_3 receptors present on the endoplasmic reticulum and opens calcium channels. This releases stored

$$Ca^{2+}$$

into the cytoplasm.

Hence,

$$\boxed{IP_3}$$

is the correct answer.

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Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: In the PIP_2 pathway,

$$\boxed{PIP_2 \rightarrow IP_3 + DAG}$$

where

$$\boxed{IP_3 \rightarrow \text{Releases } Ca^{2+} \text{ from the ER}}$$

and

$$\boxed{DAG \rightarrow \text{Activates Protein Kinase C (PKC).}}$$

---

34. Which electron transport chain complex does not pump protons across the mitochondrial inner membrane?

(A) Complex I

(B) Complex II

(C) Complex III

(D) Complex IV

Correct Answer: (B) Complex II

Solution:

Step 1: Recall the proton-pumping complexes.

In the mitochondrial electron transport chain,

$$\text{Complex I} \rightarrow \text{Pumps protons},$$

$$\text{Complex II} \rightarrow \text{Does not pump protons},$$

$$\text{Complex III} \rightarrow \text{Pumps protons},$$

$$\text{Complex IV} \rightarrow \text{Pumps protons}.$$

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Step 2: Identify the correct complex.

Complex II (Succinate dehydrogenase) transfers electrons from succinate to ubiquinone but does not contribute to the proton gradient.

Hence,

$$\boxed{\text{Complex II}}$$

is the correct answer.

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Remember:

Proton pumps : Complex I, III, IV
No proton pumping : Complex II

---

35. In what ratio does the Na^+/K^+ pump transport sodium and potassium ions?

(A) 2 Na^+ out : 2 K^+ in

(B) 3 Na^+ out : 2 K^+ in

(C) 2 Na^+ in : 3 K^+ out

(D) 1 Na^+ out : 1 K^+ in

Correct Answer: (B) 3 Na^+ out : 2 K^+ in

Solution:

Step 1: Recall the function of the Na^+/K^+-ATPase.

The sodium-potassium pump is an ATP-driven membrane protein that maintains ionic gradients across the plasma membrane.

Step 2: State the transport ratio.

For every ATP molecule hydrolyzed,

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$$\boxed{3\ Na^+ \text{ are pumped out of the cell}}$$

and

$$\boxed{2\ K^+ \text{ are pumped into the cell.}}$$

Thus, the transport ratio is

$$\boxed{3\ Na^+ \text{ out} : 2\ K^+ \text{ in.}}$$

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: The Na^+/K^+-ATPase uses

$$\boxed{1\ ATP}$$

to transport

$$\boxed{3\ Na^+ \text{ out} \quad \text{and} \quad 2\ K^+ \text{ in.}}$$

This pump is electrogenic because more positive charges leave the cell than enter.

---

36. In a population, the frequency of a recessive allele (q) is 0.4. Calculate the frequency of homozygous dominant individuals?

(A) 0.16

(B) 0.36

(C) 0.48

(D) 0.64

Correct Answer: (B) 0.36

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Solution:

Step 1: Use the Hardy–Weinberg equation.

For a population in Hardy–Weinberg equilibrium,

$$\boxed{p+q=1,}$$

where

- p = frequency of dominant allele,
- q = frequency of recessive allele.

Step 2: Calculate the dominant allele frequency.

Given,

$$q=0.4.$$

Therefore,

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

Step 3: Calculate the frequency of homozygous dominant individuals.

The frequency of homozygous dominant genotype is

$$\boxed{p^2.}$$

Hence,

$$p^2=(0.6)^2=0.36.$$

Therefore,

$$\boxed{0.36}$$

is the correct answer.

Thus,

$$\boxed{(B)}$$

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is the correct answer.

Quick Tip: Hardy–Weinberg equilibrium:

$$\boxed{p+q=1}$$

and

$$\boxed{p^2+2pq+q^2=1,}$$

where

$$\boxed{p^2 = \text{Homozygous dominant},\ 2pq = \text{Heterozygous},\ q^2 = \text{Homozygous recessive.}}$$

---

37. Consider the following and choose the correct answer

Assertion [A]: DNA replication is semiconservative in nature.

Reason [R]: Each daughter DNA molecule contains one parental strand and one newly synthesized strand.

The correct answer is

(A) Both [A] and [R] are true and [R] is the correct explanation of [A]

(B) Both [A] and [R] are true and [R] is not the correct explanation of [A]

(C) [A] is true, but [R] is false

(D) [A] is false, but [R] is true

Correct Answer: (A) Both [A] and [R] are true and [R] is the correct explanation of [A]

Solution:

Step 1: Examine the assertion.

DNA replication is said to be semiconservative because each newly formed DNA molecule conserves one of the original parental strands.

Hence,

$$\boxed{\text{Assertion [A] is true.}}$$

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Step 2: Examine the reason.

After DNA replication,

each daughter DNA molecule contains

one parental strand and one newly synthesized strand.

Thus,

Reason [R] is true.

Step 3: Establish the relationship.

The reason correctly explains why DNA replication is termed semiconservative.

Therefore,

Both [A] and [R] are true and [R] correctly explains [A].

Thus,

(*A*)

is the correct answer.

Quick Tip: Semiconservative replication was experimentally demonstrated by

Meselson and Stahl (1958).

Each daughter DNA molecule consists of

1 old strand + 1 new strand.

---

38. Enzyme responsible for transcription in prokaryotes?

(A) DNA polymerase

(B) RNA polymerase

(C) Reverse transcriptase

(D) Primase

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Correct Answer: (B) RNA polymerase

Solution:

Step 1: Recall the process of transcription.

Transcription is the synthesis of RNA using a DNA template.

Step 2: Identify the enzyme responsible.

In prokaryotes, transcription is carried out by

$$\boxed{\text{RNA polymerase.}}$$

This enzyme binds to the promoter region and synthesizes RNA in the

$$5' \rightarrow 3'$$

direction.

Hence,

$$\boxed{\text{RNA polymerase}}$$

is the correct answer.

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Functions of important enzymes:

$$\boxed{\begin{aligned} \text{DNA polymerase} &\rightarrow \text{DNA replication} \\ \text{RNA polymerase} &\rightarrow \text{Transcription} \\ \text{Primase} &\rightarrow \text{RNA primer synthesis} \\ \text{Reverse transcriptase} &\rightarrow \text{RNA} \rightarrow \text{DNA} \end{aligned}}$$

---

39. Consider the following and choose the correct answer

Assertion [A]: Peptide bond formation occurs at the P site of the ribosome.

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Reason [R]: Peptidyl transferase activity is an intrinsic property of rRNA.

The correct answer is

(A) Both [A] and [R] are true and [R] is the correct explanation of [A]

(B) Both [A] and [R] are true and [R] is not the correct explanation of [A]

(C) [A] is true, but [R] is false

(D) [A] is false, but [R] is true

Correct Answer: (D) [A] is false, but [R] is true

Solution:

Step 1: Examine the assertion.

Peptide bond formation occurs at the

Peptidyl Transferase Center (PTC)

of the large ribosomal subunit.

During elongation, the aminoacyl-tRNA enters the

A site

and the growing peptide attached to the tRNA at the P site is transferred to the amino acid in the A site.

Hence, peptide bond formation is associated with the

A site and the Peptidyl Transferase Center,

not the P site alone.

Therefore,

Assertion [A] is false.

Step 2: Examine the reason.

The peptidyl transferase activity of the ribosome is catalyzed by

23S rRNA

in prokaryotes (or 28S rRNA in eukaryotes), demonstrating that the ribosome acts as a ribozyme.

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Hence,

$$\boxed{\text{Reason [R] is true.}}$$

Step 3: Establish the relationship.

Since the assertion is false but the reason is true,

$$\boxed{(D)}$$

is the correct answer.

Quick Tip: Ribosomal sites:

A site → Entry of aminoacyl-tRNA
P site → Holds peptidyl-tRNA
E site → Exit of deacylated tRNA

Peptidyl transferase activity is an intrinsic property of

$$\boxed{\text{rRNA (Ribozyme).}}$$

---

40. In a dihybrid cross ($AaBb \times AaBb$), what is the probability of obtaining an individual heterozygous for both traits ($AaBb$)?

(A) $\frac{1}{16}$

(B) $\frac{1}{8}$

(C) $\frac{1}{4}$

(D) $\frac{1}{2}$

Correct Answer: (C) $\frac{1}{4}$

Solution:

Step 1: Consider each gene separately.

For the cross

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$$Aa \times Aa,$$

the probability of obtaining a heterozygous genotype is

$$P(Aa) = \frac{1}{2}.$$

Similarly, for

$$Bb \times Bb,$$

the probability of obtaining

$$Bb$$

is

$$P(Bb) = \frac{1}{2}.$$

Step 2: Apply the multiplication rule.

Since the two genes assort independently,

$$P(AaBb) = P(Aa) \times P(Bb) = \frac{1}{2} \times \frac{1}{2} = \frac{1}{4}.$$

Hence,

$$\boxed{\frac{1}{4}}$$

is the required probability.

Therefore,

$$\boxed{(C)}$$

is the correct answer.

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Quick Tip: For independent genes,

$$\boxed{P(AaBb) = P(Aa) \times P(Bb).}$$

Since

$$Aa \times Aa \Rightarrow P(Aa) = \frac{1}{2},$$

and

$$Bb \times Bb \Rightarrow P(Bb) = \frac{1}{2},$$

therefore,

$$\boxed{P(AaBb) = \frac{1}{4}.}$$

---

41. A phenotypic ratio of $12 : 3 : 1$ **is produced due to**

(A) Recessive epistasis

(B) Dominant epistasis

(C) Duplicate recessive epistasis

(D) Complementation

Correct Answer: (B) Dominant epistasis

Solution:

Step 1: Recall common modified dihybrid ratios.

Different gene interactions produce characteristic phenotypic ratios:

$$12 : 3 : 1 \rightarrow \text{Dominant epistasis},$$

$$9 : 3 : 4 \rightarrow \text{Recessive epistasis},$$

$$9 : 7 \rightarrow \text{Complementary genes},$$

$$15 : 1 \rightarrow \text{Duplicate dominant genes}.$$

Step 2: Identify the correct interaction.

Since the observed phenotypic ratio is

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$$12 : 3 : 1,$$

it corresponds to

$$\boxed{\text{Dominant epistasis.}}$$

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Important modified Mendelian ratios:

12 : 3 : 1	→ Dominant epistasis
9 : 3 : 4	→ Recessive epistasis
9 : 7	→ Complementary genes
15 : 1	→ Duplicate dominant genes

---

42. The following cross can never result in a recessive phenotype?

(A) Tt Pp × Tt Pp

(B) TT Pp × tt pp

(C) tt pp × TT PP

(D) tt pp × Tt Pp

Correct Answer: (C) tt pp × TT PP

Solution:

Step 1: Recall the condition for a recessive phenotype.

A recessive phenotype appears only when the genotype is homozygous recessive.

For two genes,

$$\boxed{ttpp}$$

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is the recessive phenotype.

Step 2: Check each cross.

For option (A),

$$TtPp \times TtPp$$

can produce

$$ttpp,$$

so a recessive phenotype is possible.

For option (B),

$$TTPp \times ttpp$$

all offspring are

$$TtPp \text{ or } Ttpp,$$

so recessive phenotype for both genes is not produced, but recessive phenotype for one gene is possible.

For option (C),

$$ttpp \times TTPP$$

produces only

$$TtPp.$$

Every offspring is heterozygous for both genes.

Hence,

$$\boxed{ttpp}$$

can never be produced.

For option (D),

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$$ttpp \times TtPp$$

may produce

$$ttpp.$$

Therefore,

$$\boxed{ttpp \times TTPP}$$

can never result in a recessive phenotype.

Thus,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Crossing

$$\boxed{ttpp \times TTPP}$$

always gives

$$\boxed{100\%\, TtPp,}$$

so no recessive phenotype appears.

---

43. If the percentage of crossing over between two genes is 10, then the distance between two genes will be

(A) 5 morganoid

(B) 10 centimorgans

(C) 20 centimorgans

(D) 40 map units

Correct Answer: (B) 10 centimorgans

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Solution:

Step 1: Recall the relationship between recombination frequency and map distance.

Genetic distance is measured in centimorgans (cM).

$$\boxed{1\% \text{ recombination } = 1 \text{ centimorgan.}}$$

Step 2: Calculate the map distance.

Given,

$$\text{Crossing over} = 10\%.$$

Hence,

$$\boxed{10\% = 10 \text{ cM.}}$$

Therefore,

$$\boxed{10 \text{ centimorgans}}$$

is the correct answer.

Thus,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Remember,

$$\boxed{1\% \text{ recombination} = 1 \text{ cM} = 1 \text{ map unit.}}$$

---

44. Extra-chromosomal inheritance is often called maternal inheritance because

(A) Genes are inherited from both parents equally

(B) Cytoplasm of the zygote is mainly contributed by the mother

(C) Organellar genes show dominance

(D) Only females show the trait

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Correct Answer: (B) Cytoplasm of the zygote is mainly contributed by the mother

Solution:

Step 1: Recall extra-chromosomal inheritance.

Extra-chromosomal inheritance involves genes present in

- Mitochondria,
- Chloroplasts.

These organelles are transmitted through the cytoplasm.

Step 2: Identify the reason for maternal inheritance.

During fertilization, the egg contributes almost all of the cytoplasm to the zygote, whereas the sperm contributes mainly the nucleus.

Hence,

$$\boxed{\text{Organellar DNA is usually inherited from the mother.}}$$

Therefore,

$$\boxed{\text{Cytoplasm of the zygote is mainly contributed by the mother.}}$$

Thus,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Maternal inheritance is due to inheritance of

$$\boxed{\text{mitochondrial DNA and chloroplast DNA}}$$

through the egg cytoplasm.

---

45. The following is a classic example of extra-chromosomal inheritance?

(A) Sickle cell anemia

(B) Color blindness

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(C) Variation in *Mirabilis jalapa*

(D) Hemophilia

Correct Answer: (C) Variation in *Mirabilis jalapa*

Solution:

Step 1: Recall extra-chromosomal inheritance.

Extra-chromosomal inheritance is caused by genes present outside the nucleus, mainly in

Mitochondria and Chloroplasts.

Step 2: Identify the classic example.

The leaf colour variation in

Mirabilis jalapa

(four-o'clock plant) is controlled by chloroplast genes and is inherited through the maternal parent.

Thus, it is a classic example of cytoplasmic (extra-chromosomal) inheritance.

Hence,

Variation in *Mirabilis jalapa*

is the correct answer.

Therefore,

(*C*)

is the correct answer.

Quick Tip: Common examples of extra-chromosomal inheritance are

Mirabilis jalapa

Mitochondrial inheritance in humans

Traits such as colour blindness and hemophilia are X-linked, not cytoplasmic.

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46. Identify the organism with polyploidy?

(A) Humans

(B) *Drosophila*

(C) Wheat

(D) Frog

Correct Answer: (C) Wheat

Solution:

Step 1: Recall polyploidy.

Polyploidy is the condition in which an organism possesses more than two complete sets of chromosomes.

It is commonly found in plants.

Step 2: Identify the polyploid organism.

Bread wheat (*Triticum aestivum*) is a

$$\boxed{\text{Hexaploid } (6n)}$$

plant.

Hence,

$$\boxed{\text{Wheat}}$$

is the correct answer.

Therefore,

$$\boxed{(C)}$$

is the correct answer.

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Quick Tip: Examples of polyploid crops:

$$\boxed{\begin{array}{r}\text{Wheat} \rightarrow 6n \\ \text{Potato} \rightarrow 4n \\ \text{Banana} \rightarrow 3n\end{array}}$$

Polyploidy is much more common in plants than in animals.

---

47. Consider a population of sheep to be in Hardy-Weinberg equilibrium. The allele for black wool (p) has a frequency of 0.81 while the allele for white wool (q) has a frequency of 0.19. Then the percentage of heterozygous individuals in the population is

(A) 4%

(B) 15%

(C) 31%

(D) 66%

Correct Answer: (C) 31%

Solution:

Step 1: Use the Hardy-Weinberg equation.

For a population in equilibrium,

$$\boxed{p^2 + 2pq + q^2 = 1.}$$

The frequency of heterozygous individuals is

$$\boxed{2pq.}$$

Step 2: Substitute the given values.

Given,

$$p = 0.81, \qquad q = 0.19.$$

Therefore,

$$2pq = 2(0.81)(0.19) = 0.3078 \approx 0.31.$$

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Thus,

$$\boxed{31\%}$$

of the population is heterozygous.

Hence,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Hardy-Weinberg genotype frequencies are

$$\boxed{p^2 : 2pq : q^2.}$$

Remember,

$$\boxed{\text{Heterozygous frequency} = 2pq.}$$

---

48. Choose the transposable element which moves via an RNA intermediate?

(A) Insertion sequence

(B) Composite transposon

(C) Retrotransposon

(D) DNA transposon

Correct Answer: (C) Retrotransposon

Solution:

Step 1: Recall the types of transposable elements.

Transposable elements are classified into

- DNA transposons,
- Retrotransposons.

Step 2: Identify the element moving through an RNA intermediate.

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Retrotransposons first produce an RNA intermediate.

The RNA is then converted back into DNA by

$$\boxed{\text{Reverse Transcriptase.}}$$

Thus, retrotransposons move by a

$$\boxed{\text{copy-and-paste mechanism.}}$$

Hence,

$$\boxed{\text{Retrotransposon}}$$

is the correct answer.

Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Types of transposable elements:

$$\boxed{\begin{array}{l}\text{DNA transposons} \rightarrow \text{Cut-and-paste} \\ \text{Retrotransposons} \rightarrow \text{RNA intermediate (Copy-and-paste)}\end{array}}$$

---

49. Which application is used to detect genetic disorders at the DNA level?

(A) Western blotting

(B) ELISA

(C) PCR

(D) Chromatography

Correct Answer: (C) PCR

Solution:

Step 1: Recall the applications of the given techniques.

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Western blotting → Detection of proteins,

ELISA → Detection of antigens or antibodies,

PCR → Amplification and analysis of DNA,

Chromatography → Separation of biomolecules.

Step 2: Identify the technique used for DNA diagnosis.

Polymerase Chain Reaction (PCR) amplifies specific DNA sequences and is widely used to detect mutations responsible for genetic disorders.

Hence,

$$\boxed{\text{PCR}}$$

is the correct answer.

Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Important laboratory techniques:

PCR → DNA amplification

Western blot → Protein detection

ELISA → Antigen/Antibody detection

---

50. Match the following

	Disease / Application		**Molecular basis / Use**
A	Sickle cell anemia	*I*	Frameshift mutation
B	Thalassemia	*II*	Missense point mutation
C	Duchenne muscular dystrophy	*III*	β-globin gene defect
D	PCR	*IV*	DNA amplification technique

The correct matching is

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(A) A – II, B – III, C – I, D – IV

(B) A – III, B – II, C – I, D – IV

(C) A – II, B – I, C – III, D – IV

(D) A – I, B – III, C – II, D – IV

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

Solution:

Step 1: Recall the molecular basis of each disease.

$$\begin{aligned} \text{Sickle cell anemia} &\rightarrow \text{Missense point mutation} \\ \text{Thalassemia} &\rightarrow \beta\text{-globin gene defect} \\ \text{Duchenne muscular dystrophy} &\rightarrow \text{Frameshift mutation} \\ \text{PCR} &\rightarrow \text{DNA amplification technique} \end{aligned}$$

Step 2: Match List-I with List-II.

Thus,

$$\boxed{A-\text{II},\ B-\text{III},\ C-\text{I},\ D-\text{IV}}$$

Therefore,

$$\boxed{(A)}$$

is the correct answer.

Quick Tip: Remember:

$$\begin{aligned} \text{Sickle cell anemia} &\rightarrow \text{Missense mutation} \\ \text{Thalassemia} &\rightarrow \beta\text{-globin defect} \\ \text{Duchenne muscular dystrophy} &\rightarrow \text{Frameshift mutation} \\ \text{PCR} &\rightarrow \text{DNA amplification} \end{aligned}$$

---

51. Following process is primarily employed for the aerobic stabilization of liquid waste

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(A) Anaerobic digester

(B) Activated sludge process

(C) Septic tank

(D) Methanogenesis

Correct Answer: (B) Activated sludge process

Solution:

Step 1: Recall the wastewater treatment methods.

Wastewater treatment includes:

- **Aerobic treatment** using oxygen and aerobic microbes.
- **Anaerobic treatment** without oxygen.

Step 2: Identify the aerobic process.

The

$$\boxed{\text{Activated sludge process}}$$

uses aerobic microorganisms to oxidize organic matter in sewage and stabilize liquid waste.

The remaining options are anaerobic processes.

Hence,

$$\boxed{\text{Activated sludge process}}$$

is the correct answer.

Therefore,

$$\boxed{(B)}$$

is the correct answer.

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Quick Tip: Wastewater treatment:

Activated sludge process → Aerobic treatment

Septic tank → Anaerobic treatment

Methanogenesis → Biogas production under anaerobic conditions

---

52. Final stage of anaerobic digestion is

(A) Hydrolysis

(B) Acidogenesis

(C) Acetogenesis

(D) Methanogenesis

Correct Answer: (D) Methanogenesis

Solution:

Step 1: Recall the stages of anaerobic digestion.

Anaerobic digestion proceeds through the following stages:

Hydrolysis → Acidogenesis → Acetogenesis → Methanogenesis

Step 2: Identify the final stage.

In the last stage, methanogenic archaea convert acetate, carbon dioxide and hydrogen into methane.

Hence,

Methanogenesis

is the final stage of anaerobic digestion.

Therefore,

(D)

is the correct answer.

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Quick Tip: Sequence of anaerobic digestion:

$$\boxed{\text{Hydrolysis} \rightarrow \text{Acidogenesis} \rightarrow \text{Acetogenesis} \rightarrow \text{Methanogenesis}}$$

The final product is mainly

$$\boxed{\text{Methane } (CH_4).}$$

---

53. Match the following

	List-I		List-II
A	Bioaugmentation	*I*	Nutrient addition
B	Biostimulation	*II*	Addition of specific microbes
C	Phytoremediation	*III*	Use of plants
D	Composting	*IV*	Solid waste aerobic treatment

The correct matching is

(A) A – II, B – I, C – III, D – IV

(B) A – I, B – II, C – IV, D – III

(C) A – III, B – IV, C – II, D – I

(D) A – IV, B – III, C – I, D – II

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

Solution:

Step 1: Recall the definitions.

$$\boxed{\begin{array}{r}\text{Bioaugmentation} \rightarrow \text{Addition of specific microbes} \\ \text{Biostimulation} \rightarrow \text{Nutrient addition to stimulate native microbes} \\ \text{Phytoremediation} \rightarrow \text{Use of plants to remove pollutants} \\ \text{Composting} \rightarrow \text{Aerobic treatment of solid waste}\end{array}}$$

Step 2: Match List-I with List-II.

Thus,

$$\boxed{A - \text{II},\ B - \text{I},\ C - \text{III},\ D - \text{IV}}$$

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Therefore,

$$\boxed{(A)}$$

is the correct answer.

Quick Tip: Remember:

Bioaugmentation	→ Add microbes
Biostimulation	→ Add nutrients
Phytoremediation	→ Use plants
Composting	→ Aerobic solid waste treatment

---

54. Consider the following and choose the correct answer

Assertion [A]: Bioremediation is an environmentally friendly technology.

Reason [R]: Bioremediation removes pollutants mainly by converting them into highly toxic intermediate compounds that persist in the environment.

The correct answer is

(A) Both [A] and [R] are true and [R] is the correct explanation of [A]

(B) Both [A] and [R] are true and [R] is not the correct explanation of [A]

(C) [A] is true, but [R] is false

(D) [A] is false, but [R] is true

Correct Answer: (C) [A] is true, but [R] is false

Solution:

Step 1: Examine the assertion.

Bioremediation uses microorganisms or plants to degrade pollutants into harmless or less toxic products.

Hence,

$$\boxed{\text{Assertion [A] is true.}}$$

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Step 2: Examine the reason.

Bioremediation does **not** convert pollutants into highly toxic compounds that persist in the environment.

Instead, pollutants are generally converted into harmless substances such as

$$\boxed{CO_2,\ H_2O,\ \text{and biomass.}}$$

Therefore,

$$\boxed{\text{Reason [R] is false.}}$$

Thus,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Bioremediation is an eco-friendly process that uses microorganisms or plants to convert pollutants into

$$\boxed{\text{non-toxic or less toxic products.}}$$

---

55. Identify the microorganism that is industrially used for baker's yeast production?

(A) *Aspergillus niger*

(B) *Saccharomyces cerevisiae*

(C) *Penicillium chrysogenum*

(D) *Lactobacillus*

Correct Answer: (B) *Saccharomyces cerevisiae*

Solution:

Step 1: Recall the industrial uses of microorganisms.

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Saccharomyces cerevisiae → Bread and alcohol production,

Aspergillus niger → Citric acid production,

Penicillium chrysogenum → Penicillin production,

Lactobacillus → Curd and lactic acid production.

Step 2: Identify the baker's yeast.

The organism used commercially as baker's yeast is

$$\boxed{\textit{Saccharomyces cerevisiae}.}$$

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Remember the common industrial microorganisms:

Saccharomyces cerevisiae → Baker's yeast

Aspergillus niger → Citric acid

Penicillium chrysogenum → Penicillin

---

56. Exopolysaccharides are best described as

(A) Intracellular storage polymers

(B) Cell wall components

(C) Polymers secreted outside the cell

(D) Secondary metabolites only

Correct Answer: (C) Polymers secreted outside the cell

Solution:

Step 1: Recall the definition of exopolysaccharides.

Exopolysaccharides (EPS) are high-molecular-weight polysaccharides synthesized by microor-

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ganisms.

They are secreted outside the cell and form a protective extracellular matrix.

Step 2: Identify the correct description.

Since EPS are released into the surrounding environment,

They are polymers secreted outside the cell.

Therefore,

(C)

is the correct answer.

Quick Tip: Exopolysaccharides (EPS):

Produced by microbes and secreted outside the cell

Functions include:

Biofilm formation, protection, and adhesion.

---

57. Which amino acid is produced industrially using *Corynebacterium glutamicum*?

(A) Tryptophan

(B) Lysine

(C) Methionine

(D) Histidine

Correct Answer: (B) Lysine

Solution:

Step 1: Recall the industrial applications of *Corynebacterium glutamicum*.

Corynebacterium glutamicum is widely used in industrial biotechnology for the large-scale production of amino acids.

The major products include

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Lysine and Glutamic acid.

Step 2: Identify the correct amino acid.

Among the given options, the amino acid commercially produced using

Corynebacterium glutamicum

is

Lysine.

Therefore,

(B)

is the correct answer.

Quick Tip: Industrial microorganisms:

Corynebacterium glutamicum → Lysine, Glutamic acid

Saccharomyces cerevisiae → Baker's yeast

Aspergillus niger → Citric acid

---

58. Match the following

	List-I		List-II
A	Amylase	*I*	Protein hydrolysis
B	Protease	*II*	Starch hydrolysis
C	Cellulase	*III*	Fat hydrolysis
D	Lipase	*IV*	Cellulose degradation

The correct matching is

(A) A – I, B – II, C – IV, D – III

(B) A – III, B – IV, C – I, D – II

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(C) A – IV, B – III, C – II, D – I

(D) A – II, B – I, C – IV, D – III

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

Solution:

Step 1: Recall the function of each enzyme.

Amylase → Hydrolyses starch

Protease → Hydrolyses proteins

Cellulase → Degrades cellulose

Lipase → Hydrolyses fats (lipids)

Step 2: Match List-I with List-II.

Thus,

$$A-\text{II},\ B-\text{I},\ C-\text{IV},\ D-\text{III}$$

Therefore,

$$(D)$$

is the correct answer.

Quick Tip: Remember enzyme functions:

Amylase → Starch

Protease → Protein

Cellulase → Cellulose

Lipase → Fat (Lipids)

---

59. Consider the following and choose the correct answer

Assertion [A]: Downstream processing significantly increases the cost of enzyme production.

Reason [R]: Enzymes are usually produced in very pure form during fermentation.

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The correct answer is

(A) Both [A] and [R] are true and [R] is the correct explanation of [A]

(B) Both [A] and [R] are true and [R] is not the correct explanation of [A]

(C) [A] is true, but [R] is false

(D) [A] is false, but [R] is true

Correct Answer: (C) [A] is true, but [R] is false

Solution:

Step 1: Examine the assertion.

Downstream processing involves recovery, purification, concentration and formulation of the desired product after fermentation.

These purification steps contribute significantly to the overall production cost.

Hence,

$$\boxed{\text{Assertion [A] is true.}}$$

Step 2: Examine the reason.

Enzymes are **not** produced in a pure form during fermentation.

The fermentation broth contains cells, nutrients, metabolites and other impurities, which require extensive purification.

Thus,

$$\boxed{\text{Reason [R] is false.}}$$

Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Downstream processing includes

$$\boxed{\text{Recovery} \rightarrow \text{Purification} \rightarrow \text{Formulation}}$$

and often accounts for a major portion of the production cost.

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60. Why are extracellular enzymes preferred in industrial production?

(A) Higher molecular weight

(B) Require cell disruption

(C) Easier purification

(D) Low stability

Correct Answer: (C) Easier purification

Solution:

Step 1: Recall the difference between intracellular and extracellular enzymes.

Extracellular enzymes are secreted directly into the culture medium.

Therefore, they can be recovered without breaking the cells.

Step 2: Identify the advantage.

Since cell disruption is unnecessary, downstream processing becomes simpler and purification is easier.

Hence,

$$\boxed{\text{Easier purification}}$$

is the correct answer.

Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Extracellular enzymes are preferred because they

$$\boxed{\text{are secreted into the medium and require simpler purification.}}$$

Intracellular enzymes require cell lysis before purification.

61. Which bioreactor type is most commonly used for large-scale recombinant protein production?

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(A) Packed bed reactor

(B) Stirred-tank bioreactor

(C) Airlift reactor

(D) Trickling filter

Correct Answer: (B) Stirred-tank bioreactor

Solution:

Step 1: Recall the commonly used industrial bioreactors.

Among industrial fermenters, the stirred-tank bioreactor is the most widely used because it provides efficient mixing, aeration and temperature control.

Step 2: Identify the appropriate bioreactor.

For large-scale production of recombinant proteins,

$$\boxed{\text{Stirred-tank bioreactor}}$$

is preferred due to its excellent oxygen transfer and ease of process control.

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Advantages of a stirred-tank bioreactor:

Efficient mixing
Good aeration
Uniform nutrient distribution
Easy control of pH and temperature

---

62. Which purification method is commonly used when recombinant proteins carry a His-tag?

(A) Ion exchange chromatography

(B) Gel filtration chromatography

(C) Affinity chromatography

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(D) Ultracentrifugation

Correct Answer: (C) Affinity chromatography

Solution:

Step 1: Recall the purpose of a His-tag.

A His-tag consists of several histidine residues attached to a recombinant protein to facilitate its purification.

Step 2: Identify the purification method.

Histidine residues bind specifically to immobilized metal ions such as

$$\boxed{Ni^{2+} \text{ or } Co^{2+}.}$$

This property is exploited in

$$\boxed{\text{Affinity chromatography}}$$

to selectively purify the recombinant protein.

Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: His-tagged proteins are commonly purified using

$$\boxed{\text{Immobilized Metal Affinity Chromatography (IMAC)}}$$

where the tag binds to

$$\boxed{Ni^{2+} \text{ or } Co^{2+}.}$$

---

63. In gel filtration chromatography, which molecules elute first?

(A) Small molecules

(B) Highly charged molecules

(C) Hydrophobic molecules

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(D) Large molecules

Correct Answer: (D) Large molecules

Solution:

Step 1: Recall the principle of gel filtration chromatography.

Gel filtration (size-exclusion chromatography) separates molecules based on their size.

The stationary phase contains porous beads.

Step 2: Identify which molecules elute first.

Large molecules cannot enter the pores of the beads and therefore travel a shorter path through the column.

Small molecules enter the pores and take longer to pass through.

Hence,

$$\boxed{\text{Large molecules elute first.}}$$

Therefore,

$$\boxed{(D)}$$

is the correct answer.

Quick Tip: In gel filtration chromatography,

$$\boxed{\text{Large molecules} \rightarrow \text{Elute first}}$$

$$\boxed{\text{Small molecules} \rightarrow \text{Elute later}}$$

because small molecules enter the pores of the gel beads.

---

64. Match the following

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	List-I		List-II
A	Microfiltration	*I*	Removal of salts
B	Ultrafiltration	*II*	Protein concentration
C	Reverse osmosis	*III*	Suspended solids/bacteria
D	Dialysis	*IV*	Small solute diffusion

The correct matching is

(A) A – III, B – II, C – I, D – IV

(B) A – II, B – III, C – IV, D – I

(C) A – I, B – IV, C – III, D – II

(D) A – IV, B – I, C – II, D – III

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

Solution:

Step 1: Recall the applications of membrane separation techniques.

Microfiltration → Removes suspended solids and bacteria

Ultrafiltration → Concentrates proteins

Reverse osmosis → Removes dissolved salts

Dialysis → Removes small solutes by diffusion

Step 2: Match List-I with List-II.

Thus,

$$\boxed{A-\text{III},\ B-\text{II},\ C-\text{I},\ D-\text{IV}}$$

Therefore,

$$\boxed{(A)}$$

is the correct answer.

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Quick Tip: Membrane separation techniques:

Microfiltration → Cells, bacteria

Ultrafiltration → Proteins

Reverse osmosis → Salts

Dialysis → Small molecules

---

65. Most commonly used method for enzyme immobilisation is

(A) Adsorption

(B) Denaturation

(C) Fermentation

(D) Dialysis

Correct Answer: (A) Adsorption

Solution:

Step 1: Recall enzyme immobilisation methods.

Common methods of enzyme immobilisation include:

Adsorption,

Covalent binding,

Entrapment,

Encapsulation,

Cross-linking.

Step 2: Identify the most widely used method.

Among these methods,

Adsorption

is the simplest, economical and most commonly employed technique for immobilising enzymes on solid supports.

Therefore,

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$$\boxed{(A)}$$

is the correct answer.

Quick Tip: Common enzyme immobilisation methods:

Adsorption (most common)
Covalent binding
Entrapment
Encapsulation
Cross-linking

---

66. An enzyme-based biosensor primarily consists of

(A) A catalyst and substrate

(B) A signal amplifier and detector

(C) A membrane and power source

(D) A bioreceptor and transducer

Correct Answer: (D) A bioreceptor and transducer

Solution:

Step 1: Recall the components of a biosensor.

A biosensor is an analytical device that converts a biological response into a measurable signal.

Its two essential components are

$$\boxed{\text{Bioreceptor} + \text{Transducer.}}$$

Step 2: Identify the correct option.

In an enzyme-based biosensor,

- the enzyme acts as the **bioreceptor**,
- the transducer converts the biochemical reaction into an electrical signal.

Hence,

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$$\boxed{\text{A bioreceptor and transducer}}$$

is the correct answer.

Therefore,

$$\boxed{(D)}$$

is the correct answer.

Quick Tip: Basic components of a biosensor:

$$\boxed{\text{Bioreceptor} \longrightarrow \text{Transducer} \longrightarrow \text{Signal Processor}}$$

The enzyme serves as the biological recognition element.

---

67. Which of the following is a characteristic of diauxic growth?

(A) A single exponential growth phase

(B) Two distinct exponential growth phases

(C) A prolonged lag phase

(D) A rapid death phase

Correct Answer: (B) Two distinct exponential growth phases

Solution:

Step 1: Recall the meaning of diauxic growth.

Diauxic growth occurs when microorganisms are supplied with two different carbon sources. They first consume the preferred substrate, followed by a short lag phase before utilizing the second substrate.

Step 2: Identify the growth pattern.

The growth curve therefore shows

$$\boxed{\text{Two distinct exponential growth phases}}$$

separated by a brief lag phase.

Hence,

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$\boxed{(B)}$

is the correct answer.

Quick Tip: Diauxic growth pattern:

$$\boxed{\text{Log phase} \rightarrow \text{Lag} \rightarrow \text{Second log phase}}$$

It is commonly observed when glucose and lactose are present together.

---

68. The rate at which substrate is consumed by microorganisms is directly related to

(A) Only substrate concentration

(B) Only product concentration

(C) Cell concentration

(D) Temperature only

Correct Answer: (C) Cell concentration

Solution:

Step 1: Recall substrate utilization kinetics.

The rate of substrate consumption depends primarily on the amount of active microbial biomass present.

More cells consume substrate at a faster rate.

Step 2: Identify the correct factor.

Therefore, substrate consumption is directly proportional to

$$\boxed{\text{Cell concentration.}}$$

Hence,

$\boxed{(C)}$

is the correct answer.

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Quick Tip: According to microbial growth kinetics,

$$\boxed{\text{Substrate utilization rate} \propto \text{Biomass (cell concentration)}.}$$

Increasing the number of active cells generally increases substrate consumption.

---

69. How does fed-batch fermentation help in overcoming substrate inhibition?

(A) By maintaining a high substrate concentration

(B) By maintaining a low substrate concentration

(C) By adding substrate in a single batch

(D) By not adding substrate at all

Correct Answer: (B) By maintaining a low substrate concentration

Solution:

Step 1: Recall the principle of fed-batch fermentation.

In fed-batch fermentation, fresh substrate is added gradually instead of all at once.

Step 2: Identify how substrate inhibition is prevented.

Continuous or controlled feeding prevents the substrate from accumulating to inhibitory levels.

Thus, the substrate concentration is maintained at a low optimum level.

Hence,

$$\boxed{\text{By maintaining a low substrate concentration}}$$

is the correct answer.

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Fed-batch fermentation:

$$\boxed{\text{Gradual substrate addition} \rightarrow \text{Low substrate concentration} \rightarrow \text{Reduced substrate inhibition}}$$

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70. Simple structured models are most useful for studying

(A) Heat transfer in fermenters

(B) Mixing and aeration

(C) Mechanical agitation effects

(D) Metabolic regulation during growth

Correct Answer: (D) Metabolic regulation during growth

Solution:

Step 1: Recall structured models.

Structured models divide the microbial cell into different functional components and describe intracellular metabolic activities.

Step 2: Identify their application.

These models are particularly useful for analyzing

$$\boxed{\text{Metabolic regulation during microbial growth.}}$$

Therefore,

$$\boxed{(D)}$$

is the correct answer.

Quick Tip: Model types:

$$\boxed{\begin{array}{l}\text{Unstructured models} \rightarrow \text{Treat cell as a single unit} \\ \text{Structured models} \rightarrow \text{Describe intracellular metabolism}\end{array}}$$

71. Which method is the most commonly used for sterilization of culture media?

(A) Dry heat sterilization

(B) Autoclaving

(C) UV radiation

(D) Filtration

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Correct Answer: (B) Autoclaving

Solution:

Step 1: Recall the common sterilization methods.

Different sterilization methods include:

- Dry heat,
- Moist heat (autoclaving),
- Filtration,
- Radiation.

Step 2: Identify the method used for culture media.

Most microbiological culture media are sterilized by

$$\boxed{\text{Autoclaving}}$$

using saturated steam under pressure, typically at

$$\boxed{121^\circ\text{C},\ 15\ \text{psi},\ 15\text{—}20\ \text{minutes.}}$$

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Standard autoclaving conditions:

$$\boxed{121^\circ\text{C},\quad 15\ \text{psi},\quad 15\text{—}20\ \text{minutes}}$$

Autoclaving is the most common method for sterilizing culture media.

---

72. Match the following

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	List-I		List-II
A	Batch	*I*	Steady-state operation
B	Fed-batch	*II*	Substrate feeding without outflow
C	Continuous	*III*	No input or output
D	Chemostat	*IV*	Constant dilution rate

The correct matching is

(A) A – III, B – II, C – I, D – IV

(B) A – I, B – III, C – II, D – IV

(C) A – II, B – IV, C – I, D – III

(D) A – IV, B – II, C – III, D – I

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

Solution:

Step 1: Recall the characteristics of each fermentation process.

Batch → No input or output during operation

Fed-batch → Substrate added without product outflow

Continuous → Steady-state operation

Chemostat → Constant dilution rate

Step 2: Match List-I with List-II.

Thus,

$$A-\text{III},\ B-\text{II},\ C-\text{I},\ D-\text{IV}$$

Therefore,

$$(A)$$

is the correct answer.

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Quick Tip: Fermentation processes:

Batch → Closed system

Fed-batch → Feed only

Continuous → Steady state

Chemostat → Constant dilution rate

---

73. The primary purpose of aeration in aerobic fermentation is to

(A) Control temperature

(B) Provide oxygen for microbial metabolism

(C) Prevent foaming

(D) Increase pH

Correct Answer: (B) Provide oxygen for microbial metabolism

Solution:

Step 1: Recall the role of aeration.

Aeration introduces sterile air into the bioreactor to supply oxygen required by aerobic microorganisms.

Step 2: Identify the primary purpose.

Oxygen acts as the terminal electron acceptor during aerobic respiration and is essential for microbial growth and product formation.

Hence,

Provide oxygen for microbial metabolism

is the correct answer.

Therefore,

(B)

is the correct answer.

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Quick Tip: Functions of aeration:

Supply dissolved oxygen
Support aerobic microbial growth
Enhance product formation

Aeration is usually accompanied by agitation to improve oxygen transfer.

---

74. The term $k_L a$ represents

(A) Oxygen solubility

(B) Interfacial area only

(C) Oxygen uptake rate

(D) Overall gas–liquid mass transfer coefficient

Correct Answer: (D) Overall gas–liquid mass transfer coefficient

Solution:

Step 1: Recall the meaning of $k_L a$.

In bioprocess engineering,

$$k_L a = k_L \times a$$

where

$$k_L = \text{Liquid-film mass transfer coefficient},$$

$$a = \text{Interfacial area per unit volume}.$$

Step 2: Interpret its significance.

The product $k_L a$ indicates the efficiency of oxygen transfer from the gas phase to the liquid phase.

Hence,

$$\boxed{k_L a = \text{Overall volumetric gas–liquid mass transfer coefficient}.}$$

Therefore,

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$$\boxed{(D)}$$

is the correct answer.

Quick Tip: The oxygen transfer rate (OTR) is given by

$$\boxed{\text{OTR} = k_L a\,(C^* - C_L)}$$

where C^* is the saturation dissolved oxygen concentration and C_L is the dissolved oxygen concentration in the broth.

---

75. Match the following

	List-I		List-II
A	Carbon source	*I*	Enzyme cofactor
B	Nitrogen source	*II*	Energy and cell material
C	Trace elements	*III*	Protein and nucleic acid synthesis
D	Buffer	*IV*	pH maintenance

The correct matching is

(A) A – II, B – III, C – I, D – IV

(B) A – III, B – II, C – IV, D – I

(C) A – IV, B – I, C – II, D – III

(D) A – I, B – IV, C – III, D – II

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

Solution:

Step 1: Recall the functions of medium components.

Carbon source → Energy and cell material

Nitrogen source → Protein and nucleic acid synthesis

Trace elements → Enzyme cofactors

Buffer → Maintains pH

Step 2: Match List-I with List-II.

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Thus,

$$\boxed{A-\text{II},\ B-\text{III},\ C-\text{I},\ D-\text{IV}}$$

Therefore,

$$\boxed{(A)}$$

is the correct answer.

Quick Tip: Functions of culture medium components:

Carbon	→ Energy source
Nitrogen	→ Proteins and nucleic acids
Trace elements	→ Enzyme cofactors
Buffer	→ Maintains pH

---

76. Consider the following and choose the correct answer

Assertion [A]: Ethylene is a gaseous plant hormone.

Reason [R]: Ethylene inhibits fruit ripening.

The correct answer is

(A) Both [A] and [R] are true and [R] is the correct explanation of [A]

(B) Both [A] and [R] are true and [R] is not the correct explanation of [A]

(C) [A] is true, but [R] is false

(D) [A] is false, but [R] is true

Correct Answer: (C) [A] is true, but [R] is false

Solution:

Step 1: Examine the assertion.

Ethylene is the only naturally occurring gaseous plant hormone.

Hence,

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Assertion [A] is true.

Step 2: Examine the reason.

Ethylene does **not** inhibit fruit ripening.

Instead, it promotes fruit ripening, senescence and abscission.

Therefore,

Reason [R] is false.

Thus,

(C)

is the correct answer.

Quick Tip: Major functions of ethylene:

Fruit ripening, senescence, abscission and flowering in some plants.

---

77. The genes responsible for hairy root formation are located on

(A) Ti plasmid

(B) Ri plasmid

(C) F plasmid

(D) R plasmid

Correct Answer: (B) Ri plasmid

Solution:

Step 1: Recall the plasmids of *Agrobacterium*.

Agrobacterium tumefaciens → Ti plasmid (crown gall disease)

Agrobacterium rhizogenes → Ri plasmid (hairy root disease)

Step 2: Identify the correct plasmid.

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Hairy root formation is caused by genes present on the

$$\boxed{\text{Ri plasmid.}}$$

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Remember:

$$\boxed{\begin{array}{l}\text{Ti plasmid} \rightarrow \text{Crown gall} \\ \text{Ri plasmid} \rightarrow \text{Hairy root}\end{array}}$$

---

78. Secondary metabolite production in plant suspension cultures generally occurs during

(A) Lag phase

(B) Exponential phase

(C) Stationary phase

(D) Death phase

Correct Answer: (C) Stationary phase

Solution:

Step 1: Recall primary and secondary metabolites.

Primary metabolites are synthesized during active cell growth (log phase), whereas secondary metabolites are generally produced after active growth slows.

Step 2: Identify the growth phase.

Secondary metabolite production reaches its maximum during the

$$\boxed{\text{Stationary phase.}}$$

Therefore,

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(C)

is the correct answer.

Quick Tip: Growth phase vs. metabolite production:

Log phase → Primary metabolites

Stationary phase → Secondary metabolites

---

79. Which core genes are present in the T-DNA region of the Ti plasmid of *Agrobacterium tumefaciens*?

(A) *vir* genes

(B) Opine, Auxin and Cytokinin synthesis

(C) Antibiotic resistance genes

(D) Replication origin genes

Correct Answer: (B) Opine, Auxin and Cytokinin synthesis

Solution:

Step 1: Recall the structure of the Ti plasmid.

The Ti (Tumor-inducing) plasmid contains:

- **T-DNA region** – transferred into the plant genome.
- ***vir* genes** – located outside the T-DNA and required for T-DNA transfer.

Step 2: Identify the genes present in T-DNA.

The T-DNA region contains genes responsible for:

Auxin synthesis

Cytokinin synthesis

Opine synthesis

These genes induce crown gall tumor formation and opine production in infected plant cells.

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Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Remember:

T-DNA → Auxin + Cytokinin + Opine genes

vir genes → Transfer of T-DNA

---

80. Match the following

	Technique		Description / Application
A	Agrobacterium-mediated transformation	*I*	Gene transfer using particle bombardment
B	Microinjection	*II*	Direct injection of DNA into nucleus
C	Biolistic method	*III*	Ti plasmid-based gene transfer
D	Electroporation	*IV*	DNA uptake through membrane pores

The correct matching is

(A) A – III, B – II, C – I, D – IV

(B) A – II, B – I, C – III, D – IV

(C) A – IV, B – III, C – II, D – I

(D) A – I, B – IV, C – III, D – II

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

Solution:

Step 1: Recall the principle of each gene transfer technique.

Agrobacterium-mediated transformation → Ti plasmid-mediated gene transfer

Microinjection → Direct injection of DNA into the nucleus

Biolistic method → Particle bombardment (gene gun)

Electroporation → DNA uptake through temporary membrane pores

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Step 2: Match List-I with List-II.

Thus,

$$\boxed{A-\text{III},\ B-\text{II},\ C-\text{I},\ D-\text{IV}}$$

Therefore,

$$\boxed{(A)}$$

is the correct answer.

Quick Tip: Important gene transfer methods:

Agrobacterium → Ti plasmid
Biolistic → Gene gun
Microinjection → DNA injection into nucleus
Electroporation → Electric pulse creates membrane pores

---

81. Animal cloning is commonly achieved by

(A) Embryo splitting

(B) Somatic Cell Nuclear Transfer

(C) Parthenogenesis

(D) In vitro fertilization

Correct Answer: (B) Somatic Cell Nuclear Transfer

Solution:

Step 1: Recall the method used in animal cloning.

The most common technique for cloning animals is **Somatic Cell Nuclear Transfer (SCNT)**.

In this method, the nucleus of a somatic cell is transferred into an enucleated egg cell.

Step 2: Identify the correct option.

The reconstructed egg develops into an embryo genetically identical to the nucleus donor.

Therefore,

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Somatic Cell Nuclear Transfer

is the correct answer.

Hence,

(B)

is the correct answer.

Quick Tip: Example:

Dolly the sheep

was the first mammal cloned using

Somatic Cell Nuclear Transfer (SCNT).

---

82. Which chemical is commonly used to fuse B cells and myeloma cells?

(A) Trypsin

(B) Calcium chloride

(C) Polyethylene glycol

(D) EDTA

Correct Answer: (C) Polyethylene glycol

Solution:

Step 1: Recall hybridoma technology.

Hybridoma technology produces monoclonal antibodies by fusing antibody-producing B lymphocytes with immortal myeloma cells.

Step 2: Identify the fusion agent.

The most commonly used chemical for cell fusion is

Polyethylene glycol (PEG).

Therefore,

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$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Hybridoma production:

$$\boxed{\text{B cell} + \text{Myeloma cell} \xrightarrow{\text{PEG}} \text{Hybridoma}}$$

Hybridomas produce monoclonal antibodies.

---

83. Animal cell lines are typically preserved long-term in liquid nitrogen at

(A) 0°C

(B) −20°C

(C) −80°C

(D) −196°C

Correct Answer: (D) −196°C

Solution:

Step 1: Recall the method of cryopreservation.

Long-term preservation of animal cell lines is achieved by cryopreservation in liquid nitrogen.

Step 2: Identify the storage temperature.

Liquid nitrogen has a temperature of

$$\boxed{-196^\circ\text{C}.}$$

At this temperature, cellular metabolism is effectively halted, allowing long-term storage.

Therefore,

$$\boxed{(D)}$$

is the correct answer.

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Quick Tip: Cryopreservation conditions:

$$\boxed{\text{Liquid nitrogen} = -196^\circ\text{C}}$$

Cryoprotectants such as DMSO are commonly added to prevent ice crystal damage.

---

84. Consider the following and choose the correct answer

Assertion [A]: Product inhibition can reduce overall process productivity.

Reason [R]: Accumulated products may interfere with enzyme activity or cell viability.

The correct answer is

(A) Both [A] and [R] are true and [R] is the correct explanation of [A]

(B) Both [A] and [R] are true and [R] is not the correct explanation of [A]

(C) [A] is true, but [R] is false

(D) [A] is false, but [R] is true

Correct Answer: (A) Both [A] and [R] are true and [R] is the correct explanation of [A]

Solution:

Step 1: Examine the assertion.

Accumulation of the desired product during fermentation can inhibit microbial growth or enzyme activity, thereby reducing the overall productivity of the process.

Hence,

$$\boxed{\text{Assertion [A] is true.}}$$

Step 2: Examine the reason.

Many accumulated products act as inhibitors by affecting enzyme function or decreasing cell viability.

Thus,

$$\boxed{\text{Reason [R] is true.}}$$

The reason correctly explains why product inhibition lowers process productivity.

Therefore,

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$$\boxed{(A)}$$

is the correct answer.

Quick Tip: Product inhibition occurs when the accumulated product inhibits

$$\boxed{\text{enzyme activity and/or microbial growth,}}$$

thereby reducing fermentation efficiency.

---

85. A low K_m value of an enzyme indicates

(A) Low affinity for substrate

(B) High affinity for substrate

(C) No enzyme–substrate complex formation

(D) Enzyme inhibition

Correct Answer: (B) High affinity for substrate

Solution:

Step 1: Recall the meaning of K_m.

The Michaelis constant (K_m) is the substrate concentration at which the reaction velocity is half of its maximum value (V_{max}).

Step 2: Interpret a low K_m.

A lower K_m means the enzyme reaches half-maximal velocity at a lower substrate concentration. This indicates

$$\boxed{\text{High affinity between enzyme and substrate.}}$$

Therefore,

$$\boxed{(B)}$$

is the correct answer.

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Quick Tip: Relationship between K_m and substrate affinity:

$$\boxed{\begin{array}{l}\text{Low } K_m \rightarrow \text{High affinity} \\ \text{High } K_m \rightarrow \text{Low affinity}\end{array}}$$

---

86. Which of the following is a component of innate immunity?

(A) Antibodies

(B) Memory cells

(C) T lymphocytes

(D) Phagocytes

Correct Answer: (D) Phagocytes

Solution:

Step 1: Recall the components of innate immunity.

Innate immunity is the body's first line of defense and includes physical barriers and immune cells such as neutrophils and macrophages.

These cells remove pathogens by phagocytosis.

Step 2: Identify the innate immune component.

Among the given options,

$$\boxed{\text{Phagocytes}}$$

belong to the innate immune system.

Antibodies, memory cells and T lymphocytes are components of adaptive immunity.

Therefore,

$$\boxed{(D)}$$

is the correct answer.

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Quick Tip: Innate immunity includes:

Skin and mucous membranes
Neutrophils
Macrophages
Natural killer (NK) cells

Adaptive immunity includes B cells, T cells and antibodies.

---

87. Match the following

	List-I		List-II
A	Thymus	*I*	B-cell maturation
B	Bone marrow	*II*	T-cell maturation
C	Spleen	*III*	Blood filtration
D	Lymph node	*IV*	Lymph filtration

The correct matching is

(A) A – II, B – I, C – III, D – IV

(B) A – II, B – I, C – IV, D – III

(C) A – III, B – IV, C – I, D – II

(D) A – IV, B – III, C – II, D – I

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

Solution:

Step 1: Recall the functions of lymphoid organs.

Thymus → T-cell maturation
Bone marrow → B-cell maturation
Spleen → Blood filtration
Lymph node → Lymph filtration

Step 2: Match List-I with List-II.

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Thus,

$$\boxed{A-\text{II},\ B-\text{I},\ C-\text{III},\ D-\text{IV}}$$

Therefore,

$$\boxed{(A)}$$

is the correct answer.

Quick Tip: Primary lymphoid organs:

$$\boxed{\begin{aligned}\text{Bone marrow} &\rightarrow \text{B-cell maturation}\\ \text{Thymus} &\rightarrow \text{T-cell maturation}\end{aligned}}$$

Secondary lymphoid organs:

$$\boxed{\begin{aligned}\text{Spleen} &\rightarrow \text{Filters blood}\\ \text{Lymph node} &\rightarrow \text{Filters lymph}\end{aligned}}$$

---

88. Which immunoglobulin is produced first during a primary immune response?

(A) IgG

(B) IgA

(C) IgM

(D) IgE

Correct Answer: (C) IgM

Solution:

Step 1: Recall the primary immune response.

During the first exposure to an antigen, naïve B lymphocytes are activated and initially produce

$$\boxed{\text{IgM.}}$$

Step 2: Identify the correct immunoglobulin.

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After class switching, antibodies such as IgG, IgA or IgE may be produced depending on the immune response.

Therefore, the first antibody produced during a primary immune response is

$$\boxed{\text{IgM.}}$$

Hence,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Remember:

$$\boxed{\begin{aligned}\text{Primary immune response} &\rightarrow \text{IgM}\\ \text{Secondary immune response} &\rightarrow \text{IgG}\end{aligned}}$$

Mnemonic:

$$\boxed{\textbf{M = Made first}}$$

---

89. Which cells constitutively express MHC class I molecules?

(A) Only antigen-presenting cells

(B) Only T lymphocytes

(C) All nucleated cells

(D) Red blood cells

Correct Answer: (C) All nucleated cells

Solution:

Step 1: Recall the distribution of MHC Class I molecules.

MHC Class I molecules are expressed on

$$\boxed{\text{All nucleated cells.}}$$

Their function is to present endogenous peptides to $CD8^{+}$ cytotoxic T cells.

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Step 2: Eliminate the incorrect options.

- Antigen-presenting cells express both MHC Class I and Class II.
- T lymphocytes are not the only cells expressing MHC Class I.
- Mature red blood cells lack a nucleus and therefore do not express MHC Class I.

Hence,

$$\boxed{\text{All nucleated cells}}$$

is the correct answer.

Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Remember:

$$\boxed{\begin{array}{l}\text{MHC Class I} \rightarrow \text{All nucleated cells} \rightarrow \text{CD8}^+ \text{ T cells} \\ \text{MHC Class II} \rightarrow \text{Professional APCs} \rightarrow \text{CD4}^+ \text{ T cells}\end{array}}$$

---

90. Consider the following and choose the correct answer

Assertion [A]: MHC Class I presents endogenous antigens to $CD8^+$ T cells.

Reason [R]: Endogenous peptides are generated in lysosomes.

The correct answer is

(A) Both [A] and [R] are true and [R] is the correct explanation of [A]

(B) Both [A] and [R] are true and [R] is not the correct explanation of [A]

(C) [A] is true, but [R] is false

(D) [A] is false, but [R] is true

Correct Answer: (C) [A] is true, but [R] is false

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Solution:

Step 1: Examine the assertion.

MHC Class I molecules present endogenous (intracellular) peptides to

$$\boxed{\text{CD8}^+ \text{ cytotoxic T lymphocytes.}}$$

Hence,

$$\boxed{\text{Assertion [A] is true.}}$$

Step 2: Examine the reason.

Endogenous peptides are generated mainly by

$$\boxed{\text{Proteasomal degradation in the cytoplasm,}}$$

not in lysosomes.

Lysosomes generate peptides for the MHC Class II pathway.

Therefore,

$$\boxed{\text{Reason [R] is false.}}$$

Thus,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Antigen processing pathways:

$$\boxed{\begin{array}{l}\text{MHC Class I} \rightarrow \text{Proteasome} \rightarrow \text{CD8}^+ \text{ T cells} \\ \text{MHC Class II} \rightarrow \text{Lysosome} \rightarrow \text{CD4}^+ \text{ T cells}\end{array}}$$

---

91. Antibodies are synthesized by

(A) T lymphocytes

(B) Macrophages

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(C) NK cells

(D) Plasma cells

Correct Answer: (D) Plasma cells

Solution:

Step 1: Recall the function of plasma cells.

Activated B lymphocytes differentiate into plasma cells.

These plasma cells synthesize and secrete large quantities of antibodies (immunoglobulins).

Step 2: Identify the correct cell.

Therefore,

$$\boxed{\text{Plasma cells}}$$

are responsible for antibody production.

Hence,

$$\boxed{(D)}$$

is the correct answer.

Quick Tip: B-cell differentiation:

$$\boxed{\text{B lymphocyte} \longrightarrow \text{Plasma cell} \longrightarrow \text{Antibody secretion}}$$

Memory B cells provide long-term immunity after antigen exposure.

---

92. Somatic hypermutation mainly contributes to

(A) Antibody class change

(B) Increased affinity of antibodies

(C) T-cell activation

(D) Isotype switching

Correct Answer: (B) Increased affinity of antibodies

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Solution:

Step 1: Recall somatic hypermutation.

Somatic hypermutation introduces point mutations in the variable (V) regions of immunoglobulin genes in activated B cells.

Step 2: Identify its significance.

B cells producing antibodies with higher affinity are selected during affinity maturation.

Thus, somatic hypermutation mainly results in

$$\boxed{\text{Increased affinity of antibodies.}}$$

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Remember:

$$\boxed{\begin{aligned}\text{Somatic hypermutation} &\rightarrow \text{Affinity maturation}\\ \text{Class switching} &\rightarrow \text{Change in antibody isotype}\end{aligned}}$$

---

93. Consider the following and choose the correct answer

Assertion [A]: Monoclonal antibodies have higher specificity than polyclonal antibodies.

Reason [R]: They recognize only one epitope on an antigen.

The correct answer is

(A) Both [A] and [R] are true and [R] is the correct explanation of [A]

(B) Both [A] and [R] are true and [R] is not the correct explanation of [A]

(C) [A] is true, but [R] is false

(D) [A] is false, but [R] is true

Correct Answer: (A) Both [A] and [R] are true and [R] is the correct explanation of [A]

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Solution:

Step 1: Examine the assertion.

Monoclonal antibodies are produced by a single clone of B cells and therefore have very high specificity toward a single antigenic determinant.

Hence,

$$\boxed{\text{Assertion [A] is true.}}$$

Step 2: Examine the reason.

Monoclonal antibodies recognize

$$\boxed{\text{only one epitope on an antigen.}}$$

This explains why they are more specific than polyclonal antibodies, which recognize multiple epitopes.

Therefore,

$$\boxed{\text{Both [A] and [R] are true, and [R] correctly explains [A].}}$$

Hence,

$$\boxed{(A)}$$

is the correct answer.

Quick Tip: Comparison of antibodies:

$$\boxed{\begin{array}{l}\text{Monoclonal} \rightarrow \text{One epitope, high specificity} \\ \text{Polyclonal} \rightarrow \text{Multiple epitopes}\end{array}}$$

---

94. Identify the cytokine which is primarily immunosuppressive?

(A) IL-2

(B) IFN-γ

(C) IL-10

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(D) TNF-α

Correct Answer: (C) IL-10

Solution:

Step 1: Recall the functions of major cytokines.

$$\text{IL}-2 \rightarrow \text{T-cell proliferation},$$
$$\text{IFN}-\gamma \rightarrow \text{Macrophage activation},$$
$$\text{TNF}-\alpha \rightarrow \text{Pro-inflammatory cytokine},$$
$$\text{IL}-10 \rightarrow \text{Anti-inflammatory / Immunosuppressive}.$$

Step 2: Identify the immunosuppressive cytokine.

IL-10 suppresses inflammatory cytokine production and limits excessive immune responses.

Hence,

$$\boxed{\text{IL}-10}$$

is the correct answer.

Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Remember the important cytokines:

$$\boxed{\begin{aligned}\text{IL}-2 &\rightarrow \text{T-cell growth}\\ \text{IFN}-\gamma &\rightarrow \text{Cell-mediated immunity}\\ \text{TNF}-\alpha &\rightarrow \text{Inflammation}\\ \text{IL}-10 &\rightarrow \text{Immunosuppression}\end{aligned}}$$

---

95. Anaphylaxis is an example of

(A) Type I hypersensitivity

(B) Type II hypersensitivity

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(C) Type III hypersensitivity

(D) Type IV hypersensitivity

Correct Answer: (A) Type I hypersensitivity

Solution:

Step 1: Recall anaphylaxis.

Anaphylaxis is a rapid, severe allergic reaction mediated by IgE antibodies.

Upon re-exposure to an allergen, IgE bound to mast cells triggers the release of histamine and other inflammatory mediators.

Step 2: Identify the type of hypersensitivity.

Since it is an immediate IgE-mediated reaction,

$$\boxed{\text{Anaphylaxis is a Type I hypersensitivity reaction.}}$$

Therefore,

$$\boxed{(A)}$$

is the correct answer.

Quick Tip: Types of hypersensitivity:

$$\boxed{\begin{array}{l}\text{Type I} \rightarrow \text{IgE-mediated (Allergy, Anaphylaxis)}\\ \text{Type II} \rightarrow \text{Antibody-mediated cytotoxicity}\\ \text{Type III} \rightarrow \text{Immune complex-mediated}\\ \text{Type IV} \rightarrow \text{Delayed, T-cell mediated}\end{array}}$$

---

96. Which enzyme protects host DNA from restriction digestion?

(A) DNA ligase

(B) Restriction endonuclease

(C) DNA methyltransferase

(D) DNA polymerase

Correct Answer: (C) DNA methyltransferase

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Solution:

Step 1: Recall the restriction-modification system.

Bacteria possess restriction enzymes that cleave foreign DNA and methyltransferases that methylate their own DNA.

Step 2: Identify the protective enzyme.

DNA methyltransferase modifies specific recognition sites on host DNA, preventing restriction endonucleases from cutting it.

Thus,

$$\boxed{\text{DNA methyltransferase}}$$

protects host DNA.

Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Restriction-modification system:

$$\boxed{\begin{array}{r}\text{Restriction enzyme} \rightarrow \text{Cuts foreign DNA} \\ \text{DNA methyltransferase} \rightarrow \text{Protects host DNA}\end{array}}$$

---

97. Bacteriophage λ vectors can accommodate foreign DNA of about

(A) 2–5 kb

(B) 15–20 kb

(C) 50 kb

(D) 300 kb

Correct Answer: (B) 15–20 kb

Solution:

Step 1: Recall the cloning capacity of common vectors.

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Different cloning vectors accommodate different insert sizes.

$$\text{Plasmids} \rightarrow 2\text{–}10 \text{ kb}$$

$$\lambda \text{ phage vectors} \rightarrow 15\text{–}20 \text{ kb}$$

$$\text{Cosmids} \rightarrow 35\text{–}45 \text{ kb}$$

$$\text{BACs} \rightarrow 100\text{–}300 \text{ kb}$$

Step 2: Choose the correct insert size.

Hence, bacteriophage λ vectors can carry approximately

$$\boxed{15\text{–}20 \text{ kb}}$$

of foreign DNA.

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Approximate cloning capacities:

$$\boxed{\begin{aligned} &\text{Plasmid} \rightarrow 2\text{–}10 \text{ kb} \\ &\lambda \text{ phage} \rightarrow 15\text{–}20 \text{ kb} \\ &\text{Cosmid} \rightarrow 35\text{–}45 \text{ kb} \\ &\text{BAC} \rightarrow 100\text{–}300 \text{ kb} \\ &\text{YAC} \rightarrow 200\text{–}1000 \text{ kb} \end{aligned}}$$

---

98. Which vector can carry the largest DNA inserts?

(A) Plasmid

(B) Cosmid

(C) BAC

(D) YAC

Correct Answer: (D) YAC

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Solution:

Step 1: Recall the cloning capacities of common vectors.

Different cloning vectors can accommodate different sizes of foreign DNA.

$$\boxed{\begin{aligned}\text{Plasmid} &\rightarrow 2\text{–}10 \text{ kb}\\ \text{Cosmid} &\rightarrow 35\text{–}45 \text{ kb}\\ \text{BAC} &\rightarrow 100\text{–}300 \text{ kb}\\ \text{YAC} &\rightarrow 200\text{–}1000 \text{ kb}\end{aligned}}$$

Step 2: Identify the vector with the highest capacity.

Among the given vectors,

$$\boxed{\text{Yeast Artificial Chromosome (YAC)}}$$

can accommodate the largest DNA inserts.

Therefore,

$$\boxed{(D)}$$

is the correct answer.

Quick Tip: Vector capacity (increasing order):

$$\boxed{\text{Plasmid} < \text{Cosmid} < \text{BAC} < \text{YAC}}$$

---

99. Consider the following and choose the correct answer

Assertion [A]: Type II restriction enzymes are preferred in recombinant DNA technology.

Reason [R]: They cleave DNA at random sites far away from their recognition sequences.

The correct answer is

(A) Both [A] and [R] are true and [R] is the correct explanation of [A]

(B) Both [A] and [R] are true and [R] is not the correct explanation of [A]

(C) [A] is true, but [R] is false

(D) [A] is false, but [R] is true

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Correct Answer: (C) [A] is true, but [R] is false

Solution:

Step 1: Examine the assertion.

Type II restriction enzymes are widely used in recombinant DNA technology because they recognize specific DNA sequences and cleave at predictable positions.

Hence,

$$\boxed{\text{Assertion [A] is true.}}$$

Step 2: Examine the reason.

Type II restriction enzymes do **not** cut DNA at random sites far from their recognition sequences. Instead, they cleave within or very close to their specific recognition sites.

Therefore,

$$\boxed{\text{Reason [R] is false.}}$$

Hence,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Restriction enzymes:

$$\boxed{\begin{array}{l}\text{Type II} \rightarrow \text{Cuts at/near recognition site} \\ \qquad\quad \rightarrow \text{Most commonly used in genetic engineering}\end{array}}$$

---

100. A major advantage of a cDNA library over a genomic library is that cDNA

(A) Contains introns

(B) Represents non-coding regions

(C) Contains only expressed genes

(D) Is identical in all tissues

Correct Answer: (C) Contains only expressed genes

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Solution:

Step 1: Recall the origin of a cDNA library.

A cDNA library is prepared from mature mRNA using the enzyme reverse transcriptase.

Since mature mRNA has already undergone splicing, cDNA contains only expressed genes without introns.

Step 2: Compare with a genomic library.

A genomic library contains the entire genome, including coding regions, introns, promoters and intergenic sequences.

Thus, the major advantage of a cDNA library is that it

$$\boxed{\text{contains only expressed genes.}}$$

Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Comparison of libraries:

$$\boxed{\begin{array}{l}\text{Genomic library} \rightarrow \text{Entire genome} \\ \text{cDNA library} \rightarrow \text{Only expressed genes (no introns)}\end{array}}$$

---

101. Insertional inactivation is commonly used for screening recombinants in

(A) YAC vectors

(B) BAC vectors

(C) Cosmid vectors

(D) pBR322 plasmid

Correct Answer: (D) pBR322 plasmid

Solution:

Step 1: Recall insertional inactivation.

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Insertional inactivation is a method of identifying recombinant DNA by inserting foreign DNA into a marker gene, thereby disrupting its normal function.

Step 2: Identify the appropriate vector.

The plasmid **pBR322** contains antibiotic resistance genes (Amp^R and Tet^R).

Insertion of foreign DNA into one of these genes inactivates it, allowing recombinant colonies to be distinguished from non-recombinants.

Hence,

$$\boxed{\text{pBR322 plasmid}}$$

is the correct answer.

Therefore,

$$\boxed{(D)}$$

is the correct answer.

Quick Tip: Common screening methods:

$$\boxed{\begin{array}{l}\text{pBR322} \rightarrow \text{Insertional inactivation} \\ \text{pUC vectors} \rightarrow \text{Blue-white screening}\end{array}}$$

---

102. Which promoter is commonly used for high-level expression in *E. coli*?

(A) Lac promoter

(B) T7 promoter

(C) SV40 promoter

(D) CMV promoter

Correct Answer: (B) T7 promoter

Solution:

Step 1: Recall promoters used in expression systems.

The **T7 promoter** is specifically recognized by T7 RNA polymerase and drives very high levels

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of transcription in engineered *E. coli* strains.

Step 2: Eliminate other options.

- Lac promoter gives moderate expression.
- SV40 and CMV promoters are used mainly in mammalian cells.

Thus,

$$\boxed{\text{T7 promoter}}$$

is commonly used for high-level protein expression in *E. coli*.

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Expression promoters:

$$\boxed{\begin{array}{l}\text{T7 promoter} \rightarrow \textit{E. coli} \\ \text{CMV promoter} \rightarrow \text{Mammalian cells} \\ \text{SV40 promoter} \rightarrow \text{Mammalian expression}\end{array}}$$

---

103. Which nucleotide lacks a 3′-OH group?

(A) ddTTP

(B) dATP

(C) dGTP

(D) dCTP

Correct Answer: (A) ddTTP

Solution:

Step 1: Recall dNTPs and ddNTPs.

Normal deoxynucleotides (dNTPs) possess a free 3′-OH group required for DNA chain elonga-

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tion.

Dideoxynucleotides (ddNTPs) lack this 3′-OH group.

Step 2: Identify the correct nucleotide.

Since ddTTP lacks the 3′-OH group, DNA polymerase cannot extend the DNA chain after its incorporation.

Thus,

$$\boxed{\text{ddTTP}}$$

is the correct answer.

Therefore,

$$\boxed{(A)}$$

is the correct answer.

Quick Tip:

$$\boxed{\begin{array}{l}\text{dNTP} \rightarrow \text{Has } 3'\text{-OH} \\ \text{ddNTP} \rightarrow \text{No } 3'\text{-OH} \rightarrow \text{Chain termination}\end{array}}$$

ddNTPs are used in the Sanger DNA sequencing method.

---

104. Which isotope is commonly used for radioactive DNA labelling?

(A) ^{12}C

(B) ^{32}P

(C) ^{14}N

(D) ^{16}O

Correct Answer: (B) ^{32}P

Solution:

Step 1: Recall radioactive DNA labelling.

DNA contains phosphate groups in its backbone. Therefore, radioactive phosphorus isotopes are commonly used for DNA labelling.

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Step 2: Identify the commonly used isotope.

The isotope

$$\boxed{^{32}\text{P}}$$

is widely used because it emits high-energy β-particles and can be readily incorporated into DNA.

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Common radioactive isotopes in molecular biology:

$$\boxed{\begin{array}{l} ^{32}\text{P} \rightarrow \text{DNA/RNA labelling} \\ ^{35}\text{S} \rightarrow \text{Protein labelling} \\ ^{3}\text{H} \rightarrow \text{DNA and metabolic studies} \end{array}}$$

---

105. Southern blotting is used to detect

(A) RNA sequences

(B) Protein molecules

(C) Specific DNA sequences

(D) Lipids

Correct Answer: (C) Specific DNA sequences

Solution:

Step 1: Recall the purpose of Southern blotting.

Southern blotting involves the transfer of DNA fragments from a gel onto a membrane followed by hybridization with a labelled DNA probe.

Step 2: Identify what it detects.

Since complementary probes bind only to matching DNA fragments,

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Southern blotting detects specific DNA sequences.

Therefore,

$$(C)$$

is the correct answer.

Quick Tip: Remember the blotting techniques:

Southern blot → DNA

Northern blot → RNA

Western blot → Protein

---

106. A key difference between Southern and Northern blotting is that Northern blotting

(A) Uses antibodies

(B) Does not involve restriction digestion

(C) Uses protein probes

(D) Transfers proteins

Correct Answer: (B) Does not involve restriction digestion

Solution:

Step 1: Recall Southern and Northern blotting.

- **Southern blotting** detects DNA. Genomic DNA is first digested using restriction enzymes.
- **Northern blotting** detects RNA. RNA is analyzed directly and therefore does not require restriction enzyme digestion.

Step 2: Identify the distinguishing feature.

Since RNA is not digested by restriction enzymes before electrophoresis,

Northern blotting does not involve restriction digestion.

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Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Comparison of blotting methods:

Southern blot → DNA + Restriction digestion
Northern blot → RNA (No restriction digestion)
Western blot → Proteins + Antibodies

---

107. A major limitation of RAPD is

(A) Low sensitivity

(B) Poor reproducibility

(C) Requirement of radioactive probes

(D) High cost

Correct Answer: (B) Poor reproducibility

Solution:

Step 1: Recall RAPD.

RAPD (Random Amplified Polymorphic DNA) is a PCR-based technique that uses short arbitrary primers to amplify random DNA segments.

Step 2: Identify its limitation.

Because RAPD is highly sensitive to PCR conditions such as DNA quality, primer concentration and annealing temperature, its results are often difficult to reproduce.

Thus,

$$\boxed{\text{Poor reproducibility}}$$

is the major limitation of RAPD.

Therefore,

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$\boxed{(B)}$

is the correct answer.

Quick Tip: RAPD characteristics:

PCR-based marker
No prior sequence information required
Major limitation: Poor reproducibility

---

108. Match the following

	List-I		List-II
A	RAPD	*I*	Plant gene transfer
B	RFLP	*II*	Specific base change
C	Site-directed mutagenesis	*III*	Restriction-based polymorphism
D	Agrobacterium-mediated transformation	*IV*	Random PCR markers

The correct matching is

(A) A – IV, B – II, C – III, D – I

(B) A – II, B – I, C – IV, D – III

(C) A – III, B – IV, C – I, D – II

(D) A – IV, B – III, C – II, D – I

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

Solution:

Step 1: Recall the applications of each technique.

RAPD → Random PCR markers

RFLP → Restriction-based polymorphism

Site-directed mutagenesis → Specific base change

Agrobacterium-mediated transformation → Plant gene transfer

Step 2: Match List-I with List-II.

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Thus,

$$\boxed{A-\text{IV},\ B-\text{III},\ C-\text{II},\ D-\text{I}}$$

Therefore,

$$\boxed{(D)}$$

is the correct answer.

Quick Tip: Remember:

RAPD	→ Random PCR marker
RFLP	→ Restriction polymorphism
Site-directed mutagenesis	→ Specific mutation
Agrobacterium	→ Plant transformation

---

109. Which of the following is NOT a challenge in gene therapy?

(A) Immune response

(B) Targeted delivery

(C) Ethical concerns

(D) PCR amplification

Correct Answer: (D) PCR amplification

Solution:

Step 1: Recall the major challenges in gene therapy.

Gene therapy faces several challenges, including:

Immune response against vectors
Targeted delivery of therapeutic genes
Ethical and safety concerns

Step 2: Identify the option that is not a challenge.

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PCR amplification is a laboratory technique used to amplify DNA and is not considered a challenge in gene therapy.

Therefore,

$$\boxed{(D)}$$

is the correct answer.

Quick Tip: Major challenges in gene therapy:

$$\boxed{\text{Immune response, targeted delivery, vector safety and ethical concerns}}$$

---

110. What does a genomic DNA library represent?

(A) Only expressed genes

(B) Only protein-coding sequences

(C) The entire genome of an organism

(D) Only mRNA sequences

Correct Answer: (C) The entire genome of an organism

Solution:

Step 1: Recall the definition of a genomic library.

A genomic DNA library is prepared from the total genomic DNA of an organism.

It includes

$$\boxed{\text{coding sequences, introns, promoters and intergenic regions.}}$$

Step 2: Identify the correct option.

Thus, a genomic library represents

$$\boxed{\text{the entire genome of an organism.}}$$

Therefore,

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$\boxed{(C)}$

is the correct answer.

Quick Tip: Comparison of DNA libraries:

Genomic library → Entire genome

cDNA library → Only expressed genes

---

111. Which resource is NOT primarily used for protein analysis?

(A) ExPASy

(B) UniProt

(C) InterPro

(D) GenBank

Correct Answer: (D) GenBank

Solution:

Step 1: Recall the purpose of each database.

ExPASy → Protein analysis tools

UniProt → Protein sequence and function database

InterPro → Protein families and domains

GenBank → Nucleotide sequence database

Step 2: Identify the database not primarily used for protein analysis.

Since GenBank is mainly a repository of nucleotide (DNA/RNA) sequences rather than protein analysis,

$\boxed{\text{GenBank}}$

is the correct answer.

Therefore,

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$\boxed{(D)}$

is the correct answer.

Quick Tip: Important biological databases:

GenBank → DNA/RNA sequences

UniProt → Protein sequences

InterPro → Protein domains

ExPASy → Protein analysis tools

---

112. Which database stores 3D structures of biomolecules?

(A) GenBank

(B) UniProt

(C) PDB

(D) KEGG

Correct Answer: (C) PDB

Solution:

Step 1: Recall the purpose of major biological databases.

Different databases store different types of biological information.

GenBank → Nucleotide sequences

UniProt → Protein sequences and annotation

PDB → Three-dimensional structures of biomolecules

KEGG → Metabolic pathways

Step 2: Identify the correct database.

The Protein Data Bank (PDB) stores experimentally determined 3D structures of proteins, nucleic acids and other biomolecules.

Hence,

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$$\boxed{\text{PDB}}$$

is the correct answer.

Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Important databases:

PDB → 3D structures
GenBank → DNA/RNA sequences
UniProt → Protein information
KEGG → Pathways

---

113. Which database provides non-redundant protein sequences?

(A) GenBank

(B) UniProt

(C) PDB

(D) KEGG

Correct Answer: (B) UniProt

Solution:

Step 1: Recall the purpose of UniProt.

UniProt is a comprehensive protein database that provides curated, non-redundant protein sequence and functional information.

Step 2: Eliminate the other options.

- GenBank stores nucleotide sequences.
- PDB stores three-dimensional structures.
- KEGG provides metabolic and signaling pathways.

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Thus,

$$\boxed{\text{UniProt}}$$

is the correct answer.

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Remember:

$$\boxed{\begin{aligned}\text{UniProt} &\rightarrow \text{Protein sequences}\\ \text{PDB} &\rightarrow \text{Protein structures}\\ \text{KEGG} &\rightarrow \text{Biological pathways}\end{aligned}}$$

---

114. FASTA format contains

(A) Only sequence

(B) Only annotation

(C) Header line and sequence

(D) Alignment scores

Correct Answer: (C) Header line and sequence

Solution:

Step 1: Recall the FASTA format.

A FASTA file begins with a header line starting with the symbol

$$\boxed{>}$$

followed by an identifier or description.

Step 2: Identify the remaining content.

The header is followed by the nucleotide or protein sequence.

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Thus, a FASTA file contains

$$\boxed{\text{Header line and sequence.}}$$

Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Basic FASTA format:

```
> Sequence identifier
ATGCGATCGATCG...
```

The first line is the header, and the remaining lines contain the biological sequence.

---

115. Which technique is used in proteomics?

(A) DNA sequencing

(B) PCR

(C) Mass spectrometry

(D) Southern blot

Correct Answer: (C) Mass spectrometry

Solution:

Step 1: Recall the objective of proteomics.

Proteomics is the large-scale study of proteins, including their identification, structure, abundance and post-translational modifications.

Step 2: Identify the commonly used technique.

Mass spectrometry is the principal analytical technique used for protein identification and characterization.

Hence,

$$\boxed{\text{Mass spectrometry}}$$

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is the correct answer.

Therefore,

$$\boxed{(C)}$$

is the correct answer.

Quick Tip: Common techniques:

$$\boxed{\begin{array}{c}\text{Genomics} \rightarrow \text{DNA sequencing} \\ \text{Proteomics} \rightarrow \text{Mass spectrometry}\end{array}}$$

---

116. Which is NOT a force field?

(A) CHARMM

(B) AMBER

(C) GROMOS

(D) BLAST

Correct Answer: (D) BLAST

Solution:

Step 1: Recall molecular mechanics force fields.

Force fields are mathematical models used in molecular dynamics simulations to calculate molecular energies.

Examples include:

$$\boxed{\text{CHARMM, AMBER and GROMOS.}}$$

Step 2: Identify the option that is not a force field.

BLAST (Basic Local Alignment Search Tool) is a sequence similarity search program, not a molecular mechanics force field.

Hence,

$$\boxed{\text{BLAST}}$$

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is the correct answer.

Therefore,

$$\boxed{(D)}$$

is the correct answer.

Quick Tip: Remember:

$$\boxed{\begin{array}{r}\text{Force fields} \rightarrow \text{AMBER, CHARMM, GROMOS} \\ \text{Sequence alignment} \rightarrow \text{BLAST}\end{array}}$$

---

117. Incorrectly matched pair?

(A) NCBI – GenBank

(B) EBI – EMBL

(C) ExPASy – Swiss-Prot

(D) PDB – NCBI

Correct Answer: (D) PDB – NCBI

Solution:

Step 1: Recall the associations of major biological databases.

$$\boxed{\begin{array}{r}\text{NCBI} \rightarrow \text{GenBank} \\ \text{EBI} \rightarrow \text{EMBL/ENA} \\ \text{ExPASy} \rightarrow \text{Swiss-Prot (UniProt)}\end{array}}$$

Step 2: Identify the incorrect pair.

The Protein Data Bank (PDB) is an independent international repository for three-dimensional biomolecular structures and is not associated with NCBI.

Therefore,

$$\boxed{\text{PDB – NCBI}}$$

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is the incorrectly matched pair.

Hence,

$$\boxed{(D)}$$

is the correct answer.

Quick Tip: Important database associations:

NCBI → GenBank

EBI → EMBL/ENA

ExPASy → Swiss-Prot

PDB → 3D biomolecular structures

---

118. Match the following

	List-I		List-II
A	Microarray	*I*	Whole genome study
B	RNA-Seq	*II*	Protein expression
C	Proteomics	*III*	Sequencing-based
D	Genomics	*IV*	Hybridization-based

The correct matching is

(A) A – I, B – II, C – III, D – IV

(B) A – II, B – I, C – IV, D – III

(C) A – III, B – IV, C – I, D – II

(D) A – IV, B – III, C – II, D – I

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

Solution:

Step 1: Recall the applications of each technique.

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Microarray → Hybridization-based

RNA-Seq → Sequencing-based

Proteomics → Protein expression

Genomics → Whole genome study

Step 2: Match List-I with List-II.

Thus,

$$A-\text{IV},\ B-\text{III},\ C-\text{II},\ D-\text{I}$$

Therefore,

$$(D)$$

is the correct answer.

Quick Tip: Remember:

Microarray → Hybridization

RNA-Seq → Sequencing

Proteomics → Proteins

Genomics → Whole genome

---

119. Select the technique used to predict ligand binding orientation?

(A) Molecular docking

(B) Energy minimisation

(C) Molecular dynamics

(D) Homology modelling

Correct Answer: (A) Molecular docking

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Solution:

Step 1: Recall molecular docking.

Molecular docking is a computational technique that predicts how a ligand binds to the active site of a target protein.

Step 2: Identify the correct technique.

Docking estimates the preferred binding orientation and binding affinity of a ligand with its receptor.

Hence,

$$\boxed{\text{Molecular docking}}$$

is the correct answer.

Therefore,

$$\boxed{(A)}$$

is the correct answer.

Quick Tip: Computational techniques:

$$\boxed{\begin{array}{c}\text{Homology modelling} \rightarrow \text{Predict protein structure} \\ \text{Molecular docking} \rightarrow \text{Predict ligand binding} \\ \text{Molecular dynamics} \rightarrow \text{Study molecular motion}\end{array}}$$

---

120. A gene consists of 900 nucleotide bases. How many amino acids will it code?

(A) 150

(B) 300

(C) 450

(D) 900

Correct Answer: (B) 300

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Solution:

Step 1: Recall the genetic code.

Each amino acid is specified by one codon, and each codon consists of

$$\boxed{\text{3 nucleotide bases.}}$$

Step 2: Calculate the number of amino acids.

Given,

$$\text{Total nucleotide bases} = 900.$$

Therefore,

$$\text{Number of codons} = \frac{900}{3} = 300.$$

Hence,

$$\boxed{300}$$

amino acids can be coded.

Therefore,

$$\boxed{(B)}$$

is the correct answer.

Quick Tip: Genetic code formula:

$$\boxed{\text{Number of amino acids} = \frac{\text{Number of nucleotide bases}}{3}}$$

(Assuming the entire sequence is coding and stop codon is ignored.)

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