Telangana State Council Higher Education

Biotechnology

Duration :2 HR	**Maximum Marks :**120	**Total Questions :**120

General Notes

- Options shown in green color and with ✓ icon are correct.
- Options shown in red color and with icon are incorrect.

Mathematics

1.

If $x = \alpha, y = \beta, z = \gamma$ is a positive integral solution of the equation $x + y + z = 12$, the probability that it is such that $\alpha < \beta < \gamma$ is

(a) $\frac{7}{55}$
(b) $\frac{12}{55}$
(c) $\frac{13}{55}$
(d) $\frac{8}{55}$

Correct Answer: (a) $\frac{7}{55}$

Solution: We are looking for positive integral solutions to $x + y + z = 12$. This is equivalent to distributing 12 identical items into 3 distinct boxes such that each box has at least one item. Let $x' = x - 1, y' = y - 1, z' = z - 1$. Then $x', y', z' \geq 0$. The equation becomes $(x' + 1) + (y' + 1) + (z' + 1) = 12 \Rightarrow x' + y' + z' = 12 - 3 = 9$. The number of non-negative integral solutions is given by the stars and bars formula $\binom{n+k-1}{k-1}$ or $\binom{n+k-1}{n}$, where $n = 9$ (stars) and $k = 3$ (boxes). Total number of positive integral solutions $= \binom{9+3-1}{3-1} = \binom{11}{2} = \frac{11\times10}{2\times1} = 55$. So, the size of our sample space is 55.

Now, we need to find the number of solutions such that $x < y < z$ (using x, y, z for α, β, γ). Since x, y, z are distinct positive integers and $x + y + z = 12$: Possible values for x (smallest): If $x = 1$: $y + z = 11$. We need $1 < y < z$. If $y = 2, z = 9$. (1,2,9) - Valid. If $y = 3, z = 8$. (1,3,8) - Valid. If $y = 4, z = 7$. (1,4,7) - Valid. If $y = 5, z = 6$. (1,5,6) - Valid. (If $y = 6, z = 5$, not $y < z$). (4 solutions for x=1) If $x = 2$: $y + z = 10$. We need $2 < y < z$. If $y = 3, z = 7$. (2,3,7) - Valid. If $y = 4, z = 6$. (2,4,6) - Valid. (If $y = 5, z = 5$, not $y < z$). (2 solutions for x=2) If $x = 3$: $y + z = 9$. We need $3 < y < z$. If $y = 4, z = 5$. (3,4,5) - Valid. (If $y \geq 5$, then $z \leq 4$, not $y < z$). (1 solution for x=3) If $x = 4$: $y + z = 8$. We need $4 < y < z$. Smallest y is 5. Then $z = 3$, which violates $y < z$. No solutions. (Alternatively, for $x < y < z$, minimum sum is $1 + 2 + 3 = 6$. Max x can be is when $x \approx 12/3 = 4$. If $x = 3$, min $y = 4, z = 5$. Sum=12. If $x = 4$, then $y \geq 5, z \geq 6$. Min sum $4 + 5 + 6 = 15 > 12$. So x cannot be 4 or more). The number of solutions with $x < y < z$ are: (1,2,9), (1,3,8), (1,4,7), (1,5,6), (2,3,7), (2,4,6), (3,4,5). There are 7 such solutions.

The probability is $\frac{\text{Number of favorable solutions}}{\text{Total number of positive integral solutions}} = \frac{7}{55}$. This matches option (a).

$$\boxed{\frac{7}{55}}$$

Quick Tip

Quick Tip:

- Number of positive integral solutions to $x_1 + ... + x_k = n$ is $\binom{n-1}{k-1}$.
- For solutions with $x < y < z$, list them systematically starting with the smallest possible value for x.
- Alternatively, for distinct solutions, the number of partitions of n into k distinct parts is related to partitions into parts of any size. For $x < y < z$, it's about partitions into 3 distinct parts.

2.

Which of the following pairs of numbers is possible to be the regression coefficients for a data of two variables

(a) (0.7, 3.2)

(b) (–0.6, 0.5)

(c) (0.85, 0.9)

(d) (0.4, 2.6)

Correct Answer: (c) (0.85, 0.9)

Solution: Let the two regression coefficients be b_{yx} (regression of y on x) and b_{xy} (regression of x on y). There are two important properties for regression coefficients: 1. Both coefficients must have the same sign (either both positive or both negative). This is because their sign depends on the sign of the covariance between x and y, while standard deviations are always positive. $b_{yx} = r\frac{\sigma_y}{\sigma_x}$ and $b_{xy} = r\frac{\sigma_x}{\sigma_y}$, where r is the correlation coefficient. 2. The product of the regression coefficients must be less than or equal to 1, if they are based on the correlation coefficient r. Specifically, $b_{yx} \cdot b_{xy} = r^2$. Since $|r| \leq 1$, it must be that $r^2 \leq 1$. Therefore, $|b_{yx} \cdot b_{xy}| \leq 1$. Also, if one coefficient is numerically greater than 1, the other must be numerically less than 1 (unless $r = \pm 1$, then $|b_{yx}| \cdot |b_{xy}| = 1$). More strictly, if $|r| \leq 1$, then $|b_{yx}| \leq |\sigma_y/\sigma_x|$ and $|b_{xy}| \leq |\sigma_x/\sigma_y|$. The condition $b_{yx} \cdot b_{xy} = r^2 \leq 1$ is key.

Let's check the options: (a) (0.7, 3.2): Signs are the same (both positive). Product = $0.7 \times 3.2 = 2.24$. Since $2.24 > 1$, this pair is NOT possible. (r^2 cannot be > 1).

(b) (–0.6, 0.5): Signs are different (one negative, one positive). This is NOT possible.

(c) (0.85, 0.9): Signs are the same (both positive). Product = $0.85 \times 0.9 = 0.765$. Since $0.765 \leq 1$, this pair IS possible. ($r^2 = 0.765 \implies |r| = \sqrt{0.765} \approx 0.87 < 1$).

(d) (0.4, 2.6): Signs are the same (both positive). Product = $0.4 \times 2.6 = 1.04$. Since $1.04 > 1$, this pair is NOT possible.

Therefore, the only possible pair is (0.85, 0.9).

$$\boxed{(0.85,\ 0.9)}$$

Quick Tip

Quick Tip:

- Regression coefficients b_{yx} and b_{xy} must have the same sign (same as correlation coefficient r).
- The product of the regression coefficients is equal to the square of the correlation coefficient: $b_{yx} \cdot b_{xy} = r^2$.
- Since $|r| \leq 1$, it must be that $0 \leq r^2 \leq 1$. So, $0 \leq b_{yx} \cdot b_{xy} \leq 1$.
- This also implies that if one regression coefficient is numerically greater than 1, the other must be numerically less than 1 (unless $|r| = 1$, in which case $|b_{yx}| = 1/|b_{xy}|$).

3.

The order of convergence of the Newton's Raphson's method is

(a) linear

(b) quadratic

(c) biquadratic

(d) cubic

Correct Answer: (b) quadratic

Solution: The Newton-Raphson method is an iterative method for finding the roots of a real-valued function $f(x) = 0$. The iterative formula is:

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

The order of convergence of an iterative method describes how quickly the sequence of approximations x_n converges to the true root α. If $e_n = x_n - \alpha$ is the error at the nth iteration, then for a method with order of convergence p, we have $|e_{n+1}| \approx C|e_n|^p$ for some constant $C \neq 0$, as $n \to \infty$. For the Newton-Raphson method, under certain conditions (such as the root being simple and $f'(x)$ being non-zero near the root, and

$f''(x)$ being continuous), the order of convergence is $p = 2$. This is known as **quadratic convergence**. This means that the number of correct decimal places roughly doubles with each iteration, once the approximation is close enough to the root. Linear convergence: $p = 1$. Cubic convergence: $p = 3$. Biquadratic convergence: $p = 4$.

$$\boxed{\text{quadratic}}$$

Quick Tip

Quick Tip:

- Newton-Raphson method generally has quadratic convergence (order 2) for simple roots, provided $f'(root) \neq 0$.
- This means $|x_{n+1} - \alpha| \leq K|x_n - \alpha|^2$.
- Quadratic convergence is considered fast.
- If the root has multiplicity $m > 1$, the convergence of Newton's method reduces to linear.

4.

Which of the following numerical method is a multistep method to solve IVP or BVP's (IVP: Initial Value Problem, BVP: Boundary Value Problem. Multistep methods are typically for IVPs of ODEs.)

(a) Successive approximation method

(b) Adams - Bashforth method

(c) Runge - Kutta method

(d) Euler's method

Correct Answer: (b) Adams - Bashforth method

Solution: Numerical methods for solving ordinary differential equations (ODEs) can be classified as single-step or multistep methods.

- **Single-step methods:** Use information only from the previous point (y_n, t_n) to compute the next point (y_{n+1}, t_{n+1}). Examples include Euler's method and Runge-Kutta methods.

- **Multistep methods:** Use information from several previous points (e.g., $y_n, y_{n-1}, y_{n-2}, \ldots$) to compute the next point y_{n+1}. Examples include Adams-Bashforth methods (explicit) and Adams-Moulton methods (implicit).

Let's analyze the options: (a) Successive approximation method (e.g., Picard's iteration): This is an iterative method for solving ODEs or integral equations, generally considered single-step in its basic form of progression. (b) **Adams-Bashforth method:** This is a family of explicit multistep methods for solving ODEs. For example, the two-step Adams-Bashforth method uses y_n and y_{n-1} (and their derivatives) to find y_{n+1}. (c) **Runge-Kutta method:** This is a family of single-step methods. They achieve higher accuracy by evaluating the derivative function $f(t, y)$ at multiple intermediate points within a single step. (d) **Euler's method:** This is the simplest single-step method: $y_{n+1} = y_n + hf(t_n, y_n)$. Therefore, the Adams-Bashforth method is a multistep method. (Note: While some methods listed can be adapted for BVPs, multistep methods are primarily developed for IVPs of ODEs. The question wording is a bit broad.)

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

Quick Tip

Quick Tip:

- Single-step methods (for $y' = f(t, y)$): y_{n+1} depends only on y_n and values from the interval $[t_n, t_{n+1}]$. Examples: Euler, Modified Euler, Runge-Kutta.

- Multistep methods: y_{n+1} depends on $y_n, y_{n-1}, \ldots, y_{n-k+1}$ and possibly derivatives at these points. Examples: Adams-Bashforth (explicit), Adams-Moulton (implicit).

5.

If the Laplace transform of $\int_0^t \frac{((1+2t)^2-1)e^{3t}}{t}dt = \frac{A}{S-3} + \frac{B}{(S-3)^2} + \frac{C}{(S-3)^3}$ **then** $3(A+B+C) =$ (Typo: S should be s in Laplace domain variables)

(a) 8

(b) 4

(c) 12

(d) 15

Correct Answer: (b) 4 (This needs verification. The $3(A+B+C)$ looks like it might be related to $3 \times F(s)$ at some specific s, or a coefficient sum).

Solution: Let $g(t) = ((1+2t)^2-1)e^{3t}$. The given expression is $\mathcal{L}\left\{\int_0^t \frac{g(\tau)}{\tau}d\tau\right\}$. This is complicated. Let's first simplify $g(t)/t$.
$(1+2t)^2 - 1 = 1 + 4t + 4t^2 - 1 = 4t + 4t^2 = 4t(1+t)$. So,
$\frac{(1+2t)^2-1}{t} = \frac{4t(1+t)}{t} = 4(1+t) = 4+4t$. (This is valid for $t \neq 0$, and for Laplace transform starting from $t=0$, this simplification is fine). Let
$f(t) = \frac{((1+2t)^2-1)e^{3t}}{t} = (4+4t)e^{3t}$. We need to find $F(s) = \mathcal{L}\{f(t)\} = \mathcal{L}\{(4+4t)e^{3t}\}$.
Using the frequency shifting property: If $\mathcal{L}\{h(t)\} = H(s)$, then $\mathcal{L}\{e^{at}h(t)\} = H(s-a)$.
Let $h(t) = 4+4t$. $\mathcal{L}\{4\} = \frac{4}{s}$. $\mathcal{L}\{4t\} = 4\mathcal{L}\{t\} = 4\frac{1}{s^2} = \frac{4}{s^2}$. So,
$H(s) = \mathcal{L}\{4+4t\} = \frac{4}{s} + \frac{4}{s^2} = \frac{4s+4}{s^2}$. Then, $F(s) = \mathcal{L}\{(4+4t)e^{3t}\} = H(s-3)$.
$F(s) = \frac{4(s-3)+4}{(s-3)^2} = \frac{4s-12+4}{(s-3)^2} = \frac{4s-8}{(s-3)^2}$.
The question states: $\mathcal{L}\left\{\int_0^t \frac{((1+2\tau)^2-1)e^{3\tau}}{\tau}d\tau\right\} = \frac{A}{s-3} + \frac{B}{(s-3)^2} + \frac{C}{(s-3)^3}$. Let
$k(t) = \int_0^t f(\tau)d\tau$. Then $\mathcal{L}\{k(t)\} = \frac{F(s)}{s}$. So, the Laplace transform we need to equate is $\frac{F(s)}{s} = \frac{1}{s}\frac{4s-8}{(s-3)^2}$. Let $K(s) = \frac{4s-8}{s(s-3)^2}$. We need to perform partial fraction expansion for $K(s)$: $\frac{4s-8}{s(s-3)^2} = \frac{A'}{s} + \frac{B'}{s-3} + \frac{C'}{(s-3)^2}$. (Note: The question uses A, B, C for a different form, implying the initial integral was perhaps not divided by 's' in the Laplace domain. The structure $\frac{A}{S-3} + \frac{B}{(S-3)^2} + \frac{C}{(S-3)^3}$ means the original function $F(s)$ (Laplace of $f(t)$) itself should have this form. The given transform structure is
$\frac{A}{s-3} + \frac{B}{(s-3)^2} + \frac{C}{(s-3)^3}$. This implies the function whose Laplace transform is taken, say $m(t)$, would be like $(At^0/0! + Bt^1/1! + Ct^2/2!)e^{3t}$.
Let's re-read: "If the Laplace transform of $\int_0^t \frac{((1+2\tau)^2-1)e^{3\tau}}{\tau}d\tau$ is ..." Let
$f(t) = \frac{((1+2t)^2-1)e^{3t}}{t} = (4+4t)e^{3t}$. Then we are looking for $\mathcal{L}\left\{\int_0^t f(\tau)d\tau\right\}$. This is

$\frac{1}{s}\mathcal{L}\{f(t)\}$. We found $\mathcal{L}\{f(t)\} = F(s) = \frac{4s-8}{(s-3)^2}$. So we need to expand $\frac{1}{s}F(s) = \frac{4s-8}{s(s-3)^2}$. $\frac{4s-8}{s(s-3)^2} = \frac{D}{s} + \frac{E}{s-3} + \frac{F}{(s-3)^2}$. $4s - 8 = D(s-3)^2 + Es(s-3) + Fs$. Set $s = 0 \Rightarrow -8 = D(-3)^2 = 9D \Rightarrow D = -8/9$. Set $s = 3 \Rightarrow 4(3) - 8 = F(3) \Rightarrow 12 - 8 = 3F \Rightarrow 4 = 3F \Rightarrow F = 4/3$. Equate coefficients of s^2: $0 = D + E \Rightarrow E = -D = 8/9$. So, $\mathcal{L}\{\dots\} = -\frac{8}{9s} + \frac{8}{9(s-3)} + \frac{4}{3(s-3)^2}$. This form does not match the given form $\frac{A}{s-3} + \frac{B}{(s-3)^2} + \frac{C}{(s-3)^3}$. This means my interpretation of "Laplace transform of $\int_0^t \dots$" using the $F(s)/s$ property is not leading to the target form.

Perhaps the question implies that $f(t) = \frac{((1+2t)^2-1)}{t}$ itself is transformed, and then the e^{3t} is applied by shifting s to $s-3$, and the integral $\int_0^t$ means division by s. This is getting very convoluted.

Let's assume the expression on the LHS whose Laplace Transform is given is actually simpler and just $f(t) = ((A_0 + B_0 t + C_0 t^2/2)e^{3t})$ such that its transform is $\frac{A_0}{s-3} + \frac{B_0}{(s-3)^2} + \frac{C_0}{(s-3)^3}$, and relate these A, B, C. If $\mathcal{L}\{q(t)\} = \frac{A}{s-3} + \frac{B}{(s-3)^2} + \frac{C}{(s-3)^3}$, then $q(t) = (A \cdot \frac{t^0}{0!} + B \cdot \frac{t^1}{1!} + C \cdot \frac{t^2}{2!})e^{3t} = (A + Bt + \frac{C}{2}t^2)e^{3t}$. And this $q(t)$ is supposed to be $\int_0^t \frac{((1+2\tau)^2-1)e^{3\tau}}{\tau} d\tau = \int_0^t (4+4\tau)e^{3\tau} d\tau$. Let $I(t) = \int_0^t (4+4\tau)e^{3\tau} d\tau$. We need to evaluate this integral. $\int (4+4\tau)e^{3\tau} d\tau$. Use integration by parts: $\int u dv = uv - \int v du$. Let $u = 4 + 4\tau \Rightarrow du = 4d\tau$. Let $dv = e^{3\tau} d\tau \Rightarrow v = \frac{1}{3}e^{3\tau}$.

$\int (4+4\tau)e^{3\tau} d\tau = (4+4\tau)\frac{1}{3}e^{3\tau} - \int \frac{1}{3}e^{3\tau}(4d\tau)$

$= \frac{4+4\tau}{3}e^{3\tau} - \frac{4}{3}\int e^{3\tau} d\tau = \frac{4+4\tau}{3}e^{3\tau} - \frac{4}{3}\frac{1}{3}e^{3\tau} = (\frac{4}{3} + \frac{4}{3}\tau - \frac{4}{9})e^{3\tau}$

$= (\frac{12-4}{9} + \frac{4}{3}\tau)e^{3\tau} = (\frac{8}{9} + \frac{4}{3}\tau)e^{3\tau}$. Now evaluate

$I(t) = [(\frac{8}{9} + \frac{4}{3}x)e^{3x}]_0^t = (\frac{8}{9} + \frac{4}{3}t)e^{3t} - (\frac{8}{9} + 0)e^0 = (\frac{8}{9} + \frac{4}{3}t)e^{3t} - \frac{8}{9}$. This $I(t)$ is not in the form $(A + Bt + \frac{C}{2}t^2)e^{3t}$ due to the constant term $-\frac{8}{9}$. The Laplace transform of $-\frac{8}{9}u(t)$ is $-\frac{8}{9s}$. So, $\mathcal{L}\{I(t)\} = \mathcal{L}\{(\frac{8}{9} + \frac{4}{3}t)e^{3t}\} - \mathcal{L}\{\frac{8}{9}u(t)\}$.

$\mathcal{L}\{(\frac{8}{9} + \frac{4}{3}t)e^{3t}\} = \frac{8/9}{s-3} + \frac{4/3}{(s-3)^2}$. So, $\mathcal{L}\{I(t)\} = \frac{8/9}{s-3} + \frac{4/3}{(s-3)^2} - \frac{8}{9s}$. This is the same result as $\frac{1}{s}F(s)$ we got earlier: $-\frac{8}{9s} + \frac{8/9}{s-3} + \frac{4/3}{(s-3)^2}$. This means the given form on the RHS $\frac{A}{s-3} + \frac{B}{(s-3)^2} + \frac{C}{(s-3)^3}$ is the Laplace Transform of $\frac{((1+2t)^2-1)e^{3t}}{t}$ itself, NOT its integral. So, we are given $F(s) = \mathcal{L}\left\{\frac{((1+2t)^2-1)e^{3t}}{t}\right\} = \mathcal{L}\{(4+4t)e^{3t}\}$. We found $F(s) = \frac{4s-8}{(s-3)^2}$. We need to express this as $\frac{A}{s-3} + \frac{B}{(s-3)^2} + \frac{C}{(s-3)^3}$. This form implies that the highest power of $(s-3)$ in the denominator of $F(s)$ is 3. But our $F(s)$ has power 2. This means C must be 0. So, we need to write $\frac{4s-8}{(s-3)^2} = \frac{A}{s-3} + \frac{B}{(s-3)^2}$. $\frac{4s-8}{(s-3)^2} = \frac{A(s-3)+B}{(s-3)^2}$.

$4s - 8 = A(s-3) + B = As - 3A + B$. Equating coefficients of s: $A = 4$. Equating constant terms: $-8 = -3A + B = -3(4) + B = -12 + B$. $B = -8 + 12 = 4$. So $A = 4, B = 4, C = 0$. Then $3(A + B + C) = 3(4 + 4 + 0) = 3(8) = 24$. Option (b) is 4. Option (a) is 8. Option (c) is 12. Option (d) is 15. None of these match 24.
There is a fundamental misunderstanding of the question or a significant error in it or the options. "Laplace transform of $\int_0^t$ stuff $d\tau$" usually means apply $\mathcal{L}$ to the result of the integration, or use the property $\mathcal{L}\{\int_0^t f(\tau)d\tau\} = F(s)/s$. If the question actually meant: "If $f(t) = \frac{((1+2t)^2-1)e^{3t}}{t}$ and its Laplace Transform $\mathcal{L}\{f(t)\} = \frac{A}{s-3} + \frac{B}{(s-3)^2} + \frac{C}{(s-3)^3}$, then..." Then my calculation $A = 4, B = 4, C = 0$ holds. $3(A + B + C) = 24$. Still not an option.
Let's re-read "Laplace transform of $\int_0^t \frac{g(\tau)}{\tau} d\tau$". If $h(t) = g(t)/t$, then we are finding $\mathcal{L}\{\int_0^t h(\tau)d\tau\} = \frac{1}{s}\mathcal{L}\{h(t)\}$. And $\mathcal{L}\{g(t)/t\} = \int_s^\infty G(\sigma)d\sigma$, where $G(s) = \mathcal{L}\{g(t)\}$. This is becoming too complex. The form on RHS $\frac{A}{s-3} + \frac{B}{(s-3)^2} + \frac{C}{(s-3)^3}$ strongly suggests that the time domain function (whose LT is this) is $(A + Bt + \frac{C}{2}t^2)e^{3t}$. Let this time domain function be $y(t)$. So $y(t) = \int_0^t (4 + 4\tau)e^{3\tau}d\tau$. We calculated $y(t) = (\frac{8}{9} + \frac{4}{3}t)e^{3t} - \frac{8}{9}$. This $y(t)$ needs to be of the form $(A + Bt + \frac{C}{2}t^2)e^{3t}$. It is not, due to the $-\frac{8}{9}$ term. If we ignore the $-\frac{8}{9}$ term (e.g. if considering the particular integral part related to e^{3t}), then we would compare $(\frac{8}{9} + \frac{4}{3}t)e^{3t}$ with $(A + Bt + \frac{C}{2}t^2)e^{3t}$. Then $A = 8/9$, $B = 4/3$, $C/2 = 0 \implies C = 0$.
$3(A + B + C) = 3(\frac{8}{9} + \frac{4}{3} + 0) = 3(\frac{8+12}{9}) = 3(\frac{20}{9}) = \frac{20}{3}$. Not an option.
The question is most likely flawed. The provided solution (checkmark on 4) might relate to a vastly simplified or different version. If we assume the problem actually stated: Let $f(t) = (4 + 4t)e^{3t}$. Its Laplace transform is $F(s) = \frac{4}{(s-3)} + \frac{4}{(s-3)^2}$. So, $A = 4, B = 4, C = 0$. Then $3(A + B + C) = 3(4 + 4 + 0) = 24$. This is not 4.
What if $f(t) = \frac{((1+2t)^2-1)}{t}$ and $\mathcal{L}\{f(t)e^{3t}\}$ is given by the partial fraction form? $f(t) = \frac{4t+4t^2}{t} = 4 + 4t$. $\mathcal{L}\{(4 + 4t)e^{3t}\} = \frac{4}{s-3} + \frac{4}{(s-3)^2}$. Comparing this to $\frac{A}{s-3} + \frac{B}{(s-3)^2} + \frac{C}{(s-3)^3}$, we have $A = 4, B = 4, C = 0$. Then $3(A + B + C) = 3(4 + 4 + 0) = 24$. This is the most straightforward interpretation of the terms, but the integral sign on the LHS is ignored. If the answer is indeed 4, then $A + B + C = 4/3$. This would require, for example, $A = 4/3, B = 0, C = 0$. So $\mathcal{L}\{f(t)\} = \frac{4/3}{s-3}$. Then $f(t) = \frac{4}{3}e^{3t}$. Then

$(4+4t)e^{3t} = \frac{4}{3}e^{3t} \implies 4+4t = 4/3 \implies 1+t = 1/3 \implies t = -2/3$. Not possible.

Given the difficulty and inconsistencies, I cannot rigorously derive any of the options.

I will assume the marked answer implies $A+B+C = 4/3$.

$$\boxed{4 \text{ (cannot be rigorously derived from the problem statement as written)}}$$

Quick Tip

Quick Tip:

- Simplify the time-domain function first before attempting Laplace Transform.
- $\mathcal{L}\{t^n e^{at}\} = \frac{n!}{(s-a)^{n+1}}$.
- $\mathcal{L}\{\int_0^t f(\tau)d\tau\} = \frac{F(s)}{s}$.
- $\mathcal{L}\{f(t)/t\} = \int_s^\infty F(\sigma)d\sigma$ (if limit exists).
- Ensure the structure of the given partial fraction expansion matches the expected form of the Laplace Transform.

6.

Consider the following problem of vibration of a string. A tightly stretched string with fixed end points $x = 0$ and $x = L$ is initially in a position given by $y(x,0) = f(x)$. It is released from this rest position and allowed to vibrate. The mathematical representation of this problem which depicts the displacement of the string $y(x,t)$ at different times for different values of $x, 0 \le x \le L$ is

(a) $\frac{\partial y}{\partial x} = C^2 \frac{\partial^2 y}{\partial t^2}, y(x,0) = f(x), y(0,t) = 0, y(L,t) = 0$

(b) $\frac{\partial y}{\partial t} = C^2 \frac{\partial^2 y}{\partial x^2}, y(0,t) = f(x), y(0,L) = 0, y(L,0) = 0, (\frac{\partial y}{\partial t})_{t=0} = 0$

(c) $\frac{\partial^2 y}{\partial x^2} = C^2 \frac{\partial^2 y}{\partial t^2}, y(x,0) = f(x), (\frac{\partial y}{\partial x})_{x=0} = 0, y(0,L) = 0$

(d) $\frac{\partial^2 y}{\partial t^2} = C^2 \frac{\partial^2 y}{\partial x^2}, y(x,0) = f(x), y(0,t) = 0, y(L,t) = 0, (\frac{\partial y}{\partial t})_{t=0} = 0$

Correct Answer: (d) $\frac{\partial^2 y}{\partial t^2} = C^2 \frac{\partial^2 y}{\partial x^2}, y(x,0) = f(x), y(0,t) = 0, y(L,t) = 0, (\frac{\partial y}{\partial t})_{t=0} = 0$

Solution: The problem describes the vibration of a string, which is governed by the one-dimensional wave equation. The standard form of the 1D wave equation for displacement $y(x,t)$ is:

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

where c is the wave speed (here denoted as C).
Boundary Conditions (fixed end points): Since the string is fixed at $x = 0$ and $x = L$, the displacement at these points must be zero for all time t: $y(0,t) = 0$ for $t \geq 0$
$y(L,t) = 0$ for $t \geq 0$
Initial Conditions: 1. Initial position (displacement) is given by $y(x,0) = f(x)$. 2. The string is "released from this rest position". This means its initial velocity is zero. The initial velocity is $\frac{\partial y}{\partial t}$ at $t = 0$. So, $\left(\frac{\partial y}{\partial t}\right)_{t=0} = 0$ for $0 \leq x \leq L$.
Let's check the options: (a) Equation is wrong ($\frac{\partial y}{\partial x}$ vs $\frac{\partial^2 y}{\partial t^2}$). (b) Equation is of heat equation type ($\frac{\partial y}{\partial t}$). Boundary conditions are incorrectly stated. (c) Equation form is incorrect ($\frac{\partial^2 y}{\partial x^2} = C^2 \frac{\partial^2 y}{\partial t^2}$ should be $\frac{\partial^2 y}{\partial t^2} = C^2 \frac{\partial^2 y}{\partial x^2}$). Boundary conditions are mixed/incorrect. (d) Equation: $\frac{\partial^2 y}{\partial t^2} = C^2 \frac{\partial^2 y}{\partial x^2}$ (Correct wave equation). Initial position: $y(x,0) = f(x)$ (Correct). Boundary conditions: $y(0,t) = 0, y(L,t) = 0$ (Correct for fixed ends). Initial velocity: $(\frac{\partial y}{\partial t})_{t=0} = 0$ (Correct for release from rest). Option (d) correctly represents the mathematical model for this problem.

$$\boxed{\frac{\partial^2 y}{\partial t^2} = C^2 \frac{\partial^2 y}{\partial x^2}, y(x,0) = f(x), y(0,t) = 0, y(L,t) = 0, (\frac{\partial y}{\partial t})_{t=0} = 0}$$

Quick Tip

Quick Tip:

- 1D Wave Equation: $y_{tt} = c^2 y_{xx}$.
- Fixed ends at $x = 0, x = L \implies y(0,t) = 0, y(L,t) = 0$.
- Initial displacement: $y(x,0) = f(x)$.
- Released from rest $\implies$ initial velocity $y_t(x,0) = 0$.

7.

If $x = f(t)$ changes the interval $\alpha \leq t \leq \alpha + 2C$ to $\beta \leq x \leq \beta + 2\pi$, then $\frac{f(t)}{\beta} =$ (The question is asking for $f(t)/\beta$. This seems to imply a linear transformation. $f(t)$ here is actually x.) Let $x = f(t) = At + B$. When $t = \alpha$, $x = \beta \implies \beta = A\alpha + B$. When $t = \alpha + 2C$, $x = \beta + 2\pi \implies \beta + 2\pi = A(\alpha + 2C) + B = A\alpha + 2AC + B$. Subtracting the first from the second: $(\beta + 2\pi) - \beta = (A\alpha + 2AC + B) - (A\alpha + B)$ $2\pi = 2AC \implies AC = \pi \implies A = \pi/C$. Substitute A back into $\beta = A\alpha + B$: $\beta = (\pi/C)\alpha + B \implies B = \beta - (\pi/C)\alpha$. So, $x = f(t) = (\pi/C)t + (\beta - (\pi/C)\alpha) = (\pi/C)(t - \alpha) + \beta$. The question asks for $f(t)/\beta$ which is x/β. $\frac{x}{\beta} = \frac{(\pi/C)(t-\alpha)+\beta}{\beta} = \frac{\pi(t-\alpha)}{C\beta} + 1$. This doesn't match options.
The question phrasing "then $f(t)/\beta =$" is strange. Usually $f(t)$ denotes the function itself, mapping t to x. If the transformation is linear $x = mt + k$. Interval length in t: $(\alpha + 2C) - \alpha = 2C$. Interval length in x: $(\beta + 2\pi) - \beta = 2\pi$. So the scaling factor is $m = \frac{2\pi}{2C} = \frac{\pi}{C}$. $x - \beta = m(t - \alpha) \implies x = \beta + \frac{\pi}{C}(t - \alpha)$. This is $f(t)$. The question asks for $f(t)/\beta$, which is x/β. This doesn't yield simple options like t/α.
Let's look at the options: (a) $t + \alpha$, (b) t/α, (c) αt, (d) $t - \alpha$. These are very simple forms. This suggests that β might be 1 or cancel out, and C might be π. If $f(t)/\beta = t/\alpha$, then $f(t) = \beta t/\alpha$. So $x = \beta t/\alpha$. When $t = \alpha, x = \beta$. (This works: $x = \beta\alpha/\alpha = \beta$). When $t = \alpha + 2C, x = \beta + 2\pi$. $\beta + 2\pi = \beta(\alpha + 2C)/\alpha = \beta + 2C\beta/\alpha$. So $2\pi = 2C\beta/\alpha \implies \pi = C\beta/\alpha \implies \alpha\pi = C\beta$. This is a condition. If this condition holds, then $x = (\beta/\alpha)t$ is the transformation, and $x/\beta = t/\alpha$. Option (b) t/α is marked with a check. So the relationship is likely $x = k \cdot t$ and this passes through (α, β) and $(\alpha + 2C, \beta + 2\pi)$. If $x = kt$, then $\beta = k\alpha$ and $\beta + 2\pi = k(\alpha + 2C)$. From first, $k = \beta/\alpha$. Substitute into second: $\beta + 2\pi = (\beta/\alpha)(\alpha + 2C) = \beta + 2C\beta/\alpha$. $2\pi = 2C\beta/\alpha \implies \pi\alpha = C\beta$. Under this condition, $x = (\beta/\alpha)t$. Then $x/\beta = t/\alpha$. So, if $\pi\alpha = C\beta$, then $f(t)/\beta = t/\alpha$.
This requires a specific relationship between α, β, C, π. The question "If x=f(t) changes the interval... then $f(t)/\beta =$" suggests a general result. The simplicity of options implies a direct proportional scaling or simple shift. If the mapping is such that $f(t)$ is proportional to t and also scaled by β/α. If option (b) t/α is correct for $f(t)/\beta$, it means $f(t) = \frac{\beta}{\alpha}t$. This is a linear mapping passing through origin. This

works for the first point: $t = \alpha \implies f(\alpha) = \frac{\beta}{\alpha}\alpha = \beta$. For the second point: $t = \alpha + 2C \implies f(\alpha + 2C) = \frac{\beta}{\alpha}(\alpha + 2C) = \beta + \frac{2C\beta}{\alpha}$. We need this to be $\beta + 2\pi$. So, $\frac{2C\beta}{\alpha} = 2\pi \implies C\beta = \pi\alpha$. This must be an implicit condition for the problem if (b) is the answer.

$$\boxed{t/\alpha \text{ (assuming linear scaling } f(t) = kt \text{ and } C\beta = \pi\alpha)}$$

Quick Tip

Quick Tip:

- Linear transformation of an interval: $x = mt + c$. Use the endpoints to find m and c.
- $t \in [\alpha, \alpha + 2C]$ maps to $x \in [\beta, \beta + 2\pi]$.
- Length scaling: $((\alpha + 2C) - \alpha) \to ((\beta + 2\pi) - \beta) \implies 2C \to 2\pi$. So slope is π/C.
- Point-slope form: $x - \beta = (\pi/C)(t - \alpha)$.
- If the answer is one of the simple options, there might be specific implied conditions or it's a very specific type of scaling. The problem as stated is under-constrained for a general unique answer from the options without assuming the form $f(t) = kt$.

8.

Which of the following is a convergent series?

(a) $\sum_{n=0}^{\infty} \frac{3n^2+5n+6}{5n^2+6n+3}$

(b) $\sum_{n=0}^{\infty} (-1)^n \frac{2n+3}{2n}$

(c) $\sum_{n=0}^{\infty} \frac{2^n-2}{2^n+1}$

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

Correct Answer: (d) $\sum_{n=1}^{\infty} \frac{(-1)^{n+1}}{\log(n+1)}$

Solution: A necessary condition for a series $\sum a_n$ to converge is that $\lim_{n\to\infty} a_n = 0$. If this limit is not zero, the series diverges (Term Test for Divergence).
(a) $a_n = \frac{3n^2+5n+6}{5n^2+6n+3}$. $\lim_{n\to\infty} a_n = \lim_{n\to\infty} \frac{3+5/n+6/n^2}{5+6/n+3/n^2} = \frac{3}{5} \neq 0$. Diverges by Term Test.
(b) $a_n = (-1)^n \frac{2n+3}{2n}$. $\lim_{n\to\infty} \frac{2n+3}{2n} = \lim_{n\to\infty} \frac{2+3/n}{2} = \frac{2}{2} = 1$. So, $\lim_{n\to\infty} a_n$ does not exist (oscillates between approx 1 and -1). Not 0. Diverges by Term Test.
(c) $a_n = \frac{2^n-2}{2^n+1}$. $\lim_{n\to\infty} a_n = \lim_{n\to\infty} \frac{1-2/2^n}{1+1/2^n} = \frac{1-0}{1+0} = 1 \neq 0$. Diverges by Term Test.
(d) $a_n = \frac{(-1)^{n+1}}{\log(n+1)}$. This is an alternating series. Let $b_n = \frac{1}{\log(n+1)}$. 1. $\lim_{n\to\infty} b_n = \lim_{n\to\infty} \frac{1}{\log(n+1)} = 0$. (As $n \to \infty, \log(n+1) \to \infty$). 2. Is b_n decreasing? $\log(x)$ is an increasing function for $x > 0$. So $\log(n+1)$ is increasing for $n \geq 1$. Therefore, $b_n = \frac{1}{\log(n+1)}$ is a decreasing sequence for $n \geq 1$.
$(\log(n+2) > \log(n+1) \implies \frac{1}{\log(n+2)} < \frac{1}{\log(n+1)} \implies b_{n+1} < b_n)$. Since both conditions of the Alternating Series Test are met ($\lim_{n\to\infty} b_n = 0$ and b_n is decreasing), the series $\sum_{n=1}^{\infty} \frac{(-1)^{n+1}}{\log(n+1)}$ converges. (It converges conditionally, not absolutely, as $\sum 1/\log(n+1)$ diverges by comparison with $\sum 1/n$).

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

Quick Tip

Quick Tip:

- Term Test for Divergence: If $\lim_{n\to\infty} a_n \neq 0$, then $\sum a_n$ diverges.
- Alternating Series Test: If $a_n = (-1)^n b_n$ or $a_n = (-1)^{n+1} b_n$ with $b_n > 0$, then $\sum a_n$ converges if (1) $\lim_{n\to\infty} b_n = 0$ AND (2) b_n is a decreasing sequence.

9.

A and B are two nonsingular matrices. If the characteristic equation of A is $a_0\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0$ and characteristic equation of $B^{-1}AB$ is $b_0\lambda^3 + b_1\lambda^2 + b_2\lambda + b_3 = 0$, then

(a) $\frac{a_0}{b_0} = \frac{a_1}{b_1} = \frac{a_2}{b_2} = \frac{a_3}{b_3}$
(b) $\frac{a_0}{b_0} = \frac{a_1}{b_1} = \frac{a_2}{b_2} = \frac{a_3}{b_3}$

(c) $a_0 + a_1 + a_2 + a_3 = b_0 + b_1 + b_2 + b_3$

(d) $a_0 a_1 a_2 a_3 = b_0 b_1 b_2 b_3$

Correct Answer: (a) or (b) $\frac{a_0}{b_0} = \frac{a_1}{b_1} = \frac{a_2}{b_2} = \frac{a_3}{b_3}$ (since they are identical and reflect that the characteristic polynomials are proportional)

Solution: Similar matrices have the same characteristic polynomial (and thus the same eigenvalues, determinant, trace, etc.). The matrix $B^{-1}AB$ is similar to matrix A. The characteristic equation of A is $p_A(\lambda) = a_0\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0$. The characteristic equation of $B^{-1}AB$ is $p_{B^{-1}AB}(\lambda) = b_0\lambda^3 + b_1\lambda^2 + b_2\lambda + b_3 = 0$. Since A and $B^{-1}AB$ are similar, their characteristic polynomials must be the same, up to a non-zero constant multiplier. That is, $p_A(\lambda) = k \cdot p_{B^{-1}AB}(\lambda)$ for some constant $k \neq 0$. So, $a_0\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = k(b_0\lambda^3 + b_1\lambda^2 + b_2\lambda + b_3)$. Comparing coefficients of powers of λ: $a_0 = kb_0$ $a_1 = kb_1$ $a_2 = kb_2$ $a_3 = kb_3$ From these, we can write the ratios (assuming $b_i \neq 0$): $k = \frac{a_0}{b_0} = \frac{a_1}{b_1} = \frac{a_2}{b_2} = \frac{a_3}{b_3}$. This means the coefficients are proportional. Options (a) and (b) are identical in the image and state this proportionality. If the characteristic polynomial is defined as $\det(A - \lambda I)$, then the leading coefficient a_0 (coefficient of λ^3) would be $(-1)^3 = -1$ or 1 depending on convention of $\det(\lambda I - A)$. If a_0 and b_0 are chosen to be 1 (monic polynomial), then $k = 1$ and $a_i = b_i$ for all i. The given options imply that the characteristic polynomials are proportional.

$$\boxed{\frac{a_0}{b_0} = \frac{a_1}{b_1} = \frac{a_2}{b_2} = \frac{a_3}{b_3}}$$

Quick Tip

Quick Tip:

- Similar matrices A and $P^{-1}AP$ have the same characteristic polynomial, eigenvalues, determinant, and trace.
- If $p(\lambda) = c_n\lambda^n + \cdots + c_0$ and $q(\lambda) = d_n\lambda^n + \cdots + d_0$ are two characteristic polynomials for similar matrices, they must be proportional, i.e., $p(\lambda) = k \cdot q(\lambda)$ for some non-zero constant k. This means $c_i/d_i = k$ for all i.

10.

Consider the linear system of non homogeneous equation in three variables AX = B. $\rho(A)$ and $\rho([A : B])$ are roots of the equation $x^2 + bx + c = 0$. AX = B has infinite number of solutions, then the option containing two possible pairs of values of (b,c) is (Note: ρ denotes rank.)

(a) (1,1) (2,1)

(b) (1,–2) (4,–4)

(c) (–4,4) (–2,1)

(d) (1,1) (1,2)

Correct Answer: (c) (–4,4) (–2,1)

Solution: For a system of linear equations $AX = B$ in three variables (let number of variables be $n = 3$): The system has an infinite number of solutions if and only if: Rank of matrix A, $\rho(A)$, is equal to the Rank of the augmented matrix $[A : B]$, $\rho([A : B])$, AND this rank is less than the number of variables n. So, for infinite solutions: $\rho(A) = \rho([A : B]) < 3$. Let $r = \rho(A) = \rho([A : B])$. Then r can be 1 or 2 (since it must be < 3, and rank is non-negative integer. If $r = 0$, A is zero matrix, special case). The problem states that $\rho(A)$ and $\rho([A : B])$ are roots of the quadratic equation $x^2 + bx + c = 0$. Since for infinite solutions $\rho(A) = \rho([A : B]) = r$, this means the quadratic equation $x^2 + bx + c = 0$ must have equal roots, both equal to r. For a quadratic equation to have equal roots, its discriminant must be zero:
$D = b^2 - 4ac' = 0$. Here, $a' = 1, c' = c$. So, $b^2 - 4c = 0 \Rightarrow b^2 = 4c$. And the equal root is given by $x = -b/(2a') = -b/2$. So, we must have $r = -b/2$. Since r must be less than 3 (i.e., $r = 1$ or $r = 2$, assuming $r \neq 0$):
Case 1: $r = 1$. Then $1 = -b/2 \Rightarrow b = -2$. And
$b^2 = 4c \Rightarrow (-2)^2 = 4c \Rightarrow 4 = 4c \Rightarrow c = 1$. So, one possible pair for (b,c) is (–2, 1). The roots of $x^2 - 2x + 1 = 0 \Rightarrow (x - 1)^2 = 0$ are $x = 1, 1$. So $r = 1$. This is valid $(r < 3)$.
Case 2: $r = 2$. Then $2 = -b/2 \Rightarrow b = -4$. And
$b^2 = 4c \Rightarrow (-4)^2 = 4c \Rightarrow 16 = 4c \Rightarrow c = 4$. So, another possible pair for (b,c) is (–4, 4). The roots of $x^2 - 4x + 4 = 0 \Rightarrow (x - 2)^2 = 0$ are $x = 2, 2$. So $r = 2$. This is valid

$(r < 3)$.

We are looking for an option containing two possible pairs of (b,c). The possible pairs we found are (–2, 1) and (–4, 4). Option (c) is (–4,4) (–2,1). This matches our findings. Let's check other options for completeness: (a) (1,1): $b = 1, c = 1$. $b^2 = 1, 4c = 4$. $b^2 \neq 4c$. Roots are not equal. (2,1): $b = 2, c = 1$. $b^2 = 4, 4c = 4$. $b^2 = 4c$. Roots are equal. $x = -b/2 = -2/2 = -1$. Rank $r = -1$ is not possible. (b) (1,–2): $b = 1, c = -2$. $b^2 = 1, 4c = -8$. $b^2 \neq 4c$. (4,–4): $b = 4, c = -4$. $b^2 = 16, 4c = -16$. $b^2 \neq 4c$. (d) (1,1): Not valid as shown above. (1,2): $b = 1, c = 2$. $b^2 = 1, 4c = 8$. $b^2 \neq 4c$.

So, option (c) contains the two valid pairs.

$$\boxed{\text{(–4,4) (–2,1)}}$$

Quick Tip

Quick Tip:

- For infinite solutions to $AX = B$ (n variables): $\rho(A) = \rho([A : B]) = r < n$.
- If r_1, r_2 are roots of $x^2 + bx + c = 0$, and $r_1 = r_2 = r$ for infinite solutions, then the quadratic must have equal roots.
- Condition for equal roots: Discriminant $D = b^2 - 4c = 0 \implies b^2 = 4c$.
- The equal root is $x = -b/2$. So, $r = -b/2$.
- Since r is a rank, r must be a non-negative integer. For this problem, $r = 1$ or $r = 2$ as $r < 3$.

11.

Spontaneous generation or Abiogenesis was disproved by

(a) Antony van Leeuwenhoek

(b) Aristotle

(c) Louis Pasteur

(d) Ferdinand Cohn

Correct Answer: (c) Louis Pasteur

Solution: The theory of spontaneous generation (abiogenesis in its old sense, meaning life arising from non-living matter) proposed that living organisms could arise spontaneously from non-living matter. This idea was prevalent for centuries. **Louis Pasteur** conducted a series of definitive experiments in the mid-19th century (most famously his swan-neck flask experiments) that conclusively disproved the theory of spontaneous generation for microorganisms. He demonstrated that microorganisms are present in the air and can cause contamination and growth in nutrient broths, but if the broths are sterilized and protected from airborne microorganisms, no growth occurs. This supported the principle of biogenesis ("life from life").
Other scientists mentioned:

- Antony van Leeuwenhoek: Known as the "Father of Microbiology," he was one of the first to observe and describe microorganisms using his handcrafted microscopes. His observations were crucial but did not directly disprove spontaneous generation.

- Aristotle: An ancient Greek philosopher who was a proponent of the theory of spontaneous generation.

- Ferdinand Cohn: A prominent bacteriologist who made significant contributions to microbiology, including work on bacterial spores and classification, but Pasteur's experiments are most directly credited with disproving spontaneous generation.

$$\boxed{\text{Louis Pasteur}}$$

Quick Tip

Quick Tip:

- Spontaneous generation: The outdated theory that living organisms can arise directly from non-living matter.
- Biogenesis: The principle that all living things come from pre-existing living things.
- Louis Pasteur's swan-neck flask experiments were a landmark in disproving spontaneous generation and establishing biogenesis for microorganisms.

12.

Endoplasmic reticulum and Golgi bodies are present in

(a) Prokaryotic cell

(b) Animal cell only

(c) Plant cell only

(d) Both animal and plant cell

Correct Answer: (d) Both animal and plant cell

Solution: Endoplasmic reticulum (ER) and Golgi bodies (also known as Golgi apparatus or Golgi complex) are membrane-bound organelles found in eukaryotic cells.

- **Prokaryotic cells** (e.g., bacteria, archaea) lack membrane-bound organelles. Therefore, ER and Golgi bodies are absent in prokaryotic cells.
- **Eukaryotic cells** possess a nucleus and other membrane-bound organelles. This includes both animal cells and plant cells.
  - **Animal cells** have Endoplasmic reticulum and Golgi bodies, involved in protein synthesis/modification, lipid synthesis, and packaging/transport of cellular products.

  - **Plant cells** also have Endoplasmic reticulum and Golgi bodies (often referred to as dictyosomes in plants when considered as individual stacks), performing similar functions, including involvement in cell wall synthesis.

Therefore, Endoplasmic reticulum and Golgi bodies are present in both animal and plant cells (which are eukaryotic).

$$\boxed{\text{Both animal and plant cell}}$$

Quick Tip

Quick Tip:

- Key distinction: Prokaryotic cells lack membrane-bound organelles; Eukaryotic cells have them.
- Endoplasmic Reticulum (ER) and Golgi Apparatus are characteristic organelles of eukaryotic cells.
- Both animal and plant cells are eukaryotic and thus contain ER and Golgi.

13.

Fimbriae in prokaryotes is used for

(a) Motility

(b) Attachment or adhesion

(c) Conjugation

(d) Motility, attachment and conjugation

Correct Answer: (b) Attachment or adhesion

Solution: Fimbriae (singular: fimbria) are short, hair-like proteinaceous appendages found on the surface of many prokaryotic cells (bacteria). Their primary function is to enable the bacteria to **attach or adhere** to surfaces, including host tissues (in pathogenic bacteria, facilitating colonization) or other bacteria (e.g., in biofilm formation).

- (a) Motility: Motility in most bacteria is primarily achieved by flagella (singular: flagellum), which are longer, whip-like appendages. Some specialized motility like twitching motility can involve type IV pili, which are different from fimbriae.
- (c) Conjugation: Bacterial conjugation, the transfer of genetic material between bacteria, is typically mediated by specialized structures called sex pili (or F-pili), which are generally longer and fewer in number than fimbriae.
- (d) Motility, attachment and conjugation: While some pili (related structures) are involved in motility and conjugation, the primary role of fimbriae is adhesion.

Therefore, fimbriae are mainly used for attachment or adhesion.

$$\boxed{\text{Attachment or adhesion}}$$

Quick Tip

Quick Tip:

- **Fimbriae:** Short, numerous, hair-like appendages for adhesion/attachment.
- **Pili (Sex Pili/F-Pili):** Longer, less numerous than fimbriae, involved in bacterial conjugation. Some types of pili (Type IV) are involved in twitching motility.
- **Flagella:** Long, whip-like structures for motility (swimming).

14.

Transduction is a process of

(a) Uptake of exogenous DNA by microbe

(b) Sexual transfer of DNA from two microbes

(c) Transfer of genetic material through a bacteriophage or a virus

(d) Uptake of exogenous DNA by microbe and Sexual transfer of DNA from two microbes

Correct Answer: (c) Transfer of genetic material through a bacteriophage or a virus

Solution: Transduction is one of the three main mechanisms of horizontal gene transfer in bacteria, where genetic material (DNA) is transferred from one bacterium to another via a virus that infects bacteria, called a bacteriophage (or phage).

- During the lytic or lysogenic cycle of a bacteriophage, fragments of the host bacterial DNA can be accidentally packaged into newly forming phage particles.
- When such a phage (now carrying bacterial DNA instead of, or in addition to, its own viral DNA) infects a new bacterial cell, it injects this bacterial DNA into the recipient cell.
- This transferred bacterial DNA can then integrate into the recipient's chromosome, leading to genetic recombination.

Let's look at the options: (a) "Uptake of exogenous DNA by microbe": This describes transformation. (b) "Sexual transfer of DNA from two microbes": This usually refers to conjugation, which involves direct cell-to-cell contact. (c) "Transfer of genetic material through a bacteriophage or a virus": This correctly describes transduction. (d) Combination of (a) and (b).
Therefore, transduction is the process of genetic material transfer mediated by a bacteriophage.

$$\boxed{\text{Transfer of genetic material through a bacteriophage or a virus}}$$

Quick Tip

Quick Tip:

- Main mechanisms of horizontal gene transfer in bacteria:
  - **Transformation:** Uptake of naked DNA from the environment.
  - **Transduction:** Transfer of DNA by a bacteriophage.
  - **Conjugation:** Transfer of DNA through direct cell-to-cell contact (via a pilus).

15.

Axenic culture means

(a) Study of characteristics of a culture, in an environment of other living organisms

(b) Study of characteristics of a culture, in an environment free of other living organisms

(c) Study of characteristics of a culture, of living organisms without environment effect

(d) Study of characteristics of a culture, in absence of nutrients

Correct Answer: (b) Study of characteristics of a culture, in an environment free of other living organisms

Solution: An **axenic culture** (also known as a pure culture in microbiology) is a culture that contains only a single species, strain, or variety of an organism, and is entirely free of all other contaminating organisms. The term "axenic" means "without foreign guests" or "without strangers." Let's analyze the options: (a) "...in an environment of other living organisms": This describes a mixed culture or a contaminated culture, not axenic. (b) "...in an environment free of other living organisms": This correctly describes an axenic culture. It refers to the culture itself being pure (one type of organism) and uncontaminated by other living organisms. (c) "...of living organisms without environment effect": This is too general and doesn't capture the essence of "axenic" which is about purity from other organisms. (d) "...in absence of nutrients": A culture requires nutrients to grow; absence of nutrients would mean no growth. This is unrelated to being axenic.
Therefore, axenic culture means a culture that is free of other living organisms (i.e., a pure culture). The option implies studying this pure culture.

$$\boxed{\text{Study of characteristics of a culture, in an environment free of other living organisms}}$$

Quick Tip

Quick Tip:

- Axenic culture = Pure culture.
- Contains only one known species, strain, or type of microorganism.
- Free from contamination by any other living organisms.
- Essential for studying the properties of a specific microorganism.

16.

Photo lithotrophic autotroph organisms use

(a) Light energy, inorganic electron source and CO_2 as its carbon source

(b) Chemical energy, organic electron source and CO_2 as its carbon source

(c) Light energy, organic electron source and organic compounds as its carbon source

(d) Chemical energy, inorganic electron source and CO_2 as its carbon source

Correct Answer: (a) Light energy, inorganic electron source and CO_2 as its carbon source

Solution: Organisms can be classified based on their sources of energy, electrons, and carbon:

- **Energy Source:**
  - **Photo-**: Light energy
  - **Chemo-**: Chemical energy (from oxidation of chemical compounds)
- **Electron Source (Reducing Power):**
  - **-litho-**: Inorganic electron donor (e.g., H_2O, H_2S, NH_3, Fe^{2+})
  - **-organo-**: Organic electron donor (e.g., glucose, acetate)
- **Carbon Source:**

  - **-autotroph**: Uses inorganic carbon (primarily CO_2) as its main carbon source.
  - **-heterotroph**: Uses organic compounds as its main carbon source.

The term "Photo lithotrophic autotroph" (or photolithoautotroph) describes an organism that:

- **Photo-**: Uses light as its energy source.
- **-litho-**: Uses inorganic compounds as its electron source.
- **-autotroph**: Uses CO_2 (inorganic carbon) as its primary carbon source.

This matches option (a): "Light energy, inorganic electron source and CO_2 as its carbon source". Examples include plants, algae, and cyanobacteria (which use H_2O as the electron donor, producing O_2) and some photosynthetic bacteria like purple sulfur bacteria and green sulfur bacteria (which may use H_2S or other inorganic donors as electron sources).

$$\boxed{\text{Light energy, inorganic electron source and } CO_2 \text{ as its carbon source}}$$

Quick Tip

Quick Tip:

- Breakdown of metabolic classification terms:
  - Energy: Photo- (light), Chemo- (chemical).
  - Electrons: -litho- (inorganic), -organo- (organic).
  - Carbon: -autotroph (CO_2), -heterotroph (organic C).
- Plants are photolithoautotrophs (using H_2O as the electron donor).

17.

Electron transport chain mechanism for generation of ATP is carried out in

(a) Outer membrane of Endoplasmic reticulum

(b) Mitochondrial Matrix

(c) Mitochondrial folded inner membrane cristae

(d) In Golgi bodies

Correct Answer: (c) Mitochondrial folded inner membrane cristae

Solution: The electron transport chain (ETC) and oxidative phosphorylation, which are the primary mechanisms for ATP generation in aerobic cellular respiration, occur in specific locations within the mitochondria in eukaryotic cells.

- **Mitochondrial folded inner membrane cristae (Option c):** The electron transport chain complexes and ATP synthase (the enzyme that produces ATP) are embedded in the inner mitochondrial membrane. The folds of the inner membrane, called cristae, significantly increase the surface area available for these processes. Protons (H^+) are pumped from the matrix into the intermembrane space across this inner membrane, creating a proton gradient that drives ATP synthesis. This is the correct location.
- (a) Outer membrane of Endoplasmic reticulum: The ER is involved in protein and lipid synthesis, not primarily ATP generation via ETC.
- (b) Mitochondrial Matrix: The mitochondrial matrix is the site of the Krebs cycle (citric acid cycle) and pyruvate oxidation, which produce NADH and $FADH_2$ that feed electrons into the ETC. However, the ETC itself is located on the inner membrane, not within the matrix.
- (d) In Golgi bodies: The Golgi apparatus is involved in modifying, sorting, and packaging proteins and lipids for secretion or delivery to other organelles. It is not involved in ATP generation via ETC.

Therefore, the electron transport chain mechanism for ATP generation is carried out in the mitochondrial folded inner membrane (cristae).

$$\boxed{\text{Mitochondrial folded inner membrane cristae}}$$

Quick Tip

Quick Tip:

- Aerobic Respiration Stages in Eukaryotes:
  - Glycolysis: Cytoplasm
  - Pyruvate Oxidation Krebs Cycle: Mitochondrial matrix
  - Electron Transport Chain Oxidative Phosphorylation: Inner mitochondrial membrane (cristae)
- The cristae increase surface area for the ETC components and ATP synthase.

18.

Microbes at exponential growth phase will have

(a) Rate of growth is inversely proportional to division

(b) Rate of growth and division is constant and maximal

(c) Population is not uniform in terms of chemical and physical properties during this phase

(d) Population is uniform but not in terms of chemical and physical properties during this phase

Correct Answer: (b) Rate of growth and division is constant and maximal

Solution: The exponential growth phase (also known as the logarithmic or log phase) is a period in a microbial batch culture where cells are actively dividing at a constant and maximal rate under the given conditions (e.g., nutrient availability, temperature). Characteristics of the exponential phase:

- **Constant and Maximal Growth Rate:** The rate of increase in cell number (or biomass) per unit time is constant, and cell division occurs at the maximum rate possible for that organism in that specific medium and environment. This leads to an exponential increase in population size.

- **Balanced Growth:** Cells are typically in a state of balanced growth, meaning that all cellular components are synthesized at constant rates relative to each other. This results in a relatively uniform population in terms of size, chemical composition, and metabolic activity.
- **High Metabolic Activity:** Cells are metabolically very active.

Let's analyze the options: (a) "Rate of growth is inversely proportional to division": This is incorrect. Higher division rate means higher growth rate. (b) "Rate of growth and division is constant and maximal": This correctly describes the exponential phase. The specific growth rate (μ) and division rate are constant and at their peak. (c) "Population is not uniform in terms of chemical and physical properties during this phase": This is generally false. During balanced exponential growth, the population is usually most uniform. Non-uniformity is more characteristic of lag phase or stationary phase. (d) "Population is uniform but not in terms of chemical and physical properties during this phase": This is contradictory and incorrect. If it's uniform, it's generally in terms of these properties during balanced growth.
Therefore, option (b) is the correct statement.

$$\boxed{\text{Rate of growth and division is constant and maximal}}$$

Quick Tip

Quick Tip:

- Phases of Microbial Growth in Batch Culture: Lag phase → Exponential (Log) phase → Stationary phase → Death (Decline) phase.
- Exponential Phase: Cells divide at a constant, maximum rate. Population increases exponentially. Cells are generally most uniform and metabolically active.

19.

Chemoorganotrophic heterotroph organisms use (Typo in image: Chemoorganotrophic, not Chetroorganotrophic)

(a) Organic compounds as sources of energy, hydrogen, electrons and carbon

(b) Light energy, organic electron source and organic compounds as its carbon source

(c) Chemical energy, inorganic electron source and CO_2 as its carbon source

(d) Organic compounds as sources of energy, hydrogen, inorganic compounds for electrons and carbon (This option is cut off in one image, but ends like this in another)

Correct Answer: (a) Organic compounds as sources of energy, hydrogen, electrons and carbon

Solution: Breaking down the term "Chemoorganotrophic heterotroph" (or simply Chemoorganoheterotroph):

- **Chemo-**: Derives energy from chemical reactions (oxidation of chemical compounds).
- **-organo-**: Uses organic compounds as its electron source (and often also as its hydrogen source).
- **-heterotroph**: Uses organic compounds as its carbon source.

So, a chemoorganoheterotroph uses organic compounds for all three fundamental needs: energy, electrons (and hydrogen), and carbon. Let's analyze the options: (a) "Organic compounds as sources of energy, hydrogen, electrons and carbon": This perfectly matches the definition of a chemoorganoheterotroph. (b) "Light energy...": This would be "Photo-", not "Chemo-". Incorrect. (c) "Chemical energy, inorganic electron source and CO_2 as its carbon source": This describes a chemolithoautotroph. Incorrect. (d) "Organic compounds as sources of energy, hydrogen, inorganic compounds for electrons and carbon": "inorganic compounds for electrons and carbon" contradicts "-organo-" and "-heterotroph". Incorrect.
Therefore, option (a) is the correct description. Many common organisms, including most animals, fungi, and many bacteria, are chemoorganoheterotrophs.

$$\boxed{\text{Organic compounds as sources of energy, hydrogen, electrons and carbon}}$$

Quick Tip

Quick Tip:

- Metabolic classification based on:
  - Energy source: Chemo- (chemical), Photo- (light).
  - Electron source: -organo- (organic), -litho- (inorganic).
  - Carbon source: -heterotroph (organic), -autotroph (CO_2).
- Chemoorganoheterotrophs use organic compounds for energy, electrons, and carbon (e.g., humans metabolizing glucose).

20.

Fermentation is a process where

(a) Glucose is converted into pyruvate in the presence of oxygen

(b) Glucose is converted into pyruvate in the absence of oxygen

(c) Glucose is converted into lactate and / or alcohol in the absence of oxygen

(d) Glucose is converted into lactate and / or alcohol in the presence of oxygen

Correct Answer: (c) Glucose is converted into lactate and / or alcohol in the absence of oxygen

Solution: Fermentation is an anaerobic metabolic process (occurs in the absence of oxygen) that follows glycolysis. In fermentation, organic molecules (like pyruvate, the end product of glycolysis) are converted into other organic end products, such as lactic acid or ethanol and carbon dioxide. The primary purpose of fermentation in this context is to regenerate NAD^+ from NADH, which allows glycolysis to continue producing a small amount of ATP.

- **Glycolysis (common first step):** Glucose $\rightarrow$ Pyruvate + ATP + NADH. This step itself does not require oxygen.
- **Fermentation (anaerobic):** Pyruvate (or its derivatives) is then processed further without oxygen to regenerate NAD^+.

  - Lactic acid fermentation: Pyruvate → Lactic acid (e.g., in muscle cells, some bacteria).
  - Alcoholic fermentation: Pyruvate → Acetaldehyde → Ethanol + CO_2 (e.g., in yeast).

Let's analyze the options: (a) "Glucose is converted into pyruvate in the presence of oxygen": Glycolysis (glucose to pyruvate) can occur with or without oxygen. If oxygen is present, pyruvate usually enters aerobic respiration. This is not fermentation. (b) "Glucose is converted into pyruvate in the absence of oxygen": This describes glycolysis under anaerobic conditions, which is the *prelude* to fermentation, but not fermentation itself (which processes the pyruvate). (c) "Glucose is converted into lactate and / or alcohol in the absence of oxygen": This correctly describes the overall process including glycolysis followed by the fermentation steps that produce end products like lactate or alcohol, all occurring anaerobically. (d) "Glucose is converted into lactate and / or alcohol in the presence of oxygen": Fermentation is an anaerobic process. If oxygen is present, cells typically perform aerobic respiration for much higher ATP yield.
Therefore, option (c) best describes fermentation.

$$\boxed{\text{Glucose is converted into lactate and / or alcohol in the absence of oxygen}}$$

Quick Tip

Quick Tip:

- Fermentation is an anaerobic process (no oxygen required).
- It starts with glycolysis (glucose → pyruvate).
- The main purpose of the steps after glycolysis in fermentation is to regenerate NAD^+ so glycolysis can continue.
- Common end products: Lactic acid (lactic acid fermentation), Ethanol and CO_2 (alcoholic fermentation).

21.

Lyophilization or freeze-drying involves

(a) Freezing the cells in liquid nitrogen

(b) Sublimation of cells water by its drying under vacuum

(c) Making into powder by dry heat

(d) Wet heat and freezing of cells

Correct Answer: (b) Sublimation of cells water by its drying under vacuum

Solution: Lyophilization, also known as freeze-drying, is a dehydration process typically used to preserve perishable materials or make the material more convenient for transport. It works by freezing the material and then reducing the surrounding pressure to allow the frozen water in the material to sublimate directly from the solid phase to the gas phase. The key steps are: 1. **Freezing:** The material (e.g., a cell culture, food, pharmaceutical) is frozen, usually to a very low temperature. 2. **Primary Drying (Sublimation):** The frozen material is placed under a vacuum, and the pressure is reduced below the triple point of water. Heat may be gently applied to provide energy for sublimation. The ice in the material turns directly into water vapor without passing through the liquid phase. This vapor is then removed (e.g., by a condenser). 3. **Secondary Drying (Desorption):** After most of the ice has sublimated, some unfrozen water molecules may still be bound to the material. The temperature is slightly raised (while still under vacuum) to remove this residual moisture by desorption.

Let's analyze the options: (a) "Freezing the cells in liquid nitrogen": Freezing is the first step, but lyophilization is more than just freezing. (b) "Sublimation of cells water by its drying under vacuum": This correctly describes the core principle of lyophilization – removing water by sublimation under vacuum. "Cells water" implies water within the cells. (c) "Making into powder by dry heat": Dry heat would typically denature or destroy biological materials. Lyophilization aims to preserve them. (d) "Wet heat and freezing of cells": Wet heat (like autoclaving) sterilizes by killing cells. Freezing is part of lyophilization, but "wet heat" is contradictory to the preservation goal.

Therefore, option (b) best describes the process.

$$\boxed{\text{Sublimation of cells water by its drying under vacuum}}$$

Quick Tip

Quick Tip:

- Lyophilization = Freeze-drying.
- Process: Freeze the material → Reduce pressure (vacuum) → Ice sublimes (solid → gas).
- Used for preserving sensitive biological materials, pharmaceuticals, food.

22.

The following is not an inhibitor of protein synthesis

(a) Streptomycin

(b) Penicillin

(c) Tetracyclin

(d) Erythromycin

Correct Answer: (b) Penicillin

Solution: Many antibiotics work by inhibiting bacterial protein synthesis, typically by targeting the bacterial ribosome.

- **(a) Streptomycin:** An aminoglycoside antibiotic that binds to the 30S subunit of the bacterial ribosome, causing misreading of mRNA and inhibiting protein synthesis. It IS an inhibitor.
- **(b) Penicillin:** A β-lactam antibiotic. Penicillins work by inhibiting the synthesis of peptidoglycan, a crucial component of the bacterial cell wall. They do NOT directly inhibit protein synthesis.

- **(c) Tetracyclin (Tetracycline):** Binds to the 30S ribosomal subunit and blocks the attachment of aminoacyl-tRNA to the A-site of the ribosome, thus inhibiting protein synthesis. It IS an inhibitor.
- **(d) Erythromycin:** A macrolide antibiotic that binds to the 50S subunit of the bacterial ribosome and inhibits translocation (movement of the ribosome along mRNA) or peptide chain elongation. It IS an inhibitor.

Therefore, Penicillin is not an inhibitor of protein synthesis; it targets cell wall synthesis.

$$\boxed{\text{Penicillin}}$$

Quick Tip

Quick Tip:

- Antibiotics targeting bacterial protein synthesis often act on the 30S or 50S ribosomal subunits. Examples:
  - 30S inhibitors: Aminoglycosides (e.g., Streptomycin, Gentamicin), Tetracyclines.
  - 50S inhibitors: Macrolides (e.g., Erythromycin, Azithromycin), Chloramphenicol, Clindamycin, Linezolid.
- β-lactam antibiotics (e.g., Penicillins, Cephalosporins) inhibit bacterial cell wall synthesis.

23.

Which among the following is a compound lipid

(a) Fats

(b) Oils

(c) Phospholipids

(d) Waxes

Correct Answer: (c) Phospholipids

Solution: Lipids are a diverse group of hydrophobic molecules. They can be broadly classified:

- **Simple Lipids:** Esters of fatty acids with various alcohols.
  - **Fats and Oils (Triglycerides):** Esters of fatty acids with glycerol. Fats are solid at room temp, oils are liquid.
  - **Waxes:** Esters of long-chain fatty acids with long-chain alcohols (other than glycerol).
- **Compound Lipids (or Complex Lipids):** Esters of fatty acids containing groups in addition to an alcohol and fatty acids. These additional groups can be phosphate, carbohydrate, protein, etc.
  - **Phospholipids:** Lipids containing a phosphate group. They are major components of cell membranes. Examples: Lecithin, Cephalin. They typically consist of glycerol, two fatty acids, and a phosphate group often linked to another small molecule (e.g., choline, ethanolamine).
  - **Glycolipids:** Lipids containing a carbohydrate group.
  - **Lipoproteins:** Complexes of lipids and proteins.
- **Derived Lipids:** Substances derived from simple or compound lipids by hydrolysis. Examples include fatty acids, glycerol, steroids, cholesterol, lipid-soluble vitamins.

From the options: (a) Fats: Simple lipids (triglycerides). (b) Oils: Simple lipids (triglycerides). (c) Phospholipids: Contain a phosphate group in addition to fatty acids and alcohol (glycerol or sphingosine). They are compound lipids. (d) Waxes: Simple lipids.
Therefore, phospholipids are compound lipids.

$$\boxed{\text{Phospholipids}}$$

Quick Tip

Quick Tip:

- Simple lipids = Fatty acid esters with alcohol (e.g., fats, oils, waxes).
- Compound lipids = Esters of fatty acids with alcohol + additional groups (e.g., phosphate in phospholipids, carbohydrate in glycolipids).
- Phospholipids are key components of biological membranes.

24.

Select a conjugated protein

(a) Collagen

(b) Albumin

(c) Keratin

(d) Hemoglobin

Correct Answer: (d) Hemoglobin

Solution: Proteins can be classified based on their composition:

- **Simple Proteins:** On hydrolysis, yield only amino acids or their derivatives. Examples: Albumins, Globulins, Glutelins, Prolamins, Scleroproteins (like collagen, keratin, elastin).
- **Conjugated Proteins:** Proteins that are combined with a non-protein component, called a prosthetic group. On hydrolysis, they yield amino acids plus the prosthetic group. Examples:
  - **Nucleoproteins:** Protein + Nucleic acid (e.g., ribosomes, viruses).
  - **Glycoproteins:** Protein + Carbohydrate (e.g., mucin, some antibodies).
  - **Lipoproteins:** Protein + Lipid (e.g., chylomicrons, LDL, HDL).
  - **Phosphoproteins:** Protein + Phosphate group (e.g., casein in milk).

  - **Chromoproteins (Metalloproteins):** Protein + Pigment or Metal ion (e.g., Hemoglobin - contains heme group with iron; Chlorophyll-protein complexes).

Let's analyze the options: (a) Collagen: A fibrous simple protein (scleroprotein), a major component of connective tissue. (b) Albumin: A globular simple protein found in blood plasma and egg white. (c) Keratin: A fibrous simple protein (scleroprotein) found in hair, nails, skin. (d) **Hemoglobin:** A chromoprotein (specifically a metalloprotein) found in red blood cells. It consists of a protein part (globin) and a non-protein prosthetic group (heme), which contains an iron atom. The heme group is responsible for oxygen binding. Thus, hemoglobin is a conjugated protein.

$$\boxed{\text{Hemoglobin}}$$

Quick Tip

Quick Tip:

- Simple proteins: Yield only amino acids upon hydrolysis.
- Conjugated proteins: Yield amino acids + a non-protein prosthetic group.
- Hemoglobin's prosthetic group is heme (an iron-containing porphyrin).

25.

Which one is incorrect with regard to pK_a?

(a) In pK_a, K_a is acid dissociation constant

(b) pK_a is measurement of the concentration of hydrogen ions in a solution

(c) Higher the K_a the stronger the acid

(d) pK_a is used to show the strength of an acid

Correct Answer: (b) pK_a is measurement of the concentration of hydrogen ions in a solution

Solution: Let's analyze each statement regarding pK$_a$: (a) "In pK$_a$, K$_a$ is acid dissociation constant": TRUE. K$_a$ is the equilibrium constant for the dissociation of an acid HA $\rightleftharpoons$ H$^+$ + A$^-$. $K_a = \frac{[\text{H}^+][\text{A}^-]}{[\text{HA}]}$.
(b) "pK$_a$ is measurement of the concentration of hydrogen ions in a solution": FALSE. The measurement of the concentration of hydrogen ions in a solution is pH, where pH $= -\log_{10}[\text{H}^+]$. pK$_a$ is defined as $-\log_{10} K_a$. It is a measure of the acid's strength (its tendency to dissociate), not directly the [H$^+$] in a particular solution (though it's related via the Henderson-Hasselbalch equation).
(c) "Higher the K$_a$ the stronger the acid": TRUE. A larger K$_a$ value means the acid dissociates more completely, producing more H$^+$ ions, hence it is a stronger acid.
(d) "pK$_a$ is used to show the strength of an acid": TRUE. Since pK$_a$ $= -\log_{10} K_a$, there is an inverse relationship between pK$_a$ and K$_a$. A stronger acid has a larger K$_a$ and therefore a *smaller* pK$_a$. So, pK$_a$ values are indeed used to indicate acid strength (lower pK$_a$ = stronger acid).
The incorrect statement is (b).

$$\boxed{\text{pK}_a \text{ is measurement of the concentration of hydrogen ions in a solution}}$$

Quick Tip

Quick Tip:

- K_a: Acid dissociation constant. Larger $K_a \implies$ stronger acid.
- pK$_a$ $= -\log_{10} K_a$. Smaller pK$_a$ $\implies$ stronger acid.
- pH $= -\log_{10}[\text{H}^+]$. Measures hydrogen ion concentration (acidity/basicity of a solution).
- Henderson-Hasselbalch equation relates pH, pK$_a$, and the ratio of conjugate base to acid: pH = pK$_a$ + $\log_{10}(\frac{[\text{A}^-]}{[\text{HA}]})$.

26.

Which is correct for bisubstrate reactions?

(a) They are classified into sequential and double displacement reactions

(b) The most widely used rate expression for them is Michaelis- Menten kinetics

(c) Enzyme concentration is in excess of the substrate in the medium

(d) The rate is mainly limited by the substrate concentration

Correct Answer: (a) They are classified into sequential and double displacement reactions

Solution: Bisubstrate reactions are enzyme-catalyzed reactions involving two substrates and typically yielding two products (e.g., A + B $\rightleftharpoons$ P + Q). (a) "They are classified into sequential and double displacement reactions": TRUE.

- **Sequential Reactions:** All substrates must bind to the enzyme before any product is released. This can be ordered (substrates bind in a specific sequence) or random (substrates can bind in any order).
- **Double Displacement (Ping-Pong) Reactions:** One or more products are released before all substrates have bound. The enzyme is temporarily modified (e.g., by carrying a group from the first substrate to the second).

(b) "The most widely used rate expression for them is Michaelis-Menten kinetics": Michaelis-Menten kinetics was originally derived for single-substrate enzyme reactions. While the principles can be extended to bisubstrate reactions under certain simplifying assumptions (e.g., one substrate is saturating), the rate expressions for bisubstrate reactions are generally more complex (e.g., involving multiple K_m and V_{max} terms, or using Cleland notation for rate equations). So, this is generally FALSE as the "most widely used" for *bisubstrate* specifically. (c) "Enzyme concentration is in excess of the substrate in the medium": Enzyme kinetic studies, including Michaelis-Menten, are typically performed under conditions where substrate concentration [S] is much greater than enzyme concentration [E] ($[S] \gg [E]$), so that the formation of enzyme-substrate complex is dependent on [S]. This statement is FALSE. (d) "The rate is mainly limited by the substrate concentration": This is true at low substrate concentrations for Michaelis-Menten kinetics (first-order with respect to [S]). At high

substrate concentrations, the rate becomes limited by the enzyme concentration (zero-order with respect to [S]). For bisubstrate reactions, the rate depends on the concentrations of both substrates in a more complex way. This statement is too general and not always correct, especially not as a defining characteristic.
Therefore, the most accurate and defining correct statement for bisubstrate reactions among the options is (a).

$$\boxed{\text{They are classified into sequential and double displacement reactions}}$$

Quick Tip

Quick Tip:

- Bisubstrate reactions involve two substrates.
- **Sequential mechanism:** Both substrates bind before product release (can be ordered or random). Ternary complex (EAB) is formed.
- **Ping-Pong (Double Displacement) mechanism:** First substrate binds, product is released, enzyme is modified. Second substrate binds, second product is released, enzyme regenerated. No ternary complex.
- Michaelis-Menten equation is primarily for single-substrate reactions.

27.

Select the wrong option regarding enthalpy

(a) Enthalpy is the measure of total heat in a thermodynamic system where pressure is constant

(b) It is represented as $\Delta H = \Delta E + P\Delta V$

(c) It is a measure of disorder in a thermodynamic system

(d) It represents the heat constant of a system

Correct Answer: (c) It is a measure of disorder in a thermodynamic system

Solution: Enthalpy (H) is a thermodynamic property defined as $H = E + PV$, where E is internal energy, P is pressure, and V is volume. Let's analyze the options: (a) "Enthalpy is the measure of total heat in a thermodynamic system where pressure is constant": More precisely, the change in enthalpy (ΔH) of a system at constant pressure is equal to the heat absorbed or released by the system (q_p). So, $\Delta H = q_p$. While related to "total heat content" under constant pressure, this statement is largely considered TRUE in intent. (b) "It is represented as $\Delta H = \Delta E + P\Delta V$": From $H = E + PV$, if pressure P is constant, then $\Delta H = \Delta E + \Delta(PV) = \Delta E + P\Delta V + V\Delta P$. If P is constant, $\Delta P = 0$, so $\Delta H = \Delta E + P\Delta V$. This is TRUE for constant pressure processes. (Note: ΔE is often written as ΔU for internal energy). (c) "It is a measure of disorder in a thermodynamic system": This statement is FALSE. The measure of disorder or randomness in a thermodynamic system is **Entropy (S)**, not enthalpy. (d) "It represents the heat constant of a system": This phrasing is a bit vague. "Heat content" is a common informal term for enthalpy. If "heat constant" means heat content, then it aligns with the concept. Enthalpy is often referred to as the heat content at constant pressure. The statement that is definitively wrong is (c). Enthalpy is related to heat content, especially at constant pressure, while entropy is the measure of disorder.

$$\boxed{\text{It is a measure of disorder in a thermodynamic system}}$$

Quick Tip

Quick Tip:

- Enthalpy $H = E + PV$ (or $U + PV$).
- Change in enthalpy $\Delta H = q_p$ (heat exchanged at constant pressure).
- For processes at constant pressure, $\Delta H = \Delta E + P\Delta V$.
- Entropy (S) is the measure of disorder or randomness in a system.

28.

Mitochondria known as the "powerhouse" of the cell, generates ATP via oxidative phosphorylation complexes. Which among the following is known as complex I?

(a) Succinate dehydrogenase
(b) Ubiquinol-cytochrome c oxidoreductase
(c) Cytochrome c oxidase
(d) NADH: ubiquinone oxidoreductase

Correct Answer: (d) NADH: ubiquinone oxidoreductase

Solution: The electron transport chain (ETC) in mitochondria consists of a series of protein complexes (I, II, III, IV) and mobile electron carriers (Ubiquinone/Coenzyme Q, Cytochrome c) that transfer electrons from NADH and $FADH_2$ to oxygen, ultimately producing water and generating a proton gradient used by ATP synthase (Complex V) to produce ATP. The complexes are:

- **Complex I: NADH:ubiquinone oxidoreductase** (also known as NADH dehydrogenase complex). It accepts electrons from NADH and transfers them to ubiquinone (CoQ). It also pumps protons from the mitochondrial matrix to the intermembrane space.

- **Complex II: Succinate dehydrogenase** (or succinate-CoQ reductase). It accepts electrons from succinate (via $FADH_2$ which is part of the complex) and transfers them to ubiquinone. It does NOT pump protons. (Option a)

- **Complex III: Ubiquinol-cytochrome c oxidoreductase** (or cytochrome bc_1 complex). It accepts electrons from ubiquinol (reduced CoQ) and transfers them to cytochrome c. It pumps protons. (Option b)

- **Complex IV: Cytochrome c oxidase.** It accepts electrons from cytochrome c and transfers them to molecular oxygen (O_2), reducing it to water (H_2O). It pumps protons. (Option c)

- **Complex V: ATP synthase.** Uses the proton gradient generated by Complexes I, III, and IV to synthesize ATP from ADP and Pi.

Therefore, Complex I is NADH:ubiquinone oxidoreductase.

$$\boxed{\text{NADH: ubiquinone oxidoreductase}}$$

Quick Tip

Quick Tip:

- Mitochondrial Electron Transport Chain Complexes:
  - Complex I: NADH dehydrogenase (NADH:ubiquinone oxidoreductase)
  - Complex II: Succinate dehydrogenase
  - Complex III: Cytochrome bc_1 complex (Ubiquinol-cytochrome c oxidoreductase)
  - Complex IV: Cytochrome c oxidase
  - Complex V: ATP synthase
- Complexes I, III, and IV are proton pumps.

29.

Which of the following is not a transport protein?

(a) Sodium-potassium pump

(b) Mechano-Sensitive ion Channels

(c) The sodium-calcium exchanger

(d) Lactose permease

Correct Answer: (b) Mechano-Sensitive ion Channels (While they transport ions, their primary defining characteristic is gating by mechanical stimuli, not simply being a "transport protein" in the same category as pumps or carriers. All options are involved in transport, but the question asks what is "not a transport protein" perhaps implying a specific category or primary role.)

Solution: Transport proteins are proteins that facilitate the movement of substances (ions, small molecules, macromolecules) across biological membranes. Let's analyze the options: (a) **Sodium-potassium pump (Na^+/K^+-ATPase):** This is an active transport protein (an ion pump) that moves Na^+ ions out of the cell and K^+ ions into the cell against their concentration gradients, using ATP. It is a transport protein. (b) **Mechano-Sensitive ion Channels:** These are ion channels that open or close in response to mechanical stimuli (e.g., stretch, pressure, touch). When open, they allow the passage of ions across the membrane. Thus, they are involved in ion transport and are a type of transport protein (specifically, a channel protein). (c) **The sodium-calcium exchanger (NCX):** This is a transport protein that uses the electrochemical gradient of sodium ions (moving Na^+ into the cell) to drive the transport of calcium ions (Ca^{2+}) out of the cell (or vice-versa depending on conditions). It is an example of secondary active transport (an antiporter). It is a transport protein. (d) **Lactose permease:** This is a membrane transport protein (a symporter) found in bacteria like E. coli. It transports lactose across the cell membrane into the cell, along with a proton (H^+). It is a transport protein.

All the options listed are indeed types of transport proteins or are directly involved in transport across membranes. The question asks "Which of the following is **not** a transport protein?" This suggests there might be a subtlety in definition or one option is fundamentally different in classification. Mechano-sensitive ion channels are proteins that form channels for ion transport, gated by mechanical force. Pumps, exchangers, and permeases are also proteins facilitating transport. If the question is trying to distinguish between different *types* of transport mechanisms where one is not primarily "just a transporter" but a sensor-transducer that then transports: Ion channels are typically considered transport proteins.

Perhaps the question is flawed, as all listed are involved in transport. However, if "transport protein" is used in a more restrictive sense to mean carriers or pumps that bind and move specific solutes, then ion channels (which form pores) could be considered a slightly different category, though still facilitating transport. The provided checkmark is on (b) "Mechano-Sensitive ion Channels". One reason this might be considered "not a transport protein" in a very narrow sense is if the emphasis is on their gating mechanism (mechano-sensation) rather than just the transport function once gated. However, they fundamentally transport ions. This is a problematic question if all options are involved in transport. Let's assume the distinction is based on primary classification where the "mechano-sensitive" aspect is considered primary over the "ion channel/transport" aspect for the purpose of this question.

$\boxed{\text{Mechano-Sensitive ion Channels (this is debatable as they are ion transport channels)}}$

Quick Tip

Quick Tip:

- Transport proteins include:
  - **Pumps (ATPases):** Use ATP for active transport (e.g., Na^+/K^+ pump).
  - **Carriers/Transporters (Permeases, Exchangers):** Bind solute and undergo conformational changes (e.g., lactose permease, Na^+/Ca^{2+} exchanger). Can be uniport, symport, antiport; passive (facilitated diffusion) or active (secondary active transport).
  - **Channels:** Form pores for passage of ions or water (e.g., ion channels, aquaporins). Can be gated (voltage-gated, ligand-gated, mechano-sensitive).
- All listed options are involved in the transport of substances across membranes. The question might be distinguishing based on primary functional classification.

30.

Which of the following are positive regulators of cell cycle?

(a) Cyclin and cyclin dependent kinases

(b) Retinoblastoma protein

(c) P53

(d) P21

Correct Answer: (a) Cyclin and cyclin dependent kinases

Solution: The cell cycle is controlled by a complex network of regulatory proteins.

- **Positive Regulators:** These proteins promote the progression of the cell cycle.
  - **Cyclins and Cyclin-Dependent Kinases (CDKs) (Option a):** Cyclins are proteins whose concentrations fluctuate throughout the cell cycle. They bind to and activate CDKs. The cyclin-CDK complexes then phosphorylate target proteins, driving the cell cycle through its various phases (G1, S, G2, M). They are key positive regulators.
- **Negative Regulators (Tumor Suppressors/Cell Cycle Inhibitors):** These proteins halt or slow down cell cycle progression, often in response to DNA damage or unfavorable conditions.
  - **Retinoblastoma protein (Rb) (Option b):** Rb is a tumor suppressor protein. In its active (hypophosphorylated) state, it binds to E2F transcription factors, preventing them from activating genes required for S phase entry. Phosphorylation of Rb by cyclin-CDK complexes inactivates it, releasing E2F and allowing cell cycle progression. So, active Rb is a negative regulator.
  - **P53 (Option c):** P53 is a crucial tumor suppressor protein, often called the "guardian of the genome." It is activated in response to DNA damage or cellular stress. Activated p53 can halt the cell cycle (e.g., by inducing p21) to allow for DNA repair, or it can trigger apoptosis (programmed cell death) if the damage is too severe. It is a negative regulator.
  - **P21 (Option d):** P21 (also known as WAF1/CIP1) is a CDK inhibitor (CKI). Its expression is often induced by p53. P21 binds to and inhibits the activity of cyclin-CDK complexes, thereby arresting the cell cycle, typically at the G1/S checkpoint or G2/M checkpoint. It is a negative regulator.

Therefore, cyclins and cyclin-dependent kinases are the positive regulators among the given options.

Cyclin and cyclin dependent kinases

Quick Tip

Quick Tip:

- Positive cell cycle regulators promote progression (e.g., Cyclins, CDKs).
- Negative cell cycle regulators inhibit progression (e.g., Rb, p53, p21, p16).
- Many negative regulators are tumor suppressor proteins.

31.

Which among the following belongs to the class of second messengers?

(a) Hormones, neurotransmitters

(b) Pharmacological agonists

(c) cAMP, cGMP, DNA binding

(d) Ions, protein kinases

Correct Answer: (c) cAMP, cGMP, DNA binding (The part "DNA binding" is incorrect for a second messenger. However, cAMP and cGMP are key second messengers. This option is the best fit despite the error.)

Solution: Second messengers are small, non-protein, intracellular signaling molecules that are rapidly synthesized or released in response to an extracellular signal (the "first messenger," e.g., a hormone or neurotransmitter binding to a cell surface receptor). They relay the signal from the receptor to intracellular target proteins, amplifying the signal and triggering cellular responses. Common examples of second messengers include:

- Cyclic AMP (cAMP)
- Cyclic GMP (cGMP)

- Calcium ions (Ca^{2+})
- Inositol trisphosphate (IP_3)
- Diacylglycerol (DAG)
- Nitric Oxide (NO) (though it can also act as a first messenger in some contexts)

Let's analyze the options: (a) Hormones, neurotransmitters: These are typically first messengers (extracellular signals). (b) Pharmacological agonists: These are drugs that bind to receptors and activate them, mimicking the effect of natural first messengers. Not second messengers themselves. (c) cAMP, cGMP, DNA binding:

- cAMP (cyclic Adenosine Monophosphate) is a classic second messenger.
- cGMP (cyclic Guanosine Monophosphate) is also a well-known second messenger.
- "DNA binding" is a process or property of certain proteins (e.g., transcription factors), not a second messenger molecule.

Despite "DNA binding" being incorrectly included, cAMP and cGMP are definitely second messengers. (d) Ions, protein kinases:

- Certain ions (like Ca^{2+}) act as second messengers. However, "ions" in general is too broad.
- Protein kinases are enzymes that phosphorylate other proteins. They are often components of signaling pathways activated by second messengers, but they are not second messengers themselves.

Comparing the options, option (c) contains two definitive examples of second messengers (cAMP, cGMP), even though it also includes an incorrect item ("DNA binding"). Given the choices, this is the best fit.

$\boxed{\text{cAMP, cGMP, DNA binding (recognizing cAMP cGMP are key second messengers)}}$

Quick Tip

Quick Tip:

- First messengers: Extracellular signals (e.g., hormones, neurotransmitters).
- Second messengers: Intracellular signaling molecules that relay and amplify the signal from a receptor.
- Key second messengers: cAMP, cGMP, Ca^{2+}, IP_3, DAG.
- Protein kinases are enzymes involved in signal transduction, often activated by second messengers, but are not second messengers themselves.

32.

What are Alleles?

(a) two genes that occupy the different position on non-homologous chromosomes and that cover the same trait
(b) two genes that occupy the same position on homologous chromosomes and that cover the same trait
(c) two genes that occupy the same position on non-homologous chromosomes and that cover different trait
(d) two genes that occupy the same position on homologous chromosomes and that cover different trait

Correct Answer: (b) two genes that occupy the same position on homologous chromosomes and that cover the same trait

Solution: Alleles are alternative forms of a gene that arise by mutation and are found at the same place (locus) on homologous chromosomes. They control the same trait but may result in different expressions of that trait. Let's analyze the options: (a) "...different position on non-homologous chromosomes...": Incorrect. Alleles are at the same locus on homologous chromosomes. (b) "...same position (locus) on homologous chromosomes and that cover the same trait": Correct. This accurately describes

alleles. For example, the gene for flower color in peas might have an allele for purple flowers and an allele for white flowers, both located at the flower color locus on homologous chromosomes. (c) "...same position on non-homologous chromosomes...different trait": Incorrect on both counts regarding chromosome type and trait. (d) "...same position on homologous chromosomes...different trait": Incorrect. Alleles for a specific gene control the same trait (e.g., flower color), though they may lead to different phenotypes (e.g., purple vs. white).
Therefore, option (b) is the correct definition of alleles.

$\boxed{\text{two genes that occupy the same position on homologous chromosomes and that cover the same t}}$

Quick Tip

Quick Tip:

- **Gene:** A segment of DNA that codes for a functional product (e.g., a protein).
- **Locus:** The specific physical location of a gene on a chromosome.
- **Homologous Chromosomes:** Pairs of chromosomes (one from each parent) that have the same genes in the same order, but may have different alleles for those genes.
- **Alleles:** Different versions of the same gene found at the same locus on homologous chromosomes. They code for the same trait (e.g., eye color) but can produce different phenotypes (e.g., blue eyes, brown eyes).

33.

In Mendel's dihybrid cross study mating that involve parents that differ in two genes (two independent traits) the F2 generation phenotype ratio would be

(a) 1:2:1

(b) 9:3:1:3

(c) 9:3:3:1

(d) 9:1:3:3

Correct Answer: (c) 9:3:3:1

Solution: A dihybrid cross involves parents that differ in two traits, controlled by two different genes that assort independently (Mendel's Law of Independent Assortment). Let the two genes be A/a and B/b, with A and B being dominant alleles. If the parental cross is, for example, AABB (dominant for both traits) × aabb (recessive for both traits):

- **P generation:** AABB × aabb
- **Gametes from P:** AB from first parent, ab from second parent.
- **F_1 generation:** All offspring are AaBb (dihybrid, heterozygous for both genes). They will all express the dominant phenotype for both traits.

Now, consider the F_2 generation obtained by selfing or intercrossing the F_1 generation: AaBb × AaBb. The gametes produced by an AaBb individual are AB, Ab, aB, ab (each with probability 1/4, due to independent assortment). Using a Punnett square (4x4 grid) for the F_2 generation, we get 16 possible genotypic combinations. These combinations result in four distinct phenotypes in the following ratio, assuming complete dominance for both genes:

- **9/16** will have the dominant phenotype for both traits (e.g., A_B_: AABB, AABb, AaBB, AaBb)
- **3/16** will have the dominant phenotype for the first trait and recessive for the second (e.g., A_bb: AAbb, Aabb)
- **3/16** will have the recessive phenotype for the first trait and dominant for the second (e.g., aaB_: aaBB, aaBb)
- **1/16** will have the recessive phenotype for both traits (e.g., aabb)

Thus, the classic F_2 phenotypic ratio for a dihybrid cross with independent assortment and complete dominance is **9:3:3:1**. Options (b) and (d) have typographical errors in the ratio order. Option (c) correctly states 9:3:3:1.

$$\boxed{9:3:3:1}$$

Quick Tip

Quick Tip:

- Dihybrid cross: Involves two different genes controlling two different traits.
- Law of Independent Assortment: Alleles of different genes assort independently during gamete formation (if genes are on different chromosomes or far apart on the same chromosome).
- F_2 phenotypic ratio for a dihybrid cross (with complete dominance and independent assortment): 9 (Dominant-Dominant) : 3 (Dominant-Recessive) : 3 (Recessive-Dominant) : 1 (Recessive-Recessive).

34.

Polygenic Trait means

(a) Several genes influence different traits; genes for a polygenic trait may be scattered along the same chromosome

(b) Several genes influence a trait; genes for a polygenic trait are not scattered along the same chromosome or different chromosomes

(c) Several genes influence different traits; genes for a polygenic trait are not scattered along the same chromosome or on different chromosomes

(d) Several genes influence a trait; genes for a polygenic trait may be scattered along the same chromosome or located on different chromosomes

Correct Answer: (d) Several genes influence a trait; genes for a polygenic trait may be scattered along the same chromosome or located on different chromosomes

Solution: A **polygenic trait** (or quantitative trait) is a trait whose phenotype is influenced by **multiple genes** (polygenes), often in an additive manner. Each gene may contribute a small effect to the overall phenotype. These traits typically show continuous variation (e.g., height, skin color, weight in humans). The genes involved in a polygenic trait:

- Can be located on the **same chromosome** (they might be linked or assort independently if far apart).
- Can be located on **different chromosomes** (they will assort independently).

Let's analyze the options: (a) "Several genes influence *different* traits...": Incorrect. Polygenic inheritance refers to multiple genes influencing a *single* trait. Pleiotropy is when one gene influences multiple traits. (b) "Several genes influence a trait; genes for a polygenic trait are *not scattered* along the same chromosome or different chromosomes": The "not scattered" part is restrictive and likely incorrect. The genes can be scattered. (c) "Several genes influence *different* traits...": Incorrect, as in (a). (d) "Several genes influence a trait; genes for a polygenic trait may be scattered along the same chromosome or located on different chromosomes": Correct. This accurately describes that multiple genes contribute to a single trait, and these genes can be located at various positions in the genome.
Therefore, option (d) is the best description.

$$\boxed{\text{Several genes influence a trait; genes for a polygenic trait may be scattered along the same chromosome or located on different chromosomes}}$$

Quick Tip

Quick Tip:

- **Polygenic Inheritance:** A single phenotypic trait is controlled by the additive effects of two or more genes.
- Examples: Human height, skin color, intelligence, crop yield.
- These traits often exhibit continuous variation.
- The contributing genes (polygenes) can be on the same or different chromosomes.
- Contrast with **Pleiotropy**, where one gene influences multiple traits.

35.

Frequency of crossing-over between linked genes is

(a) Inversely proportional to the distance between them

(b) Proportional to the distance between them

(c) Inversely proportional to the square of the distance between them

(d) Proportional to the square of the distance between them

Correct Answer: (b) Proportional to the distance between them

Solution: Crossing-over (recombination) is the exchange of genetic material between homologous chromosomes during meiosis. Genes that are located on the same chromosome are said to be linked. The frequency of crossing-over between two linked genes is a measure of the genetic distance between them.

- Genes that are **farther apart** on a chromosome are more likely to have a crossover event occur between them.
- Genes that are **very close together** are less likely to be separated by a crossover.

Therefore, the frequency of crossing-over (recombination frequency) between linked genes is generally **proportional to the physical distance** separating them on the chromosome (at least for relatively short distances where multiple crossovers are rare or can be accounted for). This principle is the basis for constructing genetic maps, where 1 map unit (or 1 centimorgan, cM) corresponds to a 1So, as distance increases, the frequency of crossing-over increases.

$$\boxed{\text{Proportional to the distance between them}}$$

Quick Tip

Quick Tip:

- Linked genes are on the same chromosome.
- Crossing-over during meiosis can separate linked genes.
- The probability (frequency) of a crossover event occurring between two linked genes increases with the physical distance between them on the chromosome.
- Recombination frequency is used to estimate genetic map distances.

36.

Epistasis refers to

(a) No variation resulting from the interaction of alleles at different loci

(b) Variation resulting from the interaction of alleles at same loci

(c) No variation resulting from the interaction of alleles at different chromosomes

(d) Variation resulting from the interaction of alleles at different loci

Correct Answer: (d) Variation resulting from the interaction of alleles at different loci

Solution: Epistasis is a form of gene interaction where one gene (the epistatic gene) masks or modifies the phenotypic expression of another gene (the hypostatic gene) located at a different locus (i.e., they are non-allelic genes). This interaction between genes at different loci leads to variations in phenotypes that may not be predictable from considering each gene independently (e.g., modified Mendelian ratios like 9:3:4, 9:7, 12:3:1, etc.). Let's analyze the options: (a) "No variation resulting from the interaction of alleles at different loci": Incorrect. Epistasis *does* involve interaction and often leads to phenotypic variation or modified ratios. (b) "Variation resulting from the interaction of alleles at same loci": This describes dominance relationships (complete dominance, incomplete dominance, codominance) between alleles of the *same* gene, not epistasis. (c) "No variation resulting from the interaction of alleles at different chromosomes": Incorrect (similar to a). Also, the genes involved in epistasis can be on the same chromosome (linked) or on different chromosomes. The key is "different loci." (d) "Variation resulting from the interaction of alleles at different loci": Correct. Epistasis is an interaction between non-allelic genes (genes at different loci) that affects the phenotype, often leading to specific phenotypic ratios.

Therefore, epistasis refers to the interaction of alleles at different loci affecting phenotypic expression.

$$\boxed{\text{Variation resulting from the interaction of alleles at different loci}}$$

Quick Tip

Quick Tip:

- **Epistasis:** A gene at one locus alters the phenotypic expression of a gene at a second locus.
- It's an interaction between non-allelic genes.
- This can lead to modified Mendelian dihybrid ratios (e.g., 9:3:4, 9:7, 12:3:1 instead of 9:3:3:1).
- Example: Coat color in Labrador retrievers, comb shape in chickens.

37.

What is transition and transversion mutations respectively means?

(a) Purine is replaced by pyrimidine in transition and purine is replaced by purine in transversion

(b) Purine is replaced by purine in transition and purine is replaced by pyrimidine in transversion

(c) Purine is replaced by purine in transition and transversion

(d) Pyrimidine is replaced by pyrimidine in transition and in transversion

Correct Answer: (b) Purine is replaced by purine in transition and purine is replaced by pyrimidine in transversion (More completely: Transition = purine to purine OR pyrimidine to pyrimidine. Transversion = purine to pyrimidine OR pyrimidine to purine).

Solution: Point mutations are changes in a single nucleotide base in DNA. They are classified based on the type of base substitution:

- **Transition:** A type of point mutation where a purine nucleotide is replaced by another purine nucleotide (A ↔ G), OR a pyrimidine nucleotide is replaced by another pyrimidine nucleotide (C ↔ T in DNA, or C ↔ U in RNA). The type of base (purine or pyrimidine) remains the same.

- **Transversion:** A type of point mutation where a purine nucleotide is replaced by a pyrimidine nucleotide, OR a pyrimidine nucleotide is replaced by a purine nucleotide. The type of base changes. (Purine ↔ Pyrimidine; e.g., A ↔ C, A ↔ T, G ↔ C, G ↔ T).

Purines are Adenine (A) and Guanine (G). Pyrimidines are Cytosine (C) and Thymine (T) (Uracil (U) in RNA).
Let's analyze the options (interpreting "X is replaced by Y in transition" as one example of transition): (a) "Purine is replaced by pyrimidine in transition..." - Incorrect. This is transversion. "...and purine is replaced by purine in transversion" - Incorrect. This is transition. (b) "Purine is replaced by purine in transition..." - Correct (this is one type of transition, A↔G). "...and purine is replaced by pyrimidine in transversion" - Correct (this is one type of transversion, e.g., A→C or A→T). This

option captures one example of each correctly. (c) "Purine is replaced by purine in transition and transversion": Incorrect for transversion. (d) "Pyrimidine is replaced by pyrimidine in transition and in transversion": Incorrect for transversion. (Pyrimidine replaced by pyrimidine is a transition).
Option (b) provides correct examples for each: Transition: Purine ↔ Purine (e.g., A to G) OR Pyrimidine ↔ Pyrimidine (e.g., C to T). Option says "Purine is replaced by purine". Transversion: Purine ↔ Pyrimidine (e.g., A to C). Option says "purine is replaced by pyrimidine". This option best describes the two types based on the examples given.

$\boxed{\text{Purine is replaced by purine in transition and purine is replaced by pyrimidine in transversion}}$

Quick Tip

Quick Tip:

- **Transition:** Purine ↔ Purine (A ↔ G); Pyrimidine ↔ Pyrimidine (C ↔ T). (Same type of base).
- **Transversion:** Purine ↔ Pyrimidine (A/G ↔ C/T). (Different type of base).
- Remember: Pu**R**ines are **A**, **G** (Pure As Gold). Pyrimidines are **C**, **T**, **U** (CUT the Py).

38.

In structural chromosome mutations pericentric inversion mutation means

(a) A portion in the chromosome is reversed and gets inserted back into the other arm of the same chromosome

(b) Some part of the chromosome is deleted and new is added

(c) A portion in the chromosome is reversed and gets inserted back into the same arm of the chromosome

(d) A portion in the chromosome is reversed and gets inserted back into the other chromosome

Correct Answer: (a) A portion in the chromosome is reversed and gets inserted back into the other arm of the same chromosome (This implies the inversion includes the centromere, thus affecting both arms if the break points are on different arms relative to the centromere, or changing arm lengths if one break point is in one arm and other in other arm.)

Solution: Chromosomal inversions are structural mutations where a segment of a chromosome breaks off, rotates 180 degrees, and then reattaches to the same chromosome. There are two main types of inversions based on whether the inverted segment includes the centromere: 1. **Paracentric Inversion:** The inverted segment does **not** include the centromere. Both breaks occur in the same arm of the chromosome. 2. **Pericentric Inversion:** The inverted segment **does** include the centromere. The breaks occur in different arms of the chromosome (one in the short arm 'p', one in the long arm 'q'). A pericentric inversion can change the relative lengths of the chromosome arms and thus potentially alter the chromosome's morphology (e.g., from metacentric to submetacentric).
Let's analyze the options: (a) "A portion in the chromosome is reversed and gets inserted back into the other arm of the same chromosome": This phrasing is a bit imprecise. For a pericentric inversion, the segment that includes the centromere is reversed. If the breaks are on opposite sides of the centromere, then parts of "other" arms are involved in the inverted segment. This is the closest description to a pericentric inversion if "inserted back into the other arm" means the inverted segment now spans parts of what were originally different configurations of the arms relative to the centromere, or that arm lengths change. More accurately, the inverted segment *includes* the centromere. (b) "Some part of the chromosome is deleted and new is added": This describes deletion and insertion, not inversion. (c) "A portion in the chromosome is reversed and gets inserted back into the same arm of the chromosome": This describes a paracentric inversion (centromere not included). (d) "A portion in the chromosome is reversed and gets inserted back into the other chromosome": This

describes a translocation, not an inversion on the same chromosome.
Given the options, option (a) is the most plausible description intended for a pericentric inversion, focusing on the involvement of both arms (implicitly because the centromere is included in the inversion). A key feature of pericentric inversion is that the inverted segment contains the centromere. If the break points are in different arms, then the orientation of the segment containing the centromere is flipped, affecting how the arms are now constituted. The phrasing could be better, e.g., "An inversion that includes the centromere." But (a) implies the centromere is involved.

$$\boxed{\text{A portion in the chromosome is reversed and gets inserted back into the other arm of the same chromosome (implying the centromere is within the inverted segment)}}$$

Quick Tip

Quick Tip:

- **Inversion:** A chromosomal segment is detached, rotated 180 degrees, and reinserted.
- **Paracentric Inversion:** Does NOT include the centromere. Breaks are in one arm.
- **Pericentric Inversion:** DOES include the centromere. Breaks are in different arms (one on each side of the centromere). Can change arm length ratio.

39.

UV light effect the DNA by causing

(a) G-G dimerization

(b) G-C dimerization

(c) T-T dimerization

(d) A-T dimerization

Correct Answer: (c) T-T dimerization

Solution: Ultraviolet (UV) radiation, particularly UV-B, is a known mutagen that can cause specific types of DNA damage. The most common type of UV-induced DNA damage is the formation of **pyrimidine dimers**. These dimers form between adjacent pyrimidine bases (Thymine - T, or Cytosine - C) on the same DNA strand. The most frequent pyrimidine dimers are:

- **Thymine dimers (T-T dimers or T<>T):** Two adjacent thymine bases become covalently linked. This is the most common type.
- Cytosine dimers (C-C dimers) can also form.
- Thymine-cytosine dimers (T-C or C-T dimers) can also form.

These dimers distort the DNA helix and can block DNA replication and transcription if not repaired. Purine-purine (e.g., G-G, A-A) or purine-pyrimidine (e.g., A-T, G-C) dimerization is not a typical lesion caused by UV light in this manner. Therefore, UV light primarily causes pyrimidine dimerization, with T-T dimerization being very common. Option (c) "T-T dimerization" is the correct answer.

$$\boxed{\text{T-T dimerization}}$$

Quick Tip

Quick Tip:

- UV radiation is a common environmental mutagen.
- It primarily causes the formation of covalent bonds between adjacent pyrimidine bases (C or T) on the same DNA strand, forming pyrimidine dimers.
- Thymine dimers (T-T) are the most prevalent type of UV-induced DNA damage.
- These dimers can interfere with DNA replication and transcription. Cells have repair mechanisms (e.g., photoreactivation, nucleotide excision repair) to fix them.

40.

Smaller subunit of ribosomes binds to what for initiation of translation

(a) DNA

(b) mRNA

(c) tRNA

(d) microsatellite RNA

Correct Answer: (b) mRNA

Solution: Initiation of translation (protein synthesis) involves the assembly of the ribosomal subunits, mRNA, and the initiator tRNA at the start codon of the mRNA. The process typically involves these key steps (simplified): 1. The **smaller ribosomal subunit** binds to the **mRNA** molecule, usually at or near the 5' cap (in eukaryotes) or a specific ribosome-binding site (Shine-Dalgarno sequence in prokaryotes) upstream of the start codon (AUG). 2. The initiator tRNA (carrying methionine in eukaryotes, or formylmethionine in prokaryotes) binds to the start codon on the mRNA, which is positioned in the P-site of the small ribosomal subunit complex. 3. The **larger ribosomal subunit** then joins the complex, forming the functional ribosome. Therefore, the smaller subunit of the ribosome binds to mRNA for the initiation of translation. (a) DNA: DNA is transcribed into mRNA; ribosomes translate mRNA, not DNA directly. (c) tRNA: The initiator tRNA binds to the mRNA (at the start codon) within the complex formed with the small subunit, but the small subunit primarily binds the mRNA first to locate the start site. (d) microsatellite RNA: Microsatellites are repetitive DNA sequences; "microsatellite RNA" is not a standard term for a molecule that the ribosome binds to for initiation. MicroRNAs (miRNAs) are regulatory RNAs, not directly involved in ribosomal binding for initiation in this context.

$$\boxed{\text{mRNA}}$$

Quick Tip

Quick Tip:

- Translation Initiation Steps: 1. Small ribosomal subunit binds to mRNA. 2. Initiator tRNA (carrying Met or fMet) binds to the start codon (AUG) on mRNA. 3. Large ribosomal subunit joins the complex.
- mRNA (messenger RNA) carries the genetic code from DNA to the ribosome.

41.

Promotor and operator are cis sites on DNA for binding of (Typo: "Promotor" should be "Promoter")

(a) RNA polymerase binds to promotor and repressor binds to operator

(b) Repressor binds to promotor and RNA polymerase binds to operator

(c) DNA polymerase binds to promotor and repressor binds to operator

(d) DNA polymerase binds to promotor and RNA polymerase binds to operator

Correct Answer: (a) RNA polymerase binds to promotor and repressor binds to operator

Solution: In gene regulation, particularly in prokaryotic operons (like the lac operon or trp operon):

- **Promoter:** A specific DNA sequence located upstream of a gene or operon where **RNA polymerase** binds to initiate transcription. It is a cis-acting regulatory site.
- **Operator:** A specific DNA sequence, usually located near or overlapping the promoter, where a **repressor protein** can bind. Binding of the repressor to the operator typically blocks RNA polymerase from transcribing the downstream genes, thus inhibiting gene expression. It is also a cis-acting regulatory site.

Let's analyze the options: (a) "RNA polymerase binds to promotor and repressor binds to operator": Correct. This describes the standard roles. (b) "Repressor binds to promotor and RNA polymerase binds to operator": Incorrect. Roles are swapped. (c) "DNA polymerase binds to promotor...": Incorrect. DNA polymerase is involved in DNA replication, not transcription initiation at promoters. (d) "DNA polymerase binds to promotor...": Incorrect, as in (c).

Therefore, RNA polymerase binds to the promoter, and a repressor protein (if present and active) binds to the operator.

$$\boxed{\text{RNA polymerase binds to promotor and repressor binds to operator}}$$

Quick Tip

Quick Tip:

- **Cis-acting elements:** DNA sequences (like promoter, operator, enhancers) that regulate genes on the same DNA molecule.
- **Trans-acting factors:** Proteins (like RNA polymerase, repressors, activators) that bind to cis-acting elements to regulate gene expression. They are encoded by genes that can be located elsewhere.
- Promoter: Binding site for RNA polymerase (initiates transcription).
- Operator: Binding site for repressor protein (blocks transcription).

42.

Post transcriptional modification includes

(a) RNA editing

(b) Phosphorylation, Acetylation

(c) 5' capping, 3' poly adenylating and intron removal by splicing

(d) Ubiquitination

Correct Answer: (c) 5' capping, 3' poly adenylating and intron removal by splicing

Solution: Post-transcriptional modifications are changes made to the primary RNA transcript (pre-mRNA in eukaryotes) before it is translated into protein. These modifications are crucial for the stability, transport, and proper translation of mRNA in eukaryotes. Key post-transcriptional modifications in eukaryotes include: 1. **5' Capping:** Addition of a modified guanine nucleotide (7-methylguanosine cap) to the 5' end of the pre-mRNA. This protects the mRNA from degradation, aids in its export from the nucleus, and is important for ribosome binding during translation initiation. 2. **3' Polyadenylation (Poly(A) tail addition):** Addition of a long string of adenine nucleotides (poly(A) tail) to the 3' end of the pre-mRNA. This increases mRNA stability, aids in its export from the nucleus, and plays a role in translation. 3. **Splicing (Intron Removal):** Removal of non-coding intervening sequences (introns) and joining of the coding sequences (exons) to form a mature, continuous coding mRNA.

Let's analyze the options: (a) RNA editing: This is a type of post-transcriptional modification where the nucleotide sequence of an RNA molecule is altered (e.g., insertion, deletion, or substitution of bases). It is a valid modification, but option (c) lists more common and defining ones. (b) Phosphorylation, Acetylation: These are common post-translational modifications of proteins, not usually post-transcriptional modifications of RNA (though RNA can be modified in other ways, these are primarily protein mods). (c) "5' capping, 3' poly adenylating and intron removal by splicing": This lists the three major and most characteristic post-transcriptional modifications of eukaryotic pre-mRNA. (d) Ubiquitination: This is a post-translational modification of proteins, involving the attachment of ubiquitin, often targeting the protein for degradation.

Option (c) provides the most comprehensive and common set of post-transcriptional modifications.

$$\boxed{\text{5' capping, 3' poly adenylating and intron removal by splicing}}$$

Quick Tip

Quick Tip:

- Post-transcriptional modifications occur primarily in eukaryotes to convert pre-mRNA into mature mRNA.
- Major modifications:
  - 5' cap (7-methylguanosine)
  - 3' poly(A) tail
  - Splicing (removal of introns, joining of exons)
- RNA editing is another, less universal, type of modification.

43.

Function of signal sequences in translation

(a) Protein modifications

(b) Protein targeting to other organelles for further protein synthesis

(c) Protein degradation

(d) Protein transport to target specific sites for function

Correct Answer: (d) Protein transport to target specific sites for function (Option (b) is also related but (d) is more general and accurate).

Solution: A **signal sequence** (also known as a signal peptide, targeting sequence, or localization signal) is a short stretch of amino acids (typically 15-60 amino acids long) present at the N-terminus (or sometimes C-terminus or internally) of a newly synthesized polypeptide chain. The primary function of a signal sequence is to **direct the protein to its correct location or destination** within the cell or for secretion out of the cell. It acts as an "address label." Examples:

- Signal sequences can target proteins to the endoplasmic reticulum (for entry into the secretory pathway), mitochondria, chloroplasts, nucleus, peroxisomes, etc.

- Once the protein reaches its destination, the signal sequence is often cleaved off by a signal peptidase.

Let's analyze the options: (a) Protein modifications: While proteins undergo modifications, the signal sequence itself is for targeting, not the modification process itself (though it might be removed as a modification). (b) "Protein targeting to other organelles for further protein synthesis": Proteins are synthesized on ribosomes. Targeting to organelles is correct, but "for further protein synthesis" is not the general purpose; it's for the protein's function or further processing/folding in that organelle. (c) Protein degradation: Signal sequences are not primarily for degradation; specific signals (like ubiquitination tags) target proteins for degradation. (d) "Protein transport to target specific sites for function": This accurately describes the main role of signal sequences – directing proteins to their proper cellular or extracellular locations where they will perform their functions.
Option (d) is the most comprehensive and correct statement about the function of signal sequences.

$$\boxed{\text{Protein transport to target specific sites for function}}$$

Quick Tip

Quick Tip:

- Signal sequences are short amino acid stretches that act as "zip codes" or "address labels" for proteins.
- They direct newly synthesized proteins to their correct destinations (e.g., specific organelles, secretion pathway).
- This process is called protein targeting or protein sorting.

44.

Mismatch repair mechanism in DNA deals with

(a) Deamination

(b) Adducts and cross-links
(c) Double stranded breaks
(d) Replication errors

Correct Answer: (d) Replication errors

Solution: DNA repair mechanisms are crucial for maintaining the integrity of the genome. Different types of DNA damage are repaired by specific pathways.

Mismatch Repair (MMR): This system corrects errors that occur during DNA replication when an incorrect nucleotide is inserted opposite a template nucleotide, resulting in a mismatched base pair (e.g., A paired with C instead of T, or G paired with T instead of C). It also corrects small insertions or deletions (indels) that can occur in repetitive DNA sequences during replication. The MMR system recognizes the mismatch, identifies the newly synthesized strand (which contains the error), excises the incorrect segment from the new strand, and then DNA polymerase and ligase fill in the gap with the correct nucleotides.

Let's analyze the options: (a) Deamination (e.g., C to U): Often repaired by Base Excision Repair (BER). (b) Adducts and cross-links (bulky lesions): Often repaired by Nucleotide Excision Repair (NER) or other specialized pathways. (c) Double-stranded breaks: Repaired by Homologous Recombination (HR) or Non-Homologous End Joining (NHEJ). (d) Replication errors: This is precisely what mismatch repair deals with – errors made by DNA polymerase during replication that were not corrected by its proofreading activity.

Therefore, the mismatch repair mechanism deals with replication errors.

$$\boxed{\text{Replication errors}}$$

Quick Tip

Quick Tip:

- **Mismatch Repair (MMR):** Corrects base-base mismatches and small insertions/deletions that arise during DNA replication and escape the proofreading activity of DNA polymerase.
- **Base Excision Repair (BER):** Repairs damage to single bases (e.g., deamination, oxidation, alkylation).
- **Nucleotide Excision Repair (NER):** Repairs bulky lesions that distort the DNA helix (e.g., pyrimidine dimers caused by UV, large chemical adducts).
- **Double-Strand Break Repair (DSBR):** Homologous Recombination (HR) and Non-Homologous End Joining (NHEJ).

45.

Hardy-Weinberg Law / equilibrium model in population genetics means

(a) Allele and genotype frequencies in a population do not remain constant in the absence of other evolutionary influences

(b) Allele and genotype frequencies in a population remain constant in the absence of other evolutionary influences

(c) Allele and genotype frequencies in a population remain constant in the presence of other evolutionary influences

(d) Allele and genotype frequencies in a population defer in the absence of other evolutionary influences

Correct Answer: (b) Allele and genotype frequencies in a population remain constant in the absence of other evolutionary influences

Solution: The Hardy-Weinberg Law (or Hardy-Weinberg equilibrium, HWE) is a fundamental principle in population genetics. It states that in a large, randomly mating population, the allele frequencies and genotype frequencies will remain constant from generation to generation, provided that other evolutionary influences are absent. These "other evolutionary influences" (or conditions for HWE to hold) include:

- No mutation
- No gene flow (migration)
- Random mating
- No natural selection
- Very large population size (no genetic drift)

If these conditions are met, the population is said to be in Hardy-Weinberg equilibrium. Let's analyze the options: (a) "...do not remain constant in the absence of other evolutionary influences": Incorrect. HWE states they *do* remain constant. (b) "Allele and genotype frequencies in a population remain constant in the absence of other evolutionary influences": Correct. This is the essence of the Hardy-Weinberg principle. (c) "...remain constant in the *presence* of other evolutionary influences": Incorrect. Evolutionary influences (like selection, mutation, drift, migration) are what cause allele and genotype frequencies to change. (d) "...frequencies in a population *defer* (likely typo for "differ" or "deviate") in the absence of other evolutionary influences": Incorrect. They remain constant.
Therefore, option (b) accurately describes the Hardy-Weinberg Law.

$\boxed{\text{Allele and genotype frequencies in a population remain constant in the absence of other evolutio}}$

Quick Tip

Quick Tip:

- Hardy-Weinberg Equilibrium (HWE) describes a hypothetical, non-evolving population.
- Conditions for HWE: No mutation, no gene flow, random mating, no natural selection, large population size.
- If HWE holds, allele frequencies (p, q) and genotype frequencies (p^2, 2pq, q^2 for two alleles) remain constant across generations.
- Deviations from HWE indicate that evolution is occurring.

46.

Which of the following is a primary metabolite?

(a) Antibiotics

(b) Ethanol

(c) Penicillin

(d) Taxol

Correct Answer: (b) Ethanol (produced during primary metabolism of glycolysis/fermentation)

Solution: Metabolites are intermediates and products of metabolism. They are broadly classified into primary and secondary metabolites.

- **Primary Metabolites:** These are compounds that are directly involved in the normal growth, development, and reproduction of an organism. They are essential for the life of the cell and are typically produced during the exponential growth phase (trophophase). Examples include amino acids, nucleotides, vitamins, organic acids (like citric acid, lactic acid), alcohols (like ethanol from fermentation), and components of central metabolic pathways (like glucose, pyruvate).

- **Secondary Metabolites:** These are organic compounds that are not directly involved in the normal growth, development, or reproduction of the organism. They often have ecological functions (e.g., defense, signaling) or are produced during the stationary phase (idiophase) or under stress conditions. Examples include antibiotics, toxins, pigments, alkaloids, and some pharmaceuticals.

Let's analyze the options: (a) Antibiotics: These are classic examples of secondary metabolites, produced by microorganisms often to inhibit the growth of other competing microbes. (b) **Ethanol:** Ethanol is a product of alcoholic fermentation, which is a primary metabolic pathway for energy generation (from glycolysis) in some yeasts and bacteria under anaerobic conditions. It's directly linked to the central energy metabolism. (c) Penicillin: An antibiotic produced by *Penicillium* fungi. It is a secondary metabolite. (d) Taxol (Paclitaxel): A complex diterpene produced by yew trees, used as an anticancer drug. It is a secondary metabolite.
Therefore, ethanol is a primary metabolite among the given options, as it is a direct product of a primary energy-yielding pathway (fermentation linked to glycolysis).

$$\boxed{\text{Ethanol}}$$

Quick Tip

Quick Tip:

- **Primary metabolites:** Essential for growth, development, reproduction. Produced during active growth. Examples: amino acids, alcohols, organic acids, vitamins, nucleotides.
- **Secondary metabolites:** Not essential for growth. Often have ecological roles or specialized functions. Examples: antibiotics, pigments, toxins, alkaloids.

47.

Antibiotics are substances produced by microorganisms to

(a) Inhibit the growth of other microorganisms

(b) Enhance the growth of other microorganisms

(c) Act as nutrients for other microorganisms

(d) Regulate microbial metabolism

Correct Answer: (a) Inhibit the growth of other microorganisms

Solution: Antibiotics are a class of antimicrobial substances, typically produced by microorganisms (like bacteria and fungi), that in low concentrations can inhibit the growth of or kill other microorganisms. Their primary ecological role is thought to be in microbial warfare or competition, allowing the producing organism to gain an advantage over other microbes in its environment. Let's analyze the options: (a) "Inhibit the growth of other microorganisms": This is the defining characteristic and primary function of antibiotics. They target essential processes in susceptible microbes, such as cell wall synthesis, protein synthesis, DNA replication, or metabolic pathways. (b) "Enhance the growth of other microorganisms": This is the opposite of what antibiotics do. (c) "Act as nutrients for other microorganisms": While some microbes can degrade antibiotics, antibiotics themselves are not primarily produced as general nutrients. (d) "Regulate microbial metabolism": While some microbial products might regulate metabolism, antibiotics are specifically known for their inhibitory or cidal effects on other microbes.
Therefore, antibiotics are substances produced by microorganisms primarily to inhibit the growth of (or kill) other microorganisms.

$$\boxed{\text{Inhibit the growth of other microorganisms}}$$

Quick Tip

Quick Tip:

- Antibiotics are antimicrobial agents produced by microorganisms.
- They are effective against other microorganisms (usually bacteria, sometimes fungi).
- Their primary action is to kill (bactericidal/fungicidal) or inhibit the growth (bacteriostatic/fungistatic) of susceptible microbes.
- Used extensively in medicine to treat infections.

48.

Which of the following is an example of a microbial pigment used in industrial applications?

(a) Chlorophyll
(b) Melanin
(c) Carotene
(d) Hemoglobin

Correct Answer: (c) Carotene (Beta-carotene is produced by some microbes and used as a food colorant and vitamin A precursor).

Solution: Microbial pigments are colored compounds produced by microorganisms (bacteria, fungi, algae, yeasts). Some of these have industrial applications, for example, as food colorants, in cosmetics, or for pharmaceutical purposes. Let's analyze the options: (a) Chlorophyll: The primary photosynthetic pigment in plants, algae, and cyanobacteria. While produced by microbes (algae, cyanobacteria), its large-scale industrial extraction is often from plants. It is used as a food colorant (E140). This is a plausible microbial pigment with industrial use. (b) Melanin: A pigment found in animals (including humans, responsible for skin, hair, eye color) and also produced by some fungi and bacteria. It has potential applications in cosmetics (UV protection) and biomedicine, but widespread industrial use as a "pigment" for coloration might be less common than others. (c) **Carotene (β-carotene):** Carotenoids are a large class of pigments. β-carotene is produced by various microorganisms, including the alga *Dunaliella salina* and the fungus *Blakeslea trispora*, as well as by plants. It is widely used industrially as a food colorant (E160a), a feed additive (for animal coloration), and as a provitamin A source. This is a very strong candidate. (d) Hemoglobin: The iron-containing oxygen-transport protein in red blood cells of vertebrates and some invertebrates. It is not typically considered a "microbial pigment" for industrial applications in the same way as colorants.

Considering "microbial pigment used in industrial applications" specifically for coloration or as a product: β-carotene (a type of carotene) is a very prominent example of a microbial pigment with significant industrial use as a colorant and nutritional supplement. Chlorophyll from microbial sources (like algae) is also used. Between chlorophyll and carotene, β-carotene produced microbially (e.g., by *Dunaliella*) is a major industrial product. The question asks for "an example". Both (a) and (c) could fit from microbial sources. However, "Carotene" (specifically β-carotene) is a very well-established example of a microbial pigment with large-scale industrial production and application as a food colorant and vitamin precursor. If only one is to be chosen, Carotene is an excellent example.

$$\boxed{\text{Carotene}}$$

Quick Tip

Quick Tip:

- Microorganisms produce a variety of pigments (e.g., carotenoids, phycocyanins, prodigiosin, melanins, chlorophylls by algae/cyanobacteria).
- Some microbial pigments have industrial uses as natural colorants (food, cosmetics), antioxidants, or pharmaceuticals.
- β-carotene, produced by algae like *Dunaliella salina* or fungi like *Blakeslea trispora*, is a major industrial microbial pigment.

49.

Membrane-based bio separation methods rely on the principle of

(a) Centrifugation
(b) Filtration
(c) Precipitation
(d) Sedimentation

Correct Answer: (b) Filtration

Solution: Membrane-based bioseparation methods utilize semi-permeable membranes to separate components from a mixture based on differences in size, charge, or other physical/chemical properties. The driving force can be pressure, concentration gradient, or electrical potential. The fundamental principle underlying these methods is **filtration** at a molecular or particulate level. The membrane acts as a selective barrier or sieve. Examples of membrane-based separation methods include:

- Microfiltration (MF)
- Ultrafiltration (UF)
- Nanofiltration (NF)
- Reverse Osmosis (RO)

- Dialysis / Electrodialysis

Let's analyze the options: (a) Centrifugation: Separates components based on differences in density and size by applying centrifugal force. Not primarily membrane-based. (b) **Filtration:** This is the core principle. The membrane filters out particles or molecules larger than its pore size, allowing smaller ones to pass through. (c) Precipitation: Involves forming a solid (precipitate) from a solution, which can then be separated by methods like centrifugation or filtration. The membrane itself isn't the primary precipitation principle. (d) Sedimentation: Separation based on gravity causing denser particles to settle. Not primarily membrane-based. Therefore, membrane-based bioseparation methods rely on the principle of filtration.

$$\boxed{\text{Filtration}}$$

Quick Tip

Quick Tip:

- Membrane separation processes use a semi-permeable membrane as a selective barrier.
- The underlying mechanism is a form of filtration, where separation occurs based on size exclusion or other properties at the membrane interface.
- Different types (MF, UF, NF, RO) target different size ranges of particles/molecules.

50.

In immobilization of enzymes, the term "carrier" refers to

(a) The substrate of the enzyme

(b) The support material for enzyme attachment

(c) The product of enzyme catalysis

(d) The cofactor of the enzyme

Correct Answer: (b) The support material for enzyme attachment

Solution: Enzyme immobilization is a process where enzymes are confined or localized in a defined region of space with retention of their catalytic activity, allowing for their repeated or continuous use. There are several methods of immobilization, including:

- **Adsorption:** Enzyme attached to the surface of an insoluble carrier.
- **Covalent Binding:** Enzyme covalently linked to an insoluble carrier.
- **Entrapment:** Enzyme enclosed within a porous matrix or gel (e.g., alginate, polyacrylamide).
- **Encapsulation (Microencapsulation):** Enzyme enclosed within a semi-permeable membrane capsule.
- **Cross-linking:** Enzymes linked to each other to form large, insoluble aggregates, often with a bifunctional reagent.

In methods like adsorption and covalent binding, the insoluble material to which the enzyme is attached is referred to as the **carrier** or **support material**. This carrier provides a solid phase for the enzyme, facilitating its separation from the reaction mixture and reuse. Let's analyze the options: (a) The substrate of the enzyme: The substrate is the molecule upon which the enzyme acts. (b) "The support material for enzyme attachment": This correctly describes the carrier in enzyme immobilization. (c) The product of enzyme catalysis: The product is what the enzyme converts the substrate into. (d) The cofactor of the enzyme: A cofactor is a non-protein chemical compound or metallic ion required for an enzyme's activity.
Therefore, the term "carrier" in enzyme immobilization refers to the support material.

$$\boxed{\text{The support material for enzyme attachment}}$$

Quick Tip

Quick Tip:

- Enzyme immobilization restricts enzyme mobility while retaining activity.
- Advantages: Enzyme reuse, easier product separation, improved stability.
- "Carrier" or "support" is the insoluble matrix or material to which the enzyme is bound or within which it is entrapped/encapsulated.

51.

Recombinant proteins are often produced on a large scale using

(a) Conventional chemical methods
(b) Plant cells
(c) Microbial systems
(d) Inorganic catalysts

Correct Answer: (c) Microbial systems

Solution: Recombinant proteins are proteins produced by recombinant DNA technology, where a gene encoding the desired protein is inserted into a host organism's expression system. For large-scale production, various host systems are used.

- **(c) Microbial systems:** This is a very common and widely used approach. Microorganisms like bacteria (especially *E. coli*), yeast (*Saccharomyces cerevisiae*, *Pichia pastoris*), and fungi are extensively used as hosts for large-scale production of recombinant proteins due to their rapid growth, ease of genetic manipulation, high yields, and relatively low cost of cultivation in fermenters/bioreactors. Many therapeutic proteins (e.g., insulin, growth hormone) and industrial enzymes are produced this way.
- **(b) Plant cells (or whole plants):** Plant-based systems (molecular farming) are also used for producing some recombinant proteins. They offer advantages

like scalability and potentially lower cost for certain proteins, but protein folding and post-translational modifications might differ from mammalian systems.

- Mammalian cell cultures: Also widely used, especially for therapeutic proteins that require complex post-translational modifications similar to those in humans (e.g., monoclonal antibodies). However, they are generally more expensive and complex to culture than microbial systems.
- Insect cell cultures (using baculovirus expression systems): Another option.
- (a) Conventional chemical methods: While peptides can be synthesized chemically, large complex proteins are typically produced biologically using recombinant DNA technology, not by conventional chemical synthesis on a large scale.
- (d) Inorganic catalysts: These are used in chemical reactions, not for producing proteins. Enzymes (which are proteins) are biological catalysts.

Considering "often produced on a large scale," microbial systems (bacteria and yeast) are workhorses for many recombinant proteins due to cost-effectiveness and scalability. While mammalian and plant cells are also important, microbial systems are a very prominent and often preferred choice for large-scale production of many recombinant proteins. Among the given options, "Microbial systems" is the most fitting answer for common large-scale production.

$$\boxed{\text{Microbial systems}}$$

Quick Tip

Quick Tip:

- Recombinant protein production involves expressing a cloned gene in a host organism.
- Common host systems for large-scale production:
  - Microbial systems (bacteria like *E. coli*, yeasts like *S. cerevisiae* or *P. pastoris*) - often high yield, low cost.
  - Mammalian cell cultures (e.g., CHO cells) - for complex proteins requiring human-like modifications.
  - Plant cells/Transgenic plants.
  - Insect cell cultures.

52.

Citric acid is widely used in the food and beverage industry. It is primarily produced by

(a) Bacteria
(b) Yeast
(c) Fungi
(d) Algae

Correct Answer: (c) Fungi

Solution: Citric acid is an organic acid that is widely used as an acidulant, flavoring agent, and preservative in the food and beverage industry, as well as in pharmaceutical and other industrial applications. While citric acid is found naturally in citrus fruits, its large-scale industrial production is primarily achieved through microbial fermentation. The most common microorganism used for the commercial production of citric acid is the filamentous fungus ***Aspergillus niger***. This fungus is cultured under specific conditions (e.g., using molasses or other carbohydrate-rich substrates) where it efficiently converts sugars into citric acid.

Let's consider the options: (a) Bacteria: Some bacteria can produce citric acid, but *Aspergillus niger* is the dominant industrial producer. (b) Yeast: Some yeasts (e.g., *Yarrowia lipolytica*) can produce citric acid, and research is ongoing for their use, but *Aspergillus niger* remains the primary commercial source. (c) **Fungi:** This is the correct category. *Aspergillus niger* is a fungus. (d) Algae: Algae are primarily known for photosynthesis and production of other compounds, not typically for large-scale industrial citric acid production.

Therefore, citric acid is primarily produced by fungi, specifically *Aspergillus niger*.

$$\boxed{\text{Fungi}}$$

Quick Tip

Quick Tip:

- Citric acid is a common food additive (E330).
- Industrially, it is produced mainly by fermentation using the fungus *Aspergillus niger*.
- This process utilizes carbohydrate feedstocks like molasses or corn starch.

53.

What is the purpose of a fed-batch culture in bioprocess technology?

(a) To feed the cells with nutrients continuously

(b) To maintain a constant volume of the culture

(c) To induce stress on the cells

(d) To stop the bioprocess abruptly

Correct Answer: (a) To feed the cells with nutrients continuously (or intermittently, to prolong growth and product formation)

Solution: Fed-batch culture is a biotechnological process where, after an initial batch phase, one or more nutrients (substrates) are fed (either intermittently or continuously) to the bioreactor, while the products remain in the reactor until the end of the run. The volume of the culture typically increases over time due to the feed addition. The main purposes of a fed-batch culture strategy include:

- **Prolonging the productive phase of cells:** By supplying limiting nutrients, cell growth and/or product formation can be extended beyond what is possible in a simple batch culture where nutrients deplete and waste products accumulate.
- **Controlling substrate concentration:** Feeding can maintain substrate concentration at an optimal level, avoiding substrate inhibition (if substrate is toxic at high concentrations) or catabolite repression.
- **Achieving high cell densities and product yields:** By extending the growth/production phase and managing nutrient levels, higher overall productivity can often be achieved.
- **Overcoming limitations of batch culture:** Such as nutrient depletion, accumulation of toxic byproducts (though fed-batch does not remove byproducts, it can manage their formation rate relative to cell mass).

Let's analyze the options: (a) "To feed the cells with nutrients continuously" (or intermittently): This is a core aspect of fed-batch operation, aiming to supply nutrients to sustain or enhance cell activity. This is TRUE. (b) "To maintain a constant volume of the culture": This is generally FALSE. In fed-batch, volume usually increases as feed is added. Constant volume is a characteristic of a chemostat (continuous culture with outflow). (c) "To induce stress on the cells": While some bioprocesses might use controlled stress to induce product formation, the primary purpose of fed-batch nutrient feeding is generally to support or optimize growth/production, not primarily to induce stress via nutrient manipulation in a general sense. (d) "To stop the bioprocess abruptly": This is incorrect. Fed-batch aims to extend the process. Option (a) best describes a primary purpose of fed-batch culture.

$$\boxed{\text{To feed the cells with nutrients continuously}}$$

Quick Tip

Quick Tip:

- **Batch culture:** Closed system, initial nutrients, no addition/removal during run (except gas).
- **Fed-batch culture:** Nutrients are added during cultivation, volume usually increases, product harvested at end.
- **Continuous culture (e.g., chemostat):** Fresh medium continuously added, and culture (with cells and products) continuously removed to maintain constant volume and steady state.
- Fed-batch is used to achieve high cell densities, prolong production, or control substrate levels.

54.

Which of the following is a common aerobic process for the stabilization of solid wastes?

(a) Incineration

(b) Composting

(c) Landfilling

(d) Pyrolysis

Correct Answer: (b) Composting

Solution: Stabilization of solid wastes refers to processes that reduce the volume, toxicity, or reactivity of the waste, often by decomposing organic matter.

- **(a) Incineration:** A thermal process involving combustion of waste at high temperatures. It significantly reduces volume and can generate energy, but it is a combustion process, not primarily a biological stabilization method focused on decomposition by microbes. It can be aerobic in terms of combustion.

- **(b) Composting:** A biological process where organic solid wastes (e.g., food scraps, yard waste) are decomposed by aerobic microorganisms (bacteria, fungi, actinomycetes) under controlled conditions of moisture, aeration, and temperature. The end product is compost, a stable, humus-like material beneficial for soil. This is a common aerobic stabilization process.
- **(c) Landfilling:** Disposal of solid waste by burying it in land. Decomposition in landfills is largely anaerobic (especially in deeper layers), leading to methane production. It is a disposal method, and some stabilization occurs, but it's not primarily a controlled aerobic stabilization process.
- **(d) Pyrolysis:** A thermochemical decomposition of organic material at elevated temperatures in the absence of oxygen (or with very limited oxygen). It produces gas, liquid (bio-oil), and solid (char) products. It is an anaerobic thermal process.

Among the options, composting is the most common aerobic biological process specifically designed for the stabilization of organic solid wastes.

$$\boxed{\text{Composting}}$$

Quick Tip

Quick Tip:

- **Composting:** Aerobic decomposition of organic waste by microorganisms.
- **Anaerobic Digestion:** Decomposition of organic waste by microorganisms in the absence of oxygen (produces biogas).
- **Incineration:** High-temperature combustion (thermal, requires oxygen).
- **Pyrolysis:** Thermal decomposition in the absence of oxygen.
- **Landfilling:** Disposal method, primarily anaerobic decomposition occurs over time.

55.

Bioremediation can be applied to clean up contaminants in

(a) Air only

(b) Water only

(c) Soil, water, and air

(d) Metals only

Correct Answer: (c) Soil, water, and air

Solution: Bioremediation is a waste management technique that uses naturally occurring or deliberately introduced microorganisms (or sometimes plants - phytoremediation) to consume and break down environmental pollutants, transforming them into less toxic or non-toxic substances. Bioremediation can be applied to a wide range of contaminated media:

- **Soil:** To clean up soil contaminated with pesticides, hydrocarbons (e.g., oil spills), solvents, etc.
- **Water:** To treat contaminated groundwater, surface water, or wastewater (e.g., in sewage treatment plants, oil spill cleanups in marine environments).
- **Air:** Biofilters and bioscrubbers use microorganisms to remove volatile organic compounds (VOCs) and other pollutants from contaminated air streams.

Let's analyze the options: (a) "Air only": Incorrect, it's also used for soil and water. (b) "Water only": Incorrect, also used for soil and air. (c) "Soil, water, and air": Correct. Bioremediation techniques are applicable to all three environmental media. (d) "Metals only": Bioremediation can be used for organic contaminants. While some microbial processes can transform metals (e.g., change their oxidation state or immobilize them, sometimes called bioreduction or biosorption), the primary focus of "cleaning up contaminants" by degradation is usually for organic pollutants. "Metals only" is too restrictive and not entirely accurate for the broad scope of bioremediation. Therefore, bioremediation can be applied to clean up contaminants in soil, water, and air.

$$\boxed{\text{Soil, water, and air}}$$

Quick Tip

Quick Tip:

- Bioremediation uses biological agents (microorganisms, plants) to degrade or detoxify environmental pollutants.
- It can be applied *in situ* (at the contaminated site) or *ex situ* (contaminated material moved elsewhere for treatment).
- Applicable media include soil, groundwater, surface water, wastewater, and air.

56.

Reverse-phase chromatography involves the use of a stationary phase that is

(a) Nonpolar
(b) Polar
(c) Neutral
(d) Electrically charged

Correct Answer: (a) Nonpolar

Solution: Chromatography is a separation technique. In liquid chromatography, there are two main modes based on the relative polarities of the stationary phase and the mobile phase: 1. **Normal-Phase Chromatography (NPC):**

- Stationary phase: Polar (e.g., silica gel, alumina).
- Mobile phase: Nonpolar (e.g., hexane, dichloromethane).
- Principle: Polar analytes interact more strongly with the polar stationary phase and elute later. Nonpolar analytes elute earlier.

2. **Reverse-Phase Chromatography (RPC):**

- Stationary phase: **Nonpolar** (hydrophobic). Commonly silica gel modified with nonpolar alkyl chains (e.g., C18 - octadecylsilyl, C8 - octylsilyl).
- Mobile phase: Polar (e.g., water, methanol, acetonitrile, or mixtures).
- Principle: Nonpolar (hydrophobic) analytes interact more strongly with the nonpolar stationary phase and are retained longer, eluting later. Polar analytes interact more with the polar mobile phase and elute earlier.

The question asks about reverse-phase chromatography. In this mode, the stationary phase is nonpolar. Option (a) "Nonpolar" is correct. Option (b) "Polar" describes the stationary phase in normal-phase chromatography. Option (c) "Neutral" refers to pH or charge, not directly polarity in this context. Option (d) "Electrically charged" describes ion-exchange chromatography stationary phases.

$$\boxed{\text{Nonpolar}}$$

Quick Tip

Quick Tip:

- **Normal Phase:** Stationary Phase = Polar; Mobile Phase = Nonpolar. (Polar compounds stick longer).
- **Reverse Phase:** Stationary Phase = Nonpolar; Mobile Phase = Polar. (Nonpolar compounds stick longer).
- Reverse-phase HPLC (High-Performance Liquid Chromatography) is very widely used. Common stationary phases are C18 or C8 bonded silica.

57.

Penicillin belongs to which class of antibiotics?

(a) Aminoglycosides

(b) Cephalosporins

(c) Beta-lactams

(d) Tetracyclines

Correct Answer: (c) Beta-lactams

Solution: Penicillin is a group of antibiotics derived originally from *Penicillium* molds. Its core chemical structure contains a **β-lactam ring**, which is essential for its antibacterial activity. Antibiotics that share this β-lactam ring structure are classified as **β-lactam antibiotics**. This class is one of the most important and widely used groups of antibiotics. Other major β-lactam antibiotics include:

- Cephalosporins (Option b) - also β-lactams
- Carbapenems
- Monobactams

These antibiotics primarily work by inhibiting bacterial cell wall synthesis, specifically by interfering with peptidoglycan cross-linking.
Let's look at the other options: (a) Aminoglycosides (e.g., streptomycin, gentamicin): Inhibit protein synthesis by binding to the 30S ribosomal subunit. (d) Tetracyclines (e.g., tetracycline, doxycycline): Inhibit protein synthesis by binding to the 30S ribosomal subunit and preventing tRNA attachment.
Since Cephalosporins are also β-lactams, option (c) "Beta-lactams" is the broader and more fundamental classification that includes penicillin. If Penicillin is specifically asked, it *is* a β-lactam.

$$\boxed{\text{Beta-lactams}}$$

Quick Tip

Quick Tip:

- β-lactam antibiotics are characterized by the presence of a β-lactam ring in their structure.
- Major groups of β-lactams: Penicillins, Cephalosporins, Carbapenems, Monobactams.
- Mechanism of action: Inhibition of bacterial cell wall synthesis (peptidoglycan synthesis).

58.

Exopolysaccharides are often produced by microorganisms in response to

(a) Low nutrient availability
(b) High temperatures
(c) Presence of antibiotics
(d) Sunlight exposure

Correct Answer: (a) Low nutrient availability (and other stress conditions)

Solution: Exopolysaccharides (EPS) are high-molecular-weight polymers composed of sugar residues that are secreted by microorganisms (bacteria, fungi, algae) into their surrounding environment. They form a major component of biofilms. The production of EPS is often a response to various environmental conditions, including stress:

- **Nutrient Availability:**
  - **Low nutrient availability (Option a):** Under nutrient limitation (especially when carbon is available but other nutrients like nitrogen or phosphorus are limiting), many microbes switch their metabolism towards EPS production. EPS can serve as a protective barrier, help in adhesion, or act as a reserve. This is a common trigger.

  - Excess carbon source with limitation of another nutrient often stimulates EPS production.

- **Stress Conditions:** EPS production can be enhanced by various environmental stresses such as osmotic stress, desiccation, presence of toxic compounds (like antibiotics - option c, or heavy metals), extreme temperatures (option b - though specific temperature ranges might be optimal for certain EPS producers, extreme high temps are usually detrimental to growth overall).

- **Biofilm Formation:** EPS is crucial for the formation and structural integrity of biofilms, providing a protective matrix for the microbial community. Biofilm formation itself can be triggered by surface attachment or environmental cues.

- (d) Sunlight exposure: While relevant for photosynthetic microbes, it's not a universal trigger for EPS in all EPS-producing microbes in the same way nutrient stress is.

Considering the options, "Low nutrient availability" is a well-documented and significant factor that often induces or enhances exopolysaccharide production in many microorganisms as a survival or adaptive strategy. While other stresses like presence of antibiotics or temperature extremes can also influence EPS, nutrient limitation (especially an imbalance like C-excess and N/P-limitation) is a key trigger.

$$\boxed{\text{Low nutrient availability}}$$

Quick Tip

Quick Tip:

- Exopolysaccharides (EPS) are extracellular polymers, often forming capsules or slime layers.
- They play roles in adhesion, protection (against desiccation, phagocytosis, toxins, antibiotics), biofilm formation, and nutrient trapping.
- EPS production is often induced or enhanced under stress conditions, including nutrient limitation (especially when a carbon source is still abundant but other essential nutrients are scarce).

59.

Which phase of microbial growth is characterized by a balance between cell division and cell death?

(a) Lag phase

(b) Exponential phase

(c) Stationary phase

(d) Death phase

Correct Answer: (c) Stationary phase

Solution: In a batch culture, microbial growth typically follows four phases: 1. **Lag Phase:** Cells adapt to the new environment; little or no cell division. 2. **Exponential (Log) Phase:** Cells divide at a constant, maximal rate; number of cells increases exponentially. Cell division rate is much higher than cell death rate. 3. **Stationary Phase:** Growth rate slows down and becomes zero. The rate of cell division equals the rate of cell death, or cells stop dividing but remain viable for some time. This phase is usually reached due to nutrient depletion, accumulation of toxic waste products, or other limiting factors. There is no net increase in the number of viable cells. 4. **Death (Decline) Phase:** The rate of cell death exceeds the rate of cell division (if any). The number of viable cells decreases.

The phase characterized by a balance between cell division and cell death, resulting in no net change in viable cell population, is the **stationary phase**.

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

Quick Tip

Quick Tip:

- **Lag phase:** Adaptation, no significant growth.
- **Exponential (log) phase:** Maximum, constant growth rate.
- **Stationary phase:** Net growth is zero (division rate = death rate or division stops). Caused by nutrient depletion or waste accumulation.
- **Death phase:** Death rate > division rate. Viable cell count declines.

60.

The Monod equation describes the relationship between

(a) Substrate concentration and product formation rate

(b) Specific growth rate and substrate concentration

(c) Biomass concentration and time

(d) Product formation rate and biomass concentration

Correct Answer: (b) Specific growth rate and substrate concentration

Solution: The Monod equation is an empirical model that describes the relationship between the specific growth rate (μ) of a microorganism and the concentration of a single limiting substrate (S). The equation is given by:

$$\mu = \mu_{max} \frac{S}{K_s + S}$$

where:

- μ is the specific growth rate (time^{-1}).

- μ_{max} is the maximum specific growth rate (time^{-1}), achieved when substrate is not limiting ($S \gg K_s$).
- S is the concentration of the limiting substrate.
- K_s is the Monod constant or half-saturation constant, which is the substrate concentration at which $\mu = \mu_{max}/2$. It is a measure of the organism's affinity for the substrate.

The Monod equation is analogous in form to the Michaelis-Menten equation for enzyme kinetics. It describes how the specific growth rate depends on the availability of a limiting nutrient.

Let's analyze the options: (a) Substrate concentration and product formation rate: While related (product formation is often linked to growth or substrate consumption), the Monod equation directly relates to growth rate. (b) **Specific growth rate and substrate concentration:** This is precisely what the Monod equation describes. (c) Biomass concentration and time: This describes the overall growth curve, not directly the Monod relationship for specific growth rate. (d) Product formation rate and biomass concentration: This relates to specific productivity, often modeled by Luedeking-Piret or similar equations, not the Monod equation.

Therefore, the Monod equation describes the relationship between specific growth rate and substrate concentration.

$$\boxed{\text{Specific growth rate and substrate concentration}}$$

Quick Tip

Quick Tip:

- Monod Equation: $\mu = \mu_{max} \frac{S}{K_s + S}$.
- μ: Specific growth rate.
- μ_{max}: Maximum specific growth rate.
- S: Limiting substrate concentration.
- K_s: Half-saturation constant (substrate concentration at $\mu = \mu_{max}/2$).
- Describes how growth rate depends on a single limiting nutrient.

61.

The specific growth rate (μ) is defined as

(a) The rate of biomass production per unit time

(b) The rate of substrate utilization per unit biomass

(c) The rate of product formation per unit substrate

(d) The rate of nutrient consumption per unit volume

Correct Answer: (a) The rate of biomass production per unit time (More precisely, per unit biomass per unit time. Let's check options carefully.)

Solution: The specific growth rate (μ) of a microbial population is a measure of how quickly the biomass increases per unit of existing biomass. It is defined as:

$$\mu = \frac{1}{X} \frac{dX}{dt}$$

where:

- X is the biomass concentration (e.g., g/L or cells/mL).
- $\frac{dX}{dt}$ is the rate of biomass production (e.g., g/L/hr or cells/mL/hr).

So, μ has units of time^{-1} (e.g., hr^{-1}). It represents the rate of increase of biomass *per unit of biomass*.

Let's analyze the options: (a) "The rate of biomass production per unit time": This is $\frac{dX}{dt}$, which is the overall growth rate, not the specific growth rate. The specific growth rate is $\frac{dX}{dt}$ normalized by X. However, if "rate of biomass production" is interpreted as "proportional increase", this could be loosely correct. (b) "The rate of substrate utilization per unit biomass": This defines the specific substrate consumption rate, often denoted as $q_S = \frac{1}{X}\frac{dS}{dt}$. (c) "The rate of product formation per unit substrate": This is related to yield of product from substrate, not specific growth rate. (d) "The rate of nutrient consumption per unit volume": This would be a volumetric consumption rate, not specific growth rate.

Revisiting option (a): "The rate of biomass production per unit time". This is dX/dt. The definition of specific growth rate is $\mu = (1/X)(dX/dt)$. If the question implies "The rate of *increase* of biomass per unit biomass per unit time", then that's μ. Option (a) is the closest if we consider it loosely. In exponential growth, $dX/dt = \mu X$. So dX/dt is "rate of biomass production". If μ is "rate of biomass production per unit biomass", then (a) is missing the "per unit biomass". However, among the options given, it's the most related. Let's assume the question might be slightly simplified. If a population doubles in time t_d, then $\mu = \ln(2)/t_d$. "Rate of biomass production per unit time" is the absolute growth rate dX/dt. The specific growth rate μ is the *relative* rate of increase of biomass.

If the question is from a context where "rate of biomass production" is taken to mean μX, then option (a) becomes problematic as $\mu \neq \mu X$. The term "specific" usually implies "per unit biomass". So μ is the rate of biomass production *per unit biomass*. None of the options state this perfectly. Option (a) is "The rate of biomass production per unit time". This is dX/dt. If option (a) meant "the fractional rate of biomass production per unit time", then it would be $(dX/dt)/X = \mu$. The question asks for definition of μ.

Let's check standard definitions. "Specific growth rate μ is the increase in cell mass per unit of cell mass per unit time." Option (a) says "rate of biomass production per unit time". This is dX/dt. This means μ is $(dX/dt)/X$. So, option (a) defines dX/dt, not μ. This question is poorly phrased or the options are not ideal.

However, sometimes specific growth rate is also viewed as the "proportionality constant relating the rate of biomass increase to the biomass concentration" ($dX/dt = \mu X$). If "rate of biomass production per unit time" is interpreted as the constant μ in this differential equation, then it's plausible. The checkmark on (a) suggests this might be the intended (albeit imprecise) meaning. If we consider the units: dX/dt has units of mass/(volume.time). μ has units of 1/time. Option (a) describes dX/dt. This is not μ. There is a high chance of error in the question or the marked option. If "rate of biomass production" refers to μ itself as the "rate constant" for biomass production in $dX/dt = \mu X$, then (a) is a very loose interpretation. Let's assume it means the "proportional increase in biomass per unit time".

$$\boxed{\text{The rate of biomass production per unit time (interpreting this loosely as the intrinsic rate constant } \mu \text{ in } dX/dt = \mu X\text{, though technically it should be per unit biomass)}}$$

Quick Tip

Quick Tip:

- Specific growth rate $\mu = \frac{1}{X}\frac{dX}{dt}$. It is the rate of increase of biomass per unit of existing biomass, per unit time. Units: time^{-1}.
- In exponential growth phase, $dX/dt = \mu X$, where μ is constant.

62.

Agitation in a bioreactor is essential for

(a) Mixing nutrients and maintaining uniform conditions

(b) Sterilizing the medium

(c) Reducing oxygen concentration

(d) Minimizing microbial contamination

Correct Answer: (a) Mixing nutrients and maintaining uniform conditions

Solution: Agitation in a bioreactor (fermenter) refers to the stirring or mixing of the culture medium. It serves several crucial purposes: 1. **Mixing Nutrients and**

Maintaining Uniform Conditions (Homogeneity): Agitation ensures that nutrients, oxygen (if aerobic), and cells are evenly distributed throughout the bioreactor. This prevents the formation of concentration gradients (e.g., of substrate, dissolved oxygen, pH, temperature) and ensures that all cells have access to necessary resources and are exposed to uniform environmental conditions. (Option a) 2. **Enhancing Mass Transfer:**

- **Oxygen Transfer (for aerobic processes):** Agitation breaks up gas bubbles (e.g., sparged air/oxygen) into smaller ones, increasing the interfacial area for oxygen transfer from the gas phase to the liquid medium. It also helps disperse the dissolved oxygen throughout the liquid.
- **Nutrient Transfer:** It improves the transfer of nutrients from the bulk liquid to the surface of the microbial cells.
- **Heat Transfer:** It helps in maintaining a uniform temperature by improving heat distribution, especially if heating or cooling is applied.

3. **Keeping Cells Suspended (for suspension cultures):** For microbial or cell suspension cultures, agitation prevents cells from settling at the bottom of the bioreactor.

Let's analyze the options: (a) "Mixing nutrients and maintaining uniform conditions": This is a primary and essential role of agitation. (b) "Sterilizing the medium": Sterilization is done *before* inoculation or sometimes in-situ using heat (steam), but agitation itself is not the sterilizing agent. Agitation helps in uniform heating during sterilization. (c) "Reducing oxygen concentration": For aerobic processes, agitation is crucial for *increasing* dissolved oxygen concentration by enhancing oxygen transfer from gas to liquid. For anaerobic processes, agitation might still be needed for mixing but not for oxygen reduction (oxygen is excluded). (d) "Minimizing microbial contamination": Maintaining sterility prevents contamination. Agitation itself doesn't minimize contamination; proper bioreactor design and sterile operation do.

Therefore, the most essential and direct role of agitation described in the options is (a).

$$\boxed{\text{Mixing nutrients and maintaining uniform conditions}}$$

Quick Tip

Quick Tip:

- Agitation in bioreactors is crucial for:
  - Homogenization (uniform distribution of cells, nutrients, temperature, pH, DO).
  - Enhancing mass transfer (oxygen, nutrients to cells).
  - Enhancing heat transfer.
  - Keeping cells in suspension.
- Achieved by impellers (stirrers) and sometimes baffles to improve mixing efficiency.

63.

Which sterilization method is suitable for heat-sensitive media and is commonly used in the pharmaceutical industry?

(a) Autoclaving
(b) Membrane filtration
(c) Pasteurization
(d) Dry heat sterilization

Correct Answer: (b) Membrane filtration

Solution: Sterilization is the process of eliminating all forms of microbial life, including bacteria, viruses, fungi, and spores.

- **(a) Autoclaving (Steam Sterilization):** Uses high-pressure saturated steam at high temperatures (e.g., 121°C for 15-20 minutes). It is very effective but not suitable for heat-sensitive (heat-labile) materials as the high temperature can degrade them.
- **(b) Membrane Filtration (Filter Sterilization):** This method physically

removes microorganisms from liquids or gases by passing them through a filter with pore sizes small enough to retain the microbes (e.g., 0.22 µm pores for bacterial removal). It does not involve heat and is therefore ideal for sterilizing heat-sensitive solutions like pharmaceuticals (e.g., protein solutions, vaccines, some vitamin solutions) and culture media components that would be damaged by heat.

- **(c) Pasteurization:** A heat treatment process (e.g., 63°C for 30 min or 72°C for 15 sec) that kills most pathogenic microorganisms and reduces the number of spoilage organisms in liquids like milk and fruit juices. It is not sterilization, as some thermoduric organisms and spores may survive.
- **(d) Dry Heat Sterilization:** Uses high temperatures in a dry oven (e.g., 160-180°C for 1-2 hours). Suitable for heat-stable materials like glassware and metal instruments, but not for heat-sensitive liquids or media.

For heat-sensitive media, especially in the pharmaceutical industry where product integrity is critical, membrane filtration is the common method of sterilization.

$$\boxed{\text{Membrane filtration}}$$

Quick Tip

Quick Tip:

- Heat-based sterilization (autoclaving, dry heat) is effective but damages heat-sensitive materials.
- Filter sterilization (using membrane filters) physically removes microbes without heat, suitable for heat-labile liquids and gases.
- Other non-heat methods: Radiation sterilization (gamma rays, electron beams), chemical sterilization (e.g., ethylene oxide gas).
- Pasteurization reduces microbial load but is not sterilization.

64.

Rheology of fermentation fluids refers to the study of

(a) Heat transfer properties

(b) Flow and deformation characteristics

(c) Oxygen transfer rates

(d) pH variations

Correct Answer: (b) Flow and deformation characteristics

Solution: Rheology is the branch of physics (and engineering) that deals with the deformation and flow of matter, especially non-Newtonian fluids. It studies the relationship between stress, strain, and the rate of strain. Fermentation fluids (broths) can exhibit complex rheological behavior, especially at high cell densities or when microorganisms produce viscous exopolysaccharides or form filamentous structures (like some fungi or actinomycetes). The rheological properties (e.g., viscosity, shear stress vs. shear rate relationship) of the fermentation fluid are crucial because they affect:

- Mixing efficiency and power consumption for agitation.
- Mass transfer rates (e.g., oxygen transfer, nutrient distribution).
- Heat transfer rates.
- Pumping and processing of the fluid.

Therefore, rheology of fermentation fluids refers to the study of their **flow and deformation characteristics**.

Let's analyze the options: (a) Heat transfer properties: Affected by rheology, but rheology itself is not the study of heat transfer. (b) "Flow and deformation characteristics": This is the direct definition of rheology. (c) Oxygen transfer rates: Affected by rheology, but rheology is not solely the study of OTR. (d) pH variations: pH is a chemical property, not directly rheology.

Thus, option (b) is the correct definition.

Flow and deformation characteristics

Quick Tip

Quick Tip:

- Rheology: The study of how materials deform and flow under applied stress.
- Key rheological property: Viscosity.
- Newtonian fluids: Viscosity is constant (e.g., water).
- Non-Newtonian fluids: Viscosity changes with shear rate or shear stress (e.g., many fermentation broths can be shear-thinning or shear-thickening, or exhibit yield stress like Bingham plastics).
- Rheology is important in bioprocess engineering for designing and operating bioreactors and downstream processing equipment.

65.

Biot number is associated with

(a) Rheology of fluids

(b) Mass transfer

(c) Conduction

(d) Heat transfer

Correct Answer: (d) Heat transfer

Solution: The **Biot number (Bi)** is a dimensionless number used in heat transfer calculations. It represents the ratio of the internal thermal resistance of a solid body to its external thermal resistance (convective resistance at the surface).

$$Bi = \frac{hL_c}{k_s}$$

where:

- h is the convective heat transfer coefficient (W/m^{2}K) between the solid surface and the surrounding fluid.
- L_c is a characteristic length of the solid body (e.g., Volume/Surface Area).
- k_s is the thermal conductivity of the solid material (W/mK).

The Biot number is used to determine if the temperature within a solid body will vary significantly in space during transient heat conduction processes (lumped capacitance analysis).

- If $Bi \ll 0.1$, internal resistance is negligible compared to surface resistance, and the temperature within the body can be considered uniform (lumped system analysis is valid).
- If $Bi \gg 0.1$, internal temperature gradients are significant.

Therefore, the Biot number is associated with **heat transfer**, specifically transient conduction within a solid coupled with convection at its surface.
(a) Rheology of fluids: Deals with flow and deformation (e.g., Reynolds number, Deborah number). (b) Mass transfer: Analogous dimensionless numbers exist in mass transfer (e.g., Sherwood number, mass transfer Biot number), but the "Biot number" unqualified usually refers to heat transfer. (c) Conduction: Biot number involves both conduction (within the solid, related to k_s) and convection (at the surface, related to h), but it characterizes the relative importance of these in transient heat transfer. Thus, Biot number is primarily associated with heat transfer.

$$\boxed{\text{Heat transfer}}$$

Quick Tip

Quick Tip:

- Biot Number (Bi) $= \frac{\text{Internal Conductive Resistance}}{\text{External Convective Resistance}} = \frac{hL_c}{k_s}$.
- Used in transient heat conduction analysis.
- $Bi < 0.1$ often indicates that lumped capacitance method can be used (uniform temperature within the object).
- Analogous Biot numbers exist for mass transfer.

66.

Which of the following component is a common nitrogen source in fermentation media?

(a) Glucose

(b) Peptone

(c) Phosphate

(d) Ethanol

Correct Answer: (b) Peptone

Solution: Microorganisms require a source of nitrogen for the synthesis of proteins, nucleic acids, and other nitrogen-containing cellular components. Fermentation media must provide this nitrogen. Let's analyze the options: (a) Glucose ($C_6H_{12}O_6$): A common carbon and energy source. It contains C, H, O but no nitrogen. (b) **Peptone:** A complex mixture of peptides and amino acids produced by the partial hydrolysis of proteins (e.g., from meat, casein, soy). Amino acids and peptides are rich in nitrogen (due to amino groups -NH_2). Peptones are widely used as an organic nitrogen source in microbial culture media. (c) Phosphate (e.g., KH_2PO_4, K_2HPO_4): A source of phosphorus, essential for nucleic acids, ATP, phospholipids. It contains P and O, but no nitrogen. (d) Ethanol (C_2H_5OH): An organic compound containing C, H, O. Can be a carbon/energy source for some microbes or a product of fermentation.

No nitrogen.

Therefore, peptone is a common nitrogen source in fermentation media. Other common nitrogen sources include yeast extract, meat extract, ammonium salts (e.g., $(NH_4)_2SO_4$), nitrates, and urea.

$$\boxed{\text{Peptone}}$$

Quick Tip

Quick Tip:

- Microorganisms need Macronutrients (C, H, O, N, P, S, K, Mg, Ca, Fe) and Micronutrients.
- **Nitrogen sources** can be organic (e.g., amino acids, peptides from peptone, yeast extract) or inorganic (e.g., ammonium salts, nitrates).
- Peptone and yeast extract are complex nitrogen sources providing amino acids and other growth factors.

67.

The purpose of a plug-flow reactor is to

(a) Minimize reactor volume

(b) Maximize contact time between substrate and microorganisms

(c) Allow continuous addition and removal of substrate

(d) Enhance heat transfer

Correct Answer: (b) Maximize contact time between substrate and microorganisms (This needs careful consideration. PFRs provide a defined residence time distribution. "Maximize" might not be the best word, but ensuring sufficient contact time is key.)

Solution: A Plug-Flow Reactor (PFR), also known as a tubular reactor, is a type of chemical reactor or bioreactor characterized by the following idealized flow pattern:

- Fluid particles pass through the reactor in an orderly manner without overtaking or mixing with earlier or later entering fluid (no axial mixing, perfect radial mixing).

- Each fluid element has the same residence time in the reactor.
- Concentration of reactants and products changes along the length of the reactor, but is uniform across any given cross-section.

Purposes and characteristics:

- **Defined Residence Time and Contact Time:** PFRs provide a well-defined residence time for all fluid elements. This ensures that all parts of the fluid (containing reactants, substrates, microorganisms) spend a specific amount of time in the reactor, allowing for sufficient contact and reaction to occur.
- **High Conversion (for many reaction orders):** For many reaction kinetics (especially positive order reactions), PFRs can achieve higher conversion per unit volume compared to a CSTR (Continuous Stirred-Tank Reactor) of the same volume because reactants enter at high concentration and are gradually consumed, maintaining a higher average reaction rate along the length.
- **Continuous Operation:** PFRs are typically operated continuously, with reactants fed at one end and products removed at the other.

Let's analyze the options: (a) "Minimize reactor volume": For a given conversion, a PFR is often smaller in volume than a CSTR, so this can be an advantage, but not the sole "purpose". (b) "Maximize contact time between substrate and microorganisms": While PFRs ensure a specific contact time (residence time), "maximize" might be too strong unless compared to a system with severe short-circuiting. The purpose is more about providing a *controlled and sufficient* contact time for the reaction to proceed to the desired extent. As fluid flows along the PFR, substrate and microorganisms are in contact for the duration of their passage. (c) "Allow continuous addition and removal of substrate": This describes continuous operation, which is a mode PFRs operate in, but "substrate" removal is usually as product or unreacted substrate in the effluent. This is more a characteristic of continuous reactors in general. (d) "Enhance heat transfer": Heat transfer can be managed in PFRs (e.g., with jacketing), but it's not their primary defining purpose over other reactor types. The high surface-area-to-volume ratio of tubular reactors can be advantageous for heat transfer. Considering the options, option (b) "Maximize contact time between substrate and microorganisms" (interpreted as ensuring sufficient and uniform contact time for all fluid elements) is a key functional aspect directly related to the plug-flow ideal. Because there's no backmixing, all particles experience the full length of the reactor for reaction. If we rephrase (b) to "Ensure all fluid elements have a specific, defined contact time for reaction to occur effectively along the reactor length," it becomes a strong descriptor. Given the options, (b) appears to be the most relevant purpose related to the reaction process itself.

$$\boxed{\text{Maximize contact time between substrate and microorganisms}}$$

Quick Tip

Quick Tip:

- Plug Flow Reactor (PFR): Idealized reactor with no axial mixing, perfect radial mixing.
- All fluid elements have the same residence time.
- Concentration gradients exist along the length of the reactor.
- Often achieves higher conversion per unit volume than CSTR for many reaction types.
- Purpose is to provide a controlled environment for reactions to proceed over a defined path and time.

68.

Which parameter is not commonly monitored in a bioreactor?

(a) Dissolved oxygen

(b) Carbon dioxide concentration

(c) Ambient light intensity

(d) Cell density

Correct Answer: (c) Ambient light intensity

Solution: In bioreactors, several parameters are commonly monitored and controlled to optimize cell growth and product formation.

- **(a) Dissolved oxygen (DO):** Crucial for aerobic fermentations. Monitored using DO probes to ensure cells have sufficient oxygen.

- **(b) Carbon dioxide concentration:** Can be monitored in the off-gas (exit gas) as an indicator of metabolic activity and respiration rate. Sometimes dissolved CO_2 is also monitored as high levels can be inhibitory.

- **(d) Cell density:** Monitored to track growth, often using optical density (turbidity), cell counting, or online biomass sensors.

Other commonly monitored parameters include temperature, pH, substrate concentration, product concentration, agitation speed, and gas flow rates.

(c) Ambient light intensity:

- For most microbial fermentations (bacteria, yeast, fungi, animal cells) that are **not photosynthetic**, ambient light intensity is generally not a critical parameter to monitor or control, and bioreactors are often opaque or shielded from ambient light unless specific light-sensitive compounds are involved.

- For **photobioreactors** used to cultivate photosynthetic organisms (e.g., algae, cyanobacteria), light intensity (from an artificial source or sunlight) is a very critical parameter and is carefully monitored and controlled.

Since the question asks "not commonly monitored in a bioreactor" without specifying a photobioreactor, it implies general bioreactors for non-photosynthetic organisms. In that context, ambient light intensity is not a standard monitored parameter.

$$\boxed{\text{Ambient light intensity}}$$

Quick Tip

Quick Tip:

- Common parameters monitored in bioreactors: Temperature, pH, Dissolved Oxygen (DO), agitation speed, aeration rate, substrate levels, product levels, cell density/biomass, off-gas composition (O_2, CO_2).
- Light intensity is critical for photobioreactors but not for most other types of bioreactors.

69.

The concept of totipotency in plants was given by

(a) Schwan

(b) Morgan

(c) Murashige

(d) Haberlandt

Correct Answer: (d) Haberlandt

Solution: Totipotency is the ability of a single cell to divide and differentiate to produce an entire, complete organism. In plants, many differentiated cells can retain totipotency. The concept of plant cell totipotency was first proposed by the German botanist **Gottlieb Haberlandt** in 1902. He envisioned that isolated plant cells could be cultured in vitro and could potentially regenerate into whole plants, although he himself was not successful in achieving this with single cells at the time. His ideas laid the theoretical foundation for plant tissue culture. Later experiments by others (e.g., Skoog, Miller, Steward) successfully demonstrated plant regeneration from single cells or small tissue pieces, confirming Haberlandt's concept.
Let's look at the other names: (a) Theodor Schwann: A German physiologist, co-founder of the cell theory (along with Matthias Schleiden). (b) Thomas Hunt Morgan: An American geneticist, known for his work on fruit flies (*Drosophila melanogaster*) which established the chromosomal basis of heredity (Nobel Prize

1933). (c) Toshio Murashige: Known for developing the widely used Murashige and Skoog (MS) medium for plant tissue culture (along with Folke Skoog).

Therefore, Gottlieb Haberlandt is credited with first proposing the concept of plant cell totipotency.

$\boxed{\text{Haberlandt}}$

Quick Tip

Quick Tip:

- **Totipotency (Plant Cells):** The inherent capacity of a plant cell to differentiate and regenerate into a whole plant.
- **Gottlieb Haberlandt (1902):** First to propose the concept of plant cell totipotency and attempt single-cell culture.
- Practical demonstration of totipotency (regeneration of whole plants from cultured cells/tissues) came later by other scientists.

70.

Which group of phytohormone in plants is used for shoot multiplication under in vitro conditions?

(a) Auxin

(b) Cytokinin

(c) GA_3

(d) Abscisic Acid

Correct Answer: (b) Cytokinin

Solution: Plant tissue culture involves growing plant cells, tissues, or organs in a sterile nutrient medium under controlled environmental conditions (*in vitro*). Phytohormones (plant hormones) play a crucial role in controlling growth and differentiation. For **shoot multiplication** (also known as shoot proliferation or axillary bud proliferation) in vitro, **cytokinins** are the primary group of phytohormones used.

- **Cytokinins** (e.g., Kinetin, Benzylaminopurine (BAP), Zeatin, Thidiazuron (TDZ)): Promote cell division (cytokinesis), shoot formation, and axillary bud development. They are essential for inducing multiple shoots from explants in micropropagation.
- **Auxins** (e.g., Indole-3-acetic acid (IAA), Indole-3-butyric acid (IBA), Naphthaleneacetic acid (NAA)): Primarily promote root formation (rhizogenesis), cell elongation, and apical dominance. They are also involved in callus formation.
- **GA_3 (Gibberellic Acid, a type of Gibberellin):** Promote stem elongation, seed germination, and flowering. Sometimes used in tissue culture but not the primary hormone for shoot multiplication itself.
- **Abscisic Acid (ABA):** Generally a growth inhibitor, involved in stress responses, dormancy, and abscission. Not used for shoot multiplication.

The ratio of auxins to cytokinins is critical in determining the type of development in plant tissue culture:

- High cytokinin to auxin ratio: Favors shoot development.
- High auxin to cytokinin ratio: Favors root development.
- Intermediate ratio: Favors callus (undifferentiated cell mass) proliferation.

Therefore, cytokinins are used for shoot multiplication.

$$\boxed{\text{Cytokinin}}$$

Quick Tip

Quick Tip:

- **Cytokinins:** Promote cell division and shoot formation. Key for shoot multiplication in micropropagation.
- **Auxins:** Promote root formation and cell elongation.
- The auxin:cytokinin ratio is crucial for morphogenesis in plant tissue culture.

71.

Hairy root cultures in plants are induced by infection with which bacterial sps

(a) Bacillus
(b) Agrobacterium
(c) Staphylococcus
(d) Pseudomonas

Correct Answer: (b) Agrobacterium

Solution:

Hairy root disease is caused by *Agrobacterium rhizogenes*, which transfers root-inducing (Ri) plasmid DNA to plant cells:

- **Mechanism:**
  1. Bacteria infect wounded plant tissue
  2. T-DNA from Ri plasmid integrates into plant genome
  3. Genes for auxin production are expressed
  4. Results in prolific root proliferation
- **Key Features:**
  - Contains *rol* (root loci) genes (A, B, C, D)

  - Used for production of secondary metabolites
  - Shows high genetic stability

- **Why not others?**
  - *Bacillus*: Forms endospores, no natural gene transfer
  - *Staphylococcus*: Human pathogen
  - *Pseudomonas*: Causes leaf spots, not root modification

$\boxed{\text{(b) Agrobacterium}}$

72.

In the production of transgenic plants the following technique is used for DNA transfer

(a) Gene Gun

(b) PCR

(c) RT PCR

(d) Electrophoresis

Correct Answer: (a) Gene Gun

Solution:

Method	**Principle**	**Application**
Gene Gun	Biolistic particle delivery	Hard-to-transform species
PCR	DNA amplification	Not a transfer method
Electrophoresis	DNA separation	Analysis only

Gene Gun Specifics:

- Uses 0.6-1.0m gold/tungsten particles
- Helium pressure: 900-2200 psi
- Transformation efficiency: 1-100 stable transformants/shot

- Advantages:
  - No vector requirements
  - Organelle transformation possible

$$\boxed{\text{(a) Gene Gun}}$$

73.

Cell suspension cultures are grown in

(a) Semisolid media

(b) Liquid media

(c) Solid media

(d) Gaseous media

Correct Answer: (b) Liquid media

Solution:

- **Liquid Media Characteristics:**
  - Continuous agitation (80-120 rpm)
  - Dissolved oxygen >40% saturation
  - Typical composition:
    - MS basal salts
    - 2-4% sucrose
    - 0.1-1.0 mg/L 2,4-D
- **Growth Parameters:**

$$\mu = \frac{ln(X_t/X_0)}{t} \tag{1}$$

  Where μ=specific growth rate, X=cell density

- **Why not others?**
  - Solid media: For callus induction (0.8% agar)

  - Semisolid: For organogenesis
  - Gaseous: No practical application

$$\boxed{\text{(b) Liquid media}}$$

74.

Contact Inhibition means

(a) Cells stop growing without any reason

(b) Cells stop growing once the entire surface is spread

(c) Uninhibited growth

Correct Answer: (b) Cells stop growing once the entire surface is spread

Solution:

Mechanism of Contact Inhibition:

- Mediated by:
  - Cadherin interactions
  - Hippo signaling pathway
  - $p27^{Kip1}$ cyclin-dependent kinase inhibitor
- **Key Features:**
  - Density-dependent inhibition
  - Requires functional p53
  - Lost in cancer cells (transformants)
- **Experimental Evidence:**
  - Normal fibroblasts stop at 1-2 layers
  - Transformed cells form foci (3D clusters)

$\boxed{\text{(b) Cells stop growing once the entire surface is spread}}$

75.

L-Glutamine amino acid is added in the animal cell media because

(a) It is an energy source

(b) It is a carbon source for nucleic acid for synthesis

(c) It is an energy and carbon source for cell culture

(d) Cells cannot produce it

Correct Answer: (d) Cells cannot produce it

Solution:

L-Glutamine in Cell Culture:

- **Key Roles:**
  - Essential for nucleotide synthesis
  - Primary nitrogen donor
  - Maintains intracellular glutamate pools
- **Why Cells Can't Produce Enough:**
  - Glutamine synthetase activity insufficient
  - Rapid consumption (0.3-0.5 mM/day)
  - Degrades spontaneously in media ($t_{1/2} = 7$ days at 37°C)
- **Typical Concentration:**
  - DMEM: 4 mM
  - RPMI: 2 mM

$\boxed{\text{(d) Cells cannot produce it}}$

76.

Finite cell lines are known as

(a) Fresh cell lines

(b) Immortal cell lines

(c) Cell lines which grow through a limited number of cell generation

(d) Secondary cell lines

Correct Answer: (c) Cell lines which grow through a limited number of cell generation

Solution:

Characteristic	**Finite Lines**	**Continuous Lines**
Lifespan	20-80 divisions	Unlimited
Telomerase	Absent	Present
Transformation	Normal	Immortalized
Examples	WI-38, MRC-5	HeLa, CHO

Hayflick Limit:

- Due to telomere shortening (50-200 bp/division)
- Senescence markers:
  - -galactosidase activity
  - p16^{INK4a} expression

$\boxed{\text{(c) Cell lines which grow through a limited number of cell generation}}$

77.

Humanized monoclonal antibodies are a combination of

(a) Heavy and light chain constant domains are from human and variable from mouse

(b) Heavy chain constant domain from mouse and light chain constant domain from human

(c) Heavy and light chain constant domains and variable from mouse

(d) Heavy and light chain constant domains are from mouse and variable from human

Correct Answer: (a) Heavy and light chain constant domains are from human and variable from mouse

Solution: Monoclonal antibodies (mAbs) produced entirely from non-human sources (e.g., mouse) can elicit an immune response (HAMA - Human Anti-Mouse Antibody response) when administered to humans, reducing their efficacy and potentially causing side effects. To overcome this, various types of engineered antibodies have been developed:

- **Chimeric Antibodies:** Combine the variable regions (which bind to the antigen) of a mouse antibody with the constant regions of a human antibody. (60-70
- **Humanized Antibodies:** These are more extensively "humanized." They typically consist of the constant regions from a human antibody, and only the Complementarity Determining Regions (CDRs) – the hypervariable loops within the variable regions that are directly involved in antigen binding – are derived from the mouse antibody. The framework regions (FRs) of the variable domains are also of human origin or modified to be more human-like. (90-95
- **Fully Human Antibodies:** Produced using transgenic mice engineered to produce human antibodies, or by phage display technologies.

The question asks about "Humanized monoclonal antibodies." Option (a) states: "Heavy and light chain constant domains are from human and variable [domains] from mouse". This is a description more aligned with chimeric antibodies or a simplified view of humanized antibodies where the entire variable region is from mouse. However, for "humanized," usually only the CDRs are mouse-derived, grafted onto human variable region frameworks, and then combined with human constant regions. Let's re-evaluate options based on the most common understanding of "humanized": The variable domains (V$_H$ and V$_L$) are responsible for antigen binding. The constant domains (C_H and C_L) determine the antibody's effector functions and are major contributors to immunogenicity if foreign. In humanized antibodies, the aim is to make them mostly human. This means:

- Constant domains (Fc region, parts of Fab) are human.
- Variable domains: The antigen-binding specificity comes from the mouse (or other non-human) antibody. So, the critical parts of the variable domains (the CDRs) are from mouse, grafted onto human variable domain frameworks.

Option (a) "Heavy and light chain constant domains are from human and variable from mouse" implies the entire variable regions (V_H and V_L) are from mouse. This is closer to chimeric, but sometimes "humanized" is used more broadly if significant parts of variable regions are human frameworks. Option (c) "Heavy and light chain constant domains and variable from mouse" - this is even more mouse content. Option (d) "...constant domains are from mouse and variable from human" - this is the opposite of humanization.
If the options are simplified: (a) "Heavy and light chain constant domains are from human and variable [regions] from mouse." This makes the antibody mostly human with mouse antigen-binding parts. This is the most plausible description among the choices for a humanized antibody, where "variable from mouse" implies the antigen-binding specificity derived from mouse (primarily the CDRs). The key is that the constant regions are human to reduce immunogenicity, and the antigen-binding parts (variable regions or just CDRs) are from the non-human source. Considering the simplification in MCQs, option (a) is the best fit. It correctly identifies human constant domains and mouse variable (antigen-binding) domains.

$$\boxed{\text{Heavy and light chain constant domains are from human and variable from mouse}}$$

Quick Tip

Quick Tip:

- **Murine mAb:** All mouse.
- **Chimeric mAb:** Mouse Variable regions + Human Constant regions.
- **Humanized mAb:** Mostly Human Variable region frameworks + Mouse CDRs + Human Constant regions. (Minimizes mouse content to just the essential antigen-binding loops).
- **Fully Human mAb:** Entirely human sequences.
- The goal of humanization is to reduce immunogenicity while retaining antigen-binding specificity.

78.

Transgenic and knock out animal's means

(a) Gene knocked out and new gene added animals

(b) Gene knocked out but no new gene added animals

(c) Gene not removed but new gene added animals

(d) New Gene added and existing gene knocked out animals

Correct Answer: (a) or (d) (These options are essentially the same. The checkmark in the image is on (d). "Transgenic" implies gene added. "Knockout" implies gene inactivated/deleted. The question combines them.)

Solution: The question asks about "Transgenic **and** knock out animal's means". This suggests animals that are both transgenic (have an added foreign gene) and have an existing gene knocked out. Let's define the terms:

- **Transgenic Animal:** An animal that has had a foreign gene (a transgene) deliberately inserted into its genome. This results in the animal expressing a new trait or protein. (e.g., Option c describes only this part).

- **Knockout Animal:** An animal in which one or more specific endogenous genes have been inactivated or "knocked out" (often by replacing it or disrupting it with an artificial piece of DNA). This is done to study the function of the gene by observing the effect of its absence. (e.g., Option b describes only this part).

The phrase "Transgenic and knock out animal's" implies an animal that has undergone both modifications: a new gene has been added (making it transgenic) AND an existing gene has been knocked out. Options: (a) "Gene knocked out and new gene added animals": This fits the combined definition. (b) "Gene knocked out but no new gene added animals": This is only a knockout animal. (c) "Gene not removed but new gene added animals": This is only a transgenic animal. (d) "New Gene added and existing gene knocked out animals": This is the same as option (a) and fits the combined definition.

Since options (a) and (d) are identical in meaning and both describe an animal that is both transgenic (new gene added) and has a gene knocked out, they are correct. Given the checkmark in the image is on (d) (though it's a bit faint), we select that. It's also possible the question meant to ask for definitions separately or meant "Transgenic *or* knockout animals means...". But "and" implies both conditions are met in the same animal.

$$\boxed{\text{New Gene added and existing gene knocked out animals}}$$

Quick Tip

Quick Tip:

- **Transgenic:** Contains an added foreign gene (transgene).
- **Knockout:** Has a specific endogenous gene inactivated/deleted.
- **Knock-in:** An endogenous gene is replaced with a modified version or another gene is inserted at a specific locus.
- An animal can be engineered to be both transgenic (for one gene) and a knockout (for another gene).

79.

Is immunity hereditary?

(a) Yes, maternal derived

(b) Yes, paternal derived

(c) Non-hereditary

(d) Maternal and paternal derived

Correct Answer: (c) Non-hereditary (This refers to acquired immunity's specificity. Innate immunity components are genetically determined, but "immunity" as a whole, especially adaptive, is not simply inherited like a Mendelian trait.)

Solution: Immunity is a complex biological state of having sufficient biological defenses to avoid infection, disease, or other unwanted biological invasion. It has different components:

- **Innate Immunity:** Non-specific defense mechanisms that act immediately or within hours of an antigen's appearance. The components of innate immunity (e.g., physical barriers, phagocytic cells, complement system proteins) are genetically determined and thus "hereditary" in the sense that the genes encoding these components are inherited.
- **Adaptive (Acquired) Immunity:** Antigen-specific immune response that develops over time after exposure to a specific pathogen or antigen. It involves lymphocytes (B cells and T cells) and is characterized by immunological memory.
  - The *capacity* to mount an adaptive immune response (i.e., having functional immune cells and genes for antibodies/TCRs) is hereditary.
  - However, the specific antibodies or sensitized T cells developed against specific pathogens during an individual's lifetime are **not directly inherited** by their offspring (except for passive transfer of maternal antibodies). Each individual develops their own adaptive immunity through exposure.

- **Passive Immunity:** Temporary immunity conferred by receiving antibodies from another source (e.g., maternal antibodies passed to fetus/newborn, or injection of antiserum). This is passively acquired, not actively generated by the individual's immune system, and is not "hereditary" in the genetic sense. Option (a) "Yes, maternal derived" could refer to this passive transfer.

The question "Is immunity hereditary?" is broad. If "immunity" refers to the general ability to have an immune system, then yes, the genes for the immune system components are inherited (maternal and paternal derived - option d). If "immunity" refers to specific acquired immunities (e.g., immunity to measles after infection), then these are generally non-hereditary (option c), though passive maternal antibody transfer provides temporary immunity.
Considering the options: (a) "Yes, maternal derived": This is true for passive immunity (e.g., IgG via placenta, IgA via breast milk), but this is temporary and not genetic inheritance of adaptive responses. (b) "Yes, paternal derived": Paternal genes contribute to the immune system's genetic makeup, but specific acquired immunities are not passed this way typically. (c) "Non-hereditary": This is largely true for specific adaptive immune responses developed during one's lifetime. (d) "Maternal and paternal derived": The genetic basis for the immune system (genes for immune cells, receptors, cytokines etc.) is inherited from both parents.
The checkmark in the image is on (c) "Non-hereditary". This interpretation likely focuses on the fact that *specific acquired immunities* (e.g., having had chickenpox and being immune to it) are not passed down genetically to offspring. While the genetic capacity for an immune response is inherited, the actual "memory" of past infections is not. This is often what is meant in simple terms when asking if immunity is hereditary.

$$\boxed{\text{Non-hereditary (referring to specific acquired immunity)}}$$

Quick Tip

Quick Tip:

- The genetic blueprint for the immune system is inherited from both parents.
- Innate immunity components are genetically determined.
- Specific adaptive immunity (e.g., antibodies against a particular virus after infection or vaccination) is acquired during an individual's lifetime and is generally not passed on genetically to offspring.
- Passive immunity involves transfer of pre-formed antibodies (e.g., maternal antibodies to child), which is temporary.

80.

What are Haptens?

(a) Antigens which induce low immune response

(b) Antigens which are not immunogenic on their own

(c) Antigens which induce high immune response

(d) Antigens which are nonspecific stimulators of immune response

Correct Answer: (b) Antigens which are not immunogenic on their own

Solution: A **hapten** is a small molecule that can elicit an immune response (e.g., antibody production) only when attached to a larger carrier molecule, such as a protein. Key characteristics of haptens:

- **Antigenic but not Immunogenic on their own:** Haptens can be recognized by antibodies (they are antigenic or can act as epitopes), but they are too small to induce an immune response (i.e., stimulate antibody production or T-cell activation) by themselves (they are not immunogenic alone).
- **Require a Carrier:** To become immunogenic, a hapten must be covalently bound to a larger carrier molecule (usually a protein like albumin or keyhole limpet hemocyanin - KLH). The hapten-carrier conjugate is then immunogenic.

- Antibodies produced against the hapten-carrier conjugate can include antibodies specific for the hapten, antibodies specific for the carrier, and antibodies specific for the conjugate.

Let's analyze the options: (a) "Antigens which induce low immune response": Some antigens are weakly immunogenic, but this doesn't define a hapten. Haptens are *not* immunogenic *at all* on their own. (b) "Antigens which are not immunogenic on their own": This correctly describes haptens. They can bind to antibodies (are antigenic) but need a carrier to stimulate an immune response. (c) "Antigens which induce high immune response": This describes strong immunogens, not haptens. (d) "Antigens which are nonspecific stimulators of immune response": This might describe adjuvants or polyclonal activators (like mitogens), not haptens.
Therefore, haptens are antigens that are not immunogenic by themselves but become immunogenic when conjugated to a carrier.

$$\boxed{\text{Antigens which are not immunogenic on their own}}$$

Quick Tip

Quick Tip:

- **Antigen:** Any substance that can be bound by an antibody or T-cell receptor.
- **Immunogen:** An antigen that can elicit an immune response (antibody production, T-cell activation).
- **Hapten:** A small molecule that is antigenic (can bind to antibodies) but not immunogenic on its own. It becomes immunogenic when coupled to a larger carrier molecule.
- Example: Penicillin can act as a hapten, leading to allergic reactions in some individuals when it binds to host proteins.

81.

Best antigen presenting cell is

(a) Mast cell

(b) B cell

(c) Neutrophils

(d) Dendritic cells

Correct Answer: (d) Dendritic cells

Solution: Antigen-Presenting Cells (APCs) are specialized cells that capture, process, and present antigens (fragments of pathogens or foreign substances) on their cell surface in conjunction with Major Histocompatibility Complex (MHC) molecules for recognition by T lymphocytes (T cells). This is crucial for initiating adaptive immune responses. There are several types of APCs:

- **Professional APCs:** These are highly efficient at antigen presentation and T cell activation. They include:
  - **Dendritic Cells (DCs):** Considered the most potent and effective professional APCs, especially for activating naive T cells and initiating primary immune responses. They are found in tissues and migrate to lymph nodes upon antigen capture. (Option d)
  - **Macrophages:** Phagocytic cells that can present antigens to T cells, particularly important in ongoing immune responses and for activating effector T cells.
  - **B cells (B lymphocytes):** Can internalize specific antigens via their B cell receptors (antibodies), process them, and present them to helper T cells. This T cell help is often required for B cell activation and antibody production. (Option b)
- **Non-professional (Atypical) APCs:** Some other cell types (e.g., fibroblasts, thymic epithelial cells) can express MHC class II molecules under certain conditions (e.g., inflammation) and present antigens, but this is not their primary role.

Among the professional APCs, **dendritic cells are generally considered the "best" or most potent** at initiating T cell responses, especially for naive T cells, due to their high expression of MHC molecules, co-stimulatory molecules, and their migratory capacity.

Let's analyze the options: (a) Mast cell: Primarily involved in allergic reactions and defense against parasites by releasing histamine and other mediators. Not considered a primary APC for T cell activation. (b) B cell: A professional APC, but dendritic cells are generally more potent for initiating T cell responses. (c) Neutrophils: Phagocytic cells crucial in innate immunity and acute inflammation. They are not typically considered professional APCs for T cell activation in the same way as DCs, macrophages, or B cells, though they can present some antigens. (d) Dendritic cells: The most potent professional APCs.

Therefore, dendritic cells are considered the best antigen-presenting cells for initiating adaptive immunity.

$$\boxed{\text{Dendritic cells}}$$

Quick Tip

Quick Tip:

- Professional Antigen-Presenting Cells (APCs): Dendritic cells, Macrophages, B cells.
- They express MHC class II molecules (for presenting to CD4+ T helper cells) and MHC class I molecules (on all nucleated cells, for presenting to CD8+ cytotoxic T cells).
- Dendritic cells are particularly specialized and efficient at capturing antigens in peripheral tissues and migrating to lymphoid organs to activate naive T cells.

82.

Hypersensitivity - I is associated with what type of immune complex?

(Note: Type I Hypersensitivity is immediate hypersensitivity / allergy.)

(a) IgM antibody + Protein antigen complex

(b) IgG antibody + Protein antigen complex

(c) IgE antibody + Allergen complex

(d) IgA antibody + antigen complex

Correct Answer: (c) IgE antibody + Allergen complex

Solution: Hypersensitivity reactions are exaggerated or inappropriate immune responses to antigens that can cause tissue damage. They are classified into four main types (Gell and Coombs classification):

- **Type I Hypersensitivity (Immediate or Allergic Hypersensitivity):** This type is mediated by **IgE antibodies**. Mechanism: 1. Initial exposure to an allergen (an antigen that causes allergy) leads to sensitization, where IgE antibodies specific to the allergen are produced and bind to Fc receptors on the surface of mast cells and basophils. 2. Upon re-exposure to the same allergen, the allergen cross-links the IgE antibodies bound to mast cells/basophils. 3. This cross-linking triggers the degranulation of these cells, releasing pre-formed mediators (like histamine, tryptase) and newly synthesized mediators (like prostaglandins, leukotrienes). 4. These mediators cause the symptoms of allergy (e.g., vasodilation, smooth muscle contraction, mucus secretion), such as in hay fever, asthma, food allergies, anaphylaxis. So, Type I involves "IgE antibody + Allergen complex" triggering mast cell degranulation.

Let's look at other types briefly for context:

- **Type II Hypersensitivity (Antibody-mediated Cytotoxic Hypersensitivity):** Mediated by IgG or IgM antibodies directed against antigens on cell surfaces or in the extracellular matrix. Leads to cell destruction (e.g., autoimmune hemolytic anemia, transfusion reactions). Forms antibody-cell surface antigen complexes.

- **Type III Hypersensitivity (Immune Complex-mediated Hypersensitivity):** Mediated by the formation of antigen-antibody (immune) complexes (usually IgG or IgM with soluble antigens) that deposit in tissues (e.g., blood vessels, kidneys, joints) and activate complement and inflammatory responses. (e.g., Serum sickness, Arthus reaction, some forms of glomerulonephritis).
- **Type IV Hypersensitivity (Cell-mediated or Delayed-Type Hypersensitivity - DTH):** Mediated by T lymphocytes (specifically T_H1 cells and cytotoxic T lymphocytes - CTLs), not antibodies. Takes 24-72 hours to develop. (e.g., Tuberculin skin test reaction, contact dermatitis like poison ivy, graft rejection).

The question asks about Type I Hypersensitivity. This is associated with IgE antibodies reacting with an allergen. Option (c) "IgE antibody + Allergen complex" correctly describes the key components involved in triggering Type I hypersensitivity.

$$\boxed{\text{IgE antibody + Allergen complex}}$$

Quick Tip

Quick Tip:

- **Type I (Allergy/Anaphylaxis):** IgE-mediated, mast cell degranulation (Histamine). Allergen binds to IgE on mast cells.
- **Type II (Cytotoxic):** IgG/IgM against cell surface/matrix antigens. Complement activation, phagocytosis.
- **Type III (Immune Complex):** IgG/IgM immune complexes deposit in tissues. Complement, inflammation.
- **Type IV (Delayed-Type):** T cell-mediated (T_H1, CTLs). Cytokines, inflammation. No antibodies involved directly.

83.

Antibody can become a killer when it is bound with

(a) Cytokines

(b) Interleukins

(c) Chemokines

(d) Complement

Correct Answer: (d) Complement

Solution: Antibodies themselves do not directly kill cells or pathogens in most cases. Their primary roles are neutralization (binding to toxins or pathogens to block their activity/entry) and opsonization (coating pathogens to enhance phagocytosis). However, antibodies can trigger "killing" mechanisms when bound to antigens, particularly on cell surfaces, by activating other components of the immune system: 1. **Complement System Activation (Option d):** Certain antibodies (IgM and some IgG subclasses), when bound to antigens on a cell surface, can activate the classical pathway of the complement system. Activated complement components can:

- Form a Membrane Attack Complex (MAC) that creates pores in the target cell membrane, leading to cell lysis (killing).
- Act as opsonins (C3b) to enhance phagocytosis.
- Promote inflammation.

This is a major way antibodies can lead to cell killing. 2. **Antibody-Dependent Cell-mediated Cytotoxicity (ADCC):** Cells like Natural Killer (NK) cells have Fc receptors that can bind to antibodies (typically IgG) coated on a target cell. This binding activates the NK cell to release cytotoxic granules that kill the target cell. Let's look at other options: (a) Cytokines: Signaling molecules that modulate immune responses. They don't directly make an antibody a "killer" by binding to it. Antibodies can influence cytokine production. (b) Interleukins: A type of cytokine. (c) Chemokines: A type of cytokine that directs cell migration.

Among the options, binding of an antibody (to an antigen on a target) and subsequent activation of the **complement system** is a direct way an antibody can lead to the killing/lysis of the target cell. ADCC is another mechanism, but "Complement" is listed as an option. So, when an antibody is bound to an antigen (e.g., on a bacterial cell) and then binds/activates complement, the complement cascade can lead to lysis of the cell.

$$\boxed{\text{Complement}}$$

Quick Tip

Quick Tip:

- Antibodies primarily neutralize or opsonize.
- Effector functions triggered by antigen-bound antibodies leading to killing:
  - **Complement Activation (Classical Pathway):** Leads to MAC formation and cell lysis.
  - **Antibody-Dependent Cell-mediated Cytotoxicity (ADCC):** NK cells, eosinophils, macrophages kill antibody-coated target cells.

84.

Chronic rejection mechanism in host vs graft is caused by (Host vs Graft implies transplant rejection)

(a) CD4+ T cells

(b) Antibody

(c) CD8+ T cells

(d) Macrophages

Correct Answer: (a) CD4+ T cells (Though chronic rejection is complex and involves both cellular and humoral (antibody) mechanisms. CD4+ T cells play a central orchestrating role).

Solution: Transplant rejection is an immune response by the recipient (host) against the transplanted organ or tissue (graft). Rejection can be classified based on timing and mechanisms:

- **Hyperacute Rejection:** Occurs within minutes to hours. Mediated by pre-existing recipient antibodies against donor antigens (e.g., ABO blood group antigens, HLA antigens).
- **Acute Rejection:** Occurs within days to weeks (or later if immunosuppression is inadequate). Primarily mediated by T cells (both CD4+ helper T cells and CD8+ cytotoxic T cells) recognizing donor MHC molecules (alloantigens). Antibodies can also contribute (acute humoral rejection).
- **Chronic Rejection:** Develops slowly over months to years. It is a complex process involving both cell-mediated immunity (T cells, macrophages) and humoral immunity (antibodies against donor HLA or other antigens, complement activation). It leads to gradual fibrosis, vascular damage (arteriosclerosis), and loss of graft function.

The question asks about the "Chronic rejection mechanism". (a) **CD4+ T cells (Helper T cells):** Play a crucial role in orchestrating both cellular and humoral immune responses. They help activate CD8+ T cells and B cells. In chronic rejection, CD4+ T cells recognizing donor antigens (often via the indirect pathway of allorecognition) contribute to inflammation, cytokine production, and help for antibody production. They are central to the chronic inflammatory process. (b) **Antibody:** Alloantibodies (antibodies against donor HLA or non-HLA antigens) play a significant role in chronic humoral rejection, leading to endothelial damage, complement activation, and chronic inflammation in graft vasculature. (c) **CD8+ T cells (Cytotoxic T cells):** Can directly kill graft cells expressing foreign MHC class I molecules. They are major effectors in acute cellular rejection and can contribute to chronic rejection. (d) **Macrophages:** Involved in both acute and chronic rejection as effector cells and by producing cytokines and growth factors that contribute to inflammation and tissue remodeling (fibrosis).
Chronic rejection is multifactorial, involving T cells (CD4+ and CD8+), B cells/antibodies, and macrophages. However, CD4+ T cells are key initiators and orchestrators of the alloimmune response that drives chronic damage. They provide help for B cell antibody production and activate macrophages and CD8+ T cells.

Given the options, and considering the central coordinating role: If only one primary cause is to be selected from the list for "mechanism", the options are all involved. The checkmark is on (a) CD4+ T cells. This highlights their central role in driving the chronic immune response, including help for antibody production and activation of other effector cells. While antibodies are also key effectors in chronic humoral rejection, the T cell response, particularly CD4+ T cell-mediated inflammation and help, is fundamental.

$$\boxed{\text{CD4+ T cells (play a central role in orchestrating chronic rejection)}}$$

Quick Tip

Quick Tip:

- **Chronic Graft Rejection:** Slow, progressive loss of graft function over months/years.
- Involves both cellular (T cells, macrophages) and humoral (antibodies) immune mechanisms.
- Characterized by fibrosis, vascular damage (graft arteriosclerosis), and chronic inflammation.
- CD4+ T cells are critical in initiating and sustaining the alloimmune responses leading to chronic rejection.

85.

Plasma treatment used for covid patients provides (Referring to Convalescent Plasma treatment)

(a) Blood

(b) Fibrinogen

(c) Antibodies for CoV-2 virus

(d) Immune tolerance to CoV-2 virus

Correct Answer: (c) Antibodies for CoV-2 virus

Solution: Convalescent plasma therapy involves transfusing plasma from individuals who have recovered from an infection (in this case, COVID-19, caused by SARS-CoV-2 virus) into patients who are currently suffering from the same infection or are at high risk. The rationale behind this therapy is that the plasma from recovered individuals (convalescent plasma) contains **antibodies** that their immune system produced against the pathogen (SARS-CoV-2 virus). When this plasma is transfused into an infected patient, these pre-formed antibodies can:

- Neutralize the virus, preventing it from infecting new cells.
- Help clear the virus from the body.
- Modulate the immune response.

This is a form of **passive immunity**, providing immediate but temporary protection or therapeutic effect.
Let's analyze the options: (a) Blood: Plasma is a component of blood (the liquid part without blood cells), but the key therapeutic component here is what's in the plasma, not whole blood. (b) Fibrinogen: A clotting factor present in plasma, but not the primary therapeutic agent for COVID-19 in this context. (c) "Antibodies for CoV-2 virus": Correct. Convalescent plasma contains antibodies specific to the SARS-CoV-2 virus. (d) "Immune tolerance to CoV-2 virus": This is incorrect. Plasma therapy provides antibodies for immediate action, it does not typically induce long-term immune tolerance in the recipient. Tolerance is a state of unresponsiveness of the immune system.
Therefore, convalescent plasma treatment for COVID-19 patients provides antibodies against the SARS-CoV-2 virus.

$$\boxed{\text{Antibodies for CoV-2 virus}}$$

Quick Tip

Quick Tip:

- **Convalescent Plasma Therapy:** Uses plasma from recovered patients.
- The therapeutic benefit comes from the **neutralizing antibodies** present in the donor plasma.
- It is a form of **passive antibody therapy**, providing immediate but temporary immunity/treatment.
- Used (or investigated) for various infectious diseases, including COVID-19 during the pandemic.

86.

Which one of the following is an autoimmune disease?

(a) Tuberculosis
(b) Covid-19
(c) Common cold
(d) Type 1 Diabetes

Correct Answer: (d) Type 1 Diabetes

Solution: An **autoimmune disease** is a condition in which the body's immune system mistakenly attacks its own healthy cells, tissues, or organs, recognizing them as foreign. Let's analyze the options: (a) **Tuberculosis (TB):** An infectious disease caused by the bacterium *Mycobacterium tuberculosis*. It primarily affects the lungs. The immune system fights the bacteria, but it's an infection, not an autoimmune disease. (b) **Covid-19:** An infectious disease caused by the SARS-CoV-2 virus. While severe COVID-19 can involve dysregulated immune responses (e.g., cytokine storm), the disease itself is initiated by a viral infection, not by the immune system attacking self-antigens without an external trigger. (c) **Common cold:** A viral infectious disease of the upper respiratory tract, most commonly caused by rhinoviruses or coronaviruses (other than SARS-CoV-2). (d) **Type 1 Diabetes (mellitus):** An autoimmune disease in which the immune system (specifically T cells) attacks and destroys the insulin-producing beta cells in the islets of Langerhans in the pancreas. This leads to a deficiency of insulin and an inability to regulate blood glucose levels properly.

Therefore, Type 1 Diabetes is an autoimmune disease. Other examples of autoimmune diseases include rheumatoid arthritis, systemic lupus erythematosus (SLE), multiple sclerosis, Hashimoto's thyroiditis, Graves' disease, and celiac disease.

$\boxed{\text{Type 1 Diabetes}}$

Quick Tip

Quick Tip:

- **Autoimmune Disease:** The immune system fails to distinguish between self and non-self antigens, leading to an attack on the body's own tissues.
- Infectious diseases are caused by pathogens (bacteria, viruses, fungi, parasites).
- Type 1 Diabetes results from autoimmune destruction of pancreatic beta cells.

87.

Covaxin, a vaccine developed by Bharat Biotech for covid-19 is

(a) DNA based vaccine

(b) Protein based Vaccine

(c) Inactivated Virus based vaccine

(d) mRNA based vaccine

Correct Answer: (c) Inactivated Virus based vaccine

Solution: Covaxin (BBV152) is an indigenous COVID-19 vaccine developed by Bharat Biotech in collaboration with the Indian Council of Medical Research (ICMR)

- National Institute of Virology (NIV). Covaxin is an **inactivated virus based vaccine**. This type of vaccine uses the killed (inactivated) version of the germ that causes a disease. The process involves: 1. Growing the SARS-CoV-2 virus in cell culture. 2. Chemically inactivating the virus so it can no longer replicate or cause disease. 3. Formulating the inactivated virus (which still contains its antigens, like the spike protein) into a vaccine, often with an adjuvant to enhance the immune response. When administered, the immune system recognizes the antigens on the inactivated virus and mounts an immune response (producing antibodies and T cells) without causing the disease, thus providing protection against future infection.

Let's look at other vaccine types: (a) DNA based vaccine: Uses genetically engineered DNA to instruct host cells to produce an antigen (e.g., ZyCoV-D for COVID-19). (b) Protein based Vaccine (Subunit vaccine): Uses specific purified proteins (antigens) from the pathogen, rather than the whole pathogen (e.g., Novavax vaccine (NVX-CoV2373), Hepatitis B vaccine). (d) mRNA based vaccine: Uses messenger RNA (mRNA) encoding a specific antigen. The mRNA is taken up by host cells, which then produce the antigen, triggering an immune response (e.g., Pfizer-BioNTech and Moderna COVID-19 vaccines).

Covaxin specifically uses the inactivated whole virion approach.

$$\boxed{\text{Inactivated Virus based vaccine}}$$

Quick Tip

Quick Tip:

- **Inactivated Vaccines:** Use killed versions of the pathogen. Cannot cause disease. Often require multiple doses (boosters). Example: Polio (Salk), Flu shot, Covaxin.
- **Live-Attenuated Vaccines:** Use weakened (attenuated) versions of the living pathogen. Strong, long-lasting immune response. Small risk of causing mild illness or reverting to virulence (rare). Example: MMR, Chickenpox, Polio (Sabin).
- **Subunit/Recombinant/Polysaccharide/Conjugate Vaccines:** Use specific pieces of the pathogen (like proteins, sugars). Strong immune response to key antigens. Example: Hepatitis B, Pertussis (acellular), Shingles.
- **Toxoid Vaccines:** Use inactivated toxins produced by bacteria. Example: Tetanus, Diphtheria.
- **Viral Vector Vaccines:** Use a harmless virus to deliver genetic material from the target pathogen. Example: Johnson & Johnson/Janssen, AstraZeneca COVID-19 vaccines.
- **mRNA/DNA Vaccines (Nucleic Acid Vaccines):** Deliver genetic instructions (mRNA or DNA) for host cells to make a specific antigen. Example: Pfizer, Moderna (mRNA); ZyCoV-D (DNA).

88.

Which type of restriction enzymes are used in genetic engineering work

(a) Type I

(b) Type II

(c) Type III

(d) Type IV

Correct Answer: (b) Type II

Solution: Restriction enzymes (or restriction endonucleases) are enzymes that cut DNA at or near specific recognition nucleotide sequences known as restriction sites. They are crucial tools in molecular biology and genetic engineering. There are several types of restriction enzymes, classified based on their structure, cofactor requirements, and cleavage properties:

- **Type I Restriction Enzymes:** Complex, multisubunit enzymes. They recognize specific DNA sequences but cleave DNA at random sites, often far from the recognition sequence. They require ATP, S-adenosylmethionine (SAM), and Mg^{2+} for activity. Due to their non-specific cleavage site relative to the recognition site, they are generally **not useful** for routine genetic engineering work that requires precise cutting.

- **Type II Restriction Enzymes:** These are the most commonly used restriction enzymes in molecular cloning and genetic engineering. They recognize specific (often palindromic) DNA sequences (typically 4-8 base pairs long) and cleave the DNA **at or very near** these recognition sites in a predictable and reproducible manner. They usually require only Mg^{2+} as a cofactor. Their predictable cleavage makes them ideal for creating specific DNA fragments. Examples: EcoRI, HindIII, BamHI.

- **Type III Restriction Enzymes:** Complex enzymes that recognize specific DNA sequences but cleave DNA at a defined distance (e.g., 24-26 bp) away from the recognition site. They require ATP and Mg^{2+}, and SAM can stimulate activity. Their cleavage pattern is less straightforward than Type II, making them less commonly used in routine cloning.

- **Type IV Restriction Enzymes:** Recognize modified (e.g., methylated) DNA and cleave it.

- **Type V Restriction Enzymes:** Utilize guide RNAs (gRNAs) to target specific DNA sequences for cleavage (e.g., Cas9 from CRISPR-Cas system).

For most genetic engineering applications that require precise and predictable cutting of DNA at specific sites (e.g., for cloning, DNA mapping, RFLP analysis), **Type II restriction enzymes** are the workhorses.

$$\boxed{\text{Type II}}$$

Quick Tip

Quick Tip:

- **Type II Restriction Enzymes** are most widely used in genetic engineering because:
  - They recognize specific DNA sequences (restriction sites).
  - They cleave DNA at or very near these specific sites in a predictable manner.
  - They generally require only Mg^{2+} for activity (simpler cofactor requirements).
- Type I and Type III enzymes have cleavage sites distant from their recognition sites, making them less useful for precise DNA manipulation.

89.

Identify the vector which is not a phage vector among the following?

(a) pBR322

(b) MP13MP2

(c) λgt 10

(d) λZAPII

Correct Answer: (a) pBR322

Solution: Vectors are DNA molecules used as vehicles to carry foreign genetic material into another cell, where it can be replicated and/or expressed.

- **Phage Vectors (Bacteriophage Vectors):** These are cloning vectors derived from bacteriophages (viruses that infect bacteria). They are used for cloning larger DNA fragments than plasmids can typically accommodate. Examples:
    - **Lambda (λ) phage vectors:** Such as λgt10, λgt11, λZAPII, EMBL vectors. Used for constructing genomic libraries and cDNA libraries. (Options c and d are lambda phage vectors).
    - **M13 phage vectors:** Filamentous phages that infect *E. coli.* Used for obtaining single-stranded DNA (useful for sequencing and site-directed mutagenesis). Examples include M13mp series like M13mp18, M13mp19. (Option b, "MP13MP2", is likely a typo for an M13 derivative).
- **Plasmid Vectors:** Small, circular, extrachromosomal DNA molecules found naturally in bacteria. They are widely used for cloning smaller DNA fragments (typically up to 10-15 kb). Example: **pBR322** (Option a) is one of the earliest and classic *E. coli* plasmid cloning vectors. It contains an origin of replication, selectable markers (e.g., antibiotic resistance genes like amp^R, tet^R), and multiple cloning sites.
- Other vectors include Cosmids, BACs (Bacterial Artificial Chromosomes), YACs (Yeast Artificial Chromosomes), etc.

The question asks to identify the vector which is NOT a phage vector. pBR322 is a plasmid vector. MP13MP2 (likely M13mp series) is an M13 phage vector. λgt10 and λZAPII are lambda phage vectors. Therefore, pBR322 is not a phage vector.

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

Quick Tip

Quick Tip:

- **Plasmid vectors:** Circular DNA, common for routine cloning (e.g., pBR322, pUC series).
- **Bacteriophage vectors:** Derived from viruses infecting bacteria.
  - **Lambda (λ) phage vectors:** For larger inserts, genomic/cDNA libraries.
  - **M13 phage vectors:** For single-stranded DNA production.
- **Cosmids:** Hybrid of plasmid and lambda phage features, for large inserts.
- **Artificial Chromosomes (BACs, YACs):** For very large DNA fragments.

90.

pBluescript II KS is a

(a) Plasmid

(b) Cosmid

(c) Phagemid

(d) Artificial chromosome

Correct Answer: (c) Phagemid

Solution: pBluescript II KS (and its counterpart SK) are commercially available cloning vectors that are classified as **phagemids**. A **phagemid** is a type of plasmid vector that contains an origin of replication for a filamentous bacteriophage (like M13 or f1) in addition to its own plasmid origin of replication. Key features of phagemids like pBluescript:

- They can replicate as a normal plasmid in *E. coli*.
- When the *E. coli* host containing the phagemid is infected with a helper phage (which provides the necessary phage proteins), the phagemid can be packaged

into phage particles as single-stranded DNA (ssDNA).

- This ability to produce ssDNA is useful for DNA sequencing (Sanger method), site-directed mutagenesis, and constructing probes.
- pBluescript vectors also typically contain a multiple cloning site (MCS) within the *lacZ*α gene for blue-white screening, ampicillin resistance gene for selection, and promoters (e.g., T7 and T3 RNA polymerase promoters) flanking the MCS for *in vitro* RNA synthesis.

Let's analyze the options: (a) Plasmid: While a phagemid functions as a plasmid for general replication, its defining feature is the phage origin that allows ssDNA production. So, "phagemid" is more specific and accurate. (b) Cosmid: A hybrid vector containing lambda phage *cos* sites and a plasmid origin, used for cloning large DNA fragments (30-45 kb). Not pBluescript. (c) **Phagemid:** Correct. pBluescript is a classic example of a phagemid. (d) Artificial chromosome (e.g., YAC, BAC): Vectors designed to clone very large DNA fragments (hundreds of kb to Mb). Not pBluescript. Therefore, pBluescript II KS is a phagemid.

$$\boxed{\text{Phagemid}}$$

Quick Tip

Quick Tip:

- **Phagemid:** A plasmid vector that also contains an origin of replication from a filamentous bacteriophage (e.g., M13, f1).
- Allows for replication as a double-stranded plasmid and, upon infection with a helper phage, packaging of single-stranded DNA into phage particles.
- Useful for ssDNA production for sequencing, mutagenesis, etc.
- pBluescript is a common example.

91.

Which among the following is incorrect with reference to Yeast Artificial Chromosomes?

(a) YACs have ORS, Telomere and Centromere

(b) They are used for physical mapping of complex genomes

(c) They can be used to express eukaryotic proteins that require post translational modifications

(d) YAC do not favor cloning of large fragments of DNA

Correct Answer: (d) YAC do not favor cloning of large fragments of DNA

Solution: Yeast Artificial Chromosomes (YACs) are cloning vectors designed to clone very large fragments of DNA (typically 100 kb to over 1 Mb) in yeast (*Saccharomyces cerevisiae*) host cells. Key features and uses of YACs:

- **(a) YACs have ORS, Telomere and Centromere:** TRUE. To function as a chromosome in yeast, a YAC vector must contain:
    - **ARS (Autonomously Replicating Sequence):** Yeast origin of replication. (ORS might be a typo for ARS, or Origin of Replication Site).
    - **TEL (Telomeres):** Sequences at the ends of linear chromosomes, required for stability and complete replication.
    - **CEN (Centromere):** Sequence required for proper segregation of the chromosome during yeast cell division.
    - They also contain selectable markers for yeast and often for *E. coli* (for initial cloning steps).
- **(b) They are used for physical mapping of complex genomes:** TRUE. Due to their ability to clone very large DNA fragments, YACs were crucial in early genome mapping projects (e.g., the Human Genome Project) for creating ordered libraries of large genomic segments.
- **(c) They can be used to express eukaryotic proteins that require post translational modifications:** TRUE. Since yeast is a eukaryotic host, it

possesses the cellular machinery for many post-translational modifications (e.g., glycosylation, phosphorylation) that are common in other eukaryotes, including mammals. This makes YACs (and yeast expression systems in general) suitable for expressing some complex eukaryotic proteins that might not fold or modify correctly in prokaryotic hosts like *E. coli*.

- **(d) YAC do not favor cloning of large fragments of DNA:** FALSE. This is the opposite of their main advantage. YACs are specifically designed and used because they **do favor** and can accommodate very large DNA fragments, much larger than plasmids, phages, or cosmids.

The question asks for the incorrect statement. Statement (d) is incorrect.

$$\boxed{\text{YAC do not favor cloning of large fragments of DNA}}$$

Quick Tip

Quick Tip:

- **Yeast Artificial Chromosomes (YACs):** Cloning vectors that replicate as linear chromosomes in yeast.
- **Key features:** ARS (origin), CEN (centromere), TEL (telomeres), selectable markers.
- **Main advantage:** Can clone very large DNA inserts (hundreds of kilobases to megabases).
- Used for genomic libraries of complex genomes, physical mapping, and expressing large genes or eukaryotic proteins.

92.

For expression of eukaryotic gene in a prokaryotic system, which sequence has to be inserted from its first codon? (The question phrasing "inserted from its first codon" is a bit unusual. It likely means "inserted *before* its first codon" or what sequence is needed upstream for prokaryotic expression machinery to recognize it.)

(a) Kozak sequence

(b) Shine Dalgarno sequence

(c) Enhancers

(d) Silencers

Correct Answer: (b) Shine Dalgarno sequence

Solution: For the expression of a gene in a host system, specific regulatory sequences are required for transcription and translation initiation.

- **Prokaryotic Translation Initiation:** In prokaryotes (like *E. coli*), the ribosome (specifically the 16S rRNA in the 30S small subunit) binds to a specific sequence on the mRNA called the **Shine-Dalgarno (SD) sequence**. This sequence is typically located a few nucleotides upstream (5') of the start codon (usually AUG). The SD sequence helps to correctly position the ribosome on the mRNA for translation initiation.

- **Eukaryotic Translation Initiation:** In eukaryotes, the small ribosomal subunit (40S) typically binds at the 5' cap of the mRNA and then scans along the mRNA until it encounters the start codon (AUG). The efficiency of initiation can be influenced by the sequence context around the start codon, known as the **Kozak sequence** (e.g., (gcc)gccRccAUGG, where R is a purine).

The question asks about expressing a eukaryotic gene in a **prokaryotic system**. Therefore, for the prokaryotic ribosome to recognize and translate the eukaryotic mRNA (produced from the eukaryotic gene), a prokaryotic ribosome binding site, i.e., a Shine-Dalgarno sequence, must be present upstream of the start codon of the eukaryotic coding sequence. This SD sequence needs to be engineered into the expression vector if the eukaryotic gene's natural context doesn't provide one that works in prokaryotes.
Let's analyze the options: (a) Kozak sequence: Important for translation initiation in *eukaryotes*. (b) **Shine Dalgarno sequence:** Required for ribosome binding and

translation initiation in *prokaryotes*. This is the correct answer. (c) Enhancers: DNA sequences that increase the rate of transcription of a gene in *eukaryotes*. They are cis-acting regulatory elements for transcription, not directly translation initiation. (d) Silencers: DNA sequences that decrease or repress the transcription of a gene in *eukaryotes*.

Therefore, for expression of a eukaryotic gene in a prokaryotic system, a Shine-Dalgarno sequence needs to be appropriately positioned upstream of the start codon.

$\boxed{\text{Shine Dalgarno sequence}}$

Quick Tip

Quick Tip:

- **Shine-Dalgarno Sequence (Prokaryotes):** Ribosome binding site on mRNA, upstream of start codon. Pairs with 16S rRNA.
- **Kozak Sequence (Eukaryotes):** Consensus sequence around the start codon (AUG) that enhances translation initiation efficiency. Ribosome binds 5' cap and scans.
- For heterologous gene expression (e.g., eukaryotic gene in prokaryote), appropriate regulatory signals of the host system must be provided.

93.

The correct sequence of enzymes used for cDNA library preparation is

(a) Reverse transcriptase, RNAs H, DNA polymerase, Terminal transferase

(b) RNAs H, DNA polymerase, Reverse transcriptase, Terminal transferase

(c) DNA polymerase, Terminal transferase, Reverse transcriptase, RNAs H

(d) Reverse transcriptase, Terminal transferase, RNAs H, DNA polymerase

Correct Answer: (a) Reverse transcriptase, RNAs H, DNA polymerase, Terminal transferase (Terminal transferase is for specific cloning strategies, not always essential for basic cDNA synthesis, but a common step in some library preps).

Solution: A cDNA (complementary DNA) library is a collection of DNA copies made from the mRNA molecules isolated from a cell or tissue type. It represents the genes that are being expressed (transcribed into mRNA) at a particular time. The general steps and enzymes involved in cDNA synthesis and library preparation are: 1. **mRNA Isolation:** Isolate total RNA and then purify mRNA (e.g., using its poly(A) tail). 2. **First-Strand cDNA Synthesis:**

- An oligo(dT) primer (complementary to the poly(A) tail) or random primers are annealed to the mRNA.
- **Reverse Transcriptase** (an RNA-dependent DNA polymerase) synthesizes a single-stranded DNA copy (the first cDNA strand) complementary to the mRNA template. This creates an mRNA-cDNA hybrid.

3. **Second-Strand cDNA Synthesis:**

- The mRNA strand in the mRNA-cDNA hybrid is typically degraded or removed. This can be done using:
  - **RNase H (RNAs H):** An enzyme that specifically degrades the RNA strand of an RNA-DNA hybrid.
  - Alkaline hydrolysis (less common now).
- The remaining single-stranded cDNA is then used as a template to synthesize the second complementary DNA strand. This is done using:
  - **DNA Polymerase I** (often its Klenow fragment, which has polymerase and 3'→5' exonuclease activity but lacks 5'→3' exonuclease activity). Self-priming (hairpin loop formation at the 3' end of the first cDNA strand) or specific priming methods can be used.

This results in double-stranded cDNA (dsDNA). 4. **Modification of cDNA ends (for cloning):**

- The ends of the dsDNA may need to be made blunt (e.g., using T4 DNA polymerase).
- Linkers or adaptors (short, synthetic DNA sequences containing restriction enzyme sites) may be ligated to the ends of the dsDNA to facilitate cloning into a vector.
- Alternatively, homopolymer tailing can be done using **Terminal Deoxynucleotidyl Transferase (Terminal Transferase)**. This enzyme adds a string of identical nucleotides (e.g., poly(dC)) to the 3' ends of the dsDNA, which can then be annealed to a vector tailed with a complementary homopolymer (e.g., poly(dG)).

5. **Ligation into Vector and Library Construction:** The modified dsDNA fragments are ligated into a suitable cloning vector (e.g., plasmid, phage), and these recombinant molecules are introduced into host cells (e.g., *E. coli*) to create the cDNA library.

Let's evaluate the sequence in option (a): "Reverse transcriptase, RNAs H, DNA polymerase, Terminal transferase"

- Reverse transcriptase: First-strand synthesis. Correct.
- RNAs H: Degradation of mRNA template after first strand. Correct.
- DNA polymerase: Second-strand synthesis. Correct.
- Terminal transferase: End modification (tailing) for cloning. A possible subsequent step. Correct sequence.

This sequence of enzyme usage is logical and standard for many cDNA library preparation protocols. Other options reorder these in ways that are not standard. For example, DNA polymerase before Reverse Transcriptase makes no sense for starting from mRNA.

$$\boxed{\text{Reverse transcriptase, RNAs H, DNA polymerase, Terminal transferase}}$$

Quick Tip

Quick Tip:

- cDNA synthesis from mRNA: 1. Primer annealing (e.g., oligo(dT)). 2. First strand synthesis by **Reverse Transcriptase**. 3. mRNA degradation by **RNase H**. 4. Second strand synthesis by **DNA Polymerase**.
- Further steps for library construction often involve modifying cDNA ends (e.g., adding linkers, tailing with **Terminal Transferase**) and ligating into vectors.

94.

Which vector is not suitable for Genomic DNA library construction?

(a) λ replacement vector

(b) Yeast Artificial Chromosomes

(c) Bacterial Artificial Chromosomes

(d) Plasmids

Correct Answer: (d) Plasmids (Generally for smaller inserts, less suitable for representative genomic libraries of large genomes compared to others listed).

Solution: A genomic DNA library is a collection of cloned DNA fragments that ideally represents the entire genome of an organism. The choice of vector for constructing a genomic library depends on the size of the genome and the desired size of the cloned fragments. For large genomes (e.g., mammalian, plant), vectors that can accommodate large DNA inserts are preferred to ensure the library is representative and manageable in terms of the number of clones.

Let's analyze the suitability of the vectors listed:

- **(a) λ replacement vector (Lambda phage replacement vectors):** These are derived from bacteriophage lambda. They can accommodate DNA inserts typically in the range of 9-23 kb (kilobase pairs) by replacing a non-essential "stuffer" fragment of the phage genome. They are suitable for genomic libraries, especially for organisms with moderately sized genomes or for specific sub-genomic libraries.

- **(b) Yeast Artificial Chromosomes (YACs):** These vectors can clone very large DNA fragments, typically from 100 kb up to 1 Mb (megabase) or more. They are excellent for constructing genomic libraries of organisms with large, complex genomes (e.g., human, mouse) and for physical mapping.
- **(c) Bacterial Artificial Chromosomes (BACs):** These are based on the F-plasmid of *E. coli* and can stably maintain large DNA inserts, typically 100-300 kb. BACs are widely used for genomic libraries of complex genomes due to their stability and ease of manipulation compared to YACs.
- **(d) Plasmids:** Standard plasmid vectors (e.g., pBR322, pUC series) typically accommodate relatively small DNA inserts, usually up to about 10-15 kb. While they can be used for genomic libraries of organisms with very small genomes (e.g., some viruses or bacteria), they are generally **not suitable** for constructing representative genomic libraries of organisms with large genomes. This is because a very large number of plasmid clones would be required to cover the entire genome, making the library unwieldy and difficult to screen.

The question asks which vector is "not suitable" for genomic DNA library construction. While technically plasmids *can* be used for very small genomes, compared to the other options which are all designed for larger inserts (typical for "genomic library construction" in a general sense, implying larger genomes), plasmids are the least suitable or often unsuitable for representative libraries of complex genomes. Thus, plasmids are generally considered less suitable for constructing comprehensive genomic libraries of most organisms compared to lambda vectors, BACs, or YACs.

$$\boxed{\text{Plasmids}}$$

Quick Tip

Quick Tip:

- Choice of vector for genomic library depends on insert size capacity:
  - **Plasmids:** Small inserts (up to 15 kb).
  - **Lambda (λ) phage vectors:** Moderate inserts (9-23 kb for replacement vectors).
  - **Cosmids:** Larger inserts (30-45 kb).
  - **Bacterial Artificial Chromosomes (BACs):** Large inserts (100-300 kb). Stable.
  - **Yeast Artificial Chromosomes (YACs):** Very large inserts (100 kb - >1 Mb).
- For large, complex genomes, BACs and YACs are preferred for comprehensive genomic libraries. Plasmids are generally not suitable for this purpose.

95.

Match the following

X	Ribosome binding site	1	Enhance transcription
Y	Promoter	2	Shine Dalgarno Sequence
Z	Enhancer	3	Molecular Switches to turn on transcription

(a) X-2; Y-3; Z-1

(b) X-1; Y-2; Z-3

(c) X-3; Y-1; Z-2

(d) X-3; Y-2; Z-1

Correct Answer: (a) X-2; Y-3; Z-1

Solution: Let's match the terms with their descriptions:

- **X. Ribosome binding site:** This is a sequence on mRNA where the ribosome binds to initiate translation.

  - 2. Shine Dalgarno Sequence: This is the ribosome binding site in prokaryotic mRNA.

  So, X $\rightarrow$ 2.

- **Y. Promoter:** A DNA sequence where RNA polymerase binds to initiate transcription. It controls the start of gene expression.

  - 3. Molecular Switches to turn on transcription: Promoters are key molecular switches that regulate the initiation (turning on/off or modulating the level) of transcription.

  So, Y $\rightarrow$ 3.

- **Z. Enhancer:** A DNA sequence that can increase the rate of transcription of a gene. Enhancers can be located far from the gene they regulate and can function in either orientation. They are bound by activator proteins.

  - 1. Enhance transcription: This directly describes the function of an enhancer.

  So, Z $\rightarrow$ 1.

The matching is X-2, Y-3, Z-1. This corresponds to option (a).

$$\boxed{\text{X-2; Y-3; Z-1}}$$

Quick Tip

Quick Tip:

- **Ribosome Binding Site (RBS):** Sequence on mRNA for ribosome attachment to start translation (e.g., Shine-Dalgarno in prokaryotes, Kozak sequence context in eukaryotes).
- **Promoter:** DNA sequence where RNA polymerase binds to start transcription. Acts as a switch.
- **Enhancer:** DNA sequence that binds activator proteins to increase transcription rate, can be distant from the gene.

96.

Which is incorrect with reference to transposon?

(a) It is known as jumping genes
(b) It was first discovered by Barbara McClintock
(c) Retrotransposons can move through RNA intermediates
(d) 2/3 of human genome is made up of transposons

Correct Answer: (d) 2/3 of human genome is made up of transposons (The fraction is large, around 45-50

Solution: Transposons (transposable elements or "jumping genes") are DNA sequences that can change their position within a genome, either by a "cut and paste" mechanism (Class II transposons, DNA transposons) or via an RNA intermediate ("copy and paste" mechanism, Class I transposons, retrotransposons). Let's analyze the statements: (a) "It is known as jumping genes": TRUE. This is a common informal name for transposons due to their ability to move within the genome. (b) "It was first discovered by Barbara McClintock": TRUE. Barbara McClintock discovered transposable elements in maize (corn) in the 1940s and 1950s, for which she received the Nobel Prize in Physiology or Medicine in 1983. (c) "Retrotransposons can move through RNA intermediates": TRUE. Retrotransposons (Class I) move via a "copy-and-paste" mechanism that involves transcription of the retrotransposon DNA into an RNA intermediate, followed by reverse transcription of this RNA back into DNA, which then inserts at a new genomic location. (d) "2/3 of human genome is made up of transposons": FALSE. Transposable elements and their remnants make up a very significant portion of the human genome, estimated to be around 45 Therefore, the incorrect statement is (d).

$$\boxed{\text{2/3 of human genome is made up of transposons}}$$

Quick Tip

Quick Tip:

- **Transposons ("Jumping Genes"):** Mobile DNA elements.
- Discovered by Barbara McClintock in maize.
- **Class I (Retrotransposons):** Move via an RNA intermediate (copy-and-paste). E.g., LINEs, SINEs, LTR retrotransposons.
- **Class II (DNA Transposons):** Move directly as DNA (cut-and-paste or replicative transposition).
- Transposons constitute a large fraction of many eukaryotic genomes (e.g., 45-50

97.

Which one makes correct components of a PCR reaction?

(a) DNA template, Primers, DNTPs

(b) DNA polymerase, DNTPs, Primers, DNA template

(c) DNA template, Taq DNA polymerase, Primers, DNTPs

(d) DNA template, DNTPs, Taq DNA polymerase

Correct Answer: (c) DNA template, Taq DNA polymerase, Primers, DNTPs (This is the most complete standard set).

Solution: The Polymerase Chain Reaction (PCR) is a technique used to amplify a specific segment of DNA *in vitro*. The essential components of a PCR reaction mixture are: 1. **DNA Template:** The DNA molecule containing the target sequence to be amplified. 2. **Primers (Forward and Reverse):** Short, single-stranded DNA sequences (oligonucleotides) that are complementary to the sequences flanking the target region. They provide a starting point (3'-OH group) for DNA synthesis by the polymerase. Two primers are needed: one for the forward strand and one for the reverse strand. 3. **DNA Polymerase:** A thermostable DNA polymerase that can withstand the high temperatures used for DNA denaturation during PCR cycles. **Taq DNA polymerase** (from *Thermus aquaticus*) is the most commonly used. 4. **Deoxynucleotide Triphosphates (dNTPs):** The building blocks of DNA – dATP, dGTP, dCTP, and dTTP – which are incorporated by the DNA polymerase to synthesize new DNA strands. 5. **Buffer Solution:** Provides a suitable chemical environment (pH, salt concentration) for the activity of the DNA polymerase. Often contains Mg^{2+} ions, which are cofactors for DNA polymerase.

Let's analyze the options: (a) "DNA template, Primers, DNTPs": Missing DNA polymerase. (b) "DNA polymerase, DNTPs, Primers, DNA template": This is a correct set of components. "DNA polymerase" is general. (c) "DNA template, Taq DNA polymerase, Primers, DNTPs": This is also a correct set, and more specific by naming "Taq DNA polymerase," which is standard. This is the most complete and specific correct option. (d) "DNA template, DNTPs, Taq DNA polymerase": Missing primers. DNA polymerase cannot initiate synthesis without primers.

Comparing (b) and (c), option (c) is more specific and accurately lists the common thermostable polymerase used. Both list the essential components. Option (c) is generally preferred as it specifies Taq polymerase, which is key to PCR's practicality.

$$\boxed{\text{DNA template, Taq DNA polymerase, Primers, DNTPs}}$$

Quick Tip

Quick Tip:

- Essential PCR Components:
  - DNA Template (target DNA)
  - Pair of Primers (forward and reverse)
  - Thermostable DNA Polymerase (e.g., Taq polymerase)
  - Deoxynucleotide Triphosphates (dNTPs: dATP, dGTP, dCTP, dTTP)
  - Buffer (containing Mg^{2+} ions)
- PCR Cycles: Denaturation → Annealing → Extension.

98.

Which technique is not used for site directed mutagenesis?

(a) Oligonucleotide directed mutagenesis

(b) Cassette mutagenesis

(c) Physical mutagenesis

(d) SDM with PCR

Correct Answer: (c) Physical mutagenesis

Solution: Site-directed mutagenesis (SDM) is a molecular biology technique used to create specific, targeted changes (mutations) in a DNA sequence. The goal is to alter one or more specific nucleotides at a defined site within a gene or DNA fragment. Common techniques for site-directed mutagenesis include:

- **(a) Oligonucleotide-directed mutagenesis:** This is a classic and widely used method. It involves using a short, synthetic DNA oligonucleotide (primer) that contains the desired mutation. This primer is annealed to a single-stranded DNA template (e.g., from a phagemid or denatured plasmid), and DNA polymerase extends it to create a complementary strand incorporating the mutation.

Subsequent replication and selection yield DNA molecules with the specific mutation.

- **(b) Cassette mutagenesis:** Involves synthesizing a DNA fragment (cassette) containing the desired mutation(s) and then ligating this cassette into a target DNA molecule by replacing a corresponding wild-type segment between two restriction enzyme sites.
- **(d) SDM with PCR (PCR-based site-directed mutagenesis):** Various PCR-based strategies are used for SDM, often involving primers that contain mismatches to introduce the desired mutation. Examples include overlap extension PCR, megaprimer PCR, and QuikChange site-directed mutagenesis.

Let's analyze the options: (a), (b), and (d) are all established techniques for site-directed mutagenesis, aiming for specific changes at defined locations.
(c) **Physical mutagenesis:** This refers to the use of physical mutagens (e.g., UV radiation, X-rays, ionizing radiation) to induce mutations in DNA. Physical mutagens generally cause **random mutations** throughout the genome, rather than targeted changes at a specific site. While physical mutagenesis is used to create mutants for screening or research, it is **not a technique for site-directed mutagenesis**, which implies precision and control over the location and type of mutation.
Therefore, physical mutagenesis is not used for site-directed mutagenesis.

$$\boxed{\text{Physical mutagenesis}}$$

Quick Tip

Quick Tip:

- **Site-Directed Mutagenesis (SDM):** Introduces specific, desired mutations at a defined location in a DNA sequence.
- Common SDM techniques: Oligonucleotide-directed (e.g., Kunkel method), PCR-based methods, cassette mutagenesis.
- **Random Mutagenesis:** Introduces mutations non-specifically throughout a gene or genome. Can be induced by chemical mutagens (e.g., EMS, NTG) or physical mutagens (e.g., UV, X-rays).

99.

Which is an endonuclease in CRISPR Cas9 Technique?

(a) gRNA

(b) Cas 9

(c) PAM

(d) Cr RNA

Correct Answer: (b) Cas 9

Solution: The CRISPR-Cas9 system is a powerful gene editing tool derived from a bacterial adaptive immune system. It involves two key components for targeted DNA cleavage: 1. **Cas9 (CRISPR-associated protein 9):** This is an **RNA-guided DNA endonuclease**. It's an enzyme that uses a guide RNA (gRNA) molecule to find a specific target DNA sequence and then makes a double-strand break (DSB) in the DNA at that site. Cas9 has two nuclease domains (HNH and RuvC) that cut the two DNA strands. 2. **Guide RNA (gRNA):** In engineered CRISPR-Cas9 systems, this is often a synthetic single guide RNA (sgRNA), which combines the features of two natural bacterial RNAs:

- **crRNA (CRISPR RNA):** Contains a 20 nucleotide sequence (spacer) that is complementary to the target DNA sequence, providing specificity. (Option d)

- **tracrRNA (trans-activating crRNA):** Binds to the crRNA and also to the Cas9 protein, forming a scaffold for the complex.

The gRNA directs the Cas9 endonuclease to the correct target site in the genome. (Option a refers to the guide RNA).
Other terms:

- **PAM (Protospacer Adjacent Motif) (Option c):** A short DNA sequence (e.g., NGG for *Streptococcus pyogenes* Cas9) that is located immediately downstream of the target DNA sequence complementary to the gRNA spacer. The Cas9 enzyme requires the presence of a PAM site near the target sequence for efficient DNA binding and cleavage. The PAM itself is part of the target DNA, not the endonuclease.

The question asks which component is an endonuclease. The Cas9 protein is the endonuclease enzyme responsible for cutting the DNA.

$$\boxed{\text{Cas 9}}$$

Quick Tip

Quick Tip:

- **CRISPR-Cas9 System Components:**
    - **Cas9 Protein:** An RNA-guided DNA endonuclease (enzyme that cuts DNA).
    - **Guide RNA (gRNA/sgRNA):** Directs Cas9 to the target DNA sequence. Contains a crRNA-like spacer for target recognition and a tracrRNA-like scaffold for Cas9 binding.
- **PAM Sequence:** A short sequence in the target DNA, adjacent to the target site, required for Cas9 recognition and cleavage. Not part of the Cas9 enzyme or gRNA.

100.

Which is correct regarding ex vivo gene therapy?

(a) Therapeutic Genes are transferred to germ line cells

(b) Cells are modified outside body and transferred back to the body

(c) Genes are changed in cells when cells are inside the body

(d) Luxturna is an example of ex vivo gene therapy

Correct Answer: (b) Cells are modified outside body and transferred back to the body

Solution: Gene therapy involves introducing genetic material into an individual's cells to treat or cure a disease. There are two main approaches: 1. ***Ex vivo* Gene Therapy:**

- Cells are first **removed** from the patient's body (e.g., bone marrow cells, lymphocytes).
- These cells are then **genetically modified *in vitro* (outside the body)** in the laboratory, for example, by introducing a therapeutic gene using a viral vector or other gene delivery methods.
- The modified cells are selected, often expanded in culture, and then **transferred back into the patient's body**.

2. ***In vivo* Gene Therapy:**

- The therapeutic gene (often packaged in a vector) is directly delivered into cells **inside the patient's body** (e.g., by injection into a specific tissue or systemically).

Let's analyze the options: (a) "Therapeutic Genes are transferred to germ line cells": This describes germline gene therapy, which alters genes in sperm, eggs, or embryos, leading to heritable changes. Both *ex vivo* and *in vivo* approaches generally target somatic cells (non-reproductive cells) for ethical and safety reasons, though germline therapy is a separate concept. This option is not a definition of *ex vivo* specifically. (b) "Cells are modified outside body and transferred back to the body": This accurately describes the core procedure of *ex vivo* gene therapy. (c) "Genes are changed in cells when cells are inside the body": This describes *in vivo* gene therapy. (d) "Luxturna is an example of ex vivo gene therapy": Luxturna (voretigene neparvovec) is an FDA-approved gene therapy for a rare inherited retinal dystrophy. It is administered via subretinal injection, meaning the therapeutic gene (in an AAV vector) is delivered directly to cells *inside the eye*. Therefore, Luxturna is an example of ***in vivo*** gene therapy, not *ex vivo*.

Thus, option (b) correctly describes *ex vivo* gene therapy.

$$\boxed{\text{Cells are modified outside body and transferred back to the body}}$$

Quick Tip

Quick Tip:

- ***Ex vivo* Gene Therapy:** Cells removed from patient → Genetically modified in lab → Modified cells returned to patient. (Ex = Outside)
- ***In vivo* Gene Therapy:** Therapeutic gene delivered directly into patient's body. (In = Inside)
- **Somatic Gene Therapy:** Targets non-reproductive cells. Changes are not heritable. (Most current gene therapies).
- **Germline Gene Therapy:** Targets reproductive cells (sperm, egg, embryo). Changes are heritable. Raises significant ethical concerns.

101.

Which blotting technique is used for detection of proteins?

(a) Southern blotting

(b) Northern blotting

(c) Western blotting

(d) Eastern blotting

Correct Answer: (c) Western blotting

Solution: Blotting techniques are used in molecular biology to transfer macromolecules (DNA, RNA, or proteins) from a gel (after electrophoresis) to a solid membrane support, where they can then be detected using specific probes.

- **Southern Blotting (Option a):** Used for the detection of specific **DNA** sequences. DNA fragments separated by gel electrophoresis are transferred to a membrane and then probed with a labeled DNA or RNA sequence complementary to the target DNA. (Named after Edwin Southern).
- **Northern Blotting (Option b):** Used for the detection of specific **RNA** sequences (e.g., to analyze gene expression by detecting mRNA). RNA molecules separated by gel electrophoresis are transferred to a membrane and probed with a labeled DNA or RNA sequence.
- **Western Blotting (Option c):** Used for the detection of specific **proteins**. Proteins are separated by gel electrophoresis (usually SDS-PAGE), transferred to a membrane (e.g., nitrocellulose or PVDF), and then probed, typically using specific antibodies that bind to the target protein. The bound antibody is then detected (e.g., using a secondary antibody conjugated to an enzyme that produces a colored or chemiluminescent signal).
- **Eastern Blotting (Option d):** A less common term, often used to refer to techniques for analyzing post-translational modifications of proteins (e.g., glycosylation, phosphorylation) or lipid analysis after blotting. It's not as standardized as the other three.

Therefore, Western blotting is the technique used for the detection of proteins.

$$\boxed{\text{Western blotting}}$$

Quick Tip

Quick Tip:

- Mnemonic for major blotting techniques (SNoW DRoP):
  - **S**outhern blot → **D**NA
  - **N**orthern blot → **R**NA
  - **W**estern blot → **P**rotein
- (Eastern blotting is for post-translational modifications or lipids - less common).

102.

Which of the following is not a variant of BLAST?

(a) BLASTX

(b) TBLASTNX

(c) BLASTP

(d) BLASTN

Correct Answer: (b) TBLASTNX (This is usually written as TBLASTX. TBLASTN exists. Let's check common BLAST variants.)

Solution: BLAST (Basic Local Alignment Search Tool) is a suite of programs used to compare biological sequence information (DNA or protein sequences) against sequence databases to find regions of local similarity. Different BLAST programs are designed for different types of query and database sequences:

- **BLASTN (Option d):** Compares a nucleotide query sequence against a nucleotide sequence database.
- **BLASTP (Option c):** Compares an amino acid (protein) query sequence against a protein sequence database.
- **BLASTX (Option a):** Translates a nucleotide query sequence in all six

possible reading frames and compares these translated protein sequences against a protein sequence database. (Nucleotide query vs. Protein database).

- **TBLASTN:** Translates a protein query sequence against a nucleotide sequence database (where database sequences are translated in all six reading frames). (Protein query vs. Nucleotide database).
- **TBLASTX:** Translates both the nucleotide query sequence and the nucleotide database sequences in all six reading frames, and then compares the resulting protein sequences. (Translated Nucleotide query vs. Translated Nucleotide database).

Let's analyze the options: (a) BLASTX: A standard BLAST variant (Nucleotide query translated → Protein DB). (b) TBLASTNX: This is an unusual concatenation. Standard variants are TBLASTN and TBLASTX. If "TBLASTNX" is meant to be "TBLASTX", it is a valid variant. If it's a typo for "TBLASTN", that's also valid. However, "TBLASTNX" as a single program name is not standard. (c) BLASTP: A standard BLAST variant (Protein query → Protein DB). (d) BLASTN: A standard BLAST variant (Nucleotide query → Nucleotide DB).
The question asks which is "not a variant". TBLASTNX is not a standard name for a BLAST program. The components TBLASTN and TBLASTX are standard. It's likely that TBLASTNX as written is the intended "not a variant". If the options are to be taken literally, TBLASTNX is not a recognized BLAST program name.

$$\boxed{\text{TBLASTNX}}$$

Quick Tip

Quick Tip:

- Common BLAST programs:
  - **blastn:** Nucleotide query vs. nucleotide database.
  - **blastp:** Protein query vs. protein database.
  - **blastx:** Translated nucleotide query vs. protein database.
  - **tblastn:** Protein query vs. translated nucleotide database.
  - **tblastx:** Translated nucleotide query vs. translated nucleotide database.

103.

Proteomics refers to the study of

(a) Set of proteins in a specific region of the cell

(b) Biomolecules

(c) Set of proteins

(d) The entire set of expressed proteins in the cell

Correct Answer: (d) The entire set of expressed proteins in the cell

Solution: Proteomics is the large-scale study of proteins, particularly their structures, functions, interactions, and modifications. It aims to characterize the **proteome**, which is the entire complement of proteins produced or modified by an organism, system, tissue, or cell at a particular time and under specific conditions. Key aspects of proteomics include:

- Identification and quantification of proteins.
- Determination of protein structures and post-translational modifications.
- Analysis of protein interactions and protein networks.
- Study of protein function and localization.

Let's analyze the options: (a) "Set of proteins in a specific region of the cell": This is a part of proteomics (e.g., organellar proteomics), but proteomics is broader, encompassing the entire proteome. (b) "Biomolecules": Too general. Biomolecules include nucleic acids, carbohydrates, lipids, in addition to proteins. (c) "Set of proteins": This is closer, but option (d) is more precise. (d) "The entire set of expressed proteins in the cell" (or organism/tissue): This correctly defines the proteome, which is the subject of proteomics. It emphasizes "expressed" proteins, reflecting the dynamic nature of the proteome.

Therefore, proteomics refers to the study of the entire set of expressed proteins in a cell, tissue, or organism.

$$\boxed{\text{The entire set of expressed proteins in the cell}}$$

Quick Tip

Quick Tip:

- **Genome:** Entire set of genes of an organism. **Genomics:** Study of genomes.
- **Transcriptome:** Entire set of RNA transcripts in a cell/organism. **Transcriptomics:** Study of transcriptomes.
- **Proteome:** Entire set of proteins expressed by a genome, cell, tissue, or organism at a certain time. **Proteomics:** Study of proteomes.
- Proteomics is more complex than genomics because protein expression is dynamic and proteins undergo many post-translational modifications.

104.

The term Bioinformatics was coined by

(a) J.D Watson

(b) Pauline Hogeweg

(c) Margaret Dayhoff

(d) Frederic Sanger

Correct Answer: (b) Pauline Hogeweg

Solution: The term "bioinformatics" is generally credited to have been coined by **Paulien Hogeweg** and Ben Hesper in 1970 (or 1978 in some sources for its first appearance in a publication). They used it to refer to "the study of informatic processes in biotic systems." Let's consider the other individuals:

- (a) J.D. Watson: Co-discoverer of the structure of DNA (with Francis Crick, Maurice Wilkins, Rosalind Franklin). A key figure in molecular biology, but not the coiner of "bioinformatics."
- (c) Margaret Dayhoff: A pioneer in the field of bioinformatics. She created one of the first protein sequence databases (Atlas of Protein Sequence and Structure) and developed methods for sequence alignment and evolutionary analysis (e.g., PAM matrices). While a foundational figure, she did not coin the term "bioinformatics."
- (d) Frederic Sanger: A British biochemist who won two Nobel Prizes in Chemistry: one for determining the amino acid sequence of insulin, and another for developing methods for DNA sequencing (Sanger sequencing). Crucial for generating sequence data used in bioinformatics, but not the coiner of the term.

Therefore, Paulien Hogeweg (often along with Ben Hesper) is credited with coining the term bioinformatics.

$$\boxed{\text{Pauline Hogeweg}}$$

Quick Tip

Quick Tip:

- **Bioinformatics:** An interdisciplinary field that develops methods and software tools for understanding biological data, especially large and complex data sets (e.g., genomic, proteomic).
- Term coined by Paulien Hogeweg and Ben Hesper.
- Margaret Dayhoff was a pioneer in developing early bioinformatics tools and databases.

105.

Which of the alignment does not assume that the two sequences in question have similarity over the entire length?

(a) Local
(b) Global
(c) Heuristic
(d) Clustal

Correct Answer: (a) Local

Solution: Sequence alignment is a way of arranging DNA, RNA, or protein sequences to identify regions of similarity that may be a consequence of functional, structural, or evolutionary relationships. There are two main types of pairwise sequence alignment:

1. **Global Alignment:**

- Assumes that the two sequences are generally similar over their entire length.
- Attempts to align every residue in one sequence with a residue or a gap in the other sequence.
- Useful for comparing closely related sequences of similar length.
- Example algorithm: Needleman-Wunsch algorithm.

2. **Local Alignment:**

    - Does **not** assume that the two sequences are similar over their entire length.
    - Instead, it finds the regions of highest similarity between subsequences of the two sequences. It looks for conserved domains or motifs.
    - Useful for comparing more distantly related sequences, sequences of different lengths, or finding conserved domains within larger sequences.
    - Example algorithm: Smith-Waterman algorithm. BLAST is a heuristic method that performs local alignments.

Let's analyze the options: (a) **Local alignment:** This type specifically does not assume similarity over the entire length and seeks out the best matching sub-regions. This is the correct answer. (b) Global alignment: Assumes similarity over the entire length. (c) Heuristic: This refers to an approach or algorithm that finds an approximate solution, often faster than optimal algorithms (e.g., BLAST and FASTA are heuristic local alignment tools). It's a method type, not an alignment type (local vs. global) itself, though heuristic methods are often used for local alignments. (d) Clustal (e.g., ClustalW, Clustal Omega): This is a program for performing multiple sequence alignment (aligning three or more sequences), not pairwise alignment. Multiple sequence alignment often aims for a global-like alignment of the set of sequences.
Therefore, local alignment does not assume similarity over the entire length.

$$\boxed{\text{Local}}$$

Quick Tip

Quick Tip:

- **Global Alignment (e.g., Needleman-Wunsch):** Aligns sequences from end to end. Assumes overall similarity.
- **Local Alignment (e.g., Smith-Waterman, BLAST, FASTA):** Finds best matching segments/regions within sequences. Does not assume overall similarity. Useful for finding conserved domains or motifs.

106.

Clustal W is a ____ multiple alignment program available either as a stand-alone or on-line program.

(a) exhaustive

(b) block based

(c) progressive

(d) iterative

Correct Answer: (c) progressive

Solution: Clustal W (and its successor Clustal Omega) is a widely used computer program for performing **multiple sequence alignment (MSA)**. Multiple sequence alignment aligns three or more biological sequences (DNA, RNA, or protein). Clustal W employs a **progressive alignment** heuristic method. The main steps are: 1. **Pairwise Alignments:** All pairs of sequences are aligned (e.g., using a global alignment algorithm like Needleman-Wunsch) to calculate pairwise similarity scores. 2. **Guide Tree Construction:** A guide tree (phylogenetic tree or dendrogram) is constructed based on the pairwise similarity scores. This tree represents the presumed evolutionary relationships between the sequences, with more similar sequences clustering together. 3. **Progressive Alignment:** The sequences are then progressively aligned according to the branching order of the guide tree. Starting with the most closely related pairs, alignments are performed, and then these alignments (or consensus sequences/profiles derived from them) are aligned with other sequences or alignments, moving up the guide tree until all sequences are incorporated into the final multiple alignment. This progressive approach is a heuristic, meaning it does not guarantee finding the mathematically optimal multiple alignment (which is computationally very expensive for many sequences), but it generally produces good quality alignments in a reasonable amount of time.

Let's analyze the options: (a) exhaustive: Exhaustive methods (like dynamic programming for MSA) are computationally too intensive for more than a few sequences. Clustal W is heuristic. (b) block based: While MSA can identify conserved blocks, Clustal W's overall strategy is progressive, not primarily "block based" in the sense of programs like DIALIGN or Block Maker. (c) **progressive:** This accurately describes the core algorithmic strategy of Clustal W. (d) iterative: While some MSA programs use iterative refinement (e.g., MUSCLE, MAFFT, and Clustal Omega does incorporate iterative steps), the fundamental approach of Clustal W (the original) is primarily progressive based on a fixed guide tree. Iterative methods refine an initial alignment through multiple cycles.

Therefore, Clustal W is a progressive multiple alignment program.

$$\boxed{\text{progressive}}$$

Quick Tip

Quick Tip:

- **Clustal W / Clustal Omega:** Popular programs for multiple sequence alignment.
- Employ a **progressive alignment** strategy: 1. Calculate all pairwise alignments and similarities. 2. Construct a guide tree based on similarities. 3. Align sequences progressively following the guide tree ("once a gap, always a gap" for simple progressive).
- This is a heuristic approach, not guaranteed to find the optimal MSA.
- More advanced MSA tools may use iterative refinement or other algorithms.

107.

Which of the following is not a sequence alignment tool

(a) BLAST

(b) FASTA

(c) CLUSTAL

(d) ROSMAL

Correct Answer: (d) ROSMAL (Assuming ROSMAL is not a recognized sequence alignment tool. Others are well-known.)

Solution: Sequence alignment tools are software programs used to align biological sequences (DNA, RNA, or protein) to identify regions of similarity. Let's analyze the options: (a) **BLAST (Basic Local Alignment Search Tool):** A very widely used heuristic algorithm and program suite for finding regions of local similarity between sequences. It compares a query sequence against a database. It IS a sequence alignment tool. (b) **FASTA:** Another popular heuristic algorithm and program suite for sequence database searching and local sequence alignment. It was developed before BLAST but uses similar principles. It IS a sequence alignment tool. (c) **CLUSTAL**

(e.g., ClustalW, Clustal Omega): A widely used program for performing multiple sequence alignment (aligning three or more sequences). It IS a sequence alignment tool (specifically for multiple sequences). (d) **ROSMAL:** This term does not correspond to a well-known or standard sequence alignment tool in bioinformatics. There might be very specialized or obscure tools with similar names, but in the context of common bioinformatics tools, BLAST, FASTA, and CLUSTAL are standard.
Therefore, ROSMAL is the one that is likely "not a sequence alignment tool" among the common, widely recognized options.

$$\boxed{\text{ROSMAL}}$$

Quick Tip

Quick Tip:

- Common Sequence Alignment Tools:
  - **Pairwise Local Alignment:** BLAST, FASTA, Smith-Waterman algorithm implementations.
  - **Pairwise Global Alignment:** Needleman-Wunsch algorithm implementations.
  - **Multiple Sequence Alignment:** CLUSTAL (ClustalW, Clustal Omega), MUSCLE, MAFFT, T-Coffee.
- Always check for commonly known tools first when asked to identify one that doesn't belong.

108.

Which of the following is a data bank exclusively for proteins?

(a) DDBJ

(b) EMBL

(c) Genbank

(d) PDB

Correct Answer: (d) PDB (Protein Data Bank is for 3D structures, which implies protein or nucleic acid structures. If "exclusively for proteins" means primary sequence, then UniProt/Swiss-Prot would be better, but PDB is primarily protein structures.)

Solution: Biological sequence and structure databases are essential resources in bioinformatics.

- **Nucleotide Sequence Databases:** These store DNA and RNA sequence data. The major primary nucleotide sequence databases are:
  - **GenBank (Option c):** Maintained by NCBI (National Center for Biotechnology Information) in the USA.
  - **EMBL (European Molecular Biology Laboratory) Nucleotide Sequence Database (Option b):** Maintained by EBI (European Bioinformatics Institute). Now part of ENA (European Nucleotide Archive).
  - **DDBJ (DNA Data Bank of Japan) (Option a):** Maintained in Japan.

  These three databases (GenBank, EMBL/ENA, DDBJ) form the International Nucleotide Sequence Database Collaboration (INSDC) and exchange data daily.
- **Protein Sequence Databases:**
  - **UniProt (Universal Protein Resource):** A comprehensive resource for protein sequences and functional information, resulting from the merger of Swiss-Prot, TrEMBL, and PIR-PSD.
    - **Swiss-Prot:** Manually curated, high-quality protein sequences with rich annotation.
    - **TrEMBL:** Computationally annotated translations of EMBL/GenBank/DDBJ coding sequences.
  - NCBI Protein database (derived from GenBank translations etc.)
- **Protein Structure Databases:**
  - **PDB (Protein Data Bank) (Option d):** The primary international repository for 3D structural data of large biological molecules, including

proteins and nucleic acids, determined by methods like X-ray crystallography, NMR spectroscopy, and cryo-electron microscopy. While it contains nucleic acid structures too, it is overwhelmingly dominated by protein structures.

The question asks for a data bank "exclusively for proteins." (a) DDBJ: Nucleotide sequences. (b) EMBL: Nucleotide sequences. (c) Genbank: Nucleotide sequences (though it contains coding sequence annotations that translate to proteins). (d) PDB: Primarily 3D structures of proteins (and nucleic acids). If "exclusively for proteins" refers to its main content focus in terms of macromolecules being studied for structure, PDB fits well, although it also has some RNA/DNA structures. If it means primary sequences, then UniProt/Swiss-Prot would be the answer, but they are not options. Among the given options, PDB is the most appropriate answer as its primary focus is on protein (and nucleic acid) 3D structures, and thus implicitly on the proteins themselves as entities with structure. Options a, b, c are definitively nucleotide sequence databases. If "exclusively for proteins" means primary sequence, then this question is poorly optioned. If it means "primarily about protein information (structure in this case)", then PDB. Given the checkmark is on PDB, this latter interpretation is likely.

$$\boxed{\text{PDB (Protein Data Bank - primarily for 3D structures of proteins)}}$$

Quick Tip

Quick Tip:

- **INSDC (GenBank, ENA/EMBL, DDBJ):** Primary nucleotide sequence databases.
- **UniProt (Swiss-Prot, TrEMBL):** Primary protein sequence databases.
- **PDB (Protein Data Bank):** Database of 3D macromolecular structures (proteins and nucleic acids).
- Pay attention to "sequence" vs. "structure" and "nucleotide" vs. "protein".

109.

Which method is commonly employed for predicting the energetically favorable binding pose of a ligand with a target protein?

(a) Molecular dynamics simulation

(b) Quantum mechanics

(c) Docking simulation

(d) Monte Carlo simulation

Correct Answer: (c) Docking simulation

Solution: Predicting the binding pose (orientation and conformation) of a ligand (e.g., a drug molecule) within the binding site of a target protein, and estimating the strength of their interaction (binding affinity), is a central task in structure-based drug design and molecular modeling.

- **(c) Docking simulation (Molecular Docking):** This is a computational method specifically designed to predict the preferred binding orientation(s) of one molecule (ligand) to a second (receptor, typically a protein or nucleic acid) when they form a stable complex. Docking algorithms explore various possible poses of the ligand in the receptor's binding site and use scoring functions to rank these poses based on their predicted binding energy or fitness. This directly addresses finding an "energetically favorable binding pose."

- **(a) Molecular dynamics (MD) simulation:** MD simulates the time-dependent motion of atoms and molecules based on classical mechanics (Newton's laws of motion) and a force field that describes interatomic interactions. MD can be used to study the stability of a pre-docked ligand-protein complex, refine docked poses, explore conformational changes, or calculate binding free energies (e.g., using MM/PBSA, MM/GBSA, or free energy perturbation methods), but it's not primarily a method for *predicting the initial binding pose* from scratch in the same way docking is. It's often used after an initial pose is found.

- **(b) Quantum mechanics (QM):** QM methods provide a more accurate description of electronic structure and interatomic interactions than classical force fields. They can be used for very accurate energy calculations or to study reaction mechanisms, but they are computationally very expensive for large systems like protein-ligand complexes. QM might be used to parameterize force fields or to score a few select poses (e.g., QM/MM methods), but not typically for the extensive conformational search involved in predicting the binding pose initially.

- **(d) Monte Carlo (MC) simulation:** MC methods use random sampling to explore the conformational space of molecules or systems. MC can be used in docking algorithms (e.g., for conformational search of the ligand) or for other types of molecular simulations (e.g., protein folding, free energy calculations). While MC is a component of some docking strategies, "docking simulation" is the more specific term for the overall process of predicting binding poses.

Therefore, docking simulation is the method commonly employed for predicting the energetically favorable binding pose of a ligand with a target protein.

$$\boxed{\text{Docking simulation}}$$

Quick Tip

Quick Tip:

- **Molecular Docking:** Predicts how a ligand binds to a receptor (binding pose and affinity). Involves conformational search and scoring.
- **Molecular Dynamics (MD):** Simulates atomic motions over time. Used for studying dynamics, stability, conformational changes, refining structures, free energy calculations.
- **Quantum Mechanics (QM):** High-accuracy electronic structure calculations. Computationally expensive for large systems.
- **Monte Carlo (MC):** Stochastic simulation method using random sampling. Can be applied in various contexts, including docking.

110.

Which type of molecular modeling method is particularly suitable for studying large biomolecular systems, such as proteins and nucleic acids?

(a) Quantum mechanics

(b) Molecular dynamics simulation

(c) Docking simulation

(d) Energy minimization

Correct Answer: (b) Molecular dynamics simulation

Solution: Studying the behavior, dynamics, and conformational changes of large biomolecular systems like proteins and nucleic acids often requires methods that can handle many atoms over biologically relevant timescales.

- **(a) Quantum mechanics (QM):** QM methods (e.g., ab initio, DFT) provide very accurate descriptions of electronic structure and bonding but are computationally extremely expensive. They are generally limited to relatively small systems (hundreds of atoms at most for high-level QM, maybe a few thousand for simpler QM methods) or specific regions of interest within a larger system (e.g., active sites using QM/MM). Not typically suitable for studying the overall dynamics of large entire proteins or nucleic acids over long times.

- **(b) Molecular dynamics (MD) simulation:** MD uses classical mechanics (Newton's laws) and empirical force fields to simulate the motion of atoms in a system over time. Force fields are much simpler and computationally cheaper than QM, allowing MD simulations to be performed on very large systems (tens of thousands to millions of atoms, e.g., proteins in solvent, membranes, ribosomes) for timescales from picoseconds to microseconds or even longer. This makes MD particularly suitable for studying the dynamics, conformational changes, folding, and interactions of large biomolecules.
- **(c) Docking simulation:** As discussed previously, docking is primarily for predicting the binding pose of a ligand to a receptor. While it deals with biomolecules, it's focused on the binding event, not the general study of the biomolecular system's overall dynamics or behavior in isolation.
- **(d) Energy minimization:** This is a computational technique used to find a local minimum energy conformation (a stable structure) of a molecule or system by adjusting atomic coordinates to reduce potential energy. It is often used to prepare structures for MD or docking, or to refine models, but it does not simulate dynamics over time. It finds a static low-energy structure.

Therefore, molecular dynamics simulation is particularly suitable for studying the dynamics and behavior of large biomolecular systems.

$$\boxed{\text{Molecular dynamics simulation}}$$

Quick Tip

Quick Tip:

- **Molecular Dynamics (MD):** Simulates atomic motion using classical physics and force fields. Suitable for large systems and studying dynamics over time.
- **Quantum Mechanics (QM):** High accuracy for electronic properties, but computationally intensive, limited to smaller systems.
- **Docking:** Predicts ligand-receptor binding.
- **Energy Minimization:** Finds low-energy static conformations.

111.

What type of controller is commonly used to regulate temperature in a bioreactor?

(a) PID controller
(b) ON/OFF controller
(c) Bang-bang controller
(d) Proportional controller

Correct Answer: (a) PID controller

Solution: Regulating temperature accurately and stably is crucial in most bioreactor operations.

- **(b) ON/OFF controller (or Bang-bang controller - option c):** This is the simplest type of controller. It switches the heating or cooling element fully ON when the temperature deviates beyond a setpoint by a certain amount, and fully OFF when it returns within a range. This can lead to oscillations (overshoot and undershoot) around the setpoint and may not provide very precise temperature control.

- **(d) Proportional (P) controller:** The controller output is proportional to the error (difference between setpoint and measured temperature). It reduces oscillations compared to ON/OFF but can result in a steady-state error (offset).
- **(a) PID controller (Proportional-Integral-Derivative):** This is a widely used and effective feedback controller that combines three control actions:
    - **Proportional (P):** Responds to the current error.
    - **Integral (I):** Accumulates past errors to eliminate steady-state error (offset).
    - **Derivative (D):** Responds to the rate of change of error, anticipating future error and improving stability and transient response (reducing overshoot).

  PID controllers provide robust and precise control for many processes, including temperature regulation in bioreactors, where maintaining a stable and accurate temperature is often critical for optimal cell growth and product formation.

While simpler controllers like ON/OFF or P might be used in some less critical applications, for precise and stable temperature control in bioreactors, PID controllers are very commonly employed due to their ability to handle disturbances, eliminate steady-state error, and provide good transient response.

$$\boxed{\text{PID controller}}$$

Quick Tip

Quick Tip:

- **ON/OFF (Bang-Bang) Controller:** Simple, but causes oscillations.
- **Proportional (P) Controller:** Reduces error, but may have steady-state offset.
- **Proportional-Integral (PI) Controller:** Eliminates steady-state error, but can slow response or increase overshoot.
- **Proportional-Integral-Derivative (PID) Controller:** Combines benefits of P, I, and D actions for good stability, accuracy (no offset), and transient response. Widely used for process control.

112.

In a bioreactor, what is the term used to describe the resistance to mass transfer across the gas-liquid interface?

(a) Interfacial tension

(b) Gas holdup

(c) Mass transfer coefficient

(d) Film thickness

Correct Answer: (d) Film thickness (More precisely, the resistance is related to the film, and $1/k_L a$ is a resistance. $k_L a$ is volumetric mass transfer coefficient. "Film thickness" directly relates to the conceptual resistance of the film.)

Solution: Mass transfer across a gas-liquid interface (e.g., oxygen transfer from air bubbles to the liquid medium in an aerobic bioreactor) is often described by the two-film theory. This theory postulates the existence of stagnant or slow-moving films on either side of the interface (a gas film and a liquid film) through which the solute must diffuse. The **resistance to mass transfer** is considered to reside primarily within these films.

- The thickness of these hypothetical films influences the resistance. A thicker film means a longer diffusion path and thus higher resistance to mass transfer.
- The overall mass transfer rate is often characterized by a volumetric mass transfer coefficient ($k_L a$), where k_L is the liquid-side mass transfer coefficient and a is the interfacial area per unit volume.
- The reciprocal of the mass transfer coefficient ($1/k_L$) can be considered a measure of the resistance in the liquid film. Similarly for the gas film ($1/k_G$).

Let's analyze the options: (a) Interfacial tension: A property of the interface between two immiscible phases (like gas and liquid). It affects bubble size and interfacial area, but it is not directly "the resistance" itself, though it influences a. (b) Gas holdup: The volume fraction of gas in the gas-liquid dispersion. It relates to interfacial area a, but is not the resistance. (c) Mass transfer coefficient (k_L or $k_L a$): This coefficient quantifies the *rate* of mass transfer, not the resistance itself. Resistance is inversely proportional to the coefficient (e.g., $1/k_L$). (d) **Film thickness:** According to the two-film theory, the primary resistance to mass transfer lies within thin stagnant films at the gas-liquid interface. The thickness of these films directly contributes to the diffusional resistance. (Resistance $\propto$ thickness / diffusivity).
Therefore, "film thickness" is the term most directly related to the concept of resistance to mass transfer across the interface according to the film theory. A greater film thickness implies greater resistance. While $1/k_L a$ is the overall volumetric mass transfer resistance, "film thickness" is a more fundamental concept from the theory explaining this resistance.

$$\boxed{\text{Film thickness}}$$

Quick Tip

Quick Tip:

- **Two-Film Theory:** Assumes stagnant films on gas and liquid sides of the interface, where mass transfer occurs by molecular diffusion.
- Resistance to mass transfer is primarily within these films.
- Factors affecting film thickness (and thus k_L): Agitation, turbulence, fluid properties.
- Overall Volumetric Mass Transfer Coefficient ($k_L a$): Combines liquid-side coefficient (k_L) and interfacial area per unit volume (a). Higher $k_L a$ means better mass transfer (lower resistance).

113.

Which of the following is an example of in-situ bioremediation?

(a) Pumping contaminated groundwater to the surface for treatment

(b) Excavating contaminated soil and treating it in a bioreactor

(c) Injecting microorganisms directly into the contaminated site

(d) Spraying chemical agents onto polluted surfaces

Correct Answer: (c) Injecting microorganisms directly into the contaminated site

Solution: Bioremediation techniques can be broadly classified as *in-situ* or *ex-situ*:

- ***In-situ* Bioremediation:** Involves treating the contaminated material (soil, groundwater) **at its original location**, without excavation or removal. This often involves stimulating the activity of indigenous microorganisms or introducing specialized microbes directly into the contaminated zone.
- ***Ex-situ* Bioremediation:** Involves removing the contaminated material from its original location and treating it elsewhere, e.g., in bioreactors, landfarms, or biopiles.

Let's analyze the options: (a) "Pumping contaminated groundwater to the surface for treatment": This is an *ex-situ* method (specifically, "pump-and-treat"). The water is removed from its site for treatment. (b) "Excavating contaminated soil and treating it in a bioreactor": This is an *ex-situ* method. The soil is removed. (c) "Injecting microorganisms directly into the contaminated site": This describes an *in-situ* approach. The treatment occurs at the location of contamination. This can involve bioaugmentation (adding microbes) or biostimulation (adding nutrients/oxygen to enhance indigenous microbes). (d) "Spraying chemical agents onto polluted surfaces": This describes chemical remediation, not bioremediation (which uses biological agents). Therefore, injecting microorganisms directly into the contaminated site is an example of in-situ bioremediation.

$$\boxed{\text{Injecting microorganisms directly into the contaminated site}}$$

Quick Tip

Quick Tip:

- ***In-situ* bioremediation:** Treatment occurs at the contaminated site itself (e.g., bioventing, biosparging, bioaugmentation by injection). Latin "in situ" means "in the original place."
- ***Ex-situ* bioremediation:** Contaminated material is excavated/removed and treated elsewhere (e.g., landfarming, biopiles, bioreactors). Latin "ex situ" means "out of place."

114.

Which of the following is an example of a primary metabolite?

(a) Antibiotics

(b) Alkaloids

(c) Amino acids

(d) Flavonoids

Correct Answer: (c) Amino acids

Solution: Metabolites are classified as primary or secondary:

- **Primary Metabolites:** Directly involved in normal growth, development, and reproduction. Essential for cell survival. Produced during the active growth phase (trophophase). Examples include amino acids, nucleotides, simple sugars, organic acids of central pathways (like citric acid, pyruvate), lipids, vitamins, ethanol (from primary fermentation).
- **Secondary Metabolites:** Not directly involved in growth or reproduction but often have ecological roles or specialized functions. Production often occurs during stationary phase or under stress. Examples include antibiotics, alkaloids, toxins, pigments, steroids, flavonoids.

Let's analyze the options: (a) Antibiotics: Secondary metabolites. (b) Alkaloids (e.g., morphine, caffeine, nicotine): Secondary metabolites, often with pharmacological activity or defense roles. (c) **Amino acids:** The building blocks of proteins, essential for all living cells. They are primary metabolites. (d) Flavonoids: A large class of plant secondary metabolites, often pigments, with roles in signaling, defense, UV protection. Therefore, amino acids are primary metabolites.

$$\boxed{\text{Amino acids}}$$

Quick Tip

Quick Tip:

- Primary metabolites are essential for basic life functions and growth (e.g., amino acids, sugars, ATP).
- Secondary metabolites are not essential for basic growth but often have specialized roles (e.g., antibiotics, toxins, pigments, alkaloids).

115.

Which NCBI database is used for searching and retrieving biomedical literature?

(a) GenBank

(b) PubMed

(c) UniProt

(d) BLAST

Correct Answer: (b) PubMed

Solution: The National Center for Biotechnology Information (NCBI) hosts a variety of important biological databases and tools.

- **(a) GenBank:** A primary nucleotide sequence database containing publicly available DNA sequences.
- **(b) PubMed:** A free search engine accessing primarily the MEDLINE database of references and abstracts on life sciences and biomedical topics. It provides access to biomedical literature, including journal articles, and links to full-text content where available (e.g., via PubMed Central).
- **(c) UniProt (Universal Protein Resource):** A comprehensive database of protein sequence and functional information. It's a collaboration between Swiss Institute of Bioinformatics (SIB), European Bioinformatics Institute (EBI), and Protein Information Resource (PIR). NCBI also has its own protein database.
- **(d) BLAST (Basic Local Alignment Search Tool):** A suite of programs used to compare biological sequences (DNA or protein) against sequence databases to find regions of similarity. It's a search tool for sequences, not primarily for literature.

Therefore, PubMed is the NCBI database (or more accurately, a search interface to databases like MEDLINE) used for searching and retrieving biomedical literature.

$$\boxed{\text{PubMed}}$$

Quick Tip

Quick Tip:

- **PubMed:** Literature database (MEDLINE abstracts, links to full text).
- **GenBank:** DNA/RNA sequences.
- **UniProt/Swiss-Prot/NCBI Protein DB:** Protein sequences and information.
- **BLAST:** Sequence similarity search tool.
- **PDB:** 3D structures of macromolecules.

116.

Nucleosome a repeating structural unit within eukaryotic chromatin is made up of

(a) 140 bp of DNA making 1.65 negative super helical turn wrapped around a hexamer of histones

(b) 146 bp of DNA making 1.65 negative super helical turn wrapped around a dimer of histones

(c) 140 bp of DNA making 1.65 negative super helical turn wrapped around an octamer of histones

(d) 146 bp of DNA making 1.65 negative super helical turn wrapped around an octamer of histones

Correct Answer: (d) 146 bp of DNA making 1.65 negative super helical turn wrapped around an octamer of histones

Solution: The nucleosome is the fundamental repeating unit of chromatin in eukaryotic cells. It plays a crucial role in packaging DNA into a compact structure within the nucleus. A nucleosome core particle consists of:

- **DNA:** Approximately **146-147 base pairs (bp)** of DNA.

- **Histone Octamer:** This DNA is wrapped around a core complex of eight histone proteins. The histone octamer is composed of two copies each of four core histone proteins: **H2A, H2B, H3, and H4**.
- The DNA wraps around the histone octamer approximately **1.65 to 1.7 times** in a left-handed (negative) superhelical turn.

Linker DNA connects adjacent nucleosome core particles. Histone H1 (linker histone) is often associated with the linker DNA and helps in further compaction of chromatin. Let's analyze the options: (a) "140 bp ... hexamer of histones": Incorrect DNA length (closer to 146/147 bp) and histone core is an octamer. (b) "146 bp ... dimer of histones": Histone core is an octamer. (c) "140 bp ... octamer of histones": DNA length is slightly off. (d) "146 bp of DNA making 1.65 negative super helical turn wrapped around an octamer of histones": This is the most accurate description among the options. The DNA length is approximately 146-147 bp, it wraps about 1.65 times, and the core is an octamer of histones.

Therefore, option (d) is the correct description.

$$\boxed{\text{146 bp of DNA making 1.65 negative super helical turn wrapped around an octamer of histones}}$$

Quick Tip

Quick Tip:

- **Nucleosome Core Particle:**
  - DNA: 146-147 bp wrapped 1.65 times.
  - Histone Octamer: 2x(H2A + H2B + H3 + H4).
- Histone H1 (linker histone) binds to linker DNA and helps compact nucleosomes further.
- This "beads-on-a-string" structure is the first level of chromatin organization.

117.

Which sequencing technique relies on the synthesis of complementary strands in the presence of chain-terminating dideoxynucleotides?

(a) Sanger sequencing

(b) Next-generation sequencing

(c) Polymerase Chain Reaction (PCR)

(d) Pyrosequencing

Correct Answer: (a) Sanger sequencing

Solution: The sequencing technique described is **Sanger sequencing**, also known as the chain-termination method or dideoxy sequencing method. Key principles of Sanger sequencing: 1. It involves *in vitro* DNA synthesis of a complementary strand using a DNA template, a primer, DNA polymerase, normal deoxynucleotide triphosphates (dNTPs: dATP, dGTP, dCTP, dTTP), and a small amount of chain-terminating dideoxynucleotide triphosphates (ddNTPs: ddATP, ddGTP, ddCTP, ddTTP). 2. Dideoxynucleotides (ddNTPs) lack the 3'-hydroxyl (3'-OH) group that is necessary for the formation of a phosphodiester bond with the next incoming nucleotide. 3. When a ddNTP is incorporated by DNA polymerase into a growing DNA strand, synthesis of that strand is terminated at that point. 4. By running four separate reactions, each containing a different ddNTP (or using fluorescently labeled ddNTPs in a single reaction for automated sequencing), a set of DNA fragments of varying lengths is generated, each terminated at a specific base. 5. These fragments are then separated by size (e.g., by gel electrophoresis or capillary electrophoresis), and the sequence is read from the order of the terminated fragments.

Let's analyze the options: (a) **Sanger sequencing:** This directly matches the description. (b) Next-generation sequencing (NGS): A broad term for several high-throughput sequencing technologies (e.g., Illumina sequencing, Ion Torrent sequencing, PacBio SMRT sequencing). While they involve DNA synthesis, their core mechanisms are different from dideoxy chain termination (e.g., sequencing by synthesis with reversible terminators, sequencing by ligation, single-molecule real-time sequencing). (c) Polymerase Chain Reaction (PCR): Used to amplify DNA, not primarily for sequencing (though PCR products are often sequenced). (d) Pyrosequencing: A sequencing-by-synthesis method that detects the release of pyrophosphate (PPi) upon nucleotide incorporation. It does not use chain-terminating dideoxynucleotides.

Therefore, Sanger sequencing relies on chain-terminating dideoxynucleotides.

$$\boxed{\text{Sanger sequencing}}$$

Quick Tip

Quick Tip:

- **Sanger Sequencing (Dideoxy / Chain-Termination Method):**
  - Uses DNA polymerase, template, primer, dNTPs, and chain-terminating ddNTPs.
  - ddNTPs lack a 3'-OH group, so their incorporation stops DNA synthesis.
  - Generates a set of DNA fragments of different lengths, each ending with a specific ddNTP.
- This method was the dominant DNA sequencing technology for decades.

118.

Which among the following is true for RFLP?

(a) It cannot be used as a genetic marker

(b) It refers to differences (or variations) in the DNA sequences at sites recognized by restriction enzymes

(c) Restriction enzymes are not used for digesting DNA in this process

(d) It is a PCR based marker

Correct Answer: (b) It refers to differences (or variations) in the DNA sequences at sites recognized by restriction enzymes

Solution: RFLP (Restriction Fragment Length Polymorphism) is a type of polymorphism (variation in DNA sequence among individuals) that results in differences in the lengths of DNA fragments produced when DNA is digested with specific restriction enzymes. Mechanism:

- Restriction enzymes cut DNA at specific recognition sequences.
- If a mutation (e.g., a single nucleotide polymorphism - SNP) occurs within a restriction site, it can abolish that site, preventing the enzyme from cutting there.
- Alternatively, a mutation can create a new restriction site.
- These changes alter the lengths of the DNA fragments generated by restriction enzyme digestion.
- These different-sized fragments can be detected by techniques like Southern blotting (after gel electrophoresis) using a probe that hybridizes to the region containing the polymorphism.

RFLPs are used as genetic markers for linkage analysis, gene mapping, DNA fingerprinting, and disease diagnosis.
Let's analyze the options: (a) "It cannot be used as a genetic marker": FALSE. RFLPs were one of the first widely used types of DNA-based genetic markers. (b) "It refers to differences (or variations) in the DNA sequences at sites recognized by restriction enzymes": TRUE. These sequence differences can create or abolish restriction sites, leading to fragments of different lengths. (c) "Restriction enzymes are not used for digesting DNA in this process": FALSE. The "R" in RFLP stands for Restriction. Digestion with restriction enzymes is a fundamental step. (d) "It is a PCR based marker": While PCR can be used to amplify the DNA region containing an RFLP before restriction digestion (PCR-RFLP), RFLP itself is defined by restriction enzyme digestion patterns and was originally detected by Southern blotting without PCR. PCR is not an inherent part of the definition of RFLP, though it can be incorporated into the detection method. RFLP is based on sequence variation affecting restriction sites.

Therefore, option (b) is the true statement for RFLP.

It refers to differences (or variations) in the DNA sequences at sites recognized by restriction en

Quick Tip

Quick Tip:

- **RFLP:** Restriction Fragment Length Polymorphism.
- Variation in DNA sequence (e.g., SNP) that creates or abolishes a restriction enzyme recognition site.
- Leads to different lengths of DNA fragments after digestion with that restriction enzyme.
- Detected by Southern blotting or PCR-RFLP.
- Used as genetic markers.

119.

Which among the following is not a transgenic plant?

(a) Bt Cotton

(b) Golden Rice

(c) Samba Mahsuri

(d) FLAVR SAVR

Correct Answer: (c) Samba Mahsuri

Solution: A transgenic plant is a plant that has been genetically engineered to contain and express one or more genes from another organism (a transgene). Let's analyze the options: (a) **Bt Cotton:** A well-known transgenic plant. It is genetically modified to express a gene from the bacterium *Bacillus thuringiensis* (Bt) that encodes an insecticidal protein (Bt toxin), providing resistance to certain insect pests like bollworms. (b) **Golden Rice:** A transgenic rice variety genetically engineered to

produce beta-carotene (a precursor of Vitamin A) in its edible endosperm. This was done to combat Vitamin A deficiency in populations that rely heavily on rice. (c) **Samba Mahsuri (BPT 5204):** This is a popular, high-yielding rice variety developed in India through conventional plant breeding methods (hybridization and selection). It is known for its fine grain quality and good cooking characteristics but is susceptible to some diseases like bacterial blight. Improved versions (e.g., Improved Samba Mahsuri) have been developed using marker-assisted selection and may involve genes from wild relatives, but the original Samba Mahsuri is a product of conventional breeding, not a transgenic plant created by direct insertion of a foreign gene through genetic engineering techniques discussed for GMOs. (d) **FLAVR SAVR Tomato:** One of the first commercially grown genetically engineered foods. It was modified to have a longer shelf life by suppressing the gene responsible for producing an enzyme (polygalacturonase) that causes fruit softening. It is a transgenic plant.
Therefore, Samba Mahsuri (the original variety) is not a transgenic plant in the sense of being a GMO created by direct gene insertion. It's a product of conventional breeding.

$$\boxed{\text{Samba Mahsuri}}$$

Quick Tip

Quick Tip:

- **Transgenic Plant (GMO Plant):** Contains gene(s) introduced from another species using recombinant DNA technology.
- **Bt Crops (e.g., Bt Cotton, Bt Corn):** Express insecticidal protein from *Bacillus thuringiensis.*
- **Golden Rice:** Engineered to produce beta-carotene (pro-vitamin A).
- **FLAVR SAVR Tomato:** Engineered for delayed ripening/softening.
- Conventional breeding uses hybridization and selection within or between related species, not direct insertion of isolated genes from unrelated organisms.

120.

Cells signalling between distant cells mediated by hormones released from specific cells that travel to target cells, producing a slower, long-lasting response is known as

(a) Paracrine signalling
(b) Endocrine signalling
(c) Autocrine signalling
(d) Direct signalling

Correct Answer: (b) Endocrine signalling

Solution: Cell signaling can occur over different distances and via different mechanisms:

- **(a) Paracrine Signalling:** Cells release signaling molecules (local mediators) that act on **nearby target cells**. The signals diffuse over short distances through the extracellular fluid. Example: Growth factors acting on neighboring cells.
- **(b) Endocrine Signalling:** Specialized endocrine cells secrete signaling molecules called **hormones** into the **bloodstream**. These hormones travel throughout the body via the circulatory system and act on **distant target cells** that possess specific receptors for them. Endocrine signaling is typically slower to initiate but can produce widespread and long-lasting responses. This matches the description in the question.
- **(c) Autocrine Signalling:** Cells release signals that bind to receptors on the **same cell** that secreted them, or on nearby cells of the same type. The cell signals itself. Example: Some growth factors.
- **(d) Direct Signalling (Contact-Dependent or Juxtacrine Signalling):** Requires direct physical contact between the signaling cell and the target cell. Signaling molecules on the surface of one cell bind to receptors on the surface of the other (e.g., Notch signaling), or signals pass through gap junctions connecting adjacent cells.

- **Synaptic Signalling (Neuronal Signalling):** Neurons transmit signals electrically along their axons and release chemical signals (neurotransmitters) at synapses, which act on specific target cells (neurons, muscle cells, gland cells) over a very short distance across the synaptic cleft. This is fast and precise.

The description "signalling between distant cells mediated by hormones released ... that travel to target cells, producing a slower, long-lasting response" clearly defines **endocrine signalling**.

$$\boxed{\text{Endocrine signalling}}$$

Quick Tip

Quick Tip:

- **Endocrine:** Long distance, via bloodstream, hormones, slow, long-lasting (e.g., insulin, growth hormone).
- **Paracrine:** Local, acts on nearby cells, short diffusion (e.g., growth factors, some neurotransmitters outside synapse).
- **Autocrine:** Acts on the same cell that secreted it.
- **Synaptic:** Neuronal, fast, precise, across synapse via neurotransmitters.
- **Contact-Dependent (Juxtacrine):** Requires direct cell-cell contact.
