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GATE BT · 2026

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GATE BT 2026 Solved Paper

INSIDE

- All 65 questions, in the order of the paper
- The official answer to every question
- Step-by-step worked solutions
- The answer key on one page

Question paper and official answer key: IIT Guwahati

Online, with the questions linked to their topic notes: **iaeacademy.in/study/papers/bt-2026**

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About this paper

65 questions, 100 marks. Question types: 31 MCQ · 14 MSQ · 20 NAT.

Official answer key: IIT Guwahati · https://gate2026.iitg.ac.in/doc/download/2026/Keys/BT_Keys.pdf

We placed each question under a subject and topic ourselves; the exam paper does not label them.

This paper online, with the questions linked to their topic notes:
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Answer key

Q	TYPE	MARKS	ANSWER
Q.1	MCQ	1	**A**
Q.2	MCQ	1	**B**
Q.3	MCQ	1	**A**
Q.4	MCQ	1	**B**
Q.5	MCQ	1	**C**
Q.6	MCQ	2	**D**
Q.7	MCQ	2	**A**
Q.8	MCQ	2	**D**
Q.9	MCQ	2	**C**
Q.10	MCQ	2	**C**
Q.11	MCQ	1	**B**
Q.12	MCQ	1	**C**
Q.13	MCQ	1	**B**
Q.14	MCQ	1	**B**
Q.15	MCQ	1	**C**
Q.16	MCQ	1	**B**
Q.17	MCQ	1	**A**
Q.18	MCQ	1	**B**
Q.19	MCQ	1	**B**
Q.20	MCQ	1	**C**
Q.21	MCQ	1	**C**
Q.22	MCQ	1	**B**
Q.23	MCQ	1	**C**
Q.24	MCQ	1	**A**
Q.25	MCQ	1	**C**
Q.26	MCQ	1	**D**
Q.27	MSQ	1	**B, C**
Q.28	MSQ	1	**B, D**
Q.29	MSQ	1	**B, D**
Q.30	MSQ	1	**A**
Q.31	NAT	1	**0.505**
Q.32	NAT	1	**20**
Q.33	NAT	1	**40000**
Q.34	NAT	1	**-106.12**
Q.35	NAT	1	**0.016 to 0.017**
Q.36	MCQ	2	**B**
Q.37	MCQ	2	**C**
Q.38	MCQ	2	**B**
Q.39	MCQ	2	**D**
Q.40	MCQ	2	**A**
Q.41	MSQ	2	**C, D**
Q.42	MSQ	2	**A, C**
Q.43	MSQ	2	**B, C**
Q.44	MSQ	2	**C**
Q.45	MSQ	2	**D**
Q.46	MSQ	2	**B, C**
Q.47	MSQ	2	**B**
Q.48	MSQ	2	**A, B**
Q.49	MSQ	2	**A, D**
Q.50	MSQ	2	**A, D**
Q.51	NAT	2	**0.69 to 0.71**
Q.52	NAT	2	**8**
Q.53	NAT	2	**1.414**
Q.54	NAT	2	**59 to 61**
Q.55	NAT	2	**2.2 to 2.4**
Q.56	NAT	2	**100**
Q.57	NAT	2	**1.3 to 1.4**
Q.58	NAT	2	**8.3 to 8.7**
Q.59	NAT	2	**30**
Q.60	NAT	2	**6**
Q.61	NAT	2	**2.4 to 2.5**
Q.62	NAT	2	**3.6 to 3.8**
Q.63	NAT	2	**96**
Q.64	NAT	2	**0.5**
Q.65	NAT	2	**0.31 to 0.32**

General Aptitude Q.1 to Q.10

Q.1 MCQ · 1 MARK

General Aptitude › Grammar & vocabulary

“He often _____ the numbers. False claims are not going to help. Honesty _____ trust”, said the manager.

Choose the option with the correct order of words to fill the blanks.

(A) exaggerates; engenders

(B) excels; encourages

(C) aggravates; alleviates

(D) diminishes; eliminates

Official answer: **A**

SOLUTION

1. Blank 1 is in "He often _____ the numbers." The next sentence, "False claims are not going to help," shows the manager is criticising someone who misstates figures. So the first verb must mean to inflate or misrepresent the numbers.
2. Blank 2 is in "Honesty _____ trust." Honesty is set against false claims, so the second verb must mean to create, produce or foster trust.
3. (A) exaggerates; engenders: to exaggerate numbers is to inflate them, which is a false claim. To engender is to give rise to or produce, so "Honesty engenders trust" is sensible and fits the contrast. Both blanks fit.
4. (B) excels; encourages: "excels the numbers" is not idiomatic, since excel does not take an object this way, and it does not suggest false claims. Eliminated.
5. (C) aggravates; alleviates: "aggravates the numbers" does not fit the idea of false claims. "Honesty alleviates trust" is illogical, because alleviate means to relieve a pain or burden, not to build trust. Eliminated.
6. (D) diminishes; eliminates: "diminishes the numbers" means understating them, which does not match the context of false claims. "Honesty eliminates trust" contradicts the message. Eliminated.
7. Only (A) works in both blanks, so the answer is (A).

KEY IDEA

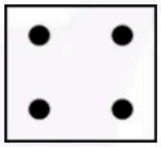
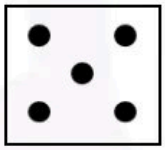
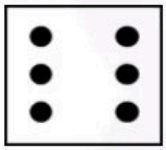
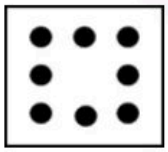
Use the context clue. "False claims are not going to help" points to a verb meaning to inflate numbers (exaggerates). Honesty, the opposite of false claims, produces trust (engenders).

WATCH OUT FOR

Picking "alleviates" or "encourages" for the second blank because they sound positive, without checking the first blank. "Excels" also takes no object here. Check both blanks together.

Q.2 MCQ · 1 MARK

General Aptitude › Spatial

Q.2	In the sequence of tiles shown below, the missing tile indicated by the question mark should be 
(A)	
(B)	
(C)	
(D)	

Official answer: **B**

SOLUTION

1. Count the dots in each known tile: tile 1 has 2, tile 2 has 3, tile 4 has $3+1+3=7$, tile 5 has $4+3+3=10$.
2. The counts are $2,\ 3,\ ?,\ 7,\ 10$. The known jumps are $+1$ (tile 1 to tile 2) and $+3$ (tile 4 to tile 5).
3. A rule that fits both known jumps is that the n-th jump equals $\lfloor n/2 \rfloor + 1$, which gives the jumps $1,\ 2,\ 2,\ 3$: each jump value from 2 upward is used twice. The first jump is 1 and the fourth is 3, as observed, so the middle two jumps are both 2.
4. So the missing tile has $3+2=5$ dots, and the next tile then has $5+2=7$ dots, which matches tile 4. The counts run $2, 3, 5, 7, 10$.

5. Count the dots in the options: (A) has 4, (B) has 5, (C) has 6, (D) has 8. Only (B), with four corner dots and one centre dot, has 5 dots, so the answer is (B).

KEY IDEA
Count the dots in each tile and study the differences between neighbouring counts. The counts 2, 3, 5, 7, 10 have differences 1, 2, 2, 3.

WATCH OUT FOR
Looking only at how the dots are arranged, or assuming the counts rise by a constant step. A constant step cannot give both the +1 at the start and the +3 at the end. Options (C) with 6 dots and (D) with 8 dots break the pattern.

Q.3 MCQ · 1 MARK

General Aptitude › Reasoning

A school has 100 students distributed among 1st to 10th standards.

Based on this, which one of the following statements is always correct?

(A) There are at least 10 students who belong to the same standard.

(B) There is at least one student in each standard.

(C) There are at most 10 students in 10th standard.

(D) The total number of students from 1st to 5th standards is at least 50.

Official answer: **A**

SOLUTION

1. Pigeonhole principle: if N objects go into k boxes, some box holds at least $\lceil N/k \rceil$ objects. Here $N = 100$ students and $k = 10$ standards.
2. So some standard has at least $\lceil 100/10 \rceil = 10$ students. Equivalently, if every standard had at most 9 students, the total would be at most $10 \times 9 = 90 < 100$, a contradiction. So (A) is always true.
3. Test (B): nothing forces every standard to be occupied. For example, put all 100 students in the 1st standard, or 12 each in nine standards and none in the 5th. Both are valid distributions, so (B) is not always true.
4. Test (C): the 10th standard could hold 50 students, or even all 100. So (C) is not always true.
5. Test (D): the 1st to 5th standards could hold only 10 students in total, with the other 90 in the 6th to 10th. So (D) is not always true.
6. Only (A) holds in every possible distribution.

KEY IDEA
Pigeonhole principle: 100 students in 10 standards forces some standard to hold at least $\lceil 100/10 \rceil = 10$ students. For "always correct", one counterexample kills an option.

WATCH OUT FOR
Assuming the students are spread evenly, so that every standard is non-empty (B) or that the 10th standard is small (C). The question asks what holds in every distribution, including very lopsided ones.

Q.4 MCQ · 1 MARK

General Aptitude › Numerical

How many 3-digit numbers can be formed using three distinct single digit prime numbers?

(A) 64

(B) 24

(C) 12

(D) 4

Official answer: **B**

SOLUTION

1. The single-digit prime numbers are 2, 3, 5 and 7. There are exactly 4 of them (0, 1, 4, 6, 8 and 9 are not prime).
2. A 3-digit number uses three distinct digits chosen from these 4. Order matters (235 and 325 are different numbers), so we count arrangements, not selections.
3. Hundreds place: 4 choices. Tens place: 3 choices remain. Units place: 2 choices remain.
4. By the multiplication principle, the count is $4 \times 3 \times 2 = 24$. This equals ${}^{4}P_{3} = \frac{4!}{(4-3)!} = 24$.
5. None of the digits is 0, so no arrangement has a leading zero and none needs to be excluded. The answer is 24, option (B).

KEY IDEA
List the single-digit primes (2, 3, 5, 7). Distinct digits with order mattering gives the number of permutations, ${}^{4}P_{3} = 24$.

WATCH OUT FOR
Counting combinations (${}^{4}C_{3} = 4$, option D) and ignoring order. Another slip is treating 1 as prime, which gives 5 digits and 60 numbers.

Q.5 MCQ · 1 MARK

General Aptitude › Numerical

In a group of students, 10 students like Mathematics, 12 students like English, 4 students like both Mathematics and English, and 6 students like neither Mathematics nor English. The number of students in the group is ____

(A) 18

(B) 20

(C) 24

(D) 32

Official answer: **C**

SOLUTION

1. Let M be the set of students who like Mathematics and E the set who like English: $|M| = 10$, $|E| = 12$, $|M \cap E| = 4$.
2. The 4 students who like both are counted once in $|M|$ and once in $|E|$, so subtract them once: $|M \cup E| = |M| + |E| - |M \cap E|$.
3. $$|M \cup E| = 10 + 12 - 4 = 18$$
4. The 6 students who like neither lie outside $M \cup E$, so they are added to get the whole group: $\text{Total} = |M \cup E| + 6$.
5. $$\text{Total} = 18 + 6 = 24$$
6. The answer is option (C).

KEY IDEA
Count the students who like at least one subject with inclusion-exclusion, $|M \cup E| = |M| + |E| - |M \cap E|$. Then add those who like neither to get the whole group.

WATCH OUT FOR
Adding 10 + 12 + 6 = 28 without subtracting the 4 students who like both, so they are counted twice. Another slip is stopping at 18 and forgetting the 6 who like neither.

Q.6 MCQ · 2 MARKS

General Aptitude › Reasoning

Charity : P :: Retaliation : Q

Choose the appropriate pair of words P and Q that fit the analogy.

(A) P = Parsimonious; Q = Vengeful

(B) P = Altruistic; Q = Amicable

(C) P = Resentful; Q = Spiteful

(D) P = Magnanimous; Q = Vindictive

Official answer: **D**

SOLUTION

1. Analogy method: first state the relationship in the first pair, then test each option for the same relationship in the same order.
2. Charity is an act of giving help generously, and it springs from a generous, noble-minded disposition. Retaliation is an act of paying back a wrong, and it springs from a revengeful disposition. So the relation is: an act, then the trait of character that drives it.
3. Option (A): Parsimonious means stingy, which is the opposite of the trait behind charity. So P does not fit the first pair.
4. Option (B): Altruistic fits Charity, but Amicable means friendly. A friendly nature does not drive retaliation, so Q does not fit.
5. Option (C): Resentful means feeling bitter about an injury. This is not the generous trait behind charity, so P does not fit. (Spiteful is close to the trait behind retaliation, but both words must fit.)
6. Option (D): Magnanimous means generous and noble-minded, which is the trait behind charity. Vindictive means keen to take revenge, which is the trait behind retaliation. Both pairs follow the same relation of act and driving trait.
7. Hence P = Magnanimous and Q = Vindictive, which is option (D).

KEY IDEA

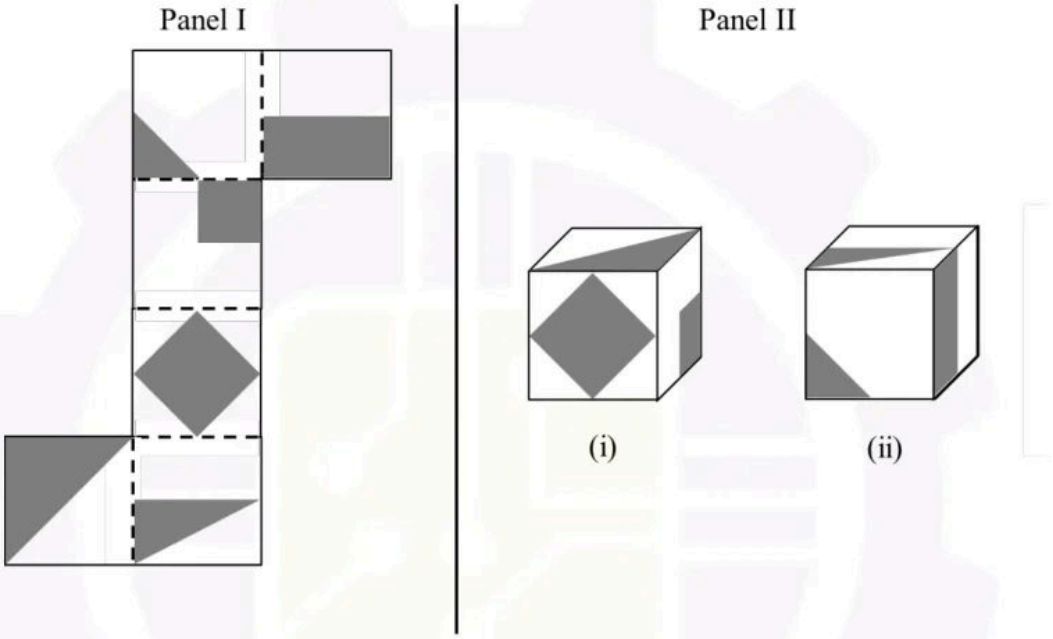
State the relation in the given pair (an act and the trait of character behind it), then choose the option in which both words follow that relation. Check both blanks, not one.

WATCH OUT FOR

Picking an option because only one word fits. In (B), Altruistic fits Charity, but Amicable does not fit Retaliation. In (A) and (C), the first word fails.

Q.7 MCQ · 2 MARKS

General Aptitude › Spatial

Q.7	A paper shown in Panel I is folded along the dashed lines (- - -) to construct a cube. The shaded regions shown in Panel I appear on the outer surface of the cube. Referring to cubes shown in Panel II, which one of the options is correct? 
(A)	Only (i) can correspond to the unfolded cube in Panel I.
(B)	Only (ii) can correspond to the unfolded cube in Panel I.
(C)	Both (i) and (ii) can correspond to the unfolded cube in Panel I.
(D)	Neither (i) nor (ii) can correspond to the unfolded cube in Panel I.

Official answer: **A**

SOLUTION

1. Label the net: the column from top to bottom is S1, S2, S3, S4. The faces S5 (right of S1) and S6 (left of S4) are the two end caps. S1, S2, S3 and S4 form the ring of four side faces, so the opposite pairs are S1-S3, S2-S4 and S5-S6.
2. Cube (i): the front face is the diamond, which is S3. The diamond is symmetric, so the cube can be turned about the front-back axis. The possible (top, right) pairs are (S2, S5), (S6, S2), (S4, S6) and (S5, S4).

3. Cube (i) shows a shaded triangle on top and only a small shaded patch on the right. The pair (S2, S5) puts a small square on top, so it fails. The pair (S4, S6) puts a half-face triangle on the right, so it fails. The pair (S5, S4) puts a wide band on top, so it fails. That leaves (top = S6, right = S2).
4. Check top = S6. S6 is the left face in the natural folding. A quarter turn takes it to the top. Its half-face triangle then covers the front-left, front-right and back-right corners of the top face and leaves the back-left corner white. This matches the top face of (i).
5. Check right = S2. S2's small square sits at the net corner shared with S1 (the back face) and S5 (which the same quarter turn moves to the bottom). So the patch lies at the back-bottom corner of the right face. This is the small patch near the far, lower part in (i). Cube (i) can therefore be folded from the net.
6. Cube (ii): the front face has a small right triangle with equal legs of half a side, in its lower-left corner. Only S1 has such a triangle. S6's triangle is half the face, and S4's triangle has legs of different lengths. So the front is S1, upright as drawn.
7. With S1 upright in front, the neighbours follow the net: S4 on top, S2 below, S5 on the right and S6 on the left.
8. S5 is shaded over its lower half, along the edge it shares with S2. That edge is the bottom edge of the right face. So the right face should carry a horizontal shaded band along its bottom half, running front to back. Cube (ii) instead shows a full-height vertical strip along the far edge. This does not match, so (ii) cannot be folded from the net.
9. Only (i) can correspond to the unfolded cube. The answer is option (A).

KEY IDEA

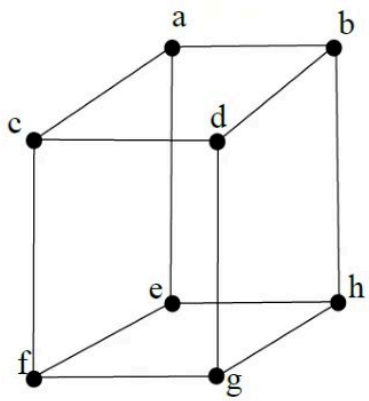
Identify opposite faces from the ring of four squares and the two end caps. Then pin down one distinctive face (the diamond, or the corner triangle) as the front. Rotate the cube about that face, matching the shading on every visible face, including its orientation.

WATCH OUT FOR

Matching only the front face and ignoring the orientation of the shading on the side faces. In (ii) the front triangle matches S1, but S5's band is horizontal along the bottom of the right face, not vertical along the far edge.

Q.8 MCQ · 2 MARKS

General Aptitude › Geometry

Q.8	Consider the cube shown below with its 8 corners labelled a, b, c, d, e, f, g, and h. The figure is representative. All corners are to be colored such that any two corners that are connected by an edge must be of different colors. The minimum number of colors required to achieve this is _____ 
(A)	8
(B)	4
(C)	3
(D)	2

Official answer: **D**

SOLUTION

1. The corners and edges of the cube form a graph. We need the smallest number of colours so that the two ends of every edge get different colours.
2. Any edge needs two different colours at its ends, so at least 2 colours are required.
3. Try 2 colours, called 1 and 2. The top face is the 4-cycle $a - b - d - c - a$. Alternating colours around it gives $a = 1,\ b = 2,\ d = 1,\ c = 2$. Each of the edges a-b, b-d, d-c, c-a joins a 1 to a 2.

4. Each bottom corner is joined by a vertical edge to the corner above it, so give it the opposite colour: $e = 2$ (below a), $h = 1$ (below b), $g = 2$ (below d), $f = 1$ (below c). The four vertical edges a-e, b-h, d-g, c-f then join different colours.
5. Check the bottom 4-cycle $e - h - g - f - e$: $e = 2,\ h = 1,\ g = 2,\ f = 1$. The edges e-h, h-g, g-f, f-e all join a 2 to a 1.
6. All 12 edges join a colour-1 corner to a colour-2 corner, so 2 colours are enough. Since at least 2 are needed, the minimum is 2. The answer is option (D).

KEY IDEA
Colouring corners so that adjacent ones differ is graph colouring. A graph needs only 2 colours when its corners can be split into two groups with every edge going between the groups. The cube is such a graph: alternate the colours around each face and flip them from the top face to the bottom face.

WATCH OUT FOR
Assuming a solid with 8 corners and 3 edges at each corner needs 3 or 4 colours. Only odd cycles, such as a triangle, force a third colour, and every cycle in a cube has even length.

Q.9 MCQ · 2 MARKS

General Aptitude › Reasoning

Four hills H1, H2, H3, and H4 are present in an area. The following observations are made about them:

i. Neither H2 nor H3 is the easternmost hill.
ii. Neither H2 nor H3 is the westernmost hill.
iii. Neither the easternmost hill nor the westernmost hill is the southernmost hill.
iv. Two hills are located to the west of H2.
v. The southernmost hill has at least two hills to its east.

The southernmost hill is _____.

(A) H1
(B) H2
(C) H3
(D) H4

Official answer: **C**

SOLUTION

1. Number the hills by position from west to east: 1 (westernmost) to 4 (easternmost).
2. By (i) and (ii), H2 and H3 are neither the easternmost nor the westernmost hill, so they occupy positions 2 and 3. H1 and H4 take the two ends, positions 1 and 4.
3. By (iv), exactly two hills lie to the west of H2, so H2 is at position 3. H3 is therefore at position 2.
4. By (iii), the southernmost hill is not an end hill, so it is H2 or H3.
5. By (v), the southernmost hill has at least two hills to its east. H2 at position 3 has only one hill to its east (position 4), so it fails. H3 at position 2 has two hills to its east (positions 3 and 4), so it satisfies the condition.
6. So the southernmost hill is H3, which is option (C).

KEY IDEA
Fix the west-to-east order using the "neither easternmost nor westernmost" and "two hills to the west" clues. Then test the remaining candidates for the southernmost hill against the clue about hills to its east.

WATCH OUT FOR
Reading "two hills are located to the west of H2" as H2 being at position 2. Two hills to its west puts H2 at position 3. Another slip is forgetting that the southernmost hill must not be an end hill, which leaves only H2 and H3.

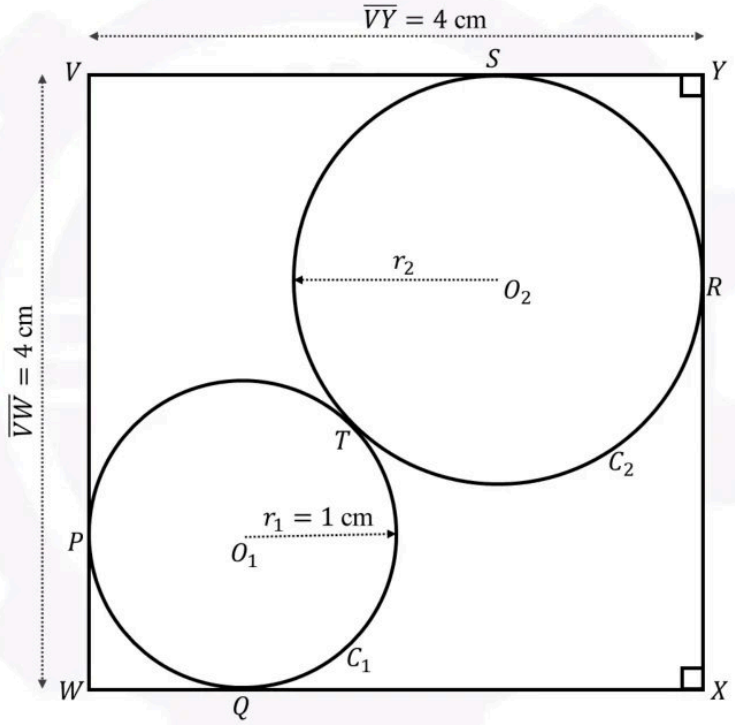
Q.10 MCQ · 2 MARKS

General Aptitude › Geometry

Q.10

As shown in the figure, circle C_1 with center O_1 and radius r_1 touches the square $VWXY$ at points P and Q while circle C_2 with center O_2 and radius r_2 touches the square $VWXY$ at points R and S. The two circles touch each other at T.

Given $r_1 = 1$ cm and $\overline{VY} = \overline{VW} = 4$ cm, $r_2 =$ _____ cm.



(A)	$4 - 3\sqrt{2}$
(B)	$1 + 2\sqrt{2}$
(C)	$7 - 4\sqrt{2}$
(D)	$5 + 3\sqrt{2}$

Official answer: **C**

SOLUTION

1. Place coordinates: $W = (0, 0)$, $X = (4, 0)$, $V = (0, 4)$, $Y = (4, 4)$. A circle touching two perpendicular sides has its centre at a distance equal to its radius from each of those sides.
2. C_1 touches the left side VW and the bottom side WX, and $r_1 = 1$, so $O_1 = (1, 1)$.
3. C_2 touches the top side VY and the right side XY, so $O_2 = (4 - r_2,\ 4 - r_2)$.

4. The circles touch externally at T, so the distance between centres is the sum of the radii: $O_1O_2 = 1 + r_2$.
5. Both centres lie on the line $y = x$, and the horizontal and vertical differences are each $(4 - r_2) - 1 = 3 - r_2$ (positive, since $r_2 < 3$). So $O_1O_2 = \sqrt{2}\,(3 - r_2)$.
6. Equate: $\sqrt{2}(3 - r_2) = 1 + r_2$, so $3\sqrt{2} - 1 = r_2(1 + \sqrt{2})$.
7. $$r_2 = \frac{3\sqrt{2} - 1}{\sqrt{2} + 1} = (3\sqrt{2} - 1)(\sqrt{2} - 1) = 6 - 3\sqrt{2} - \sqrt{2} + 1 = 7 - 4\sqrt{2}$$
8. Check: $7 - 4\sqrt{2} \approx 1.34$ cm, which is larger than r_1 and fits the figure, where C_2 is the larger circle. This is option (C).

KEY IDEA

A circle in a corner of a square has its centre on the diagonal, at a distance equal to its radius from both sides. Two circles touching externally have centre distance equal to the sum of their radii.

WATCH OUT FOR

Writing the centre distance as $\sqrt{2}(4 - r_1 - r_2)$ or using $r_2 - r_1$ (internal tangency). Another slip is forgetting the factor $\sqrt{2}$ for the diagonal distance, or leaving the answer as $\frac{3\sqrt{2}-1}{\sqrt{2}+1}$ without rationalising.

Biotechnology Q.11 to Q.65

Q.11 MCQ · 1 MARK

Engineering Mathematics › Calculus

Consider the two functions $f_1(x) = \dfrac{x^2-4}{x-2}$ and $f_2(x) = x^2 - 2x + 2$. Which of the following is the value of $(f_1(x) + f_2(x))$ as $x \to 2$?

(A) 0

(B) 6

(C) 8

(D) ∞

Official answer: **B**

SOLUTION

1. Both limits exist separately, so the limit of the sum is the sum of the limits: $\lim\limits_{x\to 2}\big(f_1(x)+f_2(x)\big) = \lim\limits_{x\to 2} f_1(x) + \lim\limits_{x\to 2} f_2(x)$.
2. At $x = 2$, $f_1(x) = \dfrac{x^2-4}{x-2}$ has the form $\frac{0}{0}$. Factorise the numerator: $x^2 - 4 = (x-2)(x+2)$.
3. As $x \to 2$ we have $x \neq 2$, so the factor $(x-2)$ cancels: $f_1(x) = x + 2$.
4. Therefore $\lim\limits_{x\to 2} f_1(x) = 2 + 2 = 4$.
5. $f_2(x) = x^2 - 2x + 2$ is a polynomial, so it is continuous: $\lim\limits_{x\to 2} f_2(x) = 4 - 4 + 2 = 2$.
6. Add the limits: $4 + 2 = 6$, which is option (B).

KEY IDEA

A $\frac{0}{0}$ form is removed by factorising and cancelling the common factor, which is allowed because $x \to 2$ means $x \neq 2$. A polynomial's limit is found by direct substitution, and the limit of a sum is the sum of the limits.

WATCH OUT FOR

Substituting $x = 2$ straight into f_1 gives $\frac{0}{0}$, and some candidates then say the limit does not exist or is ∞ (option D). Others forget to add the limit of f_2 and answer 4, which is not an option, or add wrongly and pick 0 or 8.

Q.12 MCQ · 1 MARK

Engineering Mathematics › Linear algebra

Which of the following is one of the eigenvalues for the matrix given below?

$$\begin{bmatrix} 3 & 4 \\ 4 & -3 \end{bmatrix}$$

(A) 1

(B) 3

(C) 5

(D) 7

Official answer: **C**

SOLUTION

1. Let $A = \begin{bmatrix} 3 & 4 \\ 4 & -3 \end{bmatrix}$. The eigenvalues are the roots of the characteristic equation $\det(A - \lambda I) = 0$.
2. $$\det \begin{bmatrix} 3-\lambda & 4 \\ 4 & -3-\lambda \end{bmatrix} = (3-\lambda)(-3-\lambda) - 16 = 0$$
3. Expand: $(3-\lambda)(-3-\lambda) = \lambda^2 - 9$, so $\lambda^2 - 9 - 16 = 0$, that is $\lambda^2 = 25$.
4. Hence $\lambda = \pm 5$.

5. Check with the shortcuts: the sum of the eigenvalues is the trace $3 + (-3) = 0$, and the product is the determinant $-9 - 16 = -25$. The pair $5, -5$ satisfies both.
6. Among the options only 5 is an eigenvalue, so the answer is (C).

KEY IDEA
Write down $\det(A - \lambda I) = 0$ for the 2×2 matrix. Check the roots against the trace (sum of eigenvalues) and the determinant (product of eigenvalues).

WATCH OUT FOR
Dropping a sign when expanding $(3 - \lambda)(-3 - \lambda)$ gives $\lambda^2 + 9$ instead of $\lambda^2 - 9$. The equation then has no real roots. Also easy to miss is that the -16 comes from 4×4 and enters with a minus sign.

Q.13 MCQ · 1 MARK

Engineering Mathematics › Calculus

Which of the following functions has the highest area under the curve between $x = 0$ and $x = 10$?

(A) $y = x + 8$

(B) $y = 3x$

(C) $y = 2x + 1$

(D) $y = x + 2$

Official answer: **B**

SOLUTION

1. The area under $y = f(x)$ from $x = 0$ to $x = 10$ is $\int_0^{10} f(x)\,dx$. All four functions are positive on $[0, 10]$, so each integral is an area.
2. (A) $\int_0^{10} (x + 8)\,dx = \left[\frac{x^2}{2} + 8x\right]_0^{10} = 50 + 80 = 130.$
3. (B) $\int_0^{10} 3x\,dx = \left[\frac{3x^2}{2}\right]_0^{10} = 150.$
4. (C) $\int_0^{10} (2x + 1)\,dx = \left[x^2 + x\right]_0^{10} = 100 + 10 = 110.$
5. (D) $\int_0^{10} (x + 2)\,dx = \left[\frac{x^2}{2} + 2x\right]_0^{10} = 50 + 20 = 70.$
6. Comparing: $150 > 130 > 110 > 70$, so the largest area belongs to $y = 3x$, option (B).

KEY IDEA
Area under a curve from 0 to 10 is the definite integral. For a line $y = ax + b$ it equals $50a + 10b$, so compare $50a + 10b$ for each option.

WATCH OUT FOR
Picking the line with the largest intercept (A, $y = x + 8$) or the largest value at $x = 0$. The slope matters more over a long interval: here $3x$ has intercept 0 but wins because it rises to 30 at $x = 10$.

Q.14 MCQ · 1 MARK

Recombinant DNA Technology and Tools › Assays & electrophoresis

Cancer cells display a high level of heterogeneity in the expression of TP53 protein. Which of the following techniques can be directly used to determine the intra-tumoral heterogeneity of TP53 expression in a given tumor sample, without resorting to additional cell separation techniques?

(A) Immunoblotting

(B) Flow cytometry

(C) ELISA

(D) Quantitative RT-PCR

Official answer: **B**

SOLUTION

1. Immunoblotting (A): the tumor sample is lysed and pooled before loading, so it reports a single averaged band intensity for the whole sample; heterogeneity between individual cells is lost. Not suitable.
2. ELISA (C): also requires a homogenized/pooled lysate and reports one averaged absorbance/concentration value for the sample; it cannot resolve cell-to-cell differences. Not suitable.
3. Quantitative RT-PCR (D): measures average mRNA transcript abundance from bulk-extracted RNA. Besides reading the wrong molecule (mRNA, not protein), it also yields a single pooled value rather than a per-cell readout. Not suitable.
4. Flow cytometry (B): after fixation/permeabilization, cells are stained with a fluorescently labeled anti-TP53 antibody and passed one at a time past a laser detector, so each individual cell's TP53 signal is measured separately.
5. This produces a distribution/histogram of TP53 expression across thousands of individual cells from the same tumor sample in a single run, directly revealing intra-tumoral heterogeneity.
6. No prior physical cell separation (sorting into subpopulations, microdissection, etc.) is required; heterogeneity is read out for the whole mixed cell population simultaneously.
7. Hence flow cytometry is the technique that can be directly used, satisfying the condition of not resorting to additional cell separation techniques.

KEY IDEA

Single-cell-resolved assays (flow cytometry) preserve heterogeneity information that bulk/pooled assays (immunoblotting, ELISA, qRT-PCR) inherently average away.

WATCH OUT FOR

Picking immunoblotting or ELISA because they are the standard protein-detection techniques for TP53, without noticing that both require a pooled/homogenized lysate and therefore report only an averaged, sample-level value; they cannot reveal cell-to-cell (intra-tumoral) heterogeneity.

Q.15 MCQ · 1 MARK

Fundamentals of Biological Engineering › Process control

The transfer function of a Proportional-Integral (PI) controller $G_C(s)$ is given by

$$G_C(s) = K_C\left(1 + \frac{1}{\tau_I s}\right)$$

where K_C is the controller gain, τ_I is the controller integral time constant and s is the Laplace variable. The role of the integral component of the controller is to _____.

(A) integrate the difference between the process and manipulated variable

(B) integrate the difference between the set point and disturbance variable

(C) integrate the difference between the set point and the measured variable

(D) integrate the difference between the input and output variable

Official answer: **C**

SOLUTION

1. A feedback controller acts on the **error signal**, which the comparator forms as $e(t) = y_{sp}(t) - y_m(t)$. Here y_{sp} is the set point and y_m is the measured value of the controlled variable, meaning the sensor/transmitter output.

2. The controller transfer function relates the controller output to the error: $G_C(s) = \dfrac{P'(s)}{E(s)}$, where $P'(s)$ is the Laplace transform of the deviation in controller output and $E(s)$ is the Laplace transform of the error.
3. Invert $G_C(s) = K_C\left(1 + \dfrac{1}{\tau_I s}\right)$ to get the PI law in the time domain, with K_C the controller gain, τ_I the integral time, $\bar{p}$ the controller's bias (steady-state output) and t^* a dummy integration variable:
$$p(t) = \bar{p} + K_C\, e(t) + \frac{K_C}{\tau_I}\int_0^t e(t^*)\, dt^*$$
4. The factor $\dfrac{1}{\tau_I s}$ is an integrator: for deviation variables with zero initial value, dividing by s in the Laplace domain is integration in time. It multiplies $E(s)$, so the integral action integrates $e = y_{sp} - y_m$, the set point minus the measured variable.
5. This is why integral action removes offset. As long as $e \neq 0$ the integral keeps changing, so $p(t)$ keeps changing. If the closed loop is stable and settles, $p(t)$ can only become constant when $e = 0$, which means $y_m = y_{sp}$.
6. Check the other options. (A): the manipulated variable is what the controller output adjusts. The controller never subtracts it from the process variable, and the two usually have different physical meanings and units. (B): the controller does not measure the disturbance or subtract it from the set point. The disturbance only affects the loop through its effect on y_m. (D): 'input minus output' does not identify the error signal. The controller's input minus its output means nothing physically, and neither does the process's input minus its output.
7. Only (C) names the error signal, set point minus measured variable, which the integral term accumulates. **Answer: (C)**

KEY IDEA

A controller transfer function always acts on the error $E(s)$, and $\frac{1}{\tau_I s}$ means integrate in time. So the integral term adds up $e = y_{sp} - y_m$, the set point minus the measured variable. It keeps changing the controller output until that error is zero, and that is how PI control removes steady-state offset.

WATCH OUT FOR

Picking (A) because 'manipulated variable' is confused with 'measured variable'. The manipulated variable is what the controller adjusts, not what it compares with the set point. Picking (D) because 'input minus output' sounds like an error. The error is specifically set point minus measured value, not the difference between any input and output.

Q.16 MCQ · 1 MARK

General Biology › Metabolism

Which of the following enzyme is involved in the protection of cells from reactive oxygen species?

(A) Hexokinase

(B) Glucose 6-phosphate dehydrogenase

(C) Enolase

(D) Pyruvate kinase

Official answer: **B**

SOLUTION

1. Cells defend against reactive oxygen species (ROS) with reduced glutathione and thioredoxin, together with enzymes such as catalase, superoxide dismutase and glutathione peroxidase. Regenerating the reduced forms of glutathione and thioredoxin needs a steady supply of NADPH.
2. Glutathione peroxidase uses reduced glutathione (GSH) to destroy $\mathrm{H_2O_2}$, forming oxidised glutathione (GSSG). Glutathione reductase then regenerates GSH from GSSG and needs NADPH to do so.

3. In red blood cells the oxidative (first) stage of the pentose phosphate pathway is the main source of NADPH. Its first, rate-limiting step is catalysed by glucose 6-phosphate dehydrogenase: $\text{glucose 6-phosphate} + \mathrm{NADP^+} \rightarrow \text{6-phosphogluconolactone} + \mathrm{NADPH}$.
4. Option B is correct. A deficiency of this enzyme leaves cells short of NADPH and unable to cope with oxidative stress. This causes haemolytic anaemia after exposure to oxidants such as primaquine or fava beans.
5. Option A is wrong. Hexokinase phosphorylates glucose to glucose 6-phosphate at the start of glycolysis and makes no NADPH.
6. Options C and D are wrong. Enolase (2-phosphoglycerate to phosphoenolpyruvate) and pyruvate kinase (phosphoenolpyruvate to pyruvate, with ATP formed) are glycolytic enzymes of the pay-off phase. Neither makes NADPH or takes part in ROS defence.

KEY IDEA
Antioxidant defence (glutathione, thioredoxin) runs on NADPH, and glucose 6-phosphate dehydrogenase, the first enzyme of the pentose phosphate pathway, is the main source of that NADPH.

WATCH OUT FOR
Picking a glycolytic enzyme because all four options are carbohydrate-metabolism enzymes. Only the pentose phosphate pathway makes NADPH, which ROS protection needs.

Q.17 MCQ · 1 MARK

General Biology › Pathogens & antibiotics

In nitrogen fixation, to reduce nitrogen to ammonia, which one of the following shows the correct order of electron flow?

(A) Ferredoxin → reductase → nitrogenase
(B) NADH → reductase → nitrogenase
(C) Ferredoxin → nitrogenase → reductase
(D) Reductase → NADH → nitrogenase

Official answer: **A**

SOLUTION

1. Nitrogenase is a two-component enzyme complex. The Fe protein is called dinitrogenase reductase. The MoFe protein is called dinitrogenase, and it is the site where $\mathrm{N_2}$ is reduced to $\mathrm{NH_3}$.
2. Reduced ferredoxin (or flavodoxin) is the physiological electron donor. It gives electrons to the Fe protein (the reductase).
3. The Fe protein binds ATP, and ATP hydrolysis drives electron transfer from the Fe protein to the MoFe protein. Inside the MoFe protein the electrons pass through the P-cluster to the FeMo-cofactor, where $\mathrm{N_2}$ is reduced.
4. The order of electron flow is therefore ferredoxin $\rightarrow$ reductase $\rightarrow$ nitrogenase. This is option (A).
5. Option (B) is wrong because NADH does not donate electrons directly to the Fe protein. Ferredoxin or flavodoxin is the immediate donor, and NADH is at most an indirect source further upstream.
6. Option (C) is wrong because it reverses the last two carriers. The reductase passes electrons to the nitrogenase, because the nitrogenase holds the substrate-binding site.
7. Option (D) is wrong because the reductase is not at the start of the chain, and NADH is not an electron carrier placed between the reductase and the nitrogenase.

KEY IDEA
Electrons reach nitrogenase in two stages. Reduced ferredoxin or flavodoxin reduces the Fe protein (dinitrogenase reductase). The Fe protein, driven by ATP hydrolysis, then passes electrons to the MoFe protein (dinitrogenase), which reduces N_2 to NH_3.

WATCH OUT FOR
Putting NADH at the start of the chain, or treating the reductase as the final catalytic component. The catalytic MoFe protein is the last carrier, and ferredoxin is the immediate electron donor.

Q.18 MCQ · 1 MARK

Plant, Animal and Microbial Biotechnology › Hybridomas & transgenics

For monoclonal antibody production, hypoxanthine _____.

(A) allows DNA synthesis in the absence of de novo dTMP synthesis

(B) allows purine synthesis in cells containing HGPRT

(C) induces cell fusion

(D) prevents de novo nucleotide synthesis

Official answer: **B**

SOLUTION

1. HAT medium selects hybridomas. It contains **h**ypoxanthine, **a**minopterin and **t**hymidine. Aminopterin blocks dihydrofolate reductase, so the de novo routes to purines and to dTMP are both shut.
2. Cells can then survive only through the salvage pathways. Hypoxanthine is the purine salvage substrate: HGPRT converts it to IMP, which gives AMP and GMP without the de novo route.
3. (B) is correct. Myeloma cells are HGPRT-deficient, so they cannot use hypoxanthine and die in HAT medium. Spleen B cells have HGPRT but do not grow for long in culture. Only fused hybridomas grow, because they carry HGPRT from the B cell and immortality from the myeloma cell.
4. (A) is wrong. Salvage dTMP synthesis starts from thymidine through thymidine kinase. Hypoxanthine feeds purine synthesis, not dTMP.
5. (C) is wrong. Cell fusion is induced by polyethylene glycol or Sendai virus, not by hypoxanthine.
6. (D) is wrong. Aminopterin, not hypoxanthine, blocks de novo nucleotide synthesis. Hypoxanthine supplies purines through the salvage route.

KEY IDEA
In HAT selection, aminopterin shuts the de novo pathways. Hypoxanthine supplies purines through HGPRT, and thymidine supplies dTMP through thymidine kinase. Only HGPRT-positive hybridomas survive.

WATCH OUT FOR
Giving hypoxanthine the job of thymidine (option A, dTMP synthesis), or the job of aminopterin (option D, blocking de novo synthesis).

Q.19 MCQ · 1 MARK

Fundamentals of Biological Engineering › Downstream

Which one of the following proteins would elute third in gel filtration chromatography from a mixture of four proteins given below?

(A) Insulin (6 kDa)

(B) Myoglobin (17 kDa)

(C) Thrombin (37 kDa)

(D) Albumin (66 kDa)

Official answer: **B**

SOLUTION

1. **How gel filtration (size-exclusion chromatography) works:** the column is packed with porous beads. Small molecules can enter the pores, so they have more volume to pass through and come out later. Large molecules are kept out of the pores, travel only through the space between the beads, and come out earlier. So the elution volume V_e (the volume of buffer collected before a protein comes out) goes down as molecular mass goes up.
2. For native globular proteins inside the column's fractionation range, size follows molecular mass M, and a calibrated column gives the empirical relation $V_e \approx a - b \log M$, where a and $b > 0$ are column constants. The heaviest protein therefore has the smallest V_e and comes out first.
3. Sort the four proteins by molecular mass, largest first: Albumin ($66\ \mathrm{kDa}$) > Thrombin ($37\ \mathrm{kDa}$) > Myoglobin ($17\ \mathrm{kDa}$) > Insulin ($6\ \mathrm{kDa}$).
4. So they elute in this order: 1st Albumin, 2nd Thrombin, **3rd Myoglobin**, 4th Insulin.
5. The protein that elutes third is Myoglobin ($17\ \mathrm{kDa}$), option (B).

KEY IDEA

Gel filtration separates by size. Large molecules are kept out of the bead pores and come out first. Small molecules enter the pores and come out last. For globular proteins, V_e falls roughly linearly with $\log M$, so the elution order is simply the order of decreasing molecular mass.

WATCH OUT FOR

Getting the elution order backwards. In ion-exchange or affinity chromatography, a molecule is held back by binding. In gel filtration nothing binds: the small proteins are the ones slowed down, because they wander through the pores. Students who think big molecules are 'held up' pick Thrombin (C) as the third to elute. That is the second protein counting from the small end.

Q.20 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Gene expression

Which one of the following antibiotics blocks protein chain elongation by preventing the action of peptidyl transferase ?

(A) Bleomycin

(B) Rifampicin

(C) Chloramphenicol

(D) Tetracycline

Official answer: **C**

SOLUTION

1. The question asks which antibiotic blocks translation elongation specifically by inhibiting peptidyl transferase, the ribozyme activity of the bacterial 50S ribosomal subunit that catalyzes peptide bond formation between the growing peptide chain and the incoming aminoacyl-tRNA.
2. (A) Bleomycin is an anticancer antibiotic that causes DNA strand breaks via free-radical generation. It acts on DNA, not on ribosomes or translation. Incorrect.
3. (B) Rifampicin inhibits bacterial DNA-dependent RNA polymerase, blocking transcription initiation. It does not act on the ribosome or on translation elongation. Incorrect.
4. (C) Chloramphenicol binds the 50S ribosomal subunit and directly inhibits peptidyl transferase activity, preventing peptide bond formation and thus blocking elongation. This matches the question exactly. Correct.

5. (D) Tetracycline binds the 30S ribosomal subunit and blocks binding of aminoacyl-tRNA to the ribosomal A site, preventing delivery of the incoming tRNA rather than inhibiting the peptidyl transferase reaction itself. Incorrect.
6. Only chloramphenicol's mechanism is inhibition of peptidyl transferase, so the answer is (C).

KEY IDEA
Peptidyl transferase is the ribozyme activity of the bacterial 50S subunit that catalyzes peptide bond formation; chloramphenicol specifically inhibits this step, distinguishing it from other translation-targeting antibiotics that act at different points (A-site tRNA binding, translocation, etc.).

WATCH OUT FOR
Confusing tetracycline (blocks aminoacyl-tRNA binding at the A site) with chloramphenicol (directly inhibits the peptidyl transferase reaction itself); both act on the ribosome during elongation, but only chloramphenicol targets peptidyl transferase specifically.

Q.21 MCQ · 1 MARK

Fundamentals of Biological Engineering › Enzyme kinetics

The catalytic efficiency of an enzyme following Michaelis-Menten kinetics is defined by

(A) k_{Cat}
(B) $V_{\max}/k_{\mathrm{Cat}}$
(C) $k_{\mathrm{Cat}}/K_{\mathrm{M}}$
(D) $k_{\mathrm{Cat}}/V_{\max}$

Official answer: **C**

SOLUTION

1. Michaelis-Menten rate law: $v = \dfrac{V_{\max}[S]}{K_M + [S]}$, with $V_{\max} = k_{\mathrm{cat}}[E]_0$. Here v is the initial reaction rate, $[S]$ the substrate concentration, k_{cat} the turnover number (units s^{-1}), K_M the Michaelis constant (a concentration), $V_{\max}$ the maximum rate and $[E]_0$ the total enzyme concentration. (The paper prints k_{cat} as k_{Cat}; it is the same quantity.)
2. At low substrate, $[S] \ll K_M$, the denominator is approximately K_M, so $v \approx \dfrac{k_{\mathrm{cat}}}{K_M}[E]_0[S]$. This is a second-order rate law: first order in enzyme and first order in substrate.
3. The coefficient k_{cat}/K_M (units $\mathrm{M}^{-1}\mathrm{s}^{-1}$) is the apparent second-order rate constant for free enzyme meeting free substrate and converting it to product (at $[S] \ll K_M$ almost all the enzyme is free, so $[E] \approx [E]_0$). It combines how fast the enzyme turns substrate over (k_{cat}) with how well it binds substrate ($1/K_M$). This ratio is called the catalytic efficiency, or specificity constant. Its upper limit is set by diffusion, about 10^8 to $10^9\ \mathrm{M}^{-1}\mathrm{s}^{-1}$.
4. Check the other options. (A) k_{cat} alone is the turnover number; it ignores substrate binding. (B) $V_{\max}/k_{\mathrm{cat}} = [E]_0$, which is just the enzyme concentration. (D) $k_{\mathrm{cat}}/V_{\max} = 1/[E]_0$. Neither (B) nor (D) is a property of the enzyme's efficiency.
5. So catalytic efficiency $= k_{\mathrm{cat}}/K_M$, which is option (C).

KEY IDEA
When $[S] \ll K_M$, the Michaelis-Menten equation reduces to $v = (k_{\mathrm{cat}}/K_M)[E]_0[S]$. The ratio k_{cat}/K_M therefore measures both turnover (k_{cat}) and binding ($1/K_M$) in one number, and diffusion caps it at about 10^8 to $10^9\ \mathrm{M}^{-1}\mathrm{s}^{-1}$.

WATCH OUT FOR
Choosing k_{cat} alone (A). That is the turnover number: how fast a substrate-saturated enzyme works, with binding ignored. Options (B) and (D) reduce to $[E]_0$ and $1/[E]_0$ because $V_{\max} = k_{\mathrm{cat}}[E]_0$. Both depend on how much enzyme is present, so neither describes the enzyme's efficiency.

Q.22 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Gene expression

The RNA primer synthesized during bacterial DNA replication is removed by _____.

(A) DNA gyrase

(B) DNA Polymerase I

(C) Primase

(D) DNA Polymerase III

Official answer: **B**

SOLUTION

1. DNA gyrase (A) is a type II topoisomerase that relieves supercoiling ahead of the replication fork; it plays no role in primer excision, so A is incorrect.
2. Primase (C) is the enzyme that synthesizes the RNA primers in the first place; it does not remove them, so C is incorrect.
3. DNA Polymerase III (D) is the main bacterial replicative polymerase, extending primers and synthesizing the bulk of leading- and lagging-strand DNA, but it possesses only 3'→5' proofreading exonuclease activity and lacks 5'→3' exonuclease activity, so it cannot excise primers. D is incorrect.
4. DNA Polymerase I (B) uniquely combines 5'→3' polymerase activity with 5'→3' exonuclease activity, letting it simultaneously excise the RNA primer ahead of it and fill the resulting gap with DNA. This is nick translation, the standard mechanism for primer removal during Okazaki fragment maturation.
5. The nick left after Pol I finishes is sealed by DNA ligase (not an option here), completing lagging-strand maturation.
6. Hence the correct answer is (B) DNA Polymerase I.

KEY IDEA

In bacteria, DNA Polymerase I is the only replicative polymerase with 5'→3' exonuclease activity, letting it simultaneously excise RNA primers and fill the gap with DNA (nick translation); DNA ligase then seals the remaining nick.

WATCH OUT FOR

Confusing DNA Polymerase III (the main chain-extending replicative enzyme) with DNA Polymerase I (the primer-removal/gap-filling enzyme). Students often forget Pol III lacks 5'→3' exonuclease activity and cannot excise RNA primers.

Q.23 MCQ · 1 MARK

General Biology › Biomolecules

Match the carbohydrates in Column I with the correct glycosidic linkages involved in Column II.

Column I: P. Amylose; Q. Sucrose; R. Amylopectin; S. Cellulose.
Column II: 1. β (1→4); 2. α (1→4); 3. α1→β2; 4. α (1→4), α (1→6).

(A) P-4; Q-3; R-2; S-1

(B) P-2; Q-1; R-4; S-3

(C) P-2; Q-3; R-4; S-1

(D) P-1; Q-3; R-4; S-2

Official answer: **C**

SOLUTION

1. P, Amylose: an unbranched chain of glucose units joined only by $\alpha(1 \rightarrow 4)$ bonds, so P matches 2.
2. Q, Sucrose: a disaccharide of glucose and fructose joined through both anomeric carbons, α-$\mathrm{Glc}(1 \rightarrow 2)\beta$-$\mathrm{Fru}$, written $\alpha 1 \rightarrow \beta 2$, so Q matches 3.

3. R, Amylopectin: a branched starch. The main chain is $\alpha(1 \rightarrow 4)$ and the branch points are $\alpha(1 \rightarrow 6)$ (about one in 24 to 30 residues), so R matches 4.
4. S, Cellulose: glucose units joined by $\beta(1 \rightarrow 4)$ bonds. Each residue is flipped relative to the next, giving straight chains that hydrogen-bond into fibres, so S matches 1.
5. The matching is P-2; Q-3; R-4; S-1.
6. Option A gives amylose the branched linkage 4 and amylopectin 2, so it is wrong. Option B pairs sucrose with 1 and cellulose with 3, so it is wrong. Option D pairs amylose with the β linkage and cellulose with 2, so it is wrong. Only option C matches all four.

KEY IDEA

Starch is amylose ($\alpha(1 \rightarrow 4)$ only) plus amylopectin ($\alpha(1 \rightarrow 4)$ with $\alpha(1 \rightarrow 6)$ branches). Cellulose is $\beta(1 \rightarrow 4)$. Sucrose is the odd one out, with a glycosidic bond that links the two anomeric carbons, $\alpha 1 \rightarrow \beta 2$.

WATCH OUT FOR

Giving cellulose the α linkage, or amylose the branched $\alpha(1 \rightarrow 4), \alpha(1 \rightarrow 6)$ linkage. Only amylopectin has the $\alpha(1 \rightarrow 6)$ branch points.

Q.24 MCQ · 1 MARK

Plant, Animal and Microbial Biotechnology › Microbial products

The correct sequence of the four steps involved in anaerobic production of biogas from complex organics is:

(A) Hydrolysis → Acidogenesis → Acetogenesis → Methanogenesis

(B) Methanogenesis → Acetogenesis → Acidogenesis → Hydrolysis

(C) Acidogenesis → Hydrolysis → Methanogenesis → Acetogenesis

(D) Hydrolysis → Methanogenesis → Acidogenesis → Acetogenesis

Official answer: **A**

SOLUTION

1. Anaerobic digestion converts complex organic matter to biogas ($\mathrm{CH_4}$ and $\mathrm{CO_2}$) in four consecutive stages, each feeding the next.
2. Stage 1, hydrolysis: extracellular enzymes break polymers (polysaccharides, proteins, lipids) into soluble monomers such as sugars, amino acids and fatty acids. This must come first because later microbes can only take up small soluble molecules.
3. Stage 2, acidogenesis: fermentative bacteria convert these monomers into volatile fatty acids, alcohols, $\mathrm{H_2}$ and $\mathrm{CO_2}$.
4. Stage 3, acetogenesis: acetogenic bacteria oxidise the volatile fatty acids and alcohols to acetate, $\mathrm{H_2}$ and $\mathrm{CO_2}$.
5. Stage 4, methanogenesis: methanogenic archaea make methane from acetate (acetoclastic route) and from $\mathrm{H_2}$ plus $\mathrm{CO_2}$ (hydrogenotrophic route). It is last because it needs acetate and $\mathrm{H_2}$ as substrates.
6. Option A gives exactly this order. B reverses it, so methane would be made before any substrate exists. C puts acidogenesis before hydrolysis, which is wrong because polymers must be broken down first. D puts methanogenesis before the acid and acetate stages, so it has no substrate.

KEY IDEA

Anaerobic digestion runs in a fixed chain: polymers are hydrolysed to monomers, fermented to acids and alcohols, oxidised to acetate and hydrogen, and only then converted to methane. Each stage makes the substrate the next stage needs.

WATCH OUT FOR

Putting acidogenesis before hydrolysis, or placing methanogenesis early because methane is the product people think of first. Methanogens can only use acetate, $\mathrm{H_2}$ and $\mathrm{CO_2}$, so they must come last.

Q.25 MCQ · 1 MARK

General Biology › Metabolism

Which one of the following options represents the products of light reactions of photosynthesis in plants?

(A) O2/NADH/H2

(B) O2/NADP+/CO2

(C) O2/NADPH/ATP

(D) O2/NADP+/ATP

Official answer: **C**

SOLUTION

1. The light reactions take place in the thylakoid membranes. Photosystem II splits water (photolysis), releasing O_2, protons and electrons.
2. Electrons pass along the chain to photosystem I and finally reduce $NADP^+$ to $NADPH$ (ferredoxin-NADP reductase).
3. The proton gradient across the thylakoid membrane drives ATP synthase, so ATP is made by photophosphorylation.
4. The products of the light reactions are therefore O_2, $NADPH$ and ATP, which is option C.
5. Option A is wrong. Plants make $NADPH$, not $NADH$, and no H_2 is released.
6. Option B is wrong. $NADP^+$ is the electron acceptor, so it is used up rather than made. CO_2 is a substrate of the Calvin cycle, not a product of the light reactions.
7. Option D is wrong. $NADP^+$ is the reactant. The reduced form $NADPH$ is the product, and it is used with ATP in the Calvin cycle.

KEY IDEA

The light reactions make ATP and NADPH and release O2 from water. The Calvin cycle then uses ATP and NADPH to fix CO2.

WATCH OUT FOR

Mixing up NADP+ (the oxidised acceptor) with NADPH (the product). Another slip is writing NADH, which belongs to respiration, in place of NADPH.

Q.26 MCQ · 1 MARK

Recombinant DNA Technology and Tools › Editing & interactions

Which component of the CRISPR/Cas9 gene editing system is NOT of natural origin?

(A) CAS9 protein

(B) CRISPR repeats

(C) PAM sequence

(D) sgRNA

Official answer: **D**

SOLUTION

1. Recall the natural bacterial CRISPR-Cas9 adaptive immune system: it uses the Cas9 nuclease protein, arrays of CRISPR repeat-spacer sequences in the genome, and requires a PAM (protospacer adjacent motif) sequence on the target DNA next to the protospacer.
2. Option (A) CAS9 protein: naturally produced by bacteria such as Streptococcus pyogenes as part of their native immune defense system; of natural origin. Eliminate.
3. Option (B) CRISPR repeats: naturally occurring short repeated sequences interspersed with spacers in the bacterial genome, forming the memory of past phage infections; of natural origin. Eliminate.
4. Option (C) PAM sequence: a short motif naturally present in the target genomic DNA itself (of the invading phage/plasmid), required for native Cas9 to recognize and cleave the target; of natural origin.

Eliminate.

5. Option (D) sgRNA (single guide RNA): in the natural bacterial system, Cas9 is guided by two separate RNA molecules, crRNA and tracrRNA, that base-pair with each other. The single-guide RNA used in genome-editing technology is a synthetic, laboratory-engineered fusion of these two natural RNAs into one chimeric molecule; this fused form does not exist in nature.
6. Therefore the component that is NOT of natural origin is sgRNA, option (D).

KEY IDEA
Natural CRISPR/Cas9 in bacteria uses Cas9 protein, a CRISPR repeat-spacer array, and PAM sequences on target DNA, all naturally occurring. The single-guide RNA (sgRNA) is a synthetic, laboratory-engineered fusion of the natural crRNA and tracrRNA into one chimeric molecule, created for genome-editing applications; it does not occur in this fused form in nature.

WATCH OUT FOR
Assuming any RNA involved in Cas9 targeting must be "natural" because RNA-guided cleavage itself is a natural bacterial process, and missing that the single-molecule sgRNA construct specifically is an engineered fusion (crRNA + tracrRNA) not found in native bacterial CRISPR systems.

Q.27 MSQ · 1 MARK

Engineering Mathematics › Differential equations

The equation $\frac{d^2y}{dx^2} - y = 0$ has a solution of the form $y = e^{Ax}$. The value(s) of A satisfying this is/are:

(A) 0
(B) 1
(C) -1
(D) -∞

Official answer: **B, C**

SOLUTION

1. Substitute the trial solution $y = e^{Ax}$ into the equation. Then $\frac{dy}{dx} = Ae^{Ax}$ and $\frac{d^2y}{dx^2} = A^2e^{Ax}$.
2. The equation becomes $A^2e^{Ax} - e^{Ax} = 0$, so $e^{Ax}\left(A^2 - 1\right) = 0$.
3. For $y = e^{Ax}$ to be a solution it must satisfy this for all x. Since $e^{Ax} \neq 0$ for every finite A and x, this requires $A^2 - 1 = 0$.
4. This gives $A = 1$ or $A = -1$, so the general solution is $y = c_1e^{x} + c_2e^{-x}$.
5. Check the other options. $A = 0$ gives $y = 1$, and then $\frac{d^2y}{dx^2} - y = 0 - 1 = -1 \neq 0$. $A = -\infty$ is not a finite number, so e^{Ax} is not a valid solution form for it.
6. The correct options are (B) and (C).

KEY IDEA
Put the trial solution $y = e^{Ax}$ into the equation. Because e^{Ax} is never zero, you are left with the auxiliary equation $A^2 - 1 = 0$, whose roots are the allowed values of A.

WATCH OUT FOR
Choosing only one root, usually $A = 1$, on an MSQ. A second-order equation has two roots, and both e^{x} and e^{-x} are solutions. Another slip is accepting $A = 0$ without substituting it back.

Q.28 MSQ · 1 MARK

General Biology › Metabolism

Which of the following drugs inhibit(s) ATP-ADP translocase?

(A) Oligomycin
(B) Atractyloside

(C) Amytal

(D) Bongkrekic acid

Official answer: **B, D**

SOLUTION

1. The ATP-ADP translocase (adenine nucleotide translocase, ANT) sits in the inner mitochondrial membrane. It exports ATP^{4-} from the matrix and imports ADP^{3-} in a 1:1 antiport.
2. (A) Oligomycin binds the F_0 proton channel of ATP synthase and blocks proton flow through it. It does not act on the translocase, so A is wrong.
3. (B) Atractyloside (and its relative carboxyatractyloside) binds ANT from the cytosolic side and locks it in the cytosol-facing conformation. This stops the exchange, so B is correct.
4. (C) Amytal (amobarbital) is a barbiturate that inhibits Complex I (NADH dehydrogenase) and so blocks electron transfer. It does not act on the translocase, so C is wrong.
5. (D) Bongkrekic acid binds ANT from the matrix side and locks it in the matrix-facing conformation. This also stops the exchange, so D is correct.
6. The two ANT inhibitors are therefore atractyloside and bongkrekic acid, which is options B and D.

KEY IDEA

Atractyloside and bongkrekic acid both inhibit the adenine nucleotide translocase. They lock it in opposite conformations: atractyloside in the cytosol-facing one, bongkrekic acid in the matrix-facing one. Oligomycin blocks ATP synthase and amytal blocks Complex I.

WATCH OUT FOR

Treating every mitochondrial poison as a translocase inhibitor. Oligomycin (ATP synthase F_0) and amytal (Complex I) act on other components of oxidative phosphorylation, not on the ATP-ADP exchange.

Q.29 MSQ · 1 MARK

Genetics, Cell and Molecular Biology › Cell biology

Which of the following is/are extra-cellular matrix protein(s)?

(A) Myosin

(B) Fibronectin

(C) Lamin

(D) Collagen

Official answer: **B, D**

SOLUTION

1. Myosin is a motor protein that operates in the cytoplasm, moving along actin filaments to generate force; it is never secreted into the extracellular space, so it is not an ECM protein.
2. Fibronectin is a glycoprotein secreted into the extracellular matrix, where it links cells to collagen and other matrix components via integrin receptors; a classic ECM protein.
3. Lamin is a nuclear intermediate filament protein that forms the nuclear lamina lining the inner nuclear membrane; it is strictly intracellular and structurally supports the nucleus, not the ECM.
4. Collagen is the principal fibrous structural protein of the extracellular matrix, giving connective tissue its tensile strength; a classic ECM protein.
5. Therefore the extracellular matrix proteins among the options are Fibronectin (B) and Collagen (D).

KEY IDEA
The extracellular matrix (ECM) is built mainly of structural fibrous proteins (like collagen) and adhesive glycoproteins (like fibronectin) that are secreted by cells into the space outside them; motor proteins (myosin) and nuclear lamina proteins (lamins) are intracellular, not ECM components.

WATCH OUT FOR
Confusing "structural protein" in general with "extracellular matrix protein" specifically. Students sometimes mark Lamin because it is also a structural (intermediate filament) protein, forgetting that lamins line the INNER nuclear membrane and are strictly intracellular, not secreted into the ECM.

Q.30 MSQ · 1 MARK

Recombinant DNA Technology and Tools › Bioinformatics

BLAST and its extensions can be used to determine similarity of a query protein sequence with which of the following database(s)?

(A) A database of translated nucleotide sequences

(B) A database of binding ligands and small translated peptides

(C) A database of protein structures

(D) A database of binding, linking and self-assembling proteins

Official answer: **A**

Q.31 NAT · 1 MARK

Engineering Mathematics › Probability & statistics

The mean of the following series is _____. (rounded off to three decimal places)

0.01, 0.02, 0.03, ⋯⋯, 1

Official answer: **0.505**

SOLUTION

1. The numbers $0.01, 0.02, 0.03, \ldots, 1$ form an arithmetic progression with first term $a = 0.01$ and common difference $d = 0.01$.
2. Number of terms: the last term is $l = a + (n-1)d = 0.01\,n$. Setting $0.01\,n = 1$ gives $n = 100$.
3. Sum of the AP: $S = \dfrac{n}{2}(a + l) = \dfrac{100}{2}(0.01 + 1) = 50 \times 1.01 = 50.5$.
4. Mean $= \dfrac{S}{n} = \dfrac{50.5}{100} = 0.505$.
5. Check: for an AP the mean equals the average of the first and last terms, $\dfrac{0.01 + 1}{2} = 0.505$. To three decimal places the answer is 0.505.

KEY IDEA
The series is an arithmetic progression, so its mean is the average of the first and last terms: $(0.01 + 1)/2 = 0.505$. You do not need to add up all 100 terms.

WATCH OUT FOR
Miscounting the terms. The series stops at 1, so there are 100 terms, not 99 or 101. Taking the midpoint as 0.5, or dividing the sum by the wrong count, gives a wrong mean.

Q.32 NAT · 1 MARK

Fundamentals of Biological Engineering › Enzyme kinetics

You are characterizing a new enzyme isolated and purified in the laboratory. If the maximum velocity of the enzyme is 1800 $\mu\text{moles}\ \text{L}^{-1}\ \text{min}^{-1}$ and the total concentration of the enzyme in the reaction mixture is 1.5

μM, then the turnover number of the enzyme is _____ s^{-1}. (answer in integer)

Official answer: **20**

SOLUTION

1. The turnover number k_{cat} is the number of substrate molecules one enzyme molecule converts to product per unit time when the enzyme is saturated with substrate. It is defined as $k_{cat} = \dfrac{V_{max}}{[E]_T}$, where V_{max} is the maximum velocity and $[E]_T$ is the total enzyme concentration.
2. Write both quantities in the same concentration unit. Since $1\ \mu\text{mol L}^{-1} = 1\ \mu\text{M}$, we have $V_{max} = 1800\ \mu\text{mol L}^{-1}\ \text{min}^{-1} = 1800\ \mu\text{M min}^{-1}$ and $[E]_T = 1.5\ \mu\text{M}$.
3. Divide:
$$k_{cat} = \frac{1800\ \mu\text{M min}^{-1}}{1.5\ \mu\text{M}} = 1200\ \text{min}^{-1}$$
4. Convert to per second ($1\ \text{min} = 60\ \text{s}$):
$$k_{cat} = \frac{1200}{60}\ \text{s}^{-1} = 20\ \text{s}^{-1}$$

KEY IDEA
Turnover number $k_{cat} = V_{max}/[E]_T$. It is the rate at saturation divided by the concentration of enzyme doing the work. Once the concentration units cancel, only a time unit is left, so convert it to what the question asks for.

WATCH OUT FOR
Stopping at 1200 because the question asks for s^{-1} and V_{max} was given per minute. Dividing by 60 is required. A second slip is multiplying by 60 instead of dividing, which gives 72000 s^{-1}.

Q.33 NAT · 1 MARK

General Biology › Microbiology

To determine the viable cell count of a bacterial culture, you have plated 50 µL of a 100-fold diluted sample of the culture on a nutrient agar plate and obtained 20 colonies after overnight incubation. The viable cell count of the culture is _____ CFU mL^-1. (answer in integer)

Official answer: **40000**

SOLUTION

1. Each colony grows from one viable cell, so the count of colony forming units (CFU) on the plate equals the number of viable cells in the volume plated. The viable count of the original culture is $\dfrac{\text{colonies}}{\text{volume plated}} \times \text{dilution factor}$.
2. Convert the plated volume to mL: $50\ \mu\text{L} = 0.05\ \text{mL}$.
3. Concentration of the diluted sample: $\dfrac{20\ \text{CFU}}{0.05\ \text{mL}} = 400\ \text{CFU mL}^{-1}$.
4. The sample was diluted 100-fold, so the original culture is 100 times more concentrated: $400 \times 100 = 40000\ \text{CFU mL}^{-1}$.
5. The viable cell count of the culture is $4 \times 10^4\ \text{CFU mL}^{-1}$, that is 40000 as an integer.

KEY IDEA
Viable count = colonies / volume plated (in mL) x dilution factor. Convert the volume to mL first, then multiply back by the dilution to get the concentration of the original culture.

WATCH OUT FOR
Forgetting to convert 50 microlitres to 0.05 mL (giving 20/50 = 0.4 and then 40), or forgetting to multiply by the dilution factor and stopping at 400 CFU per mL.

Q.34 NAT · 1 MARK

Q.34 Given below is the Gibbs free energy change (ΔG) in kilo Joules per electron equivalent (kJ e^-eq^{-1}) at pH 7.0, of organic and inorganic half reactions.

Acetate synthesis:

$$\frac{1}{8}CO_2 + \frac{1}{8}HCO_3^- + H^+ + e^- \rightarrow \frac{1}{8}CH_3COO^- + \frac{3}{8}H_2O \quad \Delta G=27.4 \text{ kJ } e^-eq^{-1}$$

Reduction reaction:

$$\frac{1}{4}O_2 + H^+ + e^- \rightarrow \frac{1}{2}H_2O \quad \Delta G= -78.72 \text{ kJ } e^-eq^{-1}$$

The free energy change of acetate oxidation to CO_2, H_2O and HCO_3^- is _____ kJ e^-eq^{-1}. (*rounded off to two decimal places*)

Official answer: **-106.12**

Q.35 NAT · 1 MARK

Recombinant DNA Technology and Tools › Assays & electrophoresis

You have purified an enzyme using a series of chromatographic methods. It was observed that a 10 µg mL^{-1} of this purified enzyme converted 10 mM substrate per hour at 25°C and pH 7. Its specific activity is _____ IU μg^{-1}. (rounded off to three decimal places)

Official answer: **0.016 to 0.017**

SOLUTION

1. Definition: 1 IU (International Unit) of enzyme = the amount of enzyme that converts 1 µmol of substrate per minute under the given assay conditions.
2. Choose a convenient basis, e.g. 1 mL of the enzyme solution. Enzyme mass present = 10 µg mL^{-1} × 1 mL = 10 µg.
3. Substrate converted in that 1 mL, per hour = 10 mM × 1 mL = 10 mmol L^{-1} × 0.001 L = 0.01 mmol = 10 µmol per hour.
4. Convert the rate to a per-minute basis (as required by the IU definition): 10 µmol $hour^{-1}$ ÷ 60 min $hour^{-1}$ = 0.16667 µmol min^{-1}, i.e. 0.16667 IU of total activity present in the 1 mL sample.
5. Specific activity = total activity (IU) ÷ total enzyme mass (µg) = 0.16667 IU ÷ 10 µg = 0.016667 IU μg^{-1}.
6. Rounded to three decimal places: specific activity = 0.017 IU μg^{-1}.

KEY IDEA

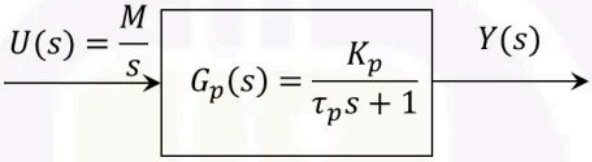
One International Unit (IU) of enzyme activity is defined as the amount of enzyme that converts 1 µmol of substrate per minute under the specified assay conditions. Specific activity is total enzyme activity (IU) divided by the total mass of enzyme protein (µg) present in the sample, so it is independent of the assay volume chosen for the calculation: any consistent volume basis (1 mL, 1 L, etc.) gives the same ratio.

WATCH OUT FOR

A common error is to divide by 1000 twice (once converting mM to M and again converting mmol to µmol) or to forget the hour-to-minute conversion (dividing/multiplying by 60 incorrectly), which changes the final specific activity by one or two orders of magnitude. Another common slip is reporting activity in IU/mL (total activity concentration) instead of IU/µg (specific activity, i.e., normalized to enzyme mass).

Q.36 MCQ · 2 MARKS

Fundamentals of Biological Engineering › Process control

Q.36	In the open-loop process shown in the figure, the input $U(s)$, the transfer function $G_p(s)$ and the output $Y(s)$ are given in the Laplace domain in terms of the Laplace variable s. For this process, which of the following is true? (where M, τ_p, K_P, are the magnitude of the input, the characteristic time and the gain for the process, respectively) 
(A)	$y(t) = K_p(1 - e^{-t/\tau_p})$
(B)	$y(t) = MK_p(1 - e^{-t/\tau_p})$
(C)	$y(t) = K_p(M - e^{-t/\tau_p})$
(D)	$y(t) = K_p(1 - Me^{-t/\tau_p})$

Official answer: **B**

SOLUTION

1. Symbols: K_p is the process gain (the stem prints it as K_P, the figure as K_p; they are the same quantity), τ_p is the characteristic time (time constant) and M is the size of the input. The input $U(s) = M/s$ is a step of magnitude M applied at $t = 0$.
2. The process is open loop, so the output is the transfer function times the input:

$$Y(s) = G_p(s)\,U(s) = \frac{K_p}{\tau_p s + 1} \cdot \frac{M}{s} = \frac{MK_p}{s(\tau_p s + 1)}$$

3. Partial fractions:
$$\frac{1}{s(\tau_p s+1)} = \frac{1}{s} - \frac{\tau_p}{\tau_p s+1} = \frac{1}{s} - \frac{1}{s+1/\tau_p}$$
(check: $\frac{(\tau_p s+1)-\tau_p s}{s(\tau_p s+1)} = \frac{1}{s(\tau_p s+1)}$).
4. Inverse Laplace, using $\mathcal{L}^{-1}\{1/s\} = 1$ and $\mathcal{L}^{-1}\{1/(s+a)\} = e^{-at}$ with $a = 1/\tau_p$:
$$y(t) = MK_p\left(1 - e^{-t/\tau_p}\right)$$
5. Check the limits. At $t = 0$ this gives $y = 0$, as it should for a first-order system starting from rest. As $t \to \infty$ it gives $y \to MK_p$, which matches the final value theorem (valid because the only pole of $sY(s)$ is at $s = -1/\tau_p < 0$): $\lim_{s\to 0} sY(s) = \lim_{s\to 0} \frac{MK_p}{\tau_p s+1} = MK_p$. The steady output is the gain times the step size.
6. Option (A) leaves out M, so it is the response to a unit step, not to a step of size M. Option (C) gives $y(0) = K_p(M-1) \neq 0$. Option (D) gives $y(0) = K_p(1-M) \neq 0$ and the wrong final value, K_p. Only (B) fits, so the answer is (B).

KEY IDEA

For a first-order process $G_p(s) = K_p/(\tau_p s+1)$ driven by a step of size M ($U(s) = M/s$), $Y(s) = MK_p/[s(\tau_p s+1)]$ and $y(t) = MK_p\left(1 - e^{-t/\tau_p}\right)$. The output starts at 0, reaches 63.2% of its final value at $t = \tau_p$, and settles at gain times step size, MK_p.

WATCH OUT FOR

Using the unit-step response $K_p\left(1 - e^{-t/\tau_p}\right)$ (option A) and forgetting that the input here has magnitude M. Because the system is linear, M scales the whole response, both the constant term and the exponential term. Options (C) and (D) put M on only one of the two terms, so they fail $y(0) = 0$.

Q.37 MCQ · 2 MARKS

General Biology › Immune system

Match the immunological terms in Column I with their function/description in the Column II. Column I: P. J gene; Q. Cyclosporin; R. Epitope; S. Hapten. Column II: 1. Suppresses immune system by blocking calcineurin; 2. Antibody binding site on a large molecule; 3. Small foreign molecule which elicits an immune response only when combined with a carrier molecule; 4. Contributes to antibody diversity.

(A) P-3; Q-4; R-2; S-1

(B) P-2; Q-4; R-1; S-3

(C) P-4; Q-1; R-2; S-3

(D) P-1; Q-3; R-4; S-2

Official answer: **C**

SOLUTION

1. **P, the J gene.** The V, D and J gene segments of the immunoglobulin genes are joined by somatic recombination. Which segments are chosen, and the imprecise joining at their ends, add to antibody diversity. So P matches 4.
2. **Q, cyclosporin.** It binds cyclophilin, and this complex inhibits calcineurin. Calcineurin is the phosphatase that activates NFAT, so IL-2 transcription and T-cell activation are blocked and the immune system is suppressed. So Q matches 1.
3. **R, epitope.** An epitope is the part of an antigen that an antibody (or a T-cell receptor) recognises. It is the antibody binding site on a large molecule. So R matches 2.
4. **S, hapten.** A hapten is a small foreign molecule that is not immunogenic alone. It elicits an immune response only when coupled to a carrier molecule such as a protein. So S matches 3.
5. **Result.** P-4; Q-1; R-2; S-3, which is option (C).

6. **Other options.** (A) fails because P-3, Q-4 and S-1 are wrong. (B) fails because P-2, Q-4 and R-1 are wrong. (D) fails because every pairing in it is wrong (P-1, Q-3, R-4, S-2).

KEY IDEA

Match each term to its defining role: the J segment is part of the V(D)J recombination that diversifies antibodies, cyclosporin blocks calcineurin, an epitope is the antibody-binding site on an antigen, and a hapten is a small molecule that is immunogenic only when attached to a carrier.

WATCH OUT FOR

Mixing up epitope and hapten (both relate to antibody binding), or linking the J gene with a suppressive role because it sounds like a regulatory element. The J segment is a diversity-generating gene segment, not an immunosuppressant target.

Q.38 MCQ · 2 MARKS

Genetics, Cell and Molecular Biology › Population & evolution

Q.38 Match the genetic disorders in **Column I** to the corresponding underlying cause in **Column II**

Column I	**Column II**
P. Klinefelter Syndrome	1. X-chromosome insufficiency
Q. Turner syndrome	2. DNA helicase mutations
R. Bloom syndrome	3. Nucleotide excision repair defects
S. Xeroderma pigmentosum	4. Extra X chromosome(s) in a male

(A) P-1; Q-3; R-4; S-2

(B) P-4; Q-1; R-2; S-3

(C) P-4; Q-2; R-3; S-1

(D) P-3; Q-2; R-4; S-1

Official answer: **B**

SOLUTION

1. Klinefelter syndrome has karyotype 47,XXY (or variants with more X chromosomes): a male with one or more extra X chromosomes → matches Column II item 4 ("Extra X chromosome(s) in a male").
2. Turner syndrome has karyotype 45,X: a female with only a single X chromosome, i.e. a deficiency of X-chromosome material → matches item 1 ("X-chromosome insufficiency").

3. Bloom syndrome is caused by mutations in the BLM gene, which encodes a RecQ-family DNA helicase; loss of helicase function causes genomic instability → matches item 2 ("DNA helicase mutations").
4. Xeroderma pigmentosum results from defects in genes of the nucleotide excision repair (NER) pathway, impairing repair of UV-induced DNA damage → matches item 3 ("Nucleotide excision repair defects").
5. Combining: P-4; Q-1; R-2; S-3, which is option (B).

KEY IDEA

Each disorder maps to one specific molecular/chromosomal defect: Klinefelter (47,XXY, extra X in a male), Turner (45,X, X insufficiency), Bloom syndrome (BLM helicase mutation causing genomic instability), and Xeroderma pigmentosum (NER pathway defect impairing repair of UV damage).

WATCH OUT FOR

Confusing Bloom syndrome (a RecQ helicase defect causing chromosome instability/sister-chromatid exchange) with Xeroderma pigmentosum (an NER defect specific to UV-damage repair); both are DNA-repair-related disorders, but only XP is a nucleotide excision repair defect, and only Bloom is a helicase mutation.

Q.39 MCQ · 2 MARKS

General Biology › Biomolecules

Q.39 Match the biomolecules in **Column I** with their function given in **Column II**

Column I	**Column II**
P. Lectins	1. Acts as ATP dependent pump to efflux out small molecules
Q. P-glycoprotein	2. Targets lysosomal enzymes to their destination
R. Digitoxigenin	3. Specific carbohydrate binding proteins
S. Mannose 6-phosphate	4. Inhibits Na^+-K^+ pump

(A) P-3; Q-2; R-1; S-4

(B) P-1; Q-3; R-4; S-2

(C) P-2; Q-1; R-3; S-4

(D) P-3; Q-1; R-4; S-2

Official answer: **D**

SOLUTION

1. **P, Lectins:** these are proteins that bind specific carbohydrate groups on glycoproteins and glycolipids, so P matches 3.
2. **Q, P-glycoprotein:** this is an ABC transporter (MDR1). It uses ATP hydrolysis to pump hydrophobic drugs and other small molecules out of the cell, which gives multidrug resistance. Q matches 1.

3. **R, Digitoxigenin:** this is the aglycone of the cardiac glycoside digitoxin. It binds the α subunit of the Na^+-K^+ ATPase and inhibits the pump. R matches 4.
4. **S, Mannose 6-phosphate:** this is the tag added to N-linked glycans of lysosomal enzymes in the Golgi. The M6P receptor recognises it and sorts the enzymes to lysosomes. S matches 2.
5. The full matching is P-3; Q-1; R-4; S-2.
6. **Option A** is wrong: it gives Q-2 and R-1. **Option B** is wrong: it gives P-1 and Q-3. **Option C** is wrong: it gives P-2 and R-3, and P is not the lysosomal targeting signal.
7. Only option D fits all four pairs.

KEY IDEA

Match each molecule to its role. Lectins bind carbohydrates, P-glycoprotein is an ATP-driven efflux pump, digitoxigenin blocks the Na+-K+ ATPase, and mannose 6-phosphate directs enzymes to lysosomes.

WATCH OUT FOR

Mixing up the lysosomal targeting signal (mannose 6-phosphate) with lectins because both involve sugars. Mannose 6-phosphate is a sorting tag, while lectins are carbohydrate-binding proteins.

Q.40 MCQ · 2 MARKS

Fundamentals of Biological Engineering › Growth kinetics

By elemental analysis of a biomass sample, it was found that the cells in the given sample are composed of (by weight) C=50%, H=8%, O=20%, N=10% and ash content=12%. Which of the following is the correct empirical formula of the ash-free cells, normalized with respect to Nitrogen?

(A) $C_{5.8}H_{11.2}O_{1.7}N$

(B) $C_{5.0}H_{10.2}O_{1.1}N$

(C) $C_{6.8}H_{12.2}O_{2.1}N$

(D) $C_{4.8}H_{9.2}O_{3.1}N$

Official answer: **A**

SOLUTION

1. Removing the ash leaves $100 - 12 = 88$ g of organic matter per 100 g of biomass (and indeed $50 + 8 + 20 + 10 = 88$). On an ash-free basis the percentages become $C = 50/0.88 = 56.8\%$, $H = 9.09\%$, $O = 22.7\%$, $N = 11.4\%$. Every element is divided by the same factor 0.88, so the ratios between them do not change, and we can work directly with the given masses.
2. Moles of each element in 100 g of the sample (mass $\div$ atomic mass, with $C = 12$, $H = 1$, $O = 16$, $N = 14$ g mol^{-1}): $C : \frac{50}{12} = 4.167$, $H : \frac{8}{1} = 8.00$, $O : \frac{20}{16} = 1.25$, $N : \frac{10}{14} = 0.714$ mol.
3. Normalise to one N atom by dividing each by the moles of N:
$$C : \frac{50/12}{10/14} = \frac{700}{120} = 5.83, \quad H : \frac{8}{10/14} = 11.2, \quad O : \frac{20/16}{10/14} = \frac{280}{160} = 1.75, \quad N : 1$$
4. The empirical formula of the ash-free cells is $C_{5.83}H_{11.2}O_{1.75}N$. Written to one decimal place, as the options are, this is $C_{5.8}H_{11.2}O_{1.7}N$. (The printed option cuts O off at 1.7 rather than rounding 1.75 up to 1.8; no option shows 1.8, so this does not change the match.)
5. Checking the others: B, C and D each have a C:N ratio (5.0, 6.8, 4.8) and an O:N ratio (1.1, 2.1, 3.1) that differ from 5.83 and 1.75, so only option (A) is consistent with the data.

KEY IDEA

Ash is inorganic and is left out of the formula. Taking it out scales every element's percentage by the same factor (1/0.88), so the atom ratios stay the same. Convert each mass to moles (divide by atomic mass), then divide every mole count by the moles of N: C/N = (50/12)/(10/14) = 5.83, H/N = 8/(10/14) = 11.2, O/N = (20/16)/(10/14) = 1.75.

WATCH OUT FOR

Using mass ratios instead of mole ratios. The mass ratio C:N = 50/10 = 5.0, which is exactly the trap in option (B). You must divide by atomic masses first. Two other mistakes: thinking the 12% ash changes the atom ratios (it only rescales every element by the same factor), and ruling out (A) because 1.75 would round to 1.8. The option truncates to 1.7, and no other option comes close on C, H or O.

Q.41 MSQ · 2 MARKS

Engineering Mathematics › Linear algebra

For the given matrix, which of the statements given below is/are true?

$$\begin{bmatrix} 3 & 1 & 5 \\ 2 & -1 & 0 \\ 5 & 2 & 9 \end{bmatrix}$$

(A) The matrix is full rank

(B) The matrix is invertible

(C) The matrix has a determinant

(D) The matrix has a transpose

Official answer: **C, D**

SOLUTION

1. Call the matrix A. A square matrix is invertible exactly when $\det A \neq 0$, and this is the same as having full rank (rank 3 here).
2. Expand along the first row:
$$\det A = 3\,[(-1)(9) - (0)(2)] - 1\,[(2)(9) - (0)(5)] + 5\,[(2)(2) - (-1)(5)].$$
3. This gives $\det A = 3(-9) - 1(18) + 5(9) = -27 - 18 + 45 = 0$.
4. Since $\det A = 0$, A is singular. So it is not invertible and not full rank. Hence (A) and (B) are false.
5. Rows 1 and 2 are not proportional: the first two entries give $3 : 2$ in column 1 but $1 : -1$ in column 2, so $\mathrm{R}_1 \neq k\,\mathrm{R}_2$. Two independent rows together with $\det A = 0$ mean the rank is exactly 2, which is less than 3.
6. Every square matrix has a determinant, and here it equals 0, so (C) is true. Every matrix has a transpose, so (D) is true.
7. Correct options: (C) and (D).

KEY IDEA

A square matrix is invertible if and only if its determinant is non-zero, and this is also the condition for full rank. Existence of a determinant (for any square matrix) and of a transpose (for any matrix) is automatic.

WATCH OUT FOR

Reading "has a determinant" as "has a non-zero determinant" and so rejecting (C). The determinant exists for every square matrix; here its value is 0. Another slip is rejecting (D) because the question seems to be about invertibility.

Q.42 MSQ · 2 MARKS

Genetics, Cell and Molecular Biology › Gene expression

Messenger RNAs (mRNAs) translate to generate polypeptides and the translation terminates at the UGA, UAG or UAA stop codons. The AGA codon acts as additional stop codon in the mitochondria. The longest possible polypeptide(s) that can be hypothetically translated in the cytosol and/or mitochondria, from the given full length mRNA sequence (36 nucleotides) is/are

5'-AACACCAUGACCCAUGUGGCGAGACGGUAGUUAAAA-3'

(A) 7 amino acids long in the cytosol

(B) 5 amino acids long in the mitochondria

(C) 6 amino acids long in the mitochondria

(D) 8 amino acids long in the cytosol

Official answer: **A, C**

SOLUTION

1. Index the 36-nt mRNA 1-36: positions 1-6 AACACC, 7-9 AUG, 10-12 ACC, 13-15 CAU, 16-18 GUG, 19-21 GCG, 22-24 AGA, 25-27 CGG, 28-30 UAG, 31-36 UUAAAA.
2. Only two AUG start codons exist in the sequence: at 7-9 and at 14-16 (no other AUG triplet occurs anywhere else).
3. ORF from AUG(7): AUG-ACC-CAU-GUG-GCG-AGA-CGG-UAG → Met-Thr-His-Val-Ala-Arg(AGA)-Arg(CGG)-stop(UAG, a universal stop in both compartments).
4. In the CYTOSOL, AGA is read as ordinary Arg (standard genetic code), so translation continues through it and stops only at the universal UAG codon: peptide = 7 amino acids (M,T,H,V,A,R,R) → matches option A.
5. In the MITOCHONDRIA, AGA is reassigned as an additional stop codon, so this same ORF halts right there, before AGA is incorporated: peptide = 5 amino acids (M,T,H,V,A) → this is option B, a genuine but shorter mitochondrial product.
6. ORF from AUG(14): re-reading the frame from position 14 gives AUG-UGG-CGA-GAC-GGU-AGU-UAA -> Met-Trp-Arg(CGA)-Asp-Gly-Ser-stop(UAA, universal). This frame contains no AGA codon at all (the shifted frame reads CGA, a distinct codon, at that position), so this 6-amino-acid product is the same, full-length product in both the cytosol and the mitochondria.
7. Longest polypeptide per compartment: cytosol = max(7 aa from AUG-7, 6 aa from AUG-14) = 7 aa (option A). Mitochondria = max(5 aa from AUG-7, truncated by AGA; 6 aa from AUG-14) = 6 aa (option C).
8. Option D (8 aa, cytosol) matches no valid ORF and is wrong. Option B is a real mitochondrial product but is not the longest one (6 aa beats it), so it is not selected. Correct options: A and C.

KEY IDEA

Mitochondrial translation reuses the universal genetic code except that AGA (and AGG) are reassigned from Arg codons to stop codons; so the same mRNA can yield different-length products in the two compartments depending on whether an in-frame AGA is read through (cytosol) or halts translation (mitochondria).

WATCH OUT FOR

Assuming there is only one reading frame (only the first AUG) to consider, and thus missing that a second, shorter-cytosolic-product ORF (from the internal AUG) becomes the LONGEST mitochondrial product once the first ORF is truncated by the AGA-as-stop rule; also assuming AGA truncation only removes the AGA and downstream residues without checking whether AGA itself even occurs in the alternate frame (it doesn't: that frame reads CGA instead).

Q.43 MSQ · 2 MARKS

Genetics, Cell and Molecular Biology › Mutation & repair

The RNA sequence below depicts the part of a 330 nucleotides long mRNA and it encodes the C-terminal portion of a protein.

5'-... ... ... AAC ACC ACG ACC CAU GUG GCG AGA CGG UAG-3'

A mutation was identified in this RNA denoted as 322A→U. This nucleotide change is represented by which of the following class(es) of mutation?

(A) Missense mutation

(B) Non-sense mutation

(C) Transversion mutation

(D) Silent mutation

Official answer: **B, C**

SOLUTION

1. The 30-nt printed sequence is 10 codons = the LAST 30 nt of the 330-nt mRNA, i.e. positions 301-330 (reading frame starting at nt 1).
2. Splitting into codons: codon8 (positions 322-324) = AGA, codon9 (325-327) = CGG, codon10 (328-330) = UAG.
3. AGA and CGG both code for Arginine (Arg); UAG is the natural stop codon that ends this protein's C-terminus.
4. Apply the mutation 322A→U: codon8 AGA becomes UGA.
5. UGA is one of the three stop codons (UAA, UAG, UGA); translation now halts at codon8 instead of continuing through Arg(CGG) to the natural UAG stop.
6. A sense codon (Arg) turned into a stop codon, causing premature chain termination, is by definition a nonsense mutation → option (B) correct. It is not missense (no substituted amino acid: translation stops) and not silent (product is truncated, not identical) → (A) and (D) are wrong.
7. Classify the base substitution itself, independent of its coding effect: A is a purine (adenine), U is a pyrimidine (uracil).
8. A purine→pyrimidine substitution is, by definition, a transversion (as opposed to a transition, which is purine↔purine or pyrimidine↔pyrimidine) → option (C) correct.
9. Since the question is MSQ (one or more correct) and both the coding-consequence classification and the base-chemistry classification describe the same single mutational event, the final answer is (B) and (C).

KEY IDEA

Classify a point mutation on two independent axes at once: (1) its effect on the encoded amino acid/reading (silent / missense / nonsense) by translating the codon before and after the change, and (2) the chemical nature of the base substitution itself (transition: purine↔purine or pyrimidine↔pyrimidine, vs transversion: purine↔pyrimidine); an MSQ can require both classifications to be marked correct simultaneously.

WATCH OUT FOR

Forgetting that the printed 30-nt segment is the LAST 10 codons of a 330-nt (110-codon) message and mis-numbering which codon contains position 322, or picking only the coding-consequence answer (nonsense, B) while overlooking that the question also independently asks about the transversion/transition nature of the base change (C), missing the second correct option in this MSQ.

Q.44 MSQ · 2 MARKS

Fundamentals of Biological Engineering › Bioreactor operation

A microbial culture is being grown in a bioreactor with continuous aeration. The dissolved oxygen probe provided with the system shows a reading of zero. In this context, which of the following inferences is/are correct?

(A) The culture has died due to absence of oxygen

(B) The culture has run out of carbon source

(C) The culture growth becomes oxygen limited

(D) The culture growth is independent of dissolved oxygen

Official answer: **C**

Q.45 MSQ · 2 MARKS

General Biology › Enzymes

For a Newtonian fluid, a plot of shear stress (on Y axis) against shear rate (on X axis) will result in a straight line _____.

(A) parallel to the X axis

(B) parallel to the Y axis

(C) with a negative slope

(D) with a positive slope

Official answer: **D**

SOLUTION

1. A Newtonian fluid obeys Newton's law of viscosity: $\tau = \mu\dot{\gamma}$, where τ is the shear stress, $\dot{\gamma}$ is the shear rate and μ is the viscosity.
2. With τ on the Y axis and $\dot{\gamma}$ on the X axis this reads $y = \mu x$. This is a straight line through the origin with slope μ.
3. For a Newtonian fluid μ is constant and does not change with shear rate, so the plot is a straight line.
4. Viscosity is always positive ($\mu > 0$), so the slope is positive. (D) is correct.
5. (A) A line parallel to the X axis has zero slope. That means the stress stays the same whatever the shear rate, so the viscosity would be zero. This is not Newtonian behaviour. Wrong.
6. (B) A line parallel to the Y axis has infinite slope, which means infinite viscosity. That describes a rigid solid, not a fluid. Wrong.
7. (C) A negative slope would mean a negative viscosity, which is physically impossible. Wrong.

KEY IDEA

A Newtonian fluid has a constant viscosity, so its shear stress against shear rate is a straight line through the origin whose slope is the viscosity. That slope is positive.

WATCH OUT FOR

Confusing the Newtonian plot with the plots of non-Newtonian fluids, which are curved (shear thinning, shear thickening) or have an intercept (Bingham plastic). Another slip is to treat the slope as shear stress instead of viscosity.

Q.46 MSQ · 2 MARKS

Fundamentals of Biological Engineering › Bioreactor operation

In an aerobic fermentation with air sparging, which of the following options can be used to increase the volumetric mass transfer coefficient for oxygen transfer?

(A) Using pure oxygen in place of air

(B) Increasing the volumetric flow rate of air

(C) Reducing the bubble diameter

(D) Decreasing the agitation rate

Official answer: **B, C**

SOLUTION

1. Oxygen transfer rate: $\mathrm{OTR} = k_L a\,(C^* - C_L)$. Here k_L is the liquid-film mass transfer coefficient, a is the gas-liquid interfacial area per unit volume of the gas-liquid dispersion, C^* is the saturation (equilibrium) dissolved-oxygen concentration and C_L is the actual dissolved-oxygen concentration. The question asks only about the product $k_L a$, not about the OTR as a whole.

2. Interfacial area of a bubble swarm: $a = \dfrac{6\,\varepsilon_G}{d_b}$, where ε_G is the gas holdup (volume fraction of gas in the dispersion) and d_b is the mean (Sauter) bubble diameter. So a, and with it k_La, goes up when ε_G goes up or d_b goes down.
3. Empirical correlation (van't Riet type) for a sparged, stirred vessel: $k_La = K\left(\dfrac{P_g}{V}\right)^{\alpha} u_G^{\beta}$, with P_g/V the gassed power input per unit volume, u_G the superficial gas velocity and K a constant for the system. Both exponents α and β are positive, so k_La rises with more power input and with more gas flow.
4. (A) Pure oxygen raises the partial pressure of O_2 in the gas about 4.8-fold ($1/0.21 \approx 4.8$), so by Henry's law C^*, and with it the driving force $(C^* - C_L)$, rises about 4.8-fold. k_L and a depend on hydrodynamics and fluid properties (bubble size, holdup, turbulence, diffusivity, viscosity), not on the composition of the gas, so k_La does not change. The OTR rises, but k_La does not. Not correct.
5. (B) A higher volumetric air flow rate means a higher superficial gas velocity u_G, which raises the gas holdup ε_G and therefore a; in the correlation $k_La \propto u_G^{\beta}$ with $\beta > 0$. k_La increases. Correct.
6. (C) A smaller d_b gives more interfacial area per unit volume ($a \propto 1/d_b$). Small bubbles also rise more slowly and stay longer in the liquid, which raises ε_G and increases a further. Very small bubbles can have a somewhat lower k_L (they behave like rigid spheres), but the rise in a outweighs it, so k_La increases. Correct.
7. (D) Less agitation means a lower P_g/V, so bubbles are broken up less (larger d_b), holdup falls and there is less turbulence at the interface. k_La decreases. Not correct.
8. Options B and C raise k_La.

KEY IDEA

k_La depends on hydrodynamics. Anything that raises the interfacial area $a = 6\varepsilon_G/d_b$ or the interfacial turbulence (more gas flow, smaller bubbles, more power input) raises it. Changing the gas composition changes only the saturation concentration C^*, so it changes the driving force in $\text{OTR} = k_La\,(C^* - C_L)$ and leaves k_La alone.

WATCH OUT FOR

Ticking (A) because pure oxygen does raise the oxygen transfer rate. It does that by raising C^* (the driving force), not the volumetric mass transfer coefficient k_La. The question asks about k_La, not OTR.

Q.47 MSQ · 2 MARKS

Q.47	For a liquid flowing in a circular cross section pipe, the transition from laminar to turbulent flow will NOT depend on which of the following factor(s)?
(A)	The diameter of the pipe
(B)	The length of the pipe
(C)	The linear velocity of the liquid
(D)	The viscosity of the liquid

Official answer: **B**

Q.48 MSQ · 2 MARKS

Genetics, Cell and Molecular Biology › Cell signalling

Which of the following is/are posttranslational modification(s) involved in epigenetic control of gene expression?

(A) Arginine methylation

(B) Lysine acetylation

(C) Cytosine methylation

(D) Cytosine deamination

Official answer: **A, B**

SOLUTION

1. Identify the question type: MSQ, 2 marks. Select all listed items that are BOTH (i) posttranslational modifications (chemical changes to a protein after it is translated) AND (ii) mechanisms of epigenetic control of gene expression.
2. Recall that the best-characterized posttranslational modifications used epigenetically are histone tail modifications (methylation, acetylation, phosphorylation, ubiquitination, sumoylation), which alter chromatin structure and gene accessibility without changing the DNA sequence.
3. (A) Arginine methylation: histone arginine residues (e.g., H3R2, H3R8, H4R3) are methylated by protein arginine methyltransferases (PRMTs). This modifies the histone protein after translation and is an established epigenetic mark that influences transcriptional activity → satisfies both criteria → CORRECT.
4. (B) Lysine acetylation: histone lysine residues (e.g., H3K9, H3K27, H4K16) are acetylated by histone acetyltransferases (HATs), neutralizing the lysine's positive charge, loosening histone-DNA contacts, and promoting an open, transcriptionally active chromatin state. This is a protein modification occurring after translation and a classic epigenetic mark → satisfies both criteria → CORRECT.
5. (C) Cytosine methylation: 5-methylcytosine is formed by DNA methyltransferases adding a methyl group directly to cytosine bases in DNA, most often at CpG sites. Although this is a major epigenetic mechanism (typically gene-silencing), it modifies DNA, not a translated protein, so it fails the 'posttranslational modification' requirement of the stem → INCORRECT for this question.
6. (D) Cytosine deamination: this converts cytosine to uracil (or 5-methylcytosine to thymine) in DNA, a chemical/mutagenic base change usually corrected by DNA repair pathways. It is neither a protein modification nor a recognized epigenetic regulatory mechanism (it is a source of mutation/damage, not gene regulation) → INCORRECT.
7. Final selection: only (A) and (B) are histone posttranslational modifications that function in epigenetic control of gene expression; (C) and (D) act on DNA rather than protein and are excluded.

KEY IDEA

Posttranslational modifications (PTMs) act on proteins (here, histones) after translation; only histone marks, not chemical changes to DNA bases, qualify as PTMs, even though DNA methylation is also an epigenetic mechanism.

WATCH OUT FOR

Treating "epigenetic" as synonymous with "posttranslational modification" and picking cytosine methylation (C) because it is a well-known epigenetic mark; it modifies DNA, not a protein, so it fails the PTM criterion in the stem even though it is epigenetic.

Q.49 MSQ · 2 MARKS

Fundamentals of Biological Engineering › Ideal reactors

For an ideal plug flow reactor, which of the following statements is/are true?

(A) It can be approximated by a large number of ideal continuous stirred tank reactors connected in series

(B) It has significant back mixing

(C) It has significant axial mixing

(D) It has a uniform velocity profile across any cross section

Official answer: **A, D**

SOLUTION

1. **What "ideal plug flow" assumes:** the fluid moves through the tube as a series of thin slices, or plugs. Every slice moves at the same velocity and does not mix with the slices ahead of it or behind it. So every fluid element spends the same time in the reactor, $\tau = V/Q$, where V is the reactor volume and Q is the volumetric flow rate.
2. **(A) True. Tanks-in-series model:** let $\theta = t/\tau$ be dimensionless time and $E(\theta)$ the residence-time distribution (RTD). For N equal ideal CSTRs in series,
$$E(\theta) = \frac{N(N\theta)^{N-1}}{(N-1)!}e^{-N\theta}, \qquad \sigma_\theta^2 = \frac{1}{N}$$
where σ_θ^2 is the dimensionless variance of the RTD. As $N \to \infty$, $\sigma_\theta^2 \to 0$ and $E(\theta)$ becomes a single spike at $\theta = 1$. That spike is the RTD of an ideal PFR, so a very large number of CSTRs in series behaves like a PFR.
3. **(B) False. Back mixing:** back mixing means material from further downstream mixes with material upstream of it. Ideal plug flow assumes there is none, so each plug keeps its own composition as it moves along the tube.
4. **(C) False. Axial mixing:** the axial dispersion model has one parameter, the dispersion number $D_{ax}/(uL)$. Here D_{ax} is the axial dispersion coefficient, u the mean velocity and L the reactor length. Ideal plug flow is the limit $D_{ax}/(uL) \to 0$, so an ideal PFR has zero axial mixing, not significant axial mixing. Back mixing is axial mixing toward the inlet, so (B) and (C) fail for the same reason.
5. **(D) True. Flat velocity profile:** "plug" means the velocity is the same at every radial position, $u(r) = \text{constant}$. Compare the parabolic laminar profile $u(r) = 2\bar{u}\left(1 - r^2/R^2\right)$, where $\bar{u}$ is the mean velocity and R the tube radius. In that profile, fluid near the wall moves more slowly and stays in the tube longer. The ideal PFR also assumes complete mixing across each cross-section, so concentration and temperature change only along the length of the reactor.
6. Correct options: **A and D**.

KEY IDEA

In ideal plug flow every fluid element has the same residence time. That means a flat velocity profile, complete mixing across each cross-section and zero mixing along the flow direction (dispersion number $D_{ax}/(uL) = 0$). The tanks-in-series RTD has variance $1/N$, which goes to zero as $N \to \infty$ and gives the same RTD.

WATCH OUT FOR

Mixing up the two directions of mixing. An ideal PFR is perfectly mixed RADIALLY, across each cross-section, but has NO mixing AXIALLY, along the flow. So 'significant axial mixing' and 'significant back mixing' are false even though mixing across the section is complete. Another mistake is to reject (A) because a single CSTR is the opposite of a PFR. It is the limit of MANY CSTRs in series that approaches plug flow.

Q.50 MSQ · 2 MARKS

General Biology › Enzymes

An enzyme-catalyzed reaction is found to have $\Delta G = -100\ \text{kJ mol}^{-1}$. Which of the following statements about this reaction is/are true?

(A) The rate of the reaction cannot be predicted

(B) The rate of the reaction is high

(C) The rate of the reaction is low

(D) The reaction is irreversible

Official answer: **A, D**

SOLUTION

1. ΔG is a thermodynamic quantity. Its sign says whether a reaction can proceed spontaneously and in which direction, and its size says how far the system is from equilibrium. It says nothing about how fast the reaction goes: speed is set by the activation energy, a kinetic property, and an enzyme only lowers that barrier.
2. (A) True. $\Delta G = -100\ \text{kJ mol}^{-1}$ gives no information about the activation barrier or the enzyme's turnover, so the rate cannot be predicted from it alone.
3. (B) False. A large negative ΔG does not imply a fast reaction. Many strongly exergonic reactions, such as the oxidation of glucose in air, are extremely slow without a catalyst.
4. (C) False. The same argument applies the other way. Nothing here shows the rate is low, because an enzyme may lower the barrier a great deal. Rate cannot be inferred either way.
5. (D) True. Write the free-energy change as $\Delta G = RT \ln \dfrac{Q}{K_{eq}}$, where Q is the mass-action ratio under the actual conditions. At about $310\ \text{K}$, $RT \approx 2.58\ \text{kJ mol}^{-1}$, so $\ln \dfrac{K_{eq}}{Q} = \dfrac{100}{2.58} \approx 39$, which gives $\dfrac{K_{eq}}{Q} \sim 10^{17}$. The system is astronomically far from equilibrium on the product-forming side, and the reverse reaction would have $\Delta G = +100\ \text{kJ mol}^{-1}$, which is not spontaneous. The reaction therefore runs only forward in practice, i.e. it is irreversible. An enzyme does not change ΔG or the direction.
6. So the correct statements are (A) and (D).

KEY IDEA

ΔG gives the direction and driving force of a reaction (thermodynamics), not its rate (kinetics). A large negative ΔG makes the reaction effectively one-way but says nothing about speed.

WATCH OUT FOR

Assuming a very negative ΔG means a fast reaction and picking (B). Exergonic does not mean fast, since the activation energy decides the rate.

Q.51 NAT · 2 MARKS

Engineering Mathematics › Numerical methods

Consider the equation $\dfrac{dy}{dx} = \dfrac{1}{x}$. The value of the integral $\int_1^2 dy$ using trapezoidal method and interval $h = 0.25$ is _____. (rounded off to two decimal places)

Official answer: **0.69 to 0.71**

SOLUTION

1. Since $dy = \dfrac{1}{x}\,dx$, the integral becomes $\int_1^2 dy = \int_1^2 \dfrac{1}{x}\,dx$, so $f(x) = \dfrac{1}{x}$.
2. With $h = 0.25$ on $[1, 2]$ there are $n = \dfrac{2-1}{0.25} = 4$ strips, with nodes $x = 1,\ 1.25,\ 1.5,\ 1.75,\ 2$.
3. Function values: $f(1) = 1$, $f(1.25) = 0.8$, $f(1.5) = 0.6667$, $f(1.75) = 0.5714$, $f(2) = 0.5$.
4. Trapezoidal rule with step $h = 0.25$:
$$\int_a^b f\,dx \approx \frac{h}{2}\left[f_0 + f_4 + 2(f_1 + f_2 + f_3)\right]$$
5. Interior sum: $f_1 + f_2 + f_3 = 0.8 + 0.6667 + 0.5714 = 2.0381$.
6. $$\frac{0.25}{2}\left[1 + 0.5 + 2(2.0381)\right] = 0.125 \times 5.5762 \approx 0.6970$$
7. Rounded to two decimal places the value is 0.70. The exact value $\ln 2 = 0.693$ is slightly lower, as expected because $f(x) = 1/x$ is convex, so the trapezoidal rule overestimates.

KEY IDEA
Rewrite dy = (1/x) dx so the integral is of f(x) = 1/x over [1, 2], then apply the composite trapezoidal rule with h = 0.25 (four strips): (h/2)[f0 + f4 + 2(f1 + f2 + f3)].

WATCH OUT FOR
Using the wrong weights, such as doubling the end ordinates or leaving the interior ones single. Another slip is using Simpson's 1/3 rule (which gives about 0.6933) instead of the trapezoidal rule, or rounding the function values too early.

Q.52 NAT · 2 MARKS

Engineering Mathematics › Linear algebra

If the straight lines given by the following two equations are parallel to each other, the value of a is _____. (answer in integer)

4x + 7y = 6; 3ax + 42y = 24

Official answer: **8**

SOLUTION

1. Write each line as $Ax + By = C$: $4x + 7y = 6$ and $3a\,x + 42y = 24$.
2. Two lines are parallel when their normal vectors (A, B) are proportional: $\frac{4}{3a} = \frac{7}{42}$.
3. Equivalently the slopes are equal: $-\frac{4}{7} = -\frac{3a}{42}$.
4. Cross-multiply: $3a \cdot 7 = 4 \cdot 42$, so $21a = 168$.
5. Hence $a = 8$.
6. Check that the lines are distinct: the second line becomes $24x + 42y = 24$, and $\frac{4}{24} = \frac{7}{42} = \frac{1}{6} \neq \frac{6}{24} = \frac{1}{4}$, so the lines are parallel and not coincident.

KEY IDEA
Parallel lines have proportional coefficients of x and y, so the ratio A1/A2 must equal B1/B2. Then confirm the constants break the proportion, so the lines are not the same line.

WATCH OUT FOR
Setting the ratio of the constants equal as well (4/(3a) = 7/42 = 6/24), which describes coincident lines and has no solution. Another slip is inverting a ratio when cross-multiplying.

Q.53 NAT · 2 MARKS

Engineering Mathematics › Calculus

A straight line $y = x - 1$ intersects a circle with center at $x = 1, y = 1$ and radius of magnitude 1 at two points. The length of the chord formed by this intersection is _____. (rounded off to three decimal places)

Official answer: **1.414**

SOLUTION

1. Write the line as $x - y - 1 = 0$. The circle has centre $C(1, 1)$ and radius $r = 1$.
2. Perpendicular distance from the centre to the line: $d = \frac{|1 - 1 - 1|}{\sqrt{1^2 + (-1)^2}} = \frac{1}{\sqrt{2}}$.
3. Since $d < r$, the line cuts the circle at two points.
4. The perpendicular from the centre bisects the chord. In the right triangle formed by the centre, the chord's midpoint and an end point, $\left(\frac{L}{2}\right)^2 = r^2 - d^2 = 1 - \frac{1}{2} = \frac{1}{2}$.
5. Chord length: $L = 2\sqrt{\frac{1}{2}} = \sqrt{2} \approx 1.414$.
6. Check: substituting $y = x - 1$ in $(x - 1)^2 + (y - 1)^2 = 1$ gives $(x - 1)^2 + (x - 2)^2 = 1$, i.e. $2x^2 - 6x + 4 = 0$, so $x = 1$ or $x = 2$. The points are $(1, 0)$ and $(2, 1)$, whose distance is $\sqrt{1 + 1} = \sqrt{2}$.

KEY IDEA

A line at perpendicular distance d from the centre of a circle of radius r cuts a chord of length $2\sqrt{r^2 - d^2}$.

WATCH OUT FOR

Using the distance formula with the line written as $y = x - 1$ without moving every term to one side, so the sign or the constant is wrong. Another slip is to forget the factor 2 and give the half-chord $\frac{1}{\sqrt{2}} \approx 0.707$.

Q.54 NAT · 2 MARKS

Engineering Mathematics › Differential equations

A heat exchanger during operation in a bioprocess has a steady temperature of 90 °C. After completion of its operation, it was shut down and it was observed that the rate of decrease of temperature at any time was directly proportional to the difference T(t) – 30 °C, where T(t) denotes temperature at time t. It was observed that it took 30 min for the temperature to drop to 70 °C. The temperature after 51.5 min will be _____ °C. (rounded off to the nearest integer)

Official answer: **59 to 61**

SOLUTION

1. Take $t = 0$ at shutdown, so $T(0) = 90\,^{\circ}\mathrm{C}$. The rate of decrease of temperature is proportional to $T - 30$, so $\dfrac{dT}{dt} = -k\,(T - 30)$ with $k > 0$.
2. Separate variables: $\dfrac{dT}{T - 30} = -k\,dt$. Integrating gives $T - 30 = Ce^{-kt}$. Using $T(0) = 90$ gives $C = 60$.
3. Use $T(30) = 70$: $40 = 60e^{-30k}$, so $e^{-30k} = \dfrac{2}{3}$.
4. At $t = 51.5$ min: $T - 30 = 60\left(e^{-30k}\right)^{51.5/30} = 60\left(\dfrac{2}{3}\right)^{1.7167}$.
5. Evaluate the exponent: $1.7167 \times \ln\dfrac{2}{3} = 1.7167 \times (-0.40547) \approx -0.6960$, so $e^{-0.6960} \approx 0.4986$.
6. Then $T - 30 \approx 60 \times 0.4986 \approx 29.9$, so $T \approx 59.9\,^{\circ}\mathrm{C}$, which rounds to $60\,^{\circ}\mathrm{C}$.

KEY IDEA

This is Newton's law of cooling, $\dfrac{dT}{dt} = -k(T - T_{\text{surroundings}})$. Its solution is $T - 30 = (T_0 - 30)e^{-kt}$. You never need k itself, because the fixed ratio $e^{-30k} = 2/3$ gives $e^{-kt} = (2/3)^{t/30}$.

WATCH OUT FOR

Writing the decay as $T = 90e^{-kt}$ and leaving out the 30 °C offset. The decaying quantity is the excess $T - 30$, not T. Another slip is to treat the cooling as linear in time (20 °C per 30 min) and get about 55 °C.

Q.55 NAT · 2 MARKS

Fundamentals of Biological Engineering › Growth kinetics

A microbial culture (following Monod model for growth) has a maximum specific growth rate of 0.1 h^{-1}, Monod constant of 1 mg L^{-1} and endogenous decay rate of 0.1 day^{-1}. At limiting substrate concentration of 23 g L^{-1}, the net specific growth rate will be _____ day^{-1}. (rounded off to one decimal place)

Official answer: **2.2 to 2.4**

SOLUTION

1. Monod model: $\mu = \dfrac{\mu_{max} S}{K_s + S}$, where μ is the specific growth rate, $\mu_{max} = 0.1\ \mathrm{h}^{-1}$ is the maximum specific growth rate, $K_s = 1\ \mathrm{mg\,L}^{-1}$ is the Monod constant and S is the limiting substrate concentration.
2. Put S and K_s in the same units: $S = 23\ \mathrm{g\,L}^{-1} = 23000\ \mathrm{mg\,L}^{-1}$.
3. $$\mu = 0.1 \times \frac{23000}{1 + 23000} = 0.1 \times 0.99996 = 0.099996\ \mathrm{h}^{-1}$$

   Because $S \gg K_s$, the culture grows at essentially μ_{max}.

4. Convert to per day so it can be combined with the decay rate, which is given per day: $\mu = 0.099996 \times 24 = 2.3999\ \text{day}^{-1}$.
5. With endogenous decay, the net specific growth rate is $\mu_{net} = \mu - k_d$, where $k_d = 0.1\ \text{day}^{-1}$ is the endogenous decay rate.
6. $$\mu_{net} = 2.3999 - 0.1 = 2.2999 \approx 2.3\ \text{day}^{-1}$$

KEY IDEA

Net specific growth rate = Monod growth rate minus the endogenous decay rate, $\mu_{net} = \dfrac{\mu_{max} S}{K_s + S} - k_d$. First put every quantity in the same units: S and K_s both in mg L^-1, and both rates in day^-1. Here S is 23000 times K_s, so the Monod term is almost exactly μ_{max}.

WATCH OUT FOR

Mixing units. If you subtract 0.1 day^-1 from 0.1 h^-1 you get zero. If you use S = 23 with K_s = 1 without converting g to mg, you get 0.0958 h^-1 and a net rate near 2.2 day^-1, which only lands in the range by luck. The right way is to convert S to 23000 mg L^-1 and mu_max to 2.4 day^-1, then subtract k_d.

Q.56 NAT · 2 MARKS

Fundamentals of Biological Engineering › Bioreactor operation

A CSTR with a volume of 100 m^3 is operated in cell recycle mode. At a volumetric flow rate of 10 m^3 day^{-1} and effluent biomass of 20 mg L^{-1}, the steady state biomass concentration is 200 mg L^{-1}. The mean cell retention time in the reactor is ____ days. (answer in integer)

Official answer: **100**

SOLUTION

1. Symbols: V = reactor volume, F = volumetric flow rate, X = steady-state biomass concentration inside the reactor, X_e = biomass concentration in the effluent, θ_c = mean cell retention time (also called solids retention time).
2. Definition: $\theta_c = \dfrac{\text{biomass held in the reactor}}{\text{rate at which biomass leaves the system}}$. The question gives no separate wastage stream, so all the biomass that leaves goes out in the effluent, at flow F and concentration X_e.
3. Biomass held in the reactor: $VX = 100\ \text{m}^3 \times 200\ \text{mg L}^{-1}$.
4. Rate at which biomass leaves: $FX_e = 10\ \text{m}^3\ \text{day}^{-1} \times 20\ \text{mg L}^{-1}$. Both concentrations are in mg L^{-1} and both volumes in m^3, so these units cancel and only day is left.
5. $$\theta_c = \frac{VX}{FX_e} = \frac{100 \times 200}{10 \times 20} = \frac{20000}{200} = 100\ \text{days}$$
6. Check: the hydraulic retention time is $V/F = 100/10 = 10$ days. Recycle keeps cells in the reactor $X/X_e = 200/20 = 10$ times longer than the liquid, so $\theta_c = 10 \times 10 = 100$ days.

KEY IDEA

Mean cell retention time is the biomass held in the reactor divided by the rate at which biomass leaves it: $\theta_c = \dfrac{VX}{FX_e}$ when cells leave only in the effluent. With cell recycle, θ_c equals the hydraulic retention time V/F multiplied by X/X_e.

WATCH OUT FOR

Answering with the hydraulic retention time $V/F = 10$ days, which is the mean cell retention time only when there is no recycle and $X_e = X$. A second mistake is to divide by FX, using the reactor concentration in place of the effluent concentration, which also gives 10 days.

Q.57 NAT · 2 MARKS

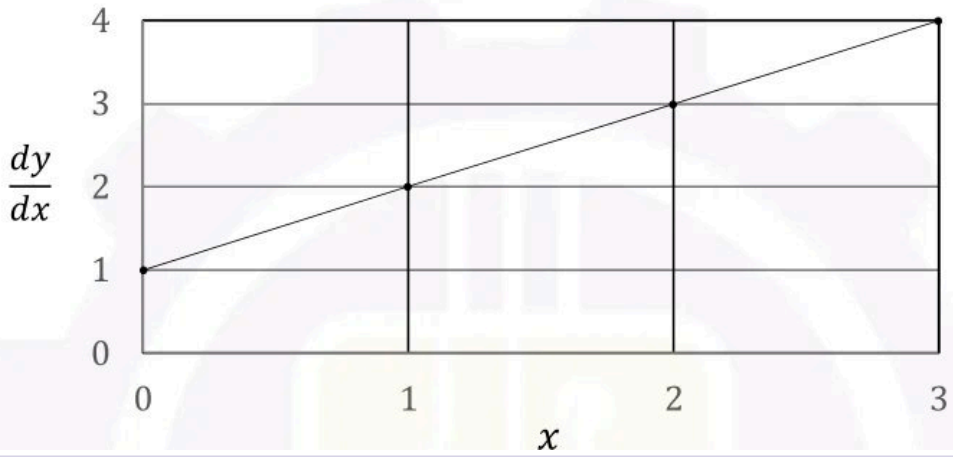
Q.57 The electron equivalent per liter ($e^-eq\ L^{-1}$) of acetate ion solution of concentration 10 g L^{-1} is _____ $e^-eq\ L^{-1}$. (*rounded off to one decimal place*)

Official answer: **1.3 to 1.4**

Q.58 NAT · 2 MARKS

Engineering Mathematics › Calculus

Q.58 From the following plot of $\frac{dy}{dx}$ versus x and if $y(2) = 5$, the value of $y(3)$ is _____. (*rounded off to one decimal place*)



Official answer: **8.3 to 8.7**

SOLUTION

1. Read the line from the plot: it passes through $(0,1)$, $(1,2)$, $(2,3)$ and $(3,4)$, so its slope is 1 and its intercept is 1. Hence $\frac{dy}{dx} = x + 1$.
2. By the fundamental theorem of calculus, the change in y equals the area under the $\frac{dy}{dx}$ curve: $y(3) - y(2) = \int_2^3 \frac{dy}{dx}\,dx$.
3. Integrate:
$$\int_2^3 (x+1)\,dx = \left[\frac{x^2}{2} + x\right]_2^3$$
4. Evaluate: $\left(\frac{9}{2} + 3\right) - (2 + 2) = 7.5 - 4 = 3.5$.
5. Check with a trapezium: the heights are 3 at $x = 2$ and 4 at $x = 3$, and the width is 1, so the area is $\frac{3+4}{2} \times 1 = 3.5$.
6. Therefore $y(3) = y(2) + 3.5 = 5 + 3.5 = 8.5$.

KEY IDEA

When the graph of the derivative is given, the change in the function between two points is the area under that graph between them. Take $y(3) = y(2) + \int_2^3 \frac{dy}{dx}\,dx$. For a straight-line graph this area is a trapezium.

WATCH OUT FOR

Reading the plot as the graph of y itself, or taking $\frac{dy}{dx}$ at $x = 3$ (which is 4) as the change. Another slip is to start the area at $x = 0$ instead of $x = 2$, which gives $y(3) = 5 + 7.5 = 12.5$.

Q.59 NAT · 2 MARKS

Fundamentals of Biological Engineering › Upstream

A batch sterilizer is being operated at 121 °C for sterilizing a medium containing microbial cells. Assume that the thermal deactivation of cells is a first order process with a death rate constant of 0.69 min^{-1} at 121 °C. If the initial concentration of microbes in the medium is 10^{10} cells m^{-3}, the time taken to reduce the microbial load to a final concentration of 10 cells m^{-3} is _____ min. (rounded off to the nearest integer)

Official answer: **30**

SOLUTION

1. Thermal death is first order: $\frac{dN}{dt} = -k_d N$, where N is the viable cell concentration and k_d is the specific death rate constant ($k_d = 0.69\ \text{min}^{-1}$ at 121 °C).
2. Integrate at constant temperature (batch holding at 121 °C): $\ln \frac{N_0}{N} = k_d t$, so $t = \frac{1}{k_d} \ln \frac{N_0}{N}$.
3. Ratio of concentrations (the medium volume cancels, so concentrations can be used directly): $\frac{N_0}{N} = \frac{10^{10}\ \text{cells m}^{-3}}{10\ \text{cells m}^{-3}} = 10^9$.
4. Del factor: $\nabla = \ln \frac{N_0}{N} = \ln(10^9) = 9 \ln 10 = 9 \times 2.3026 = 20.723$.
5. $$t = \frac{\nabla}{k_d} = \frac{20.723}{0.69\ \text{min}^{-1}} = 30.03\ \text{min}$$
6. Rounded off to the nearest integer: $t = 30$ min.

KEY IDEA

First-order death gives $\ln(N_0/N) = k_d t$ at constant temperature. The time depends only on the ratio N_0/N (here 10^9, a 9-log reduction), so the medium volume does not matter. A quick check: the decimal reduction time is $D = \ln 10 / k_d = 2.3026/0.69 = 3.34$ min, and 9 log cycles take $9 \times 3.34 \approx 30$ min.

WATCH OUT FOR

Using $\log_{10}$ where the natural log belongs: $\log_{10}(10^9)/0.69 = 13$ min is wrong, because k_d is defined through $e^{-k_d t}$. Another slip is taking the ratio as $10^{10}/1$, or mixing up which concentration goes on top, which changes the number of log cycles.

Q.60 NAT · 2 MARKS

Fundamentals of Biological Engineering › Enzyme kinetics

A substrate is consumed in a zero order reaction such that its concentration falls from 42 g L^{-1} to 14 g L^{-1} in 4 hours. The total time taken for complete utilization of substrate will be _____ hours. (*answer in integer*)

Official answer: **6**

SOLUTION

1. Zero-order rate law: $-\frac{dS}{dt} = k_0$, where S is the substrate concentration (in g L^{-1}) and k_0 is the zero-order rate constant (in g L^{-1} h^{-1}). The rate does not depend on S, so integrating from S_0 at $t = 0$ gives a straight-line fall: $S = S_0 - k_0 t$.
2. Find k_0 from the given data ($S_0 = 42$ g L^{-1}, $S = 14$ g L^{-1} at $t = 4$ h): $k_0 = \frac{S_0 - S}{t} = \frac{42 - 14}{4} = \frac{28}{4} = 7$ g L^{-1} h^{-1}.
3. Complete utilization means $S = 0$: $0 = S_0 - k_0\, t_{\text{complete}}$, so $t_{\text{complete}} = \frac{S_0}{k_0} = \frac{42}{7} = 6$ h.
4. Check: the remaining 14 g L^{-1} is consumed at the same constant rate in $14/7 = 2$ h, and $4 + 2 = 6$ h in total from the start.

KEY IDEA

In a zero-order reaction the rate is constant, so concentration falls linearly with time: $S = S_0 - k_0 t$. Get k_0 from the drop you are told about, then complete consumption takes $t = S_0/k_0$.

WATCH OUT FOR

Answering 2 h, which is only the time left after the first 4 h, when the question asks for the total time from the start. The other mistake is using first-order kinetics (a logarithmic decay), which never reaches zero concentration and so cannot give a finite time for complete utilization.

Q.61 NAT · 2 MARKS

Fundamentals of Biological Engineering › Bioreactor operation

A microbe that follows Monod growth kinetics on a limiting substrate (maximum specific growth rate of 0.5 h^{-1} and Monod constant of 0.1 $\mathrm{mg\ L}^{-1}$) is cultivated in a continuous reactor for microbial growth (chemostat) with sterile feed. Given that the chemostat volume is 5 L and inlet concentration of limiting substrate is 10 $\mathrm{g\ L}^{-1}$, the minimum inlet feed flow rate for chemostat washout is _____ $\mathrm{L\ h}^{-1}$. (rounded off to one decimal place)

Official answer: **2.4 to 2.5**

SOLUTION

1. Symbols: $\mu_{max} = 0.5\ \mathrm{h}^{-1}$ is the maximum specific growth rate, $K_s = 0.1\ \mathrm{mg\ L}^{-1}$ is the Monod constant, $S_0 = 10\ \mathrm{g\ L}^{-1}$ is the substrate concentration in the feed, S is the substrate concentration in the reactor, $V = 5\ \mathrm{L}$ is the working volume, F is the feed flow rate and $D = F/V$ is the dilution rate.
2. Put the concentrations in the same units: $K_s = 0.1\ \mathrm{mg\ L}^{-1} = 1 \times 10^{-4}\ \mathrm{g\ L}^{-1}$.
3. Steady-state biomass balance with sterile feed: $\mu = D$. With Monod kinetics, $\mu = \dfrac{\mu_{max} S}{K_s + S}$, so the substrate level in the reactor is
$$S = \frac{K_s D}{\mu_{max} - D}$$
4. The largest value S can reach is S_0, the feed value (no biomass is left to use any substrate). Washout begins when the S needed to sustain $\mu = D$ reaches S_0. Setting $S = S_0$ gives the critical dilution rate
$$D_{crit} = \frac{\mu_{max} S_0}{K_s + S_0}$$
Any $D \geq D_{crit}$ washes the culture out, so D_{crit} is the minimum dilution rate for washout.
5. Substitute:
$$D_{crit} = \frac{0.5 \times 10}{10 + 0.0001} = 0.499995\ \mathrm{h}^{-1}$$
6. Minimum feed flow rate for washout:
$$F_{crit} = D_{crit} V = 0.499995 \times 5 = 2.499975\ \mathrm{L\ h}^{-1} \approx 2.5\ \mathrm{L\ h}^{-1}$$
7. Check: K_s is 100,000 times smaller than S_0, so $D_{crit} \approx \mu_{max}$ and $F_{crit} \approx \mu_{max} V = 0.5 \times 5 = 2.5\ \mathrm{L\ h}^{-1}$.

KEY IDEA

With sterile feed, a chemostat washes out once the dilution rate D = F/V reaches D_crit = mu_max S0/(Ks + S0). This is the growth rate the cells would have if the reactor held undiluted feed. Here Ks is much smaller than S0, so D_crit is almost exactly mu_max, and F_crit = D_crit V.

WATCH OUT FOR

Mixing units: Ks is given in mg L^-1 and S0 in g L^-1. Adding 0.1 to 10 without converting gives D_crit = 0.495 h^-1 and F = 2.48 L h^-1. That happens to fall inside the key range here, but it is the wrong method. Other slips: reporting the dilution rate (0.5 h^-1) instead of the flow rate (multiply by V = 5 L), or using the approximate formula D_crit = mu_max without checking that Ks is much smaller than S0.

Q.62 NAT · 2 MARKS

Fundamentals of Biological Engineering › Upstream

It is desired to cultivate 150 mg (dry weight) microbial cells with an empirical formula of $C_5H_7O_2N$. If the phosphorus requirement for the cells is 20% of the nitrogen requirement (on a weight/weight basis), the minimum amount of phosphorous required to be added to the cultivation medium is _____ mg. (rounded off to one decimal place)

Official answer: **3.6 to 3.8**

SOLUTION

1. Molar mass of the biomass formula $C_5H_7O_2N$ (atomic masses C = 12, H = 1, O = 16, N = 14): $M = 5(12) + 7(1) + 2(16) + 14 = 113\ \text{g mol}^{-1}$.
2. Nitrogen mass fraction of the cells, w_N (mass of N per unit dry mass of cells): $w_N = \dfrac{14}{113} = 0.1239$.
3. The minimum nitrogen that must be supplied is the nitrogen that ends up inside 150 mg of cells (elemental balance, assuming all nitrogen supplied is taken up into biomass): $m_N = 150 \times \dfrac{14}{113} = 18.58\ \text{mg}$.
4. The phosphorus requirement is 20% of the nitrogen requirement on a weight/weight basis: $m_P = 0.20 \times 18.58 = 3.72\ \text{mg}$.
5. Rounded to one decimal place: $m_P \approx 3.7\ \text{mg}$. (With precise atomic masses, $M = 113.12\ \text{g mol}^{-1}$ and $m_P = 3.715\ \text{mg}$, which also rounds to 3.7.)

KEY IDEA

This is an elemental mass balance. The formula $C_5H_7O_2N$ gives the mass fraction of nitrogen in the cells, $14/113$. That fraction times the cell mass is the least nitrogen the medium must supply. Phosphorus is then 20% of that nitrogen, by weight.

WATCH OUT FOR

Taking 20% of the cell mass (30 mg) instead of 20% of the nitrogen mass. Another slip is to work on a mole basis, where 0.2 mol P per mol N would give $0.2 \times 150/113 \times 31 \approx 8.2\ \text{mg}$. The question says weight/weight, so the 20% applies to the mass of nitrogen.

Q.63 NAT · 2 MARKS

Genetics, Cell and Molecular Biology › Cell biology

In the process of generating a clonal mammalian cell line, a single cell was seeded in a well of a cell culture plate. After the first 48 hours, one of the progeny cells underwent apoptosis due to a new mutation. If the doubling time of the cells is 24 hours and no more cell death occurs, the total number of cells after a total of 7 days from seeding will be _____. (answer in integer)

Official answer: **96**

SOLUTION

1. Start: 1 cell seeded at t = 0 h, doubling time = 24 h.
2. At t = 24 h: 1 × 2 = 2 cells.
3. At t = 48 h: 2 × 2 = 4 cells (the progeny at this point).
4. At t = 48 h, one of these 4 cells undergoes apoptosis: 4 − 1 = 3 viable cells remain.
5. No further cell death occurs, so growth resumes exponentially from 3 cells with the same 24 h doubling time.
6. Total time = 7 days = 168 h; remaining time after the loss = 168 − 48 = 120 h.
7. Number of doublings in 120 h = 120 / 24 = 5.
8. Final cell number = $3 \times 2^5 = 3 \times 32 = 96$.

KEY IDEA
Track cell number through exponential doubling, applying the one-time apoptotic loss exactly when it occurs (at t = 48 h), then resume doubling from the reduced population for the remaining time.

WATCH OUT FOR
Applying the apoptosis loss at the END of the 7-day period (168 − 1 = …) instead of at t = 48 h, or forgetting that "no more cell death occurs" means only ONE cell is ever lost, not a repeated loss at every doubling.

Q.64 NAT · 2 MARKS

Genetics, Cell and Molecular Biology › Mendelian genetics

A disease-associated allele shows X-linked recessive inheritance. If the mother is a carrier of the disease, the father is genetically normal, and the child born is a son, then the probability that he is born with the disease is _____. (rounded off to one decimal place)

Official answer: **0.5**

SOLUTION

1. Mother is a carrier of the X-linked recessive disease allele: genotype X^AX^a (heterozygous, unaffected).
2. Father is genetically normal for this locus: genotype X^AY.
3. A son receives his single X chromosome only from his mother and his Y chromosome only from his father; the father's X allele is never passed to a son.
4. Because the mother is heterozygous, she transmits X^A or X^a to any child with equal probability $\frac{1}{2}$ each, and this segregation ratio does not depend on the sex of the child.
5. Given that the child born is a son, the son's genotype at this locus is determined entirely by which maternal X allele he inherited.
6. $P(\text{son is affected}, X^aY) = \frac{1}{2} = 0.5.$

KEY IDEA
For an X-linked recessive disease, a son receives his only X chromosome from his mother (his Y comes from the father), so the father's genotype is irrelevant to a son's risk; only the mother's carrier (heterozygous) genotype matters.

WATCH OUT FOR
Trying to factor in the father's genotype for a son's risk (fathers cannot pass an X-linked allele to sons), or confusing this with a daughter's risk, which would require the father's X allele and give a different probability.

Q.65 NAT · 2 MARKS

Fundamentals of Biological Engineering › Bioreactor operation

A packed bed bioreactor with length 1 m and inside diameter 10 cm has liquid flowing at an interstitial velocity of 1 cm s^{-1}. Given a volumetric flow rate of 0.025 L s^{-1}, the void fraction of the packed bed is _____. (rounded off to two decimal places)

Official answer: **0.31 to 0.32**

SOLUTION

1. Symbols: Q = volumetric flow rate, d = inside diameter of the column, A = cross-sectional area of the empty column, u_0 = superficial velocity, u_i = interstitial velocity, ε = void fraction of the bed.
2. Put everything in consistent units: $Q = 0.025\ \text{L s}^{-1} = 0.025 \times 1000\ \text{cm}^3\,\text{s}^{-1} = 25\ \text{cm}^3\,\text{s}^{-1}$, $d = 10\ \text{cm}$, $u_i = 1\ \text{cm s}^{-1}$.
3. Cross-sectional area of the empty column: $A = \frac{\pi d^2}{4} = \frac{\pi(10)^2}{4} = 78.54\ \text{cm}^2.$

4. Superficial velocity (the flow rate spread over the whole cross-section, as if the column were empty): $u_0 = \dfrac{Q}{A} = \dfrac{25}{78.54} = 0.3183\ \text{cm s}^{-1}$.
5. Dupuit relation: the liquid can pass only through the voids, which occupy a fraction ε of the cross-section, so $u_i = \dfrac{u_0}{\varepsilon}$, which gives $\varepsilon = \dfrac{u_0}{u_i}$.
6. $$\varepsilon = \frac{0.3183\ \text{cm s}^{-1}}{1\ \text{cm s}^{-1}} = 0.318 \approx 0.32$$
7. The bed length (1 m) is not needed for the void fraction. It would matter only for the bed volume or the liquid residence time in the voids, $\tau = L/u_i = 100\ \text{cm}/1\ \text{cm s}^{-1} = 100\ \text{s}$.

KEY IDEA

Superficial velocity is the flow rate divided by the area of the empty column, $u_0 = Q/A$. The liquid actually moves only through the voids, so the interstitial velocity is higher: $u_i = u_0/\varepsilon$. The void fraction is therefore the ratio u_0/u_i.

WATCH OUT FOR

Writing $\varepsilon = u_i/u_0$ (about 3.14, which cannot be right because a void fraction must be below 1), or dividing Q by A without first converting litres to cm^3 (1 L = 1000 cm^3). Some candidates also get distracted by the 1 m bed length and try to use a bed volume, but the length plays no part in the void fraction.

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