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GATE BT · 2022

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GATE BT 2022 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 Kharagpur

Online, with the questions linked to their topic notes: **iaeacademy.in/study/papers/bt-2022**

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About this paper

65 questions, 100 marks. Question types: 37 MCQ · 8 MSQ · 20 NAT.

Official answer key: IIT Kharagpur

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	**D**
Q.2	MCQ	1	**A**
Q.3	MCQ	1	**D**
Q.4	MCQ	1	**B**
Q.5	MCQ	1	**B**
Q.6	MCQ	2	**B**
Q.7	MCQ	2	**B**
Q.8	MCQ	2	**B**
Q.9	MCQ	2	**B**
Q.10	MCQ	2	**Marks to all**
Q.11	MCQ	1	**B**
Q.12	MCQ	1	**C**
Q.13	MCQ	1	**C**
Q.14	MCQ	1	**D**
Q.15	MCQ	1	**D**
Q.16	MCQ	1	**D**
Q.17	MCQ	1	**A**
Q.18	MCQ	1	**A**
Q.19	MCQ	1	**D**
Q.20	MCQ	1	**A**
Q.21	MCQ	1	**A**
Q.22	MCQ	1	**C**
Q.23	MCQ	1	**D**
Q.24	MCQ	1	**D**
Q.25	MCQ	1	**A**
Q.26	MCQ	1	**C**
Q.27	NAT	1	**64**
Q.28	NAT	1	**102**
Q.29	NAT	1	**4**
Q.30	NAT	1	**1.2 to 1.4**
Q.31	NAT	1	**0.11 to 0.13**
Q.32	NAT	1	**1**
Q.33	NAT	1	**1**
Q.34	NAT	1	**20000**
Q.35	NAT	1	**6097 to 6223**
Q.36	MCQ	2	**D**
Q.37	MCQ	2	**A**
Q.38	MCQ	2	**B**
Q.39	MCQ	2	**B**
Q.40	MCQ	2	**B**
Q.41	MCQ	2	**C**
Q.42	MCQ	2	**B**
Q.43	MCQ	2	**D**
Q.44	MCQ	2	**A**
Q.45	MCQ	2	**B**
Q.46	MCQ	2	**A**
Q.47	MSQ	2	**A, B**
Q.48	MSQ	2	**A, C, D**
Q.49	MSQ	2	**A, B**
Q.50	MSQ	2	**A, D**
Q.51	MSQ	2	**A, C**
Q.52	MSQ	2	**A, B, C**
Q.53	MSQ	2	**A, C, D**
Q.54	MSQ	2	**A, C**
Q.55	NAT	2	**0.8**
Q.56	NAT	2	**1**
Q.57	NAT	2	**2**
Q.58	NAT	2	**150**
Q.59	NAT	2	**100**
Q.60	NAT	2	**1**
Q.61	NAT	2	**291 to 293**
Q.62	NAT	2	**2420 to 2430**
Q.63	NAT	2	**17 to 19**
Q.64	NAT	2	**2**
Q.65	NAT	2	**1**

General Aptitude Q.1 to Q.10

Q.1 MCQ · 1 MARK

General Aptitude › Grammar & vocabulary

You should _____ when to say _____.

(A) no / no

(B) no / know

(C) know / know

(D) know / no

Official answer: **D**

SOLUTION

1. After the modal "should" the sentence needs a base-form verb. Whatever follows must be a verb that can take the clause "when to say ..." as its object.
2. First blank: "know" fits, because "know when to say ..." means being aware of the right moment to do something. "no" is not a verb, so it cannot follow "should".
3. Second blank: it must name the thing that is said. "say no" is the standard phrase for refusing, where "no" is the word being spoken. "say know" is ungrammatical.
4. The pair is therefore know / no, giving "You should know when to say no."
5. Check the others: (A) and (B) put "no" after "should", which is wrong. (C) ends with "say know", which is wrong. Only (D) works.

KEY IDEA

Tell apart the homophones "know" (verb, to be aware) and "no" (the word of refusal). Then fill each blank by its grammatical role.

WATCH OUT FOR

Choosing by sound alone and mixing up "know" and "no". Options (A) and (B) put "no" after "should", where a verb is needed. Options (B) and (C) put "know" after "say", where the word being said is needed.

Q.2 MCQ · 1 MARK

General Aptitude › Geometry

Two straight lines pass through the origin $(x_0, y_0) = (0, 0)$. One of them passes through the point $(x_1, y_1) = (1, 3)$ and the other passes through the point $(x_2, y_2) = (1, 2)$.

What is the area enclosed between the straight lines in the interval $[0, 1]$ on the x-axis?

(A) 0.5

(B) 1.0

(C) 1.5

(D) 2.0

Official answer: **A**

SOLUTION

1. A line through the origin has the form $y = mx$, where the slope is $m = y/x$ at any other point on it.
2. The line through $(1, 3)$ has $m_1 = 3$, so its equation is $y = 3x$.
3. The line through $(1, 2)$ has $m_2 = 2$, so its equation is $y = 2x$.
4. On $[0, 1]$ we have $3x \geq 2x$, and the two lines meet only at the origin. The enclosed region is the triangle with vertices $(0, 0)$, $(1, 2)$ and $(1, 3)$.

5. The vertical side at $x = 1$ has length $3 - 2 = 1$. The perpendicular distance from the origin to that side is 1. Area $= \frac{1}{2} \times 1 \times 1 = 0.5$.
6. Check by integration: $\int_0^1 (3x - 2x)\,dx = \int_0^1 x\,dx = \frac{1}{2}$.

KEY IDEA
Lines through the origin are $y = mx$. The area between two of them over $[0, 1]$ is $\int_0^1 (m_1 - m_2)x\,dx = \frac{m_1 - m_2}{2}$. It is also the area of a triangle whose base is the gap between the lines at $x = 1$.

WATCH OUT FOR
Taking the area as the base times the height, $1 \times 1 = 1$, and forgetting the factor $\frac{1}{2}$ for a triangle. Another slip is to use the whole area under $y = 3x$, which is 1.5.

Q.3 MCQ · 1 MARK

General Aptitude › Numerical

If

$p : q = 1 : 2$

$q : r = 4 : 3$

$r : s = 4 : 5$

and u is 50% more than s, what is the ratio $p : u$?

(A) 2 : 15

(B) 16 : 15

(C) 1 : 5

(D) 16 : 45

Official answer: **D**

SOLUTION

1. Make q the same in the first two ratios. Since $p : q = 1 : 2$ and $q : r = 4 : 3$, and the LCM of 2 and 4 is 4, scale the first ratio to $p : q = 2 : 4$.
2. Then $p : q : r = 2 : 4 : 3$.
3. Now make r the same in $p : q : r = 2 : 4 : 3$ and $r : s = 4 : 5$. The LCM of 3 and 4 is 12, so $p : q : r = 8 : 16 : 12$ and $r : s = 12 : 15$.
4. Hence $p : q : r : s = 8 : 16 : 12 : 15$. Take $p = 8k$ and $s = 15k$ for some $k > 0$.
5. u is 50% more than s, so $u = 1.5\,s = 1.5 \times 15k = 22.5k$.
6. $p : u = 8k : 22.5k = 8 : 22.5 = 16 : 45$ (multiply both terms by 2).
7. This matches option (D).

KEY IDEA
To chain ratios, rewrite them so the shared term has the same value in each (use the LCM), then read off the combined ratio. "50% more than s" means $1.5s$.

WATCH OUT FOR
Reading "50% more than s" as $0.5s$ gives $p : u = 8 : 7.5 = 16 : 15$, which is option (B). Another slip is joining the ratios without equalising q and r first.

Q.4 MCQ · 1 MARK

General Aptitude › Reasoning

Given the statements:
- P is the sister of Q.
- Q is the husband of R.
- R is the mother of S.
- T is the husband of P.

Based on the above information, T is _____ of S.

(A) the grandfather

(B) an uncle

(C) the father

(D) a brother

Official answer: **B**

SOLUTION

1. R is the mother of S and Q is the husband of R, so Q is the father of S.
2. P is the sister of Q, so P is the sister of S's father. That makes P the paternal aunt of S.
3. T is the husband of P, so T is the husband of S's paternal aunt. That makes T an uncle of S (by marriage).
4. T is not S's father, because the father is Q. T is not S's grandfather, because T is married to S's father's sister, so he belongs to the father's generation. T is not S's brother. Only option (B) fits.

KEY IDEA

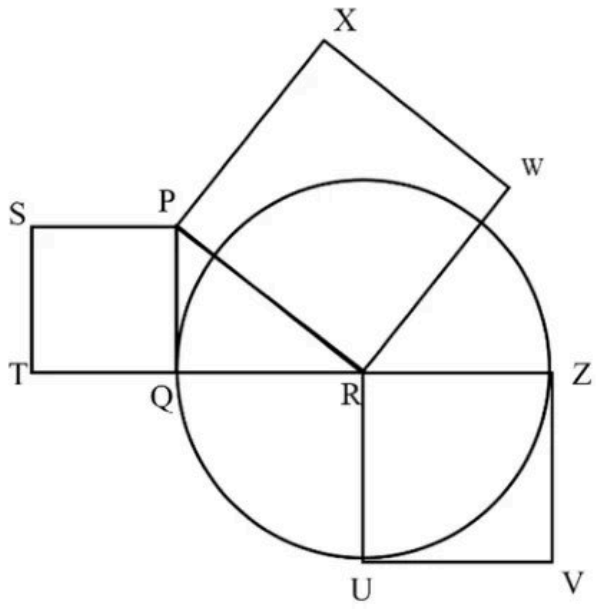
Build the family chain one statement at a time. Q is S's father, P is Q's sister so she is S's paternal aunt, and the aunt's husband is an uncle.

WATCH OUT FOR

Treating T as a blood relative of S and picking father or brother. T is related to S only through his marriage to P, so he is an uncle by marriage and not a parent or sibling.

Q.5 MCQ · 1 MARK

General Aptitude › Geometry

Q.5	In the following diagram, the point R is the center of the circle. The lines PQ and ZV are tangential to the circle. The relation among the areas of the squares, PXWR, RUVZ and SPQT is 
(A)	Area of SPQT = Area of RUVZ = Area of PXWR
(B)	Area of SPQT = Area of PXWR – Area of RUVZ
(C)	Area of PXWR = Area of SPQT – Area of RUVZ
(D)	Area of PXWR = Area of RUVZ – Area of SPQT

Official answer: **B**

SOLUTION

1. Q lies on the circle and PQ is tangent there, so the radius RQ is perpendicular to PQ. Triangle PQR is therefore right-angled at Q.
2. Let $PQ = a$ and $RQ = r$ (the radius). By Pythagoras, $PR^2 = PQ^2 + RQ^2 = a^2 + r^2$.
3. Square SPQT has side PQ, so $\text{Area}(SPQT) = a^2$.
4. Square RUVZ has side RZ. RZ is also a radius, so $\text{Area}(RUVZ) = r^2$.

5. Square PXWR has side PR, the hypotenuse, so $\text{Area}(PXWR) = PR^2 = a^2 + r^2$.
6. Hence $\text{Area}(PXWR) = \text{Area}(SPQT) + \text{Area}(RUVZ)$. Rearranging, $\text{Area}(SPQT) = \text{Area}(PXWR) - \text{Area}(RUVZ)$, which is option (B).

KEY IDEA

A tangent is perpendicular to the radius at the point of contact. This makes triangle PQR right-angled, so the squares on its three sides satisfy Pythagoras: the square on the hypotenuse equals the sum of the other two.

WATCH OUT FOR

Forgetting that RZ is a radius, equal to RQ, so RUVZ has area r^2. Another slip is choosing the option in which the hypotenuse square is not the largest, such as (C) or (D).

Q.6 MCQ · 2 MARKS

General Aptitude › Reading

Healthy eating is a critical component of healthy aging. When should one start eating healthy? It turns out that it is never too early. For example, babies who start eating healthy in the first year are more likely to have better overall health as they get older.

Which one of the following is the CORRECT logical inference based on the information in the above passage?

(A) Healthy eating is important for those with good health conditions, but not for others

(B) Eating healthy can be started at any age, earlier the better

(C) Eating healthy and better overall health are more correlated at a young age, but not older age

(D) Healthy eating is more important for adults than kids

Official answer: **B**

SOLUTION

1. The passage says healthy eating is a critical part of healthy aging. It asks when one should start and answers that it is "never too early". Its example is that babies who eat healthy in the first year are more likely to be healthier as they get older.
2. A correct inference must follow from what the passage states. It must not add restrictions or comparisons the passage never makes.
3. Option (A) says healthy eating matters only for people already in good health. The passage says healthy eating is critical for healthy aging in general and never limits it to the already healthy, so (A) is unsupported.
4. Option (C) says the link holds at a young age "but not older age". The passage never says the benefit stops later, so this claim is added from outside.
5. Option (D) says healthy eating matters more for adults than for kids. The passage gives no such comparison, and its example stresses the early years, so (D) is unsupported.
6. Option (B) says eating healthy can be started at any age, earlier the better. "Never too early" and the infant example support "earlier the better". Asking "when should one start" and answering that it is never too early points to starting at any time, with earlier being better. This follows from the passage.
7. Answer: (B).

KEY IDEA

In an inference question, choose the option the passage supports directly. Reject options that add a restriction, a comparison or a cut-off the passage never states.

WATCH OUT FOR

Picking (C) or (D) because the infant example sounds like young age matters more. The passage never says the benefit fades later or that adults need it more. Those claims come from outside the passage.

Q.7 MCQ · 2 MARKS

General Aptitude › Numerical

P invested Rs. 5000 per month for 6 months of a year and Q invested Rs. x per month for 8 months of the year in a partnership business. The profit is shared in proportion to the total investment made in that year.

If at the end of that investment year, Q receives 4/9 of the total profit, what is the value of x (in Rs.)?

(A) 2500

(B) 3000

(C) 4687

(D) 8437

Official answer: **B**

SOLUTION

1. Profit is shared in proportion to the total investment, which is the monthly amount multiplied by the number of months.
2. P's total investment is $5000 \times 6 = 30000$ (in Rs.).
3. Q's total investment is $x \times 8 = 8x$ (in Rs.).
4. Q receives $\frac{4}{9}$ of the total profit, so Q's share of the total investment is $\frac{4}{9}$:
$$\frac{8x}{30000 + 8x} = \frac{4}{9}$$
5. Cross-multiply: $9 \times 8x = 4(30000 + 8x)$, so $72x = 120000 + 32x$.
6. Hence $40x = 120000$ and $x = 3000$.
7. Check: Q invests $8 \times 3000 = 24000$ and P invests 30000, so Q's share is $\frac{24000}{54000} = \frac{4}{9}$, as required. This is option (B).

KEY IDEA

In a partnership, profit is shared in proportion to (amount invested per month) x (number of months). Set Q's investment divided by the total investment equal to Q's profit fraction and solve.

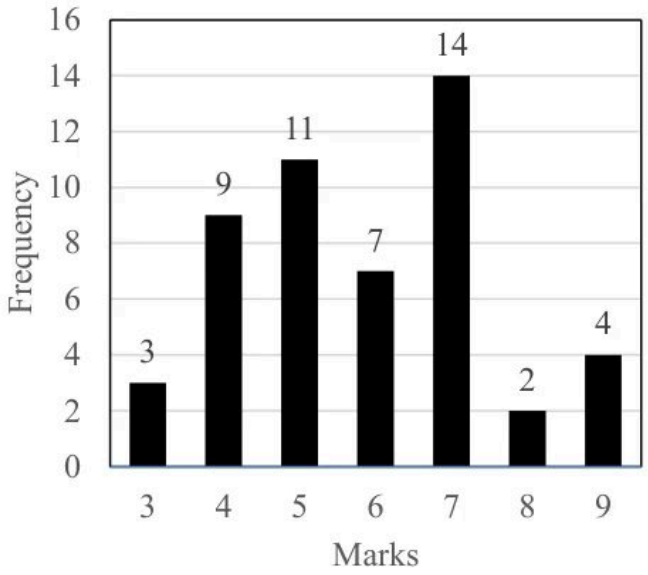
WATCH OUT FOR

Forgetting to multiply by the months, for example comparing 5000 with x directly. Another slip is setting Q's investment over P's investment equal to 4/9 instead of over the total.

Q.8 MCQ · 2 MARKS

General Aptitude › Statistics & probability

Q.8



The above frequency chart shows the frequency distribution of marks obtained by a set of students in an exam.

From the data presented above, which one of the following is CORRECT?

(A)	mean > mode > median
(B)	mode > median > mean
(C)	mode > mean > median
(D)	median > mode > mean

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Official answer: **B**

SOLUTION

1. Read the frequencies from the chart: marks $3, 4, 5, 6, 7, 8, 9$ have frequencies $3, 9, 11, 7, 14, 2, 4$. Total number of students $= 3 + 9 + 11 + 7 + 14 + 2 + 4 = 50$.
2. Mode is the mark with the highest frequency. The tallest bar is 14, at marks 7, so mode $= 7$.
3. Median of 50 values is the average of the 25th and 26th values when arranged in order. Cumulative frequencies: $3, 12, 23, 30, 44, 46, 50$. The 24th to 30th values all equal 6, so the 25th and 26th are both 6

and median $= 6$.

4. Mean $= \dfrac{\sum fx}{\sum f}$ with $\sum fx = 3 \cdot 3 + 4 \cdot 9 + 5 \cdot 11 + 6 \cdot 7 + 7 \cdot 14 + 8 \cdot 2 + 9 \cdot 4 = 9 + 36 + 55 + 42 + 98 + 16 + 36 = 292$. So mean $= \dfrac{292}{50} = 5.84$.
5. Compare: mode $7 >$ median $6 >$ mean 5.84. This is option (B).

KEY IDEA

For a frequency table, mode is the value with the largest frequency, median is found from cumulative frequencies at positions n/2 and n/2+1, and mean is the sum of f times x divided by the sum of f. A tail of low values on the left pulls the mean below the median.

WATCH OUT FOR

Taking the median as the middle of the list of marks (5 or 6 as the middle of 3 to 9) instead of using cumulative frequencies, or reading the mean off the tallest bars instead of weighting every mark by its frequency.

Q.9 MCQ · 2 MARKS

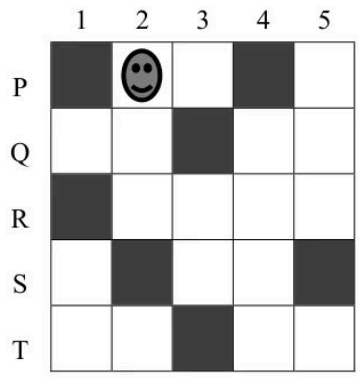
General Aptitude › Reasoning

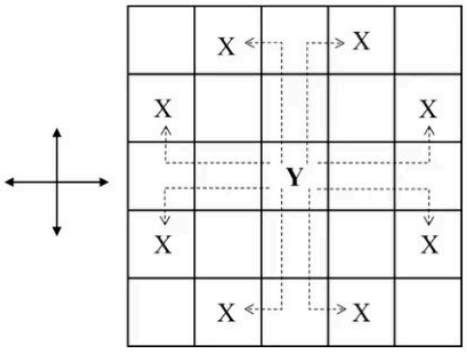
Q.9 In the square grid shown on the left, a person standing at P2 position is required to move to P5 position.

The only movement allowed for a step involves, "two moves along one direction followed by one move in a perpendicular direction". The permissible directions for movement are shown as dotted arrows in the right.

For example, a person at a given position **Y** can move only to the positions marked X on the right.

Without occupying any of the shaded squares at the end of each step, the minimum number of steps required to go from P2 to P5 is





Example: Allowed steps for a person at **Y**

(A) 4

(B) 5

(C) 6

(D) 7

Official answer: **B**

SOLUTION

1. Each step is a knight move: two squares in one direction, then one square perpendicular. Label squares by row P, Q, R, S, T (rows 1 to 5) and column 1 to 5. Shaded squares: P1, P4, Q3, R1, S2, S5, T3. A step may jump over a shaded square, but it must not end on one.
2. Work backwards from P5. The knight squares from which P5 can be reached are Q3 and R4. Q3 is shaded, so the last step must start at R4.

3. The knight squares around R4 are P3, P5, Q2, S2, T3 and T5. S2 and T3 are shaded and P5 is the target. So R4 can be reached only from P3, Q2 or T5.
4. Work forwards from P2. The knight squares from P2 are R1, R3 and Q4. R1 is shaded, so step 1 ends at R3 or Q4.
5. Step 2 from R3 gives T2, T4, Q1, Q5 and S1. The move to S5 is blocked because S5 is shaded, and the move to P4 is blocked because P4 is shaded. Step 2 from Q4 gives S3 and R2, and also P2, which is the start. So the squares reached after 2 steps are T2, T4, Q1, Q5, S1, S3 and R2. None of P3, Q2 or T5 is among them, so R4 cannot be reached in 3 steps.
6. Step 3: Q1 goes to P3. S1 goes to Q2. S3 goes to T5. So P3, Q2 and T5 are first reached at step 3.
7. Step 4: P3, Q2 or T5 goes to R4. Step 5: R4 goes to P5.
8. R4 cannot be reached before step 4, so P5 cannot be reached before step 5. The minimum number of steps is 5.

KEY IDEA

Treat each move as a knight move. Work backwards from the target to find the only squares it can be reached from. Then run a breadth-first search forward from the start, skipping squares that are shaded at the end of a step.

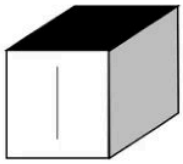
WATCH OUT FOR

Treating shaded squares as walls that cannot be jumped over, or checking only the end-point and missing that P5 can be entered only from R4 because Q3 is shaded. Another slip is adding a move that is not a knight move, for example T2 to P3, which would give a path that is too short.

Q.10 MCQ · 2 MARKS

General Aptitude › Spatial

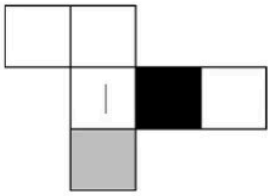
Q.10



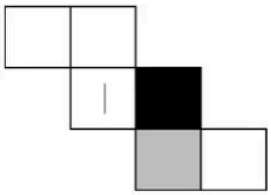
Consider a cube made by folding a single sheet of paper of appropriate shape. The interior faces of the cube are all blank. However, the exterior faces that are not visible in the above view may not be blank.

Which one of the following represents a possible unfolding of the cube?

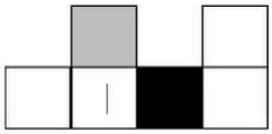
(A)



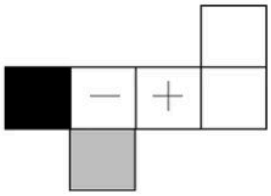
(B)



(C)



(D)



BT

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Official answer: **Marks to all**

Biotechnology Q.11 to Q.65

Q.11 MCQ · 1 MARK

Engineering Mathematics › Differential equations

What is the order of the differential equation given below?

$\frac{d^2y}{dx^2} - 6x = 3x^4 - 2x^3 + 2$

(A) 1

(B) 2

(C) 3

(D) 4

Official answer: **B**

SOLUTION

1. The order of a differential equation is the order of the highest derivative of the dependent variable that appears in it.
2. The only derivative in the equation is $\frac{d^2y}{dx^2}$, the second derivative of y with respect to x.
3. The terms $6x$, $3x^4$, $2x^3$ and 2 are polynomials in the independent variable x. They contain no derivative of y, so they do not change the order.
4. The highest derivative is of order 2, so the order of the equation is 2, which is option (B).

KEY IDEA

The order is the order of the highest derivative of y in the equation. Powers of x on either side have no effect on it.

WATCH OUT FOR

Reading the powers x^4 or x^3 as the order, or mixing up order with degree. Here the order is 2 and the degree is 1.

Q.12 MCQ · 1 MARK

Engineering Mathematics › Linear algebra

If the eigenvalues of a 2×2 matrix P are 4 and 2, then the eigenvalues of the matrix P^{-1} are

(A) 0, 0

(B) 0.0625, 0.25

(C) 0.25, 0.5

(D) 2, 4

Official answer: **C**

SOLUTION

1. Let λ be an eigenvalue of P with eigenvector $\mathbf{x} \neq 0$, so $P\mathbf{x} = \lambda\mathbf{x}$. Both eigenvalues (4 and 2) are nonzero, so $\det P = 4 \times 2 = 8 \neq 0$ and P^{-1} exists.
2. Multiply both sides by P^{-1}: $\mathbf{x} = \lambda P^{-1}\mathbf{x}$. Since $\lambda \neq 0$, $P^{-1}\mathbf{x} = \frac{1}{\lambda}\mathbf{x}$. So P^{-1} has the same eigenvectors, and its eigenvalues are the reciprocals $\frac{1}{\lambda}$.
3. For $\lambda_1 = 4$: $\frac{1}{4} = 0.25$. For $\lambda_2 = 2$: $\frac{1}{2} = 0.5$. A 2×2 matrix has exactly two eigenvalues, so these are all of them.
4. Check with the determinant: $\det P^{-1} = \frac{1}{\det P} = \frac{1}{8}$, and the product of the eigenvalues found is $0.25 \times 0.5 = 0.125 = \frac{1}{8}$. This agrees.
5. The eigenvalues of P^{-1} are 0.25 and 0.5, which is option (C).

KEY IDEA
If $P\mathbf{x} = \lambda\mathbf{x}$ and P is invertible, then P^{-1} has the same eigenvectors with eigenvalues $1/\lambda$.

WATCH OUT FOR
Taking the eigenvalues of P^{-1} to be the negatives of those of P, or squaring the reciprocals (giving 0.0625, 0.25), or leaving them unchanged as 2, 4.

Q.13 MCQ · 1 MARK

Q.13	For a double-pipe heat exchanger, the inside and outside heat transfer coefficients are 100 and 200 W m^{-2} K^{-1}, respectively. The thickness and thermal conductivity of the thin-walled inner pipe are 1 cm and 10 W m^{-1} K^{-1}, respectively. The value of the overall heat transfer coefficient is _____ W m^{-2} K^{-1}.
(A)	0.016
(B)	42.5
(C)	62.5
(D)	310

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Official answer: **C**

Q.14 MCQ · 1 MARK

Fundamentals of Biological Engineering › Upstream

Match the media component (Column I) with its role (Column II).

COLUMN I	COLUMN II
P. Sucrose	1. Anti-foam agent
Q. Zinc chloride	2. Nitrogen source
R. Ammonium sulphate	3. Carbon source
S. Silicone oil	4. Trace element

(A) P-1, Q-2, R-3, S-4
(B) P-2, Q-1, R-3, S-4
(C) P-3, Q-2, R-4, S-1

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

Official answer: **D**

SOLUTION

1. **P, sucrose:** a disaccharide ($C_{12}H_{22}O_{11}$) that invertase splits into glucose and fructose. It supplies the cell's carbon and energy, so it is the **carbon source**: P-3.
2. **Q, zinc chloride:** $ZnCl_2$ supplies Zn^{2+}, a cofactor for many metalloenzymes (for example alcohol dehydrogenase and carbonic anhydrase). Cells need it only in micromolar amounts, so it is a **trace element**: Q-4.
3. **R, ammonium sulphate:** $(NH_4)_2SO_4$ supplies NH_4^+. Cells build it into amino acids through glutamine synthetase and glutamate dehydrogenase, so it is the **nitrogen source** (it also supplies some sulphur): R-2.
4. **S, silicone oil:** polydimethylsiloxane has low surface tension and does not mix with water. It spreads over the films of foam bubbles and makes them burst, so it is added to aerated fermenters as an **anti-foam agent**: S-1.
5. The matching is P-3, Q-4, R-2, S-1, which is option (D).
6. **Quick check by elimination:** only (C) and (D) pair sucrose with 3 and silicone oil with 1. (C) makes $ZnCl_2$ the nitrogen source, but it contains no nitrogen, and it makes ammonium sulphate, a bulk salt, a trace element. So (C) is ruled out and (D) is the answer.

KEY IDEA

A fermentation medium has a job for each component. Read the chemical formula to find what each one can supply: a sugar gives carbon and energy, an ammonium salt gives nitrogen, a metal salt added in micromolar amounts gives a trace element (an enzyme cofactor), and a water-insoluble, low-surface-tension oil breaks foam.

WATCH OUT FOR

Picking (C) because zinc chloride and ammonium sulphate are both 'salts', and swapping their roles. $ZnCl_2$ contains no nitrogen, so it cannot be a nitrogen source. Ammonium sulphate is added in grams per litre as the main nitrogen supply, not in trace amounts.

Q.15 MCQ · 1 MARK

Q.15	The binding free energy of a ligand to its receptor protein is -11.5 kJ mol^{-1} at 300 K. What is the value of the equilibrium binding constant? Use R = 8.314 J mol^{-1} K^{-1}.
(A)	0.01
(B)	1.0
(C)	4.6
(D)	100.5

Official answer: **D**

Q.16 MCQ · 1 MARK

Fundamentals of Biological Engineering › Growth kinetics

The overall stoichiometry for an aerobic cell growth is

$$3C_6H_{12}O_6 + 2.5NH_3 + O_2 \rightarrow 1.5C_aH_bO_cN_d + 3CO_2 + 5H_2O$$

What is the elemental composition formula of the biomass?

(A) $C_9H_{18.2}O_5N_{1.667}$

(B) $C_9H_{22.33}O_6N_{1.667}$

(C) $C_{10}H_{18.2}O_5N_{1.667}$

(D) $C_{10}H_{22.33}O_6N_{1.667}$

Official answer: **D**

SOLUTION

1. Element balance: each of C, H, O and N must have the same number of atoms on both sides. The biomass term is $1.5\,C_aH_bO_cN_d$, so for each element, the atoms in the biomass equal (atoms in the reactants $-$ atoms in the other products), and dividing by 1.5 gives the subscript.
2. Carbon: the reactants carry $3 \times 6 = 18$; $3\,CO_2$ carries 3. So $1.5a = 18 - 3 = 15$, which gives $a = 10$.
3. Hydrogen: the reactants carry $3 \times 12 + 2.5 \times 3 = 36 + 7.5 = 43.5$; $5\,H_2O$ carries $5 \times 2 = 10$. So $1.5b = 43.5 - 10 = 33.5$, which gives $b = 22.33$.
4. Oxygen: the reactants carry $3 \times 6 + 1 \times 2 = 20$ (one O_2 molecule is 2 atoms); $3\,CO_2$ carries 6 and $5\,H_2O$ carries 5. So $1.5c = 20 - 11 = 9$, which gives $c = 6$.
5. Nitrogen: all of it comes from $2.5\,NH_3$, and no other product contains N. So $1.5d = 2.5$, which gives $d = 1.667$.
6. Biomass formula: $C_{10}H_{22.33}O_6N_{1.667}$, which is option (D). As a check, only C and D have $a = 10$, and of those only D has $b = 22.33$ and $c = 6$.

KEY IDEA

Atoms are conserved, so balance each element (C, H, O, N) separately. Whatever the reactants supply and the CO_2 and H_2O do not take away ends up in the biomass. Divide that remainder by the biomass coefficient, 1.5, to get each subscript.

WATCH OUT FOR

The common slips are counting O_2 as one oxygen atom instead of two (that gives $c = 5.33$), forgetting the hydrogen that NH_3 brings in (that gives $b = 17.33$), and forgetting to divide by the biomass coefficient 1.5 (that gives C_{15}). None of these results is among the options, so each one sends you to a wrong guess.

Q.17 MCQ · 1 MARK

General Biology › Microbiology

In binomial nomenclature, the name of a bacterial strain is written with the first letter of _____ word(s) being capitalized.

(A) first

(B) second

(C) neither

(D) first and second

Official answer: **A**

SOLUTION

1. Binomial nomenclature gives every species a two-part Latin name: the genus first, then the species epithet, for example *Escherichia coli*.
2. The genus name is always capitalized, because it names a group of related organisms.

3. The species epithet is always written in lower case, even when it honours a person or a place.
4. A bacterial strain is named by its species binomial followed by the strain designation, for example *Escherichia coli* K-12. The binomial follows the same rule, so only the first word, the genus, starts with a capital letter.
5. Option (A), first, is correct.
6. Option (B), second, is wrong because the species epithet is never capitalized.
7. Option (C), neither, is wrong because the genus is always capitalized.
8. Option (D), first and second, is wrong because the epithet stays in lower case.

KEY IDEA
In a binomial name the genus starts with a capital letter and the species epithet is all lower case. Both are italicized, and a strain designation follows after them.

WATCH OUT FOR
Capitalizing the species epithet as well, or thinking that a strain name such as K-12 changes the capitalization rule for the binomial.

Q.18 MCQ · 1 MARK

General Biology › Pathogens & antibiotics

The type of nucleic acid present in λ–phage is

(A) Double stranded DNA
(B) Single stranded circular DNA
(C) Single stranded DNA
(D) Single stranded RNA

Official answer: **A**

SOLUTION

1. Phage λ is a temperate bacteriophage of $E.coli$: after infection it can either lyse the host or integrate as a prophage (lysogeny).
2. The virion carries a linear, double-stranded DNA genome of about 48.5 kb. Each 5' end has a 12-nucleotide single-stranded overhang (the cos ends), and the two overhangs are complementary.
3. These short overhangs anneal after entry into the host, so the genome circularises inside the cell. The overhangs are only a small part of the molecule, so the genome is double stranded.
4. Option (A), double stranded DNA: correct.
5. Option (B), single stranded circular DNA: wrong. This is the genome of phages such as M13 and ϕX174, not λ.
6. Option (C), single stranded DNA: wrong. Only the 12-nucleotide cos ends are single stranded, not the genome.
7. Option (D), single stranded RNA: wrong. This is the genome of phages such as MS2 and Qβ.
8. So the answer is (A).

KEY IDEA
Phage λ has a linear dsDNA genome (about 48.5 kb) whose 12-nucleotide complementary single-stranded cos ends let it circularise in the host. Genome type is what the question asks, and that is dsDNA.

WATCH OUT FOR
Picking single stranded DNA because of the single-stranded cos overhangs, or confusing λ with M13 or ϕ X174 (single stranded DNA phages) or MS2 (RNA phage).

Q.19 MCQ · 1 MARK

Fundamentals of Biological Engineering › Enzyme kinetics

Which of the following statements about reversible enzyme inhibitors are CORRECT?

P. Uncompetitive inhibitors bind only to the enzyme-substrate complex

Q. Non-competitive inhibitors bind only at a different site from the substrate

R. Competitive inhibitors bind to the same site as the substrate

(A) P and Q only

(B) P and R only

(C) Q and R only

(D) P, Q and R

Official answer: **D**

SOLUTION

1. Write the general reversible-inhibition scheme. Free enzyme E binds substrate S to form ES, which turns over to product. v is the initial rate, V_{max} is the maximum rate at saturating $[S]$, and K_m is the Michaelis constant. A reversible inhibitor I can form EI (dissociation constant K_i), ESI (dissociation constant K_i'), or both. Which of these complexes can form is what separates the three classes.
2. **P, uncompetitive:** I binds only to ES, forming ESI. It has no affinity for free E, because its binding site only appears once substrate is bound. Taking ESI into the enzyme balance gives
$$v = \frac{V_{max}[S]}{K_m + [S]\left(1 + \frac{[I]}{K_i'}\right)}$$
Dividing top and bottom by $(1 + [I]/K_i')$ shows that the apparent V_{max} and the apparent K_m both fall by the same factor $(1 + [I]/K_i')$. This is the kinetic signature of binding to ES only. P is correct.
3. **Q, non-competitive (pure):** I binds at a site other than the active site (an allosteric site). So it can attach to free E and to ES equally, with $K_i = K_i'$:
$$v = \frac{V_{max}[S]}{\left(1 + \frac{[I]}{K_i}\right)(K_m + [S])}$$
I does not compete with S for the active site, so K_m is unchanged and V_{max} falls to $V_{max}/\left(1 + [I]/K_i\right)$. Raising $[S]$ cannot overcome it. Its binding site is always different from the substrate's, so Q is correct.
4. **R, competitive:** I resembles the substrate and occupies the active site itself. S and I exclude each other, so the inhibitor binds only free E (forming EI):
$$v = \frac{V_{max}[S]}{K_m\left(1 + \frac{[I]}{K_i}\right) + [S]}$$
The apparent K_m rises by the factor $(1 + [I]/K_i)$ and V_{max} is unchanged, because a high enough $[S]$ outcompetes I for the shared site. R is correct.
5. All three statements are correct, so the answer is **(D) P, Q and R**.

KEY IDEA

Each class of reversible inhibitor is defined by what it binds. Competitive binds free E at the active site, so K_m rises and V_{max} stays the same. Uncompetitive binds only ES, so K_m and V_{max} fall by the same factor. Pure non-competitive binds E and ES equally at a separate site, so K_m stays the same and V_{max} falls.

WATCH OUT FOR

Mixing up uncompetitive and non-competitive because the names sound alike, and so rejecting P (thinking uncompetitive inhibitors also bind free E) or rejecting Q. Another mistake is to drop a statement because it contains the word "only". Here "only" matches the textbook definition in both P and Q.

Q.20 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Cell biology

Match the component of eukaryotic cells (Column I) with its respective function (Column II).

Column I: P. Lysosome, Q. Peroxisome, R. Glyoxysome, S. Cytoskeleton

Column II: 1. Digestion of macromolecules, 2. Detoxification of harmful compounds, 3. Conversion of fatty acids to sugar, 4. Involvement in cell motility

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

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

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

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

Official answer: **A**

SOLUTION

1. Lysosome (P) contains hydrolytic (acid) enzymes such as proteases, lipases, nucleases and glycosidases that digest macromolecules delivered via endocytosis, phagocytosis and autophagy; this is its defining function, matching function 1 (Digestion of macromolecules).
2. Peroxisome (Q) houses oxidative enzymes including catalase, which breaks down hydrogen peroxide and other reactive by-products generated during metabolic oxidation reactions, a general detoxification role present in essentially all eukaryotic cell types, matching function 2 (Detoxification of harmful compounds).
3. Glyoxysome (R) is a specialized peroxisome-type organelle found in plant seeds and germinating tissue that carries out the glyoxylate cycle, converting stored fatty acids into sugars (succinate → gluconeogenesis precursors) to fuel seedling growth before photosynthesis starts, matching function 3 (Conversion of fatty acids to sugar).
4. Cytoskeleton (S) is built from microtubules, microfilaments and intermediate filaments; microtubules (in cilia/flagella) and actin microfilaments (in cell crawling) directly drive cell motility, matching function 4 (Involvement in cell motility).
5. Combining the four matches gives P-1, Q-2, R-3, S-4, which is exactly option (A).
6. Checking the distractors confirms they are wrong: (B) swaps P and Q, wrongly giving lysosome the detoxification role; (C) wrongly assigns lysosome to fatty-acid-to-sugar conversion (the glyoxysome's unique role) and glyoxysome to digestion; (D) is a fully mismatched permutation with no correct pairing.
7. Therefore the correct option is (A).

KEY IDEA

Each organelle listed is matched to its single best-known signature function: lysosome = intracellular digestion (hydrolytic enzymes), peroxisome = general detoxification (catalase breaking down H_2O_2), glyoxysome = the glyoxylate cycle converting stored fatty acids to sugars (plant seeds), cytoskeleton = structural/motility roles (microtubules, actin filaments).

WATCH OUT FOR

Confusing peroxisome's general detoxification role (H_2O_2 breakdown via catalase, found in nearly all cell types) with the glyoxysome's specialized fatty-acid-to-sugar conversion (glyoxylate cycle, restricted to plant seeds/germinating tissue): swapping Q and R, or picking option (C) which assigns lysosome to the glyoxylate function instead of digestion.

Q.21 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Gene expression

In animal cells, the endogenously produced miRNAs silence gene expression by

(A) base pairing with the 3'-untranslated region of specific mRNAs

(B) blocking mRNA synthesis

(C) binding to the operator site

(D) base pairing with the 3' region of specific rRNAs

Official answer: **A**

SOLUTION

1. miRNA-mediated silencing (RNA interference / post-transcriptional gene silencing, PTGS) in animal cells acts after transcription, not by blocking it: the mature miRNA is loaded into the RNA-induced silencing complex (RISC).
2. Option A: RISC-bound miRNA base-pairs, usually with imperfect complementarity, to the 3'-untranslated region (3'-UTR) of target mRNAs, leading to translational repression and/or mRNA degradation. This is the established mechanism of endogenous miRNA silencing, so A is correct.
3. Option B: 'Blocking mRNA synthesis' describes inhibition of transcription. miRNAs act on already-synthesized (mature) mRNA, not on RNA polymerase or transcription itself: incorrect.
4. Option C: 'Binding to the operator site' is a prokaryotic transcriptional repression mechanism (e.g., the lac repressor binding the operator), and has no role in eukaryotic miRNA-mediated gene silencing: incorrect.
5. Option D: miRNAs base-pair with the 3'-UTR of target mRNAs, not with rRNAs; ribosomal RNA is not the functional target of gene-silencing miRNAs: incorrect.
6. Hence only option A correctly describes the mechanism of endogenous miRNA-mediated gene silencing in animal cells.

KEY IDEA

Endogenous miRNAs in animal cells silence gene expression post-transcriptionally: mature miRNA loaded into the RNA-induced silencing complex (RISC) base-pairs, typically with imperfect complementarity, to the 3'-untranslated region (3'-UTR) of target mRNAs, causing translational repression and/or mRNA degradation, not transcriptional blocking.

WATCH OUT FOR

Confusing miRNA-mediated post-transcriptional silencing with transcriptional repression mechanisms (e.g., 'blocking mRNA synthesis' or 'binding to the operator site', the latter being a prokaryotic operon-repressor concept like the lac repressor, not applicable to eukaryotic miRNA action). Some students also mistakenly think miRNAs act on rRNA rather than mRNA.

Q.22 MCQ · 1 MARK

Plant, Animal and Microbial Biotechnology › Plant tissue culture

Terpenoids are made of _____ units

(A) amino acid

(B) carbohydrate

(C) isoprene

(D) triacylglycerol

Official answer: **C**

Q.23 MCQ · 1 MARK

Plant, Animal and Microbial Biotechnology › Microbial products

Match the microbial product (Column I) with its respective application (Column II).

Column I: P. Methane; Q. Glycolipids; R. Polyhydroxy alkanoate
Column II: 1. Biosurfactant; 2. Bioplastic; 3. Biofuel

(A) P-1, Q-2, R-3

(B) P-2, Q-1, R-3

(C) P-3, Q-2, R-1

(D) P-3, Q-1, R-2

Official answer: **D**

SOLUTION

1. Methane (P) is produced by methanogenic archaea during anaerobic digestion and is burned for energy, so it is a biofuel. P matches 3. This rules out options A (P-1) and B (P-2).
2. Glycolipids (Q), such as rhamnolipids made by Pseudomonas and sophorolipids made by yeasts, have a hydrophilic sugar head and a hydrophobic fatty-acid tail. They lower surface and interfacial tension, so they are biosurfactants. Q matches 1.
3. Polyhydroxyalkanoates (R), such as polyhydroxybutyrate, are storage polyesters made by bacteria such as Ralstonia and Bacillus. They are biodegradable thermoplastics, so they are bioplastics. R matches 2.
4. The full matching is P-3, Q-1, R-2. Option C fails because it pairs glycolipids with bioplastic and PHA with biosurfactant. Option D is the only option that matches all three pairs, so it is correct.

KEY IDEA

Match each microbial product to its main use. Methane is a biofuel, glycolipids are biosurfactants, and polyhydroxyalkanoates (PHA) are bioplastics.

WATCH OUT FOR

Pairing glycolipids with bioplastic because both are lipid-like or polymer-like, or pairing PHA with biosurfactant. PHA is a polyester storage polymer used for plastics. Glycolipids are amphiphilic molecules used to lower surface tension.

Q.24 MCQ · 1 MARK

Recombinant DNA Technology and Tools › Bioinformatics

Which of the following is NOT used for generating an optimal alignment of two nucleotide sequences?

(A) Gap penalties

(B) Match scores

(C) Mismatch scores

(D) Nucleotide composition

Official answer: **D**

SOLUTION

1. Optimal alignment algorithms (Needleman-Wunsch for global alignment, Smith-Waterman for local alignment) build a dynamic-programming matrix cell by cell using a fixed scoring scheme.
2. (A) Gap penalties: used; every inserted or deleted gap in the alignment is penalized (gap-open / gap-extension), directly entering the recursion and the traceback. So gap penalties ARE used, not the answer.
3. (B) Match scores: used; whenever two aligned nucleotides are identical, a positive score is added at that matrix cell. Directly used, not the answer.
4. (C) Mismatch scores: used; whenever two aligned nucleotides differ, a penalty (negative score) is applied at that cell; this is exactly as fundamental to the recursion as the match score. Used, not the answer.
5. (D) Nucleotide composition: the overall %A/%T/%G/%C content of a sequence is a global compositional statistic (relevant to things like GC-content analysis, codon usage, or compositional score-adjustment in database search statistics) but plays no role in the cell-by-cell scoring recursion or traceback of a pairwise alignment algorithm.
6. Since the algorithm needs only the match score, the mismatch score, and the gap penalty to fill and trace back the DP matrix, nucleotide composition is the one item NOT used for generating the optimal

alignment.

7. Hence the correct choice is (D) Nucleotide composition.

KEY IDEA

Optimal pairwise alignment algorithms (Needleman-Wunsch for global alignment, Smith-Waterman for local alignment) fill a dynamic-programming matrix using a fixed scoring scheme consisting only of match scores, mismatch scores, and gap penalties (gap-open/gap-extension). The overall nucleotide composition (%A/%T/%G/%C) of a sequence is a separate, global compositional statistic that plays no role in the cell-by-cell recursion or traceback of the alignment algorithm.

WATCH OUT FOR

Confusing "used in sequence analysis generally" with "used in the alignment scoring recursion specifically": nucleotide/base composition is relevant to other analyses (e.g., GC-content, codon usage bias, compositional adjustment for statistical significance) but is not one of the three parameters (match, mismatch, gap penalty) that actually build the alignment scoring matrix itself.

Q.25 MCQ · 1 MARK

Recombinant DNA Technology and Tools › Enzymes & vectors

The recognition sequences of four Type-II restriction enzymes (RE) are given below. The symbol (↓) indicates the cleavage site. Identify the RE that generates sticky ends.

(A) RE1 - 5' G↓GATCC 3'

(B) RE2 - 5' CTG↓CAG 3'

(C) RE3 - 5' CCC↓GGG 3'

(D) RE4 - 5' AG↓CT 3'

Official answer: **A**

SOLUTION

1. Each of the four recognition sequences is a palindrome (its reverse complement equals itself), so whether the cut is symmetric or offset relative to the site's own centre determines blunt vs sticky ends.
2. RE1: 5' G↓GATCC 3', a 6 bp site. The cut falls after base 1 (1 base from one end, 5 from the other), offset from the centre (which would be after base 3). Because the site is palindromic, the enzyme cuts the complementary strand at the mirror position too, leaving a 4-nucleotide single-stranded 5'-GATC overhang on each fragment → sticky (cohesive) ends. (This is the actual BamHI cutting pattern.)
3. RE2: 5' CTG↓CAG 3', a 6 bp palindromic site (reverse complement of CTGCAG is CTGCAG). The cut falls after base 3, exactly the centre of the 6-bp site → both strands are cut at the same relative position → blunt ends.
4. RE3: 5' CCC↓GGG 3', a 6 bp palindromic site (the classic SmaI site). Cut after base 3 = the exact centre → blunt ends, no overhang.
5. RE4: 5' AG↓CT 3', a 4 bp palindromic site (the classic AluI site). Cut after base 2 = the exact centre of a 4-bp site → blunt ends.
6. Only RE1 cuts off-centre relative to its site's axis of symmetry, generating a protruding single-stranded (sticky/cohesive) end; RE2, RE3 and RE4 all cut exactly at the centre of symmetry, generating flush (blunt) ends.
7. Hence the enzyme that generates sticky ends is RE1 → option (A).

KEY IDEA

For a palindromic (double-stranded-symmetric) restriction site, an enzyme produces sticky (cohesive) ends when its cleavage point on each strand is offset from the site's centre of symmetry (leaving a single-stranded overhang), and blunt ends when the cleavage point sits exactly at that centre (both strands cut in register).

WATCH OUT FOR

Assuming any recognition site with a "↓" symbol off-centre in the way it is typeset must be sticky, without actually locating the site's own centre of symmetry for each different site length (6 bp vs 4 bp), e.g. mistakenly treating CTG↓CAG (cut after base 3 of 6, i.e. exactly centred) as asymmetric because the arrow "looks" placed differently from G↓GATCC.

Q.26 MCQ · 1 MARK

Recombinant DNA Technology and Tools › PCR & sequencing

Among individuals in a human population, minor variations exist in nucleotide sequences of chromosomes. These variations can lead to gain or loss of sites for specific restriction enzymes. Which of the following technique is used to identify such variations?

(A) Polymerase dependent fragment insertion

(B) Real-time polymerase chain reaction

(C) Restriction fragment length polymorphism

(D) Reverse transcriptase polymerase chain reaction

Official answer: **C**

SOLUTION

1. The stem describes minor inter-individual nucleotide sequence variations that cause gain or loss of specific restriction enzyme recognition sites. This is the defining phenomenon detected by Restriction Fragment Length Polymorphism (RFLP) analysis.
2. Option (A) 'Polymerase dependent fragment insertion' is not an established molecular biology technique, so it is eliminated.
3. Option (B) Real-time PCR measures amplicon accumulation via fluorescence to quantify template abundance during amplification cycles; it does not detect the presence or absence of a restriction site, so it is eliminated.
4. Option (C) RFLP: genomic DNA is digested with a specific restriction enzyme; if a sequence variant creates or abolishes a cut site at that locus, the number and sizes of the resulting fragments differ between individuals. This fragment-size difference, revealed by gel electrophoresis (with or without Southern blotting/probing), is exactly the variation described in the stem. This matches.
5. Option (D) RT-PCR uses reverse transcriptase to convert RNA to cDNA before amplification, and is used to study transcripts/gene expression; it has no role in detecting genomic restriction-site variation, so it is eliminated.
6. Therefore, the technique used to identify gain/loss of restriction sites due to sequence variation is RFLP, option (C).

KEY IDEA

A DNA sequence variant (SNP or other minor change) at a restriction enzyme recognition sequence creates or destroys that cut site; digesting genomic DNA with the enzyme and comparing the resulting fragment sizes (by Southern blot or electrophoresis) between individuals reveals the variation. This is RFLP analysis.

WATCH OUT FOR

Confusing RFLP (which detects DNA sequence variation via changes in restriction-digest fragment sizes) with PCR-based quantification or amplification methods (real-time PCR, RT-PCR), which detect gene expression/RNA levels or amplify DNA but do not by themselves reveal restriction-site polymorphisms.

Q.27 NAT · 1 MARK

Genetics, Cell and Molecular Biology › Mendelian genetics

Assuming independent assortment and no recombination, the number of different combinations of maternal and paternal chromosomes in gametes of an organism with a diploid number of 12 is _____.

Official answer: **64**

SOLUTION

1. Diploid number 2n = 12, so the haploid number of chromosome pairs is n = 12 / 2 = 6.
2. Independent assortment means each of the 6 homologous pairs segregates independently during meiosis: for each pair, a gamete gets either the maternal or the paternal chromosome, giving 2 independent choices per pair.
3. With 6 independent pairs, the total number of distinct maternal/paternal combinations in a gamete is 2^6.
4. $2^6 = 64$.

KEY IDEA

With independent assortment, each homologous chromosome pair segregates independently, so a gamete can receive the maternal or paternal member of each pair; the number of distinct combinations is 2^n, where n is the haploid chromosome number.

WATCH OUT FOR

Using the diploid number (12) directly as the exponent instead of first halving it to get the haploid number of pairs (6), which gives a wrong answer of 2^{12}.

Q.28 NAT · 1 MARK

Fundamentals of Biological Engineering › Growth kinetics

A microorganism is grown in a batch culture using glucose as a carbon source. The apparent growth yield is $0.5\ \dfrac{\text{g biomass}}{\text{g substrate}}$. The initial concentrations of biomass and substrate are $2\ \text{g L}^{-1}$ and $200\ \text{g L}^{-1}$, respectively. Assuming that there is no endogenous metabolism, the maximum biomass concentration that can be achieved is _____ g L^{-1}.

Official answer: **102**

SOLUTION

1. Let X be the biomass concentration and S the substrate (glucose) concentration, both in g L^{-1}, with initial values $X_0 = 2\ \text{g L}^{-1}$ and $S_0 = 200\ \text{g L}^{-1}$. The apparent growth yield $Y_{X/S}$ is biomass formed per unit substrate consumed:
$$Y_{X/S} = \frac{X - X_0}{S_0 - S} = 0.5\ \frac{\text{g biomass}}{\text{g substrate}}$$
2. With no endogenous metabolism, no substrate is diverted to maintenance, so this yield holds unchanged until the end of the batch. Every gram of glucose consumed gives 0.5 g of new biomass.
3. Biomass is therefore highest when all the substrate has been used up ($S = 0$):
$$X_{max} = X_0 + Y_{X/S}\,(S_0 - 0)$$
4. $$X_{max} = 2 + 0.5 \times 200 = 2 + 100 = 102\ \text{g L}^{-1}$$

KEY IDEA

The yield $Y_{X/S}$ links the biomass formed to the substrate consumed. With no endogenous (maintenance) metabolism it stays constant, so the most biomass you can get is the inoculum plus the yield times all of the substrate: $X_{max} = X_0 + Y_{X/S}S_0$.

WATCH OUT FOR

Answering $100\ \text{g L}^{-1}$ (0.5×200) and leaving out the initial biomass $X_0 = 2\ \text{g L}^{-1}$. The yield gives only the biomass newly formed, not the total. A second slip is using $Y_{X/S}$ as substrate per biomass and getting 400.

Q.29 NAT · 1 MARK

Fundamentals of Biological Engineering › Growth kinetics

The degree of reduction of lactic acid ($C_3H_6O_3$) is _____.

Official answer: **4**

SOLUTION

1. The degree of reduction γ is the number of available electrons per carbon atom (per C-mole). It is measured against CO_2, H_2O and NH_3, which all count as zero. Each atom is assigned a valence: C = 4, H = 1, O = -2. For a compound $C_cH_hO_o$ with no nitrogen:
$$\gamma = \frac{4c + h - 2o}{c}$$
2. Lactic acid $C_3H_6O_3$ has $c = 3$, $h = 6$, $o = 3$.
3. Available electrons per molecule: $4(3) + 1(6) - 2(3) = 12 + 6 - 6 = 12$.
4. Divide by the number of carbons:
$$\gamma = \frac{12}{3} = 4$$
5. Check: per C-mole, lactic acid is CH_2O, the same as glucose ($C_6H_{12}O_6 \rightarrow CH_2O$), and glucose also has $\gamma = 4$. That fits homolactic fermentation (glucose to 2 lactate), which is redox-balanced and needs no external electron acceptor.

KEY IDEA

Degree of reduction means available electrons per carbon: $\gamma = (4c + h - 2o - 3n)/c$, with CO_2, H_2O and NH_3 as the zero reference. Any compound whose C-mole formula is CH_2O (glucose, lactic acid, acetic acid) has $\gamma = 4$.

WATCH OUT FOR

Giving the electron count per molecule (12) and forgetting to divide by the 3 carbons. Another slip is using O = $+2$ or leaving oxygen out, which gives 6 instead of 4.

Q.30 NAT · 1 MARK

Engineering Mathematics › Numerical methods

Consider a nonlinear algebraic equation, $x \ln x + x - 1 = 0$. Using the Newton-Raphson method, with the initial guess of $x_0 = 3$, the value of x after one iteration (rounded off to one decimal place) is _____.

Official answer: **1.2 to 1.4**

SOLUTION

1. Let $f(x) = x \ln x + x - 1$. The Newton-Raphson update is $x_1 = x_0 - \frac{f(x_0)}{f'(x_0)}$, with $x_0 = 3$.
2. Differentiate with the product rule: $f'(x) = \ln x + x \cdot \frac{1}{x} + 1 = \ln x + 2$.
3. At $x_0 = 3$: $f(3) = 3 \ln 3 + 3 - 1 = 3(1.0986) + 2 \approx 5.2958$.
4. At $x_0 = 3$: $f'(3) = \ln 3 + 2 \approx 3.0986$.
5. Then $x_1 = 3 - \frac{5.2958}{3.0986} \approx 3 - 1.7091 = 1.2909$.
6. Rounded to one decimal place, $x_1 \approx 1.3$.

KEY IDEA

Newton-Raphson: $x_{n+1} = x_n - f(x_n)/f'(x_n)$. Differentiate $x \ln x$ with the product rule to get $\ln x + 1$, so $f'(x) = \ln x + 2$.

WATCH OUT FOR

Differentiating $x \ln x$ as just $\ln x$ or $1/x$, forgetting the product rule term. Also using the natural log value of $\ln 3$ incorrectly (for example $\log_{10} 3 = 0.477$) gives a wrong iterate.

Q.31 NAT · 1 MARK

Engineering Mathematics › Probability & statistics

The probability density function of a random variable X is $p(x) = 2e^{-2x}$. The probability $P(1 \le X \le 2)$ (rounded off to two decimal places) is _____.

Official answer: **0.11 to 0.13**

SOLUTION

1. The density $p(x) = 2e^{-2x}$ is an exponential density with rate 2 (for $x \ge 0$), so it integrates to 1.
2. Use $P(a \le X \le b) = \int_a^b p(x)\,dx$, so $P(1 \le X \le 2) = \int_1^2 2e^{-2x}\,dx$.
3. The antiderivative of $2e^{-2x}$ is $-e^{-2x}$.
4. $$P = \left[-e^{-2x}\right]_1^2 = e^{-2} - e^{-4}$$
5. Numerically, $e^{-2} \approx 0.135335$ and $e^{-4} \approx 0.018316$.
6. $$P \approx 0.135335 - 0.018316 = 0.117019 \approx 0.12$$

KEY IDEA

For a density, probability over an interval is the integral of the density; for an exponential density with rate λ, $P(a \le X \le b) = e^{-\lambda a} - e^{-\lambda b}$.

WATCH OUT FOR

Writing $P = \int_1^2 e^{-2x}\,dx$ and dropping the factor 2, which gives about 0.06, or forgetting that the antiderivative of $2e^{-2x}$ is $-e^{-2x}$ with no leftover factor.

Q.32 NAT · 1 MARK

Engineering Mathematics › Calculus

The maximum value of the function $f(x) = 3x^2 - 2x^3$ for $x > 0$ is _____.

Official answer: **1**

SOLUTION

1. Differentiate: $f'(x) = 6x - 6x^2 = 6x(1 - x)$.
2. Set $f'(x) = 0$: $x = 0$ or $x = 1$. Only $x = 1$ lies in $x > 0$.
3. Second derivative: $f''(x) = 6 - 12x$, so $f''(1) = -6 < 0$, hence $x = 1$ is a local maximum.
4. Check that it is the global maximum on $x > 0$: for $0 < x < 1$, $f'(x) > 0$ so f is increasing; for $x > 1$, $f'(x) < 0$ so f is decreasing (and $f \to -\infty$ as $x \to \infty$). So f never exceeds $f(1)$ on $x > 0$.
5. Evaluate: $f(1) = 3(1)^2 - 2(1)^3 = 3 - 2 = 1$.

KEY IDEA

Find the stationary points from $f'(x) = 0$, keep those in the allowed range, and use the sign of f' on either side to confirm the point is a global maximum, not just a local one.

WATCH OUT FOR

Stopping at $f'(x) = 0$ and not discarding $x = 0$, which is outside $x > 0$. Or quoting a local maximum without checking that f does not rise again elsewhere in the range.

Q.33 NAT · 1 MARK

Fundamentals of Biological Engineering › Growth kinetics

The specific growth rate of a yeast having a doubling time of 0.693 h (rounded off to nearest integer) is _____ h^{-1}.

Official answer: **1**

SOLUTION

1. In the exponential phase, biomass grows as $\dfrac{dX}{dt} = \mu X$. Here X is the cell (biomass) concentration and μ is the specific growth rate in h^{-1}. Integrating from X_0 at $t = 0$ gives $X = X_0 e^{\mu t}$.

2. The doubling time t_d is the time it takes for X to reach $2X_0$. Putting that into the growth law gives $2 = e^{\mu t_d}$. Taking the natural log of both sides:
$$t_d = \frac{\ln 2}{\mu} \quad \Longleftrightarrow \quad \mu = \frac{\ln 2}{t_d}$$
3. Substitute $\ln 2 \approx 0.693$ and $t_d = 0.693$ h:
$$\mu = \frac{0.693}{0.693\ \text{h}} = 1\ \text{h}^{-1}$$
(Using $\ln 2 = 0.6931$ gives $1.0002\ \text{h}^{-1}$, which also rounds to 1.)
4. Rounded to the nearest integer, $\mu = 1\ \text{h}^{-1}$.

KEY IDEA

In exponential growth, $X = X_0 e^{\mu t}$, so the doubling time and the specific growth rate are linked by $t_d = \frac{\ln 2}{\mu}$. The doubling time given here, 0.693 h, is exactly $\ln 2$ hours, which makes $\mu = 1\ \text{h}^{-1}$.

WATCH OUT FOR

Taking $\mu = 1/t_d$ (which gives about $1.44\ \text{h}^{-1}$) and forgetting the $\ln 2$. Another error is using $\log_{10} 2 = 0.301$ in place of $\ln 2$, which gives about $0.43\ \text{h}^{-1}$. Growth is $e^{\mu t}$, so the natural log is the right one.

Q.34 NAT · 1 MARK

Fundamentals of Biological Engineering › Bioreactor operation

A fermentation broth of density $1000\ \text{kg m}^{-3}$ and viscosity $10^{-3}\ \text{kg m}^{-1}\ \text{s}^{-1}$ is mixed in a $100\ \text{L}$ fermenter using a $0.1\ \text{m}$ diameter impeller, rotating at a speed of $2\ \text{s}^{-1}$. The impeller Reynolds number is _____.

Official answer: **20000**

SOLUTION

1. Impeller Reynolds number: $Re_i = \frac{\rho N D_i^2}{\mu}$. Here ρ is the broth density, N is the impeller speed in revolutions per second, D_i is the impeller diameter and μ is the broth viscosity.
2. Data in SI units: $\rho = 1000\ \text{kg m}^{-3}$, $N = 2\ \text{s}^{-1}$, $D_i = 0.1\ \text{m}$ (so $D_i^2 = 0.01\ \text{m}^2$) and $\mu = 10^{-3}\ \text{kg m}^{-1}\ \text{s}^{-1}$.
3. The characteristic length is the impeller diameter, not a dimension of the tank. The $100\ \text{L}$ vessel volume therefore does not enter the calculation.
4. $$Re_i = \frac{(1000)(2)(0.1)^2}{10^{-3}} = \frac{20}{10^{-3}} = 2 \times 10^4$$
5. Units check: $\frac{\text{kg m}^{-3} \cdot \text{s}^{-1} \cdot \text{m}^2}{\text{kg m}^{-1}\ \text{s}^{-1}} = \frac{\text{kg m}^{-1}\ \text{s}^{-1}}{\text{kg m}^{-1}\ \text{s}^{-1}}$, which is dimensionless, as a Reynolds number must be.
6. $Re_i = 20000$. This is above about 10^4, the value usually taken as the start of fully turbulent flow in a stirred vessel. In a baffled vessel the power number is constant in that regime.

KEY IDEA

For a stirred tank, the Reynolds number is built from the impeller: $Re_i = \rho N D_i^2 / \mu$. N is in revolutions per second and D_i is the impeller diameter. The tank volume only tests whether you know which length to use.

WATCH OUT FOR

Three slips are common. The first is turning $N = 2\ \text{s}^{-1}$ into angular speed ($2\pi N$), which gives about 1.26×10^5; the stirred-tank Reynolds number uses revolutions per second. The second is writing D_i instead of D_i^2, which gives 200. The third is working a tank diameter out of the $100\ \text{L}$ volume and using it as the length scale.

Q.35 NAT · 1 MARK

Q.35	For a pure species, the slope of the melting line $\frac{dP}{dT}$ at $-2\ ^{\circ}C$ is -5.0665×10^{6} Pa K^{-1}. The difference between the molar volumes of the liquid and solid phase at $-2\ ^{\circ}C$ is -4.5×10^{-6} m^3 mol^{-1}. The value of the latent heat of fusion (rounded off to nearest integer) is _____ J mol^{-1}.

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Official answer: **6097 to 6223**

Q.36 MCQ · 2 MARKS

Genetics, Cell and Molecular Biology › Population & evolution

Which of the following conditions will contribute to the stability of a gene pool in a natural population?

P. Large population
Q. No net mutation
R. Non-random mating
S. No selection

(A) P only
(B) P and Q only
(C) P and R only
(D) P, Q and S only

Official answer: **D**

SOLUTION

1. Gene pool (allele frequency) stability across generations is defined by the Hardy-Weinberg equilibrium, which holds only when a specific set of disturbing forces is absent or negligible.
2. P (large population): contributes to stability. A large population size minimizes genetic drift (random, sampling-driven fluctuations in allele frequency that are pronounced in small populations), so it supports a stable gene pool.
3. Q (no net mutation): contributes to stability. Mutation is a source of new alleles and allele-frequency change; its absence is one of the Hardy-Weinberg conditions that keeps the gene pool stable.
4. R (non-random mating): does NOT contribute to stability. Hardy-Weinberg equilibrium specifically requires RANDOM mating. Non-random mating (e.g., assortative mating or inbreeding) changes genotype frequencies across generations and is one of the classical forces that can disturb equilibrium, so it is excluded from the stabilizing set.
5. S (no selection): contributes to stability. Natural selection changes allele frequencies through differential survival and reproduction; its absence is required for the gene pool to remain stable.
6. The conditions contributing to gene pool stability are therefore P, Q and S only; R does not belong, since non-random mating is a disturbing force rather than a stabilizing one.

7. This matches option (D): P, Q and S only.

KEY IDEA
A gene pool (its allele frequencies) stays stable across generations only under Hardy-Weinberg conditions: an infinitely large (in practice, sufficiently large) population, no mutation, random mating, and no selection (also no migration/gene flow).

WATCH OUT FOR
Assuming random mating and non-random mating are interchangeable, or forgetting that Hardy-Weinberg equilibrium requires RANDOM mating specifically, so "non-random mating" (R) is a disturbing force, not a stabilizing condition, and must be excluded.

Q.37 MCQ · 2 MARKS

Plant, Animal and Microbial Biotechnology › Animal cell culture

Match the media component used in mammalian cell culture (Column I) with its respective role (Column II).

Column I: P. Hydrocortisone; Q. Fibronectin; R. Epidermal growth factor; S. Riboflavin
Column II: 1. Mitogen; 2. Vitamin; 3. Hormone; 4. Cell attachment

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

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

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

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

Official answer: **A**

SOLUTION

1. Match each medium component with its role one at a time.
2. P, hydrocortisone, is a glucocorticoid steroid hormone. It is added to media for some cell types, where it promotes attachment, spreading and differentiation. So P matches 3 (Hormone).
3. Q, fibronectin, is an adhesive extracellular matrix glycoprotein. It coats culture surfaces, and anchorage-dependent cells bind it through integrins. So Q matches 4 (Cell attachment).
4. R, epidermal growth factor, binds the EGF receptor tyrosine kinase and stimulates cell division. So R matches 1 (Mitogen).
5. S, riboflavin, is vitamin B_2, a precursor of the cofactors FMN and FAD. So S matches 2 (Vitamin).
6. The combined matching is P-3, Q-4, R-1, S-2, which is option (A).
7. Check the other options. (B) calls EGF a vitamin and riboflavin a mitogen. (C) and (D) call hydrocortisone a cell attachment factor and fibronectin a hormone. Each of these contradicts at least one match above, so only (A) is correct.

KEY IDEA
In mammalian cell culture media, hormones such as hydrocortisone, growth factors such as EGF (mitogens), attachment factors such as fibronectin, and vitamins such as riboflavin each have a distinct role. Match each component by what it does for the cells.

WATCH OUT FOR
Confusing a growth factor with a vitamin or hormone, or assuming that a steroid like hydrocortisone helps cells attach to the surface because it affects spreading. Attachment is provided by matrix proteins such as fibronectin, not by hormones.

Q.38 MCQ · 2 MARKS

General Biology › Immune system

Match the cell type (Column I) with its function (Column II).

Column I: P. B cells; Q. Neutrophils; R. T cells; S. Mast cells
Column II: 1. Humoral immunity; 2. Cytotoxicity; 3. Histamine-associated allergy; 4. Phagocytosis

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

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

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

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

Official answer: **B**

SOLUTION

1. B cells differentiate into plasma cells that secrete antibodies into blood and body fluids. This is humoral immunity, so P matches 1.
2. Neutrophils are the most abundant circulating phagocytes. They engulf and destroy bacteria early in an infection, so Q matches 4 (phagocytosis).
3. Cytotoxic T cells ($\mathrm{CD8}^{+}$) kill virus-infected and tumour cells using perforin and granzymes, so R matches 2 (cytotoxicity).
4. Mast cells carry IgE bound to their surface receptors. On allergen exposure they degranulate and release histamine, so S matches 3 (histamine-associated allergy).
5. The combination is P-1, Q-4, R-2, S-3, which is option (B).
6. Option (A) fails because it pairs neutrophils with cytotoxicity (Q-2), T cells with allergy (R-3) and mast cells with phagocytosis (S-4). Option (C) fails because it pairs B cells with phagocytosis (P-4). Option (D) fails because it pairs B cells with phagocytosis (P-4) and mast cells with humoral immunity (S-1).

KEY IDEA

Match each immune cell to its signature role. B cells make antibodies (humoral immunity). Neutrophils are phagocytes. Cytotoxic T cells kill infected cells. Mast cells release histamine in IgE-mediated allergy.

WATCH OUT FOR

Giving cytotoxicity to neutrophils because they kill microbes. Neutrophils kill by phagocytosis, while cytotoxicity as a cell-type function belongs to T cells (and NK cells). Another slip is linking mast cells to humoral immunity because they carry IgE, although they only bind antibody made by B cells.

Q.39 MCQ · 2 MARKS

Engineering Mathematics › Linear algebra

A 2×2 matrix P has an eigenvalue λ1 = 2 with eigenvector x1 = (1, 0)^T and another eigenvalue λ2 = 5, with eigenvector x2 = (1, 1)^T. The matrix P is

(A) [[2, 0], [0, 5]]

(B) [[2, 3], [0, 5]]

(C) [[1, 1], [0, 1]]

(D) [[1, 1], [1, 0]]

Official answer: **B**

SOLUTION

1. A matrix with eigenpairs $(\lambda_1, \mathbf{x}_1)$ and $(\lambda_2, \mathbf{x}_2)$ satisfies $P\mathbf{x}_i = \lambda_i \mathbf{x}_i$. With the eigenvectors as the columns of V and the eigenvalues on the diagonal of D, this gives $P = VDV^{-1}$.
2. Take $V = \begin{bmatrix} 1 & 1 \\ 0 & 1 \end{bmatrix}$ and $D = \begin{bmatrix} 2 & 0 \\ 0 & 5 \end{bmatrix}$.
3. Since $\det V = 1$, the inverse is $V^{-1} = \begin{bmatrix} 1 & -1 \\ 0 & 1 \end{bmatrix}$.
4. Multiply the first two: $VD = \begin{bmatrix} 1 & 1 \\ 0 & 1 \end{bmatrix} \begin{bmatrix} 2 & 0 \\ 0 & 5 \end{bmatrix} = \begin{bmatrix} 2 & 5 \\ 0 & 5 \end{bmatrix}$.
5. Then $P = VDV^{-1} = \begin{bmatrix} 2 & 5 \\ 0 & 5 \end{bmatrix} \begin{bmatrix} 1 & -1 \\ 0 & 1 \end{bmatrix} = \begin{bmatrix} 2 & 3 \\ 0 & 5 \end{bmatrix}$, which is option (B).

6. Check: $P\begin{pmatrix}1\\0\end{pmatrix}=\begin{pmatrix}2\\0\end{pmatrix}=2\begin{pmatrix}1\\0\end{pmatrix}$ and $P\begin{pmatrix}1\\1\end{pmatrix}=\begin{pmatrix}2+3\\5\end{pmatrix}=\begin{pmatrix}5\\5\end{pmatrix}=5\begin{pmatrix}1\\1\end{pmatrix}$, so both eigenpairs hold.
7. The other options fail. The eigenvalues 2 and 5 require trace 7 and determinant 10. Option (C) has trace 2 and option (D) has trace 1, so neither has the required eigenvalues. Option (A) has the right eigenvalues, but $\begin{bmatrix}2&0\\0&5\end{bmatrix}\begin{pmatrix}1\\1\end{pmatrix}=\begin{pmatrix}2\\5\end{pmatrix}$ is not a multiple of $(1,1)^T$, so $(1,1)^T$ is not its eigenvector.

KEY IDEA

A diagonalizable matrix is rebuilt from its eigenpairs as $P=VDV^{-1}$. Alternatively, test each option on both eigenvectors, because $P\mathbf{x}=\lambda\mathbf{x}$ must hold for each pair.

WATCH OUT FOR

Choosing the diagonal matrix $\mathrm{diag}(2,5)$ because it shows the eigenvalues. That matrix has $(1,0)^T$ and $(0,1)^T$ as its eigenvectors, so it does not fit $(1,1)^T$. Matching the eigenvalues alone is not enough, because the eigenvectors must also fit.

Q.40 MCQ · 2 MARKS

Fundamentals of Biological Engineering › Downstream

Match the stationary phase (Column I) with its corresponding chromatography technique (Column II).

COLUMN I	COLUMN II
P. Protein A	1. Size exclusion chromatography
Q. Sephadex	2. Ion-exchange chromatography
R. Phenylsepharose	3. Affinity chromatography
S. Diethylaminoethyl cellulose	4. Hydrophobic interaction chromatography

(A) P-1, Q-4, R-2, S-3
(B) P-3, Q-1, R-4, S-2
(C) P-3, Q-4, R-2, S-1
(D) P-4, Q-1, R-3, S-2

Official answer: **B**

SOLUTION

1. **P. Protein A** is a cell-wall protein of *Staphylococcus aureus* that binds specifically to the Fc region of immunoglobulin G (IgG). When the stationary phase carries a ligand that binds its target through a specific biological interaction, the technique is **affinity chromatography**, so P → 3. Protein A columns are the standard capture step for monoclonal antibodies.
2. **Q. Sephadex** is a bead of cross-linked dextran with a controlled pore size, made so that it does not bind proteins. Molecules too large to enter the pores leave the column first. Smaller molecules pass through the pores, travel a longer path and come out later. Separating molecules by size in this way is **size exclusion (gel filtration) chromatography**, so Q → 1.
3. **R. Phenylsepharose** is agarose (Sepharose) carrying phenyl groups, which are hydrophobic. Proteins are loaded in high salt, which strips water from their surface so that their hydrophobic patches bind the phenyl groups. They are then eluted with a falling salt gradient. This is **hydrophobic interaction chromatography**, so R → 4.
4. **S. Diethylaminoethyl (DEAE) cellulose** is cellulose carrying the tertiary amine group $-\mathrm{O}-\mathrm{CH_2CH_2N(C_2H_5)_2}$. At working pH this group is protonated, so it is positively charged and binds negatively charged proteins. DEAE cellulose is a weak **anion exchanger**, which places it under **ion-exchange chromatography**, so S → 2.

5. The matching is P-3, Q-1, R-4, S-2, which is option **(B)**. Quick check: only (B) and (C) have P-3, and (C) puts Sephadex under hydrophobic interaction and DEAE cellulose under size exclusion, both of which are wrong.

KEY IDEA

A stationary phase is named after what it carries. A specific biological ligand (Protein A binding the Fc region of IgG) means affinity. A porous cross-linked gel with no binding groups (Sephadex) means size exclusion. Hydrophobic groups on agarose (phenyl on Sepharose) mean hydrophobic interaction. Charged groups (the protonated DEAE amine, an anion exchanger) mean ion exchange.

WATCH OUT FOR

Seeing "Sepharose" in Phenylsepharose and matching it to size exclusion, because plain Sepharose (agarose) is also used as a gel-filtration medium. The phenyl groups are what count here: they make it a hydrophobic interaction resin. Another slip is calling DEAE a cation exchanger. Its amine is positively charged, so it binds anions.

Q.41 MCQ · 2 MARKS

Fundamentals of Biological Engineering › Process control

Which of the following statements are CORRECT for a controller?

P. In a proportional controller, a control action is proportional to the error

Q. In an integral controller, a control action is proportional to the derivative of the error

R. There is no "offset" in the response of the closed-loop first-order process with a proportional controller

S. There is no "offset" in the response of the closed-loop first-order process with a proportional-integral controller

(A) P and Q only

(B) P and R only

(C) P and S only

(D) Q and S only

Official answer: **C**

SOLUTION

1. **P: true.** Proportional control: $c(t) = c_s + K_c\,\varepsilon(t)$, where $c(t)$ is the controller output, c_s its bias (the output when the error is zero), $\varepsilon = y_{sp} - y$ the error between set point y_{sp} and measured output y, and K_c the controller gain. The action is proportional to the error.
2. **Q: false.** Integral control: $c(t) = c_s + \dfrac{K_c}{\tau_I}\displaystyle\int_0^t \varepsilon\,dt$, with τ_I the integral (reset) time. The action is proportional to the *integral* of the error. Derivative action is the one proportional to $d\varepsilon/dt$.
3. Now test R and S. Take a first-order process $G_p = \dfrac{K_p}{\tau_p s + 1}$ (process gain K_p, time constant τ_p) in a unity-feedback loop with controller G_c, and apply a unit step in set point: $Y_{sp}(s) = 1/s$. The closed-loop response is $\dfrac{Y}{Y_{sp}} = \dfrac{G_c G_p}{1 + G_c G_p}$. Take $K_c K_p > 0$ (the controller acts in the correct direction), so the loop is stable and the final value theorem applies.
4. **R: false.** With a P controller, $G_c = K_c$, so $\dfrac{Y}{Y_{sp}} = \dfrac{K_c K_p}{\tau_p s + 1 + K_c K_p}$.
5. Final value theorem: $y(\infty) = \lim_{s\to 0} s \cdot \dfrac{1}{s} \cdot \dfrac{K_c K_p}{\tau_p s + 1 + K_c K_p} = \dfrac{K_c K_p}{1 + K_c K_p} < 1$. So the offset is $1 - y(\infty) = \dfrac{1}{1 + K_c K_p} \neq 0$ for any finite K_c. A P controller always leaves an offset.
6. **S: true.** With a PI controller, $G_c = K_c\left(1 + \dfrac{1}{\tau_I s}\right) = \dfrac{K_c(\tau_I s + 1)}{\tau_I s}$. The loop now contains a pure integrator ($1/s$), and

$$\frac{Y}{Y_{sp}} = \frac{K_c K_p(\tau_I s + 1)}{\tau_I s(\tau_p s + 1) + K_c K_p(\tau_I s + 1)}.$$

The characteristic equation $\tau_I \tau_p s^2 + \tau_I(1 + K_c K_p)s + K_c K_p = 0$ has all coefficients positive, so this second-order loop is stable.

7. Final value theorem: $y(\infty) = \lim_{s \to 0} s \cdot \frac{1}{s} \cdot \frac{K_c K_p(\tau_I s + 1)}{\tau_I s(\tau_p s + 1) + K_c K_p(\tau_I s + 1)} = \frac{K_c K_p}{K_c K_p} = 1$. The offset is zero, because the integral term keeps changing the output for as long as any error remains.
8. Only P and S are correct, which is option (C).

KEY IDEA

Offset is set by the loop's gain at $s = 0$. With P control, $G_c G_p(0) = K_c K_p$ is finite, so $y(\infty) = K_c K_p/(1 + K_c K_p) < 1$. Integral action puts a $1/s$ in the loop, so $G_c G_p \to \infty$ as $s \to 0$, $y(\infty) = 1$, and the offset disappears.

WATCH OUT FOR

Mixing up integral and derivative action. Q describes derivative control ($\propto d\varepsilon/dt$), not integral control. The other common slip is thinking a large enough K_c removes the P-controller offset. It only shrinks it, as $1/(1 + K_c K_p)$, and never reaches zero at any finite gain.

Q.42 MCQ · 2 MARKS

General Biology › Biomolecules

Which of the following are CORRECT about protein structure?
P. Secondary structure is formed by a repeating pattern of interactions among the polypeptide backbone atoms
Q. Tertiary structure is the three-dimensional arrangement of the polypeptide backbone atoms only
R. Quaternary structure refers to an assembly of multiple polypeptide subunits

(A) P and Q only
(B) P and R only
(C) Q and R only
(D) P, Q and R

Official answer: **B**

SOLUTION

1. Statement P: secondary structure (α-helices and β-sheets) is a regular, repeating pattern of hydrogen bonds between the backbone N-H and C=O groups. So P is correct.
2. Statement Q: tertiary structure is the full three-dimensional fold of one polypeptide chain. It includes the side chains (R groups), which are held by hydrophobic packing, disulfide bonds, ionic bonds, hydrogen bonds and van der Waals forces. Calling it the arrangement of the backbone atoms only is wrong, so Q is incorrect.
3. Statement R: quaternary structure is the assembly of two or more polypeptide subunits into one protein, for example haemoglobin ($\alpha_2\beta_2$). So R is correct.
4. P and R are correct and Q is not. This rules out (A), (C) and (D), so the answer is (B).

KEY IDEA

Secondary structure comes from backbone hydrogen bonding. Tertiary structure is the whole fold of one chain, side chains included. Quaternary structure is the assembly of several chains.

WATCH OUT FOR

Reading tertiary structure as a backbone-only arrangement and accepting Q because of the phrase "three-dimensional arrangement". The words "backbone atoms only" make it false, since side-chain interactions define the tertiary fold.

Q.43 MCQ · 2 MARKS

Genetics, Cell and Molecular Biology › Cell signalling

The enzymes involved in ubiquitinylation of cell-cycle proteins are

(A) E_1 and E_2 only

(B) E_1 and E_3 only

(C) E_1 and E_4 only

(D) E_1, E_2 and E_3

Official answer: **D**

SOLUTION

1. Cell-cycle proteins destined for proteasomal degradation (e.g., cyclin B, securin, p27/CDK inhibitors) are tagged with polyubiquitin chains via a universal three-enzyme cascade: E1, E2 and E3.
2. E1 (ubiquitin-activating enzyme) uses ATP to activate the C-terminal glycine of ubiquitin, forming a high-energy E1~ubiquitin thioester intermediate.
3. E2 (ubiquitin-conjugating enzyme) accepts the activated ubiquitin from E1 by transthioesterification, forming an E2~ubiquitin intermediate, an obligatory carrier step that cannot be skipped.
4. E3 (ubiquitin ligase, e.g., the APC/C or SCF complex acting on cell-cycle substrates) recognizes the specific substrate and mediates transfer of ubiquitin from E2 onto the substrate, building a polyubiquitin chain that the 26S proteasome recognizes.
5. Option (A) E1 and E2 only is wrong: without E3 there is no substrate recognition, so ubiquitin is never delivered to the target protein.
6. Option (B) E1 and E3 only is wrong: E2 is an obligatory intermediate between E1 and E3; the cascade cannot skip it.
7. Option (C) E1 and E4 only is wrong: E4 is only a chain-elongation factor for a subset of substrates, not a universal component, and it does not substitute for E2 or E3.
8. Option (D) E1, E2 and E3 is correct: these three enzymes acting in sequence form the minimal, universal cascade needed to ubiquitinate any cell-cycle protein for degradation.

KEY IDEA

Ubiquitin-mediated proteolysis of cell-cycle regulators (cyclins, securin, CDK inhibitors) by the proteasome always proceeds through the same enzymatic cascade: E1 (activation) → E2 (conjugation) → E3 (ligation, substrate specificity), so all three are required.

WATCH OUT FOR

Students often stop at "E1 activates, E3 ligates" and forget that E2 is an obligatory carrier intermediate between them (option B), or mistake E4 (a chain-elongation factor present only in some substrates) for a core, universal component (option C).

Q.44 MCQ · 2 MARKS

Recombinant DNA Technology and Tools › Bioinformatics

The maximum parsimony method is used to construct a phylogenetic tree for a set of sequences. Which one of the following statements about the method is CORRECT?

(A) It predicts the tree that minimizes the steps required to generate the observed variations

(B) It predicts the tree that maximizes the steps required to generate the observed variations

(C) It predicts the tree with the least number of branch points

(D) It employs probability calculations to identify the tree

Official answer: **A**

SOLUTION

1. The maximum parsimony method evaluates all candidate tree topologies for a set of aligned sequences and, for each, counts the minimum number of character-state changes (substitutions) needed along its branches to explain the observed sequence variation.
2. It then selects the tree(s) requiring the smallest total number of such changes, i.e., the tree that minimizes the steps required to generate the observed variations. This is exactly option (A), so (A) is CORRECT.
3. Option (B) states the opposite (maximizes the steps), which contradicts the parsimony principle of favoring the most economical explanation, so (B) is WRONG.
4. Option (C) refers to the number of branch points (nodes/topology), not the number of character-state changes; parsimony scores are step counts, not node counts, and a tree with fewer branch points is not what the method selects for, so (C) is WRONG.
5. Option (D) describes maximum likelihood or Bayesian phylogenetic methods, which use explicit probability/substitution models; maximum parsimony is a discrete, combinatorial counting method with no probability calculation, so (D) is WRONG.
6. Hence only (A) correctly describes maximum parsimony.

KEY IDEA

Maximum parsimony selects, among all possible tree topologies, the one(s) requiring the fewest total character-state changes (evolutionary steps) to explain the observed sequence data; it minimizes tree length, not node count, and uses no probability model.

WATCH OUT FOR

Confusing the parsimony criterion (minimum number of character-state changes/steps) with the number of branch points or nodes in the tree (option C), or mistaking parsimony for a probability-based method like maximum likelihood (option D).

Q.45 MCQ · 2 MARKS

Recombinant DNA Technology and Tools › Microscopy & spectroscopy

Which of the following spectroscopic technique(s) can be used to identify all the functional groups of an antibiotic contaminant in food?

P. Infrared

Q. Circular dichroism

R. Nuclear magnetic resonance

S. UV-Visible

(A) P only

(B) P and R only

(C) P, Q and R only

(D) P, Q, R and S

Official answer: **B**

SOLUTION

1. Work out what each technique measures. To find **every** functional group in an unknown small molecule such as an antibiotic residue, the technique must give a signal for each group, whether or not that group absorbs light or makes the molecule chiral.
2. **P. Infrared: yes.** IR absorption comes from bond vibrations (stretching and bending). Every common functional group has its own absorption band: C=O near 1650–$1780\ \mathrm{cm}^{-1}$ (amide, ester, ketone, and a strained β-lactam carbonyl at the high end), O–H and N–H stretches near 3200–$3550\ \mathrm{cm}^{-1}$, C≡N near

$2250\ \mathrm{cm^{-1}}$, and aromatic C=C near 1450–$1600\ \mathrm{cm^{-1}}$. That makes IR the standard technique for identifying functional groups.

3. **R. Nuclear magnetic resonance: yes.** In $^{1}\mathrm{H}$ and $^{13}\mathrm{C}$ NMR, the chemical shift of a nucleus depends on its electronic environment, so each functional group gives characteristic signals. Examples: aldehyde H near 9–$10\ \mathrm{ppm}$, carboxylic-acid H near 10–$13\ \mathrm{ppm}$, aromatic H near 6.5–$8.5\ \mathrm{ppm}$, and carbonyl carbons near 160–$220\ \mathrm{ppm}$ in $^{13}\mathrm{C}$ NMR. $^{13}\mathrm{C}$ NMR also detects carbons that carry no hydrogen, including quaternary and carbonyl carbons. Coupling patterns and 2D experiments then show how the groups are connected. So NMR identifies functional groups and also places them in the molecule. Together, IR and NMR are the standard pair for identifying the structure of an organic contaminant.
4. **Q. Circular dichroism: no.** CD measures the difference in absorption of left- and right-circularly polarised light ($\Delta A = A_L - A_R$). It gives a signal only for chiral chromophores and is used to study chirality and the secondary structure of proteins and nucleic acids. It does not report which functional groups are present, and a group with no chiral chromophore nearby gives no CD signal.
5. **S. UV-Visible: no.** UV-Vis measures electronic transitions, so it responds only to chromophores (conjugated π systems, aromatic rings, some carbonyls). Many functional groups, such as isolated alcohols, ethers, amines and alkyl halides, absorb little or nothing in the usable range. The spectrum is also a few broad bands, which cannot resolve a molecule's groups one by one.
6. The techniques that can identify all the functional groups are therefore P (IR) and R (NMR). The answer is **(B) P and R only**.

KEY IDEA

A technique can identify every functional group only if every group gives it a signal. IR does this through bond vibrations, and NMR does it through the chemical shifts of $^{1}\mathrm{H}$ and $^{13}\mathrm{C}$ nuclei. CD needs a chiral chromophore and UV-Vis needs a chromophore, so both miss most groups.

WATCH OUT FOR

Choosing (A) because IR is thought of as the only functional-group technique. NMR chemical shifts are just as diagnostic of functional groups ($^{13}\mathrm{C}$ NMR detects even carbonyl and quaternary carbons), and IR with NMR is the standard pair for structure elucidation. Choosing (D) is the opposite mistake: CD and UV-Vis give signals only from chiral chromophores and chromophores respectively.

Q.46 MCQ · 2 MARKS

Genetics, Cell and Molecular Biology › Mutation & repair

Adenine can undergo a spontaneous change to hypoxanthine in a cell, leading to a DNA base pair mismatch. The CORRECT combination of enzymes that are involved in repairing this damage is

(A) Nuclease, DNA polymerase, DNA ligase

(B) Nuclease, DNA ligase, helicase

(C) Primase, DNA polymerase, DNA ligase

(D) Primase, helicase, DNA polymerase

Official answer: **A**

SOLUTION

1. Adenine can spontaneously deaminate to hypoxanthine, a base not normally found in DNA; hypoxanthine base-pairs like guanine (i.e., with cytosine), so if left unrepaired it directs insertion of C at the next replication, converting the original A:T pair to G:C, a transition mutation. This creates the mismatch the question refers to.
2. Because this is damage confined to a single base within an otherwise normal duplex, it is repaired by base excision repair (BER), the pathway dedicated to removing individual damaged or abnormal bases, not by nucleotide excision repair, mismatch repair, or any replication-associated unwinding/priming step.

3. BER step 1: a DNA glycosylase specific for hypoxanthine/deaminated purines recognizes the lesion and hydrolyzes the N-glycosidic bond, excising the base and leaving an abasic (AP) site. (Note: this step cleaves a base–sugar bond, not a phosphodiester bond, so strictly it is not the 'nuclease' step.)
4. BER step 2: an AP endonuclease nicks the DNA backbone at the abasic site, and an associated exonuclease/lyase activity removes the abasic sugar-phosphate; this endonucleolytic cutting is the 'nuclease' activity option A refers to.
5. BER step 3: DNA polymerase (repair polymerase activity, e.g., Pol I-type/Pol β) fills the resulting single-nucleotide gap using the intact complementary strand as template.
6. BER step 4: DNA ligase seals the remaining nick, restoring an intact phosphodiester backbone.
7. Helicase (unwinds duplex DNA ahead of a replication fork) and primase (synthesizes RNA primers for new-strand synthesis) are replication enzymes, not required to excise and replace a single damaged base, so options B and D, which include helicase or primase, are wrong.
8. Option C substitutes primase for the nuclease/endonuclease step, but BER requires excision of the damaged base region (a nuclease-type cut) before gap-filling, not primer synthesis, so C is wrong.
9. Option A correctly lists the BER enzyme set: nuclease (AP endonuclease, for excision), DNA polymerase (gap filling), and DNA ligase (sealing).

KEY IDEA

Spontaneous deamination of adenine to hypoxanthine (which base-pairs like guanine, i.e. with cytosine) creates a base-pair mismatch that is corrected by base excision repair (BER): a DNA glycosylase excises the aberrant base, an AP endonuclease (a nuclease) nicks the backbone at the resulting abasic site, DNA polymerase fills the single-nucleotide gap, and DNA ligase seals the nick.

WATCH OUT FOR

Confusing this single-base lesion repair with replication machinery: pulling in helicase (unwinds the duplex ahead of a replication fork) or primase (lays down RNA primers for new strand synthesis) as in options B/D, neither of which is needed to excise and replace one damaged base.

Q.47 MSQ · 2 MARKS

Engineering Mathematics › Numerical methods

Consider the ordinary differential equation $\frac{dy}{dx} = f(x, y) = 2x^2 - y^2$. If $y(1) = 1$, the value(s) of $y(1.5)$, using the Euler's implicit method $[y_{n+1} = y_n + hf(x_{n+1}, y_{n+1})]$ with a step size of $h = 0.5$, is (are)

(A) $-1 - 5\sqrt{0.3}$
(B) $-1 + 5\sqrt{0.3}$
(C) $1 + 5\sqrt{0.3}$
(D) $1 - 5\sqrt{0.3}$

Official answer: **A, B**

SOLUTION

1. Start at $x_0 = 1$, $y_0 = 1$. With $h = 0.5$, one step reaches $x_1 = 1.5$, so $y(1.5) \approx y_1$.
2. Apply the implicit Euler formula with $f(x, y) = 2x^2 - y^2$ evaluated at the new point: $y_1 = y_0 + h\, f(x_1, y_1) = 1 + 0.5\left(2(1.5)^2 - y_1^2\right)$.
3. Since $2(1.5)^2 = 4.5$, this gives $y_1 = 1 + 2.25 - 0.5\, y_1^2 = 3.25 - 0.5\, y_1^2$.
4. Rearrange into a quadratic in y_1: $0.5\, y_1^2 + y_1 - 3.25 = 0$, i.e. $y_1^2 + 2y_1 - 6.5 = 0$.
5. Solve with the quadratic formula: $y_1 = \frac{-2 \pm \sqrt{4 + 26}}{2} = \frac{-2 \pm \sqrt{30}}{2} = -1 \pm \sqrt{7.5}$.
6. Since $7.5 = 25 \times 0.3$, we have $\sqrt{7.5} = 5\sqrt{0.3}$, so $y_1 = -1 \pm 5\sqrt{0.3}$.

7. The implicit equation is quadratic in y_1 and nothing in the question rules out either root, so both $-1+5\sqrt{0.3}$ and $-1-5\sqrt{0.3}$ are valid values of $y(1.5)$. These are options (B) and (A). Options (C) and (D) have $+1$ or -1 outside the root pair in the wrong form and do not satisfy $y^2+2y-6.5=0$.

KEY IDEA
In implicit Euler the unknown y_{n+1} appears on both sides, so each step means solving an equation. Here it is a quadratic, which gives two roots, and the question asks for the value(s), so both count.

WATCH OUT FOR
Using explicit Euler, $y_1 = y_0 + hf(x_0, y_0)$, which gives a single value, $1+0.5(2-1)=1.5$. Another slip is to keep only the positive root and miss that this is an MSQ with two valid roots.

Q.48 MSQ · 2 MARKS

Fundamentals of Biological Engineering › Immobilisation

Which of the following statements are CORRECT for an enzyme entrapped in a spherical particle?

(A) Effectiveness factor is ratio of the reaction rate with diffusion-limitation to the reaction rate without diffusion-limitation

(B) Internal diffusion is rate-limiting at low values of Thiele modulus

(C) Effectiveness factor increases with decrease in Thiele modulus

(D) Internal diffusion-limitation can be reduced by decreasing the size of the particle

Official answer: **A, C, D**

SOLUTION

1. Definition of the internal effectiveness factor: $\eta = \dfrac{\text{observed rate (with internal diffusion limitation)}}{\text{rate if the whole particle saw the surface concentration } S_s \text{ (no diffusion limitation)}}$, so $0 < \eta \leq 1$. Statement (A) is exactly this definition, so (A) is correct.
2. Thiele modulus for a sphere of radius R (first-order limit of Michaelis-Menten kinetics, rate constant $k_1 = V_{max}/K_m$, where V_{max} is the maximum reaction rate per unit particle volume, K_m the Michaelis constant and D_e the effective diffusivity of substrate inside the particle):
$$\phi = \frac{R}{3}\sqrt{\frac{V_{max}}{K_m D_e}}$$
It compares the intrinsic reaction rate with the rate of internal diffusion; a large ϕ means reaction is fast compared with diffusion.
3. For a sphere with first-order kinetics:
$$\eta = \frac{1}{\phi}\left(\frac{1}{\tanh 3\phi} - \frac{1}{3\phi}\right)$$
Limits: $\phi \to 0 \Rightarrow \eta \to 1$ (reaction controls, substrate reaches the whole particle); $\phi \gg 1 \Rightarrow \eta \approx 1/\phi$ (diffusion controls, only an outer shell of the particle works).
4. So internal diffusion is rate-limiting at HIGH values of ϕ, not low ones. Statement (B) is incorrect.
5. η falls steadily as ϕ rises, so a decrease in ϕ raises η toward 1. Statement (C) is correct.
6. Since $\phi \propto R$, a smaller particle gives a smaller ϕ and hence a larger η: the internal diffusion limitation is reduced (the substrate has a shorter path to the enzyme at the centre). The same direction holds for general Michaelis-Menten kinetics, whose modulus is also proportional to R. Statement (D) is correct.
7. Correct options: A, C, D.

KEY IDEA

The Thiele modulus $\phi = \frac{R}{3}\sqrt{V_{max}/(K_m D_e)}$ measures reaction speed against internal diffusion speed. The effectiveness factor η (rate with diffusion limitation divided by rate without it) equals 1 when ϕ is small and falls roughly as $1/\phi$ when ϕ is large. Since $\phi \propto R$, making the particle smaller raises η.

WATCH OUT FOR

Getting the direction of the Thiele modulus backwards and marking B: a LOW ϕ means diffusion is fast compared with reaction ($\eta \approx 1$, reaction controls). A second slip is reading the effectiveness factor the other way up (rate without limitation over rate with it), which would give a value above 1.

Q.49 MSQ · 2 MARKS

General Biology › Metabolism

Which of the following is(are) COMMON feature(s) for both aerobic and anaerobic bacterial cultures?

(A) Glycolysis

(B) NAD^+ is the oxidising agent

(C) Oxidative phosphorylation

(D) Two net ATP molecules formed per glucose molecule

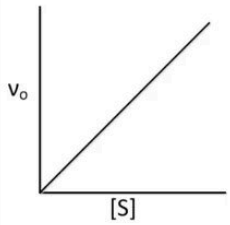
Official answer: **A, B**

Q.50 MSQ · 2 MARKS

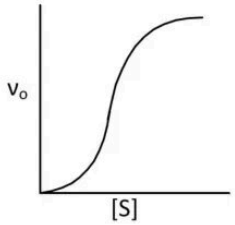
Q.50 Which of the following plot(s) is(are) CORRECT for an enzyme that obeys Michaelis-Menten kinetics, assuming $[S] \ll K_m$?

$[S]$ is the concentration of the substrate, K_m is the Michaelis constant, and v_0 is the initial reaction velocity.

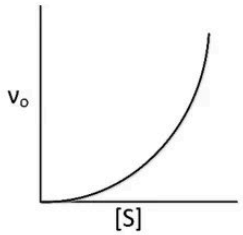
(A)



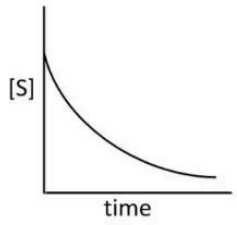
(B)



(C)



(D)



Official answer: **A, D**

SOLUTION

1. Michaelis-Menten equation:

$$v_0 = \frac{V_{max}[S]}{K_m + [S]}$$

where V_{max} is the maximum velocity (reached when the enzyme is saturated) and K_m is the Michaelis constant, the substrate concentration at which $v_0 = V_{max}/2$.

2. Limit $[S] \ll K_m$: the denominator is $K_m + [S] \approx K_m$, so
$$v_0 \approx \frac{V_{max}}{K_m}[S]$$
The rate is first order in substrate, with first-order rate constant $k = V_{max}/K_m$ (units of time^{-1}).
3. (A) $v_0 = k[S]$ is a straight line through the origin with slope V_{max}/K_m. A is CORRECT.
4. (B) A sigmoidal v_0 against $[S]$ curve is the signature of cooperative (allosteric, Hill-type) enzymes. A Michaelis-Menten enzyme gives a rectangular hyperbola, which has no inflection point, and it only approaches its plateau V_{max} when $[S] \gg K_m$, which is outside the stated condition. B is wrong.
5. (C) A concave-up curve would mean the rate rises faster than in proportion to $[S]$ (order above 1). In this limit the order is exactly 1. Over the full range the hyperbola is concave down everywhere:
$$\frac{d^2v_0}{d[S]^2} = -\frac{2V_{max}K_m}{(K_m + [S])^3} < 0$$
C is wrong.
6. (D) Substrate depletion over time. The same rate law gives the instantaneous rate at every moment, and because $[S]$ only falls, the condition $[S] \ll K_m$ keeps holding throughout. So
$$-\frac{d[S]}{dt} = \frac{V_{max}}{K_m}[S]$$
Separating variables and integrating from $[S]_0$ at $t = 0$:
$$[S] = [S]_0\, e^{-(V_{max}/K_m)t}$$
This is an exponential decay: it starts at $[S]_0$, falls steeply and then flattens toward zero, which is the shape shown. D is CORRECT.
7. Correct options: A and D.

KEY IDEA

At low substrate ($[S] \ll K_m$) the Michaelis-Menten equation reduces to first-order kinetics, $v_0 \approx (V_{max}/K_m)[S]$. A first-order rate law gives two shapes: rate linear in $[S]$ through the origin, and substrate decaying exponentially in time, $[S] = [S]_0 e^{-(V_{max}/K_m)t}$.

WATCH OUT FOR

Picking B because Michaelis-Menten kinetics 'saturates'. The hyperbolic plateau only appears at $[S] \gg K_m$, and a sigmoid (with an inflection point) belongs to cooperative enzymes, not Michaelis-Menten ones. Another trap is rejecting D because v_0 is defined as an initial velocity. The rate law holds at every instant, and $[S]$ only decreases, so the low-substrate condition stays true and first-order decay follows.

Q.51 MSQ · 2 MARKS

Genetics, Cell and Molecular Biology › Gene expression

Which of the following statement(s) is(are) CORRECT regarding the lac operon in E. coli when grown in the presence of glucose and lactose?

(A) At low glucose level, the operon is activated

(B) At high glucose level, the operon is activated to enable the utilization of lactose

(C) The lac repressor binds to operator region inactivating the operon

(D) Binding of lactose to the lac repressor induces the operon

Official answer: **A, C**

SOLUTION

1. The lac operon is under two independent controls. **Negative control:** the lac repressor (lacI product) binds the operator and blocks transcription unless an inducer is present. **Positive control:** the cAMP-CAP complex binds the CAP site upstream of the promoter and is needed for strong transcription.

Glucose acts on both: it lowers cAMP, and it causes inducer exclusion, where the glucose transport system inhibits lactose permease (LacY) so that little lactose enters the cell.

2. **(A) At low glucose level, the operon is activated. CORRECT.** When glucose is low, cAMP rises and binds CAP, and the cAMP-CAP complex binds the CAP site and recruits RNA polymerase. Lactose is also present here, so the repressor has been removed from the operator. With both controls favourable, the operon is actively transcribed. This is the second phase of diauxic growth.
3. **(B) At high glucose level, the operon is activated to enable the utilization of lactose. INCORRECT.** High glucose lowers cAMP, so there is no cAMP-CAP activation, and inducer exclusion keeps lactose out of the cell. This is catabolite repression. The cell uses glucose first and does not switch the operon on for lactose until glucose runs out.
4. **(C) The lac repressor binds to operator region inactivating the operon. CORRECT.** This is the negative-control mechanism, and it is a true statement about the operon. It also holds for the conditions in the question. While glucose is high, inducer exclusion keeps lactose out, so almost no allolactose forms and the repressor stays bound to the operator. The operon remains off even though lactose is in the medium.
5. **(D) Binding of lactose to the lac repressor induces the operon. INCORRECT.** Lactose itself is not the inducer and does not bind the repressor. A small amount of lactose is converted by beta-galactosidase (by transglycosylation) into its isomer allolactose (β-1,6 linked instead of lactose's β-1,4). Allolactose binds the repressor, changes its shape and releases it from the operator. The statement names the wrong molecule, so it is false as written.
6. So the correct statements are (A) and (C).

KEY IDEA

The lac operon has two controls: the repressor on the operator (negative control) and cAMP-CAP (positive control). Glucose lowers cAMP and blocks lactose uptake (inducer exclusion). The molecule that actually binds the repressor is allolactose, an isomer that beta-galactosidase makes from lactose.

WATCH OUT FOR

Many students mark (D) because textbooks loosely say "lactose induces the operon". But the repressor binds allolactose, not lactose. Others reject (C) because lactose is present. While glucose is high, inducer exclusion keeps lactose out of the cell, so the repressor stays on the operator.

Q.52 MSQ · 2 MARKS

Genetics, Cell and Molecular Biology › Population & evolution

Emerging viruses such as SARS-CoV2 cause epidemics. Which of the following process(es) contribute to the rise of such viruses?

(A) Mutation of existing virus

(B) Jumping of existing virus from current to new hosts

(C) Spread of virus in the new host population

(D) Replication of virus outside a host

Official answer: **A, B, C**

SOLUTION

1. Option A (mutation of existing virus): Point mutations and recombination/reassortment continually generate new viral variants with altered host range, antigenicity, or transmissibility; this is a well-documented mechanism underlying the emergence of epidemic viruses. Correct.
2. Option B (jumping of existing virus from current to new hosts): Cross-species (zoonotic) spillover is the classic first step by which a virus circulating in an animal reservoir enters a new host population, as seen with SARS-CoV-2, HIV, and influenza. Correct.

3. Option C (spread of virus in the new host population): A spillover event only becomes an epidemic if the virus subsequently achieves sustained transmission within the new host population; without this step it remains an isolated dead-end infection rather than an epidemic. Correct.
4. Option D (replication of virus outside a host): Viruses are obligate intracellular parasites with no independent metabolic or ribosomal machinery, so they cannot replicate outside a living host cell; extracellular viral replication is not a real biological process. Incorrect.
5. The processes that contribute to the rise of emerging epidemic viruses are mutation (A), host-jumping/spillover (B), and spread within the new host population (C): final answer A, B, C.

KEY IDEA

Viral emergence (the appearance/rise of "new" epidemic viruses like SARS-CoV-2) is a multi-step process: genetic change generates variant viruses, spillover moves them into a new host species, and sustained transmission within that new host population turns a spillover event into an epidemic. All three are recognized drivers; a virus replicating outside a living host cell is not a real biological process, since viruses are obligate intracellular parasites.

WATCH OUT FOR

Treating "jumping to a new host" (B) as sufficient by itself and forgetting that sustained spread within the new host population (C) is a separate, necessary step for an epidemic to result: a single spillover infection that doesn't transmit further is a dead end, not an epidemic. A second common error is assuming any exotic-sounding process (D) must be a distractor testing obscure virology rather than recognizing it contradicts the basic obligate intracellular nature of viruses.

Q.53 MSQ · 2 MARKS

Recombinant DNA Technology and Tools › Enzymes & vectors

Introduction of foreign genes into plant cells can be carried out using

(A) Agrobacterium

(B) CaCl2 mediated plasmid uptake

(C) Electroporation

(D) Gene gun

Official answer: **A, C, D**

SOLUTION

1. Agrobacterium tumefaciens naturally carries a Ti (tumor-inducing) plasmid whose T-DNA segment is transferred into and integrates with the plant cell genome; this natural gene-transfer mechanism is the most widely used vector-based method for plant transformation. Hence (A) is a valid method.
2. CaCl2-mediated plasmid uptake is the classical procedure for making bacterial cells (such as E. coli) chemically competent, relying on a brief heat shock to transiently destabilize the bacterial membrane so exogenous plasmid DNA can enter. It is a bacteria-specific technique and is not used to introduce genes into plant cells, which have a rigid cellulosic wall. Hence (B) is not a method used for plant cells.
3. Electroporation applies a short, high-voltage electric pulse to transiently create pores in the cell membrane, allowing DNA to enter. It is a standard direct-gene-transfer technique for plant protoplasts (cells with the wall removed or weakened). Hence (C) is a valid method.
4. The gene gun (biolistic or particle bombardment) method coats microscopic gold or tungsten particles with DNA and physically propels them through the plant cell wall and membrane, delivering DNA directly into cells or organelles such as chloroplasts. Hence (D) is a valid method.
5. Since the question is an MSQ asking which techniques can introduce foreign genes into plant cells, the valid methods are Agrobacterium-mediated transfer, electroporation, and the gene gun: options (A), (C), and (D). Option (B) is excluded as a bacteria-specific transformation method.

KEY IDEA

Foreign gene delivery into plant cells uses methods suited to a rigid cell wall (Agrobacterium's natural T-DNA transfer, electroporation of wall-reduced protoplasts, or physical bombardment via gene gun), never the CaCl2/heat-shock method, which is specific to making bacterial cells chemically competent.

WATCH OUT FOR

Students sometimes select CaCl2-mediated uptake by pattern-matching it to "plasmid" and "DNA transfer" language, forgetting that this technique specifically relies on transiently destabilizing a bacterial cell membrane during heat shock and has no established role in transforming plant cells, which have a cellulosic wall and different membrane biology.

Q.54 MSQ · 2 MARKS

Genetics, Cell and Molecular Biology › Cell biology

Which of the following statement(s) regarding trafficking in eukaryotic cells is(are) CORRECT?

(A) Dynamin binds GTP and is involved in vesicle budding

(B) Dynamin is involved in cytoskeletal remodelling

(C) Dynein binds ATP and is involved in movement of organelles along microtubules

(D) Dynein binds GTP and is involved in movement of organelles along microtubules

Official answer: **A, C**

SOLUTION

1. MSQ, 2 marks: the question asks which statement(s) about trafficking in eukaryotic cells are CORRECT.
2. Option A: Dynamin is a large GTPase that hydrolyzes GTP to drive the mechanical scission (pinching-off) of clathrin-coated vesicles from the plasma membrane during endocytosis, its textbook-defining function in vesicle budding. A is CORRECT.
3. Option B: Dynamin's defining trafficking role is vesicle scission, not cytoskeletal remodelling; actin/microtubule reorganisation is handled by other GTPases (e.g., Rho family) and motor proteins (myosin/kinesin/dynein), not dynamin. B is INCORRECT.
4. Option C: Dynein is an ATPase motor protein that hydrolyzes ATP to walk along microtubules, moving cargo/organelles (typically toward the microtubule minus end, i.e. retrograde transport). C is CORRECT.
5. Option D: Dynein binds and hydrolyzes ATP, not GTP. Pairing dynein with GTP-binding misassigns its nucleotide. D is INCORRECT.
6. Conclusion: A and C correctly pair each protein (dynamin, dynein) with its correct nucleotide (GTP, ATP) and correct trafficking/motor function; B and D misassign the roles. Final answer: A, C ().

KEY IDEA

Dynamin is a large GTPase that pinches off vesicles (endocytosis/budding); dynein is an ATPase motor that moves cargo/organelles along microtubules (typically toward the minus end). Kinesin, by contrast, generally moves cargo toward the microtubule plus end, and neither motor's nucleotide is interchangeable with the other's.

WATCH OUT FOR

Confusing the nucleotide used by motor/mechanoenzyme proteins: assuming all motor and trafficking proteins use ATP (missing that dynamin is a GTPase) or, conversely, assigning GTP to dynein (option D) by analogy with other GTP-binding trafficking regulators (e.g., Rab or Arf GTPases). Also mistakenly crediting dynamin with a general cytoskeletal remodelling role (option B) rather than its specific, well-defined function in vesicle scission.

Q.55 NAT · 2 MARKS

Engineering Mathematics › Probability & statistics

Consider a random variable X with mean $\mu_X = 0.1$ and variance $\sigma_X^2 = 0.2$. A new random variable $Y =$

$2X + 1$ is defined. The variance of the random variable Y (rounded off to one decimal place) is _____.

Official answer: **0.8**

SOLUTION

1. For a linear transformation $Y = aX + b$, the variance is $\mathrm{Var}(Y) = a^2\,\mathrm{Var}(X)$.
2. The constant $b = 1$ only shifts the distribution, so it does not change the spread.
3. Here $a = 2$ and $\sigma_X^2 = 0.2$, so $\mathrm{Var}(Y) = 2^2 \times 0.2$.
4. $\mathrm{Var}(Y) = 4 \times 0.2 = 0.8$.
5. The mean $\mu_X = 0.1$ is not needed for the variance.

KEY IDEA

For $Y = aX + b$, $\mathrm{Var}(Y) = a^2\,\mathrm{Var}(X)$. The shift b drops out and the scale a enters squared.

WATCH OUT FOR

Multiplying the variance by a instead of a^2 (giving 0.4), or adding the shift b to the variance (giving 1.4 or 1.8).

Q.56 NAT · 2 MARKS

Engineering Mathematics › Calculus

For $x_1 > 0$ and $x_2 > 0$, the value of $\lim\limits_{x_1 \to x_2} \dfrac{x_1 - x_2}{x_2 \ln\left(\dfrac{x_1}{x_2}\right)}$ is _____.

Official answer: **1**

SOLUTION

1. Divide numerator and denominator by x_2 (valid because $x_2 > 0$):
$$\frac{x_1 - x_2}{x_2 \ln\left(\dfrac{x_1}{x_2}\right)} = \frac{\dfrac{x_1}{x_2} - 1}{\ln\left(\dfrac{x_1}{x_2}\right)}.$$
2. Put $t = \dfrac{x_1}{x_2}$. Since $x_1 > 0$ and $x_2 > 0$, $t > 0$, so $\ln t$ is defined. As $x_1 \to x_2$, $t \to 1$, so the limit becomes
$$\lim_{t \to 1} \frac{t - 1}{\ln t}.$$
3. At $t = 1$ the numerator $t - 1$ and the denominator $\ln t$ are both 0, so the form is $\dfrac{0}{0}$ and L'Hôpital's rule applies.
4. Differentiate numerator and denominator separately:
$$\lim_{t \to 1} \frac{1}{1/t} = \lim_{t \to 1} t = 1.$$
5. Check with the standard limit: put $h = t - 1$, so $h \to 0$ and $\ln(1 + h) \approx h$ for small h. Then $\dfrac{h}{\ln(1 + h)} \to 1$, which agrees. The limit is 1.

KEY IDEA

Dividing by x_2 makes the expression depend only on the ratio $t = x_1/x_2$, which tends to 1. The limit then reduces to the standard form $\lim_{t \to 1} \dfrac{t - 1}{\ln t} = 1$ (the reciprocal of the derivative of $\ln t$ at $t = 1$).

WATCH OUT FOR

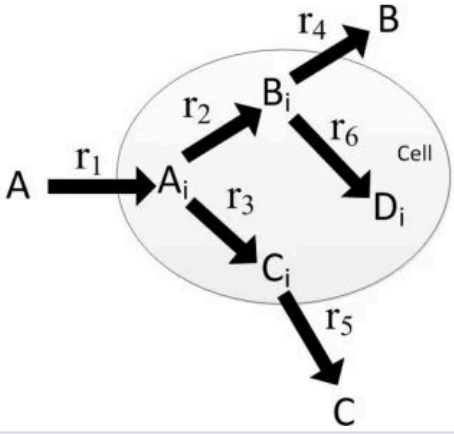
Forgetting that x_2 is a constant in this limit, or substituting $x_1 = x_2$ directly and writing $0/0$ as the answer. Another slip is applying L'Hôpital's rule to x_1 while differentiating $x_2 \ln(x_1/x_2)$ incorrectly, for example dropping the factor x_2 or the $1/x_1$ from the chain rule.

Q.57 NAT · 2 MARKS

Q.57 Figure below depicts simplified metabolic and transport reactions taking place in the production of B from A in a cell. The subscript 'i' refers to intracellular metabolites. r_j is the j^{th} reaction flux in $\frac{\text{g}}{(\text{g dry mass})\,\text{h}}$. Under pseudo-steady-state condition, the following reaction fluxes are available.

$r_1 = 4$, $r_3 = 1$ and $r_6 = 1$.

The transport flux of B, r_4, is _____ $\frac{\text{g}}{(\text{g dry mass})\,\text{h}}$.



Official answer: **2**

SOLUTION

1. Pseudo-steady state for an intracellular metabolite means it does not accumulate, so at every internal node $\sum(\text{fluxes in}) = \sum(\text{fluxes out})$. All fluxes r_j are in the same unit, $\text{g}\,(\text{g dry mass})^{-1}\,\text{h}^{-1}$, and each arrow converts one metabolite into the next, so the fluxes at a node add directly.
2. Balance on A_i (in: r_1; out: r_2 and r_3):
$$r_1 = r_2 + r_3 \;\Rightarrow\; r_2 = 4 - 1 = 3$$
3. Balance on B_i (in: r_2; out: the transport flux r_4 across the membrane and the conversion r_6 to D_i):
$$r_2 = r_4 + r_6 \;\Rightarrow\; r_4 = 3 - 1 = 2$$
4. Check on C_i: $r_5 = r_3 = 1$. Of the $r_1 = 4$ units of A taken up, $r_4 = 2$ leave the cell as B, $r_5 = 1$ leaves as C, and $r_6 = 1$ is drawn off to D_i. No reaction out of D_i is drawn, so no balance is written on it: r_6 is simply a drain on B_i. The totals agree, $4 = 2 + 1 + 1$, so the network closes.
5. Therefore the transport flux of B is $r_4 = 2\ \frac{\text{g}}{(\text{g dry mass})\,\text{h}}$.

KEY IDEA

In metabolic flux analysis at pseudo-steady state, no intracellular metabolite accumulates, so at each branch point the fluxes in equal the fluxes out. Work node by node, from the uptake flux towards the product: A_i gives $r_2 = r_1 - r_3$, then B_i gives $r_4 = r_2 - r_6$.

WATCH OUT FOR

Forgetting the second branch at B_i and taking $r_4 = r_2 = 3$. Part of B_i is diverted to D_i by r_6, so it never leaves the cell as B. Another mistake is to treat D_i as a balanced node. No reaction out of it is shown, so it only acts as a drain.

Q.58 NAT · 2 MARKS

Fundamentals of Biological Engineering › Bioreactor operation

The amount of biomass in a reactor at the end of the batch process is 50 g. Fed-batch operation is initiated by feeding the substrate solution at a constant rate of $1\ \mathrm{L\ h^{-1}}$. The concentration of substrate in the feed is $50\ \mathrm{g\ L^{-1}}$. The maximum biomass yield (Y_{XS}^{M}) is $0.4\ \dfrac{\text{g biomass}}{\text{g substrate}}$. Assuming the system is at quasi-steady state, the maximum amount of biomass after 5 h of feeding is _____ g.

Official answer: **150**

SOLUTION

1. Symbols: $X_0 = 50\ \mathrm{g}$ is the total biomass in the reactor when feeding starts, $F = 1\ \mathrm{L\ h^{-1}}$ is the volumetric feed rate, $S_0 = 50\ \mathrm{g\ L^{-1}}$ is the substrate concentration in the feed, $Y_{XS}^{M} = 0.4\ \mathrm{g\ biomass\ (g\ substrate)^{-1}}$ is the maximum biomass yield on substrate, and X_t is the total biomass (in grams, not a concentration) at time t.
2. Quasi-steady state in fed-batch: the cells consume substrate as fast as it is fed, so the substrate concentration in the reactor stays close to zero ($S \approx 0$). Every gram of substrate fed is therefore converted into biomass at the yield Y_{XS}^{M}.
3. The total biomass then grows at a constant rate: $\dfrac{dX_t}{dt} = Y_{XS}^{M} F S_0$. Integrating from $X_t = X_0$ at $t = 0$ gives $X_t = X_0 + Y_{XS}^{M} F S_0\, t$, so total biomass rises linearly with time. The growing culture volume does not enter, because the question asks for the total amount of biomass, not its concentration.
4. Substrate fed in 5 h: $F S_0 t = 1\ \mathrm{L\ h^{-1}} \times 50\ \mathrm{g\ L^{-1}} \times 5\ \mathrm{h} = 250\ \mathrm{g}$.
5. Biomass formed from this substrate: $Y_{XS}^{M} F S_0 t = 0.4 \times 250 = 100\ \mathrm{g}$.
6. $$X_t = X_0 + Y_{XS}^{M} F S_0\, t = 50 + 100 = 150\ \mathrm{g}$$
   This is the maximum possible amount because the maximum yield was used, which assumes no substrate is diverted to maintenance or product formation.

KEY IDEA

At quasi-steady state in fed-batch operation, the residual substrate stays near zero, so all substrate fed becomes biomass at the yield. Total biomass then rises linearly: $X_t = X_0 + Y_{XS}^{M} F S_0\, t$.

WATCH OUT FOR

Answering 100 g by leaving out the 50 g already in the reactor when feeding starts. Another mistake is working with biomass concentration and dividing by a volume the question never gives, when it asks for the total amount of biomass.

Q.59 NAT · 2 MARKS

Fundamentals of Biological Engineering › Ideal reactors

An enzyme catalyzes the conversion of substrate A into product B. The rate equation for this reaction is

$$-r_A = \frac{C_A}{5 + C_A}\ \mathrm{mol\ L^{-1}\ min^{-1}}$$

Substrate A at an initial concentration of $10\ \mathrm{mol\ L^{-1}}$ enters an ideal mixed flow reactor (MFR) at a flow rate of $10\ \mathrm{L\ min^{-1}}$. The volume of the MFR required for 50% conversion of substrate to product is _____ L.

Official answer: **100**

SOLUTION

1. Symbols: $C_{A0} = 10\ \mathrm{mol\ L^{-1}}$ is the feed concentration of A, $v_0 = 10\ \mathrm{L\ min^{-1}}$ the volumetric flow rate, $X_A = 0.5$ the fractional conversion, C_A the concentration of A in the tank (and at its exit), and $-r_A$ the rate of disappearance of A. The rate law is of Michaelis-Menten form $-r_A = \dfrac{V_{max} C_A}{K_m + C_A}$ with maximum rate $V_{max} = 1\ \mathrm{mol\ L^{-1}\ min^{-1}}$ and Michaelis constant $K_m = 5\ \mathrm{mol\ L^{-1}}$.

2. Exit concentration (no density change in a liquid enzyme reaction): $C_A = C_{A0}(1 - X_A) = 10(1 - 0.5) = 5\ \text{mol L}^{-1}$.
3. An ideal MFR is perfectly mixed, so the concentration everywhere in the tank equals the exit concentration, and the whole tank reacts at the exit rate: $-r_A = \dfrac{5}{5+5} = 0.5\ \text{mol L}^{-1}\,\text{min}^{-1}$.
4. MFR design equation (steady-state mole balance on A, in = out + consumed): $v_0 C_{A0} = v_0 C_A + (-r_A)V$, so $V = \dfrac{v_0\,(C_{A0} - C_A)}{-r_A} = \dfrac{F_{A0} X_A}{(-r_A)_{\text{exit}}}$, where $F_{A0} = v_0 C_{A0} = 100\ \text{mol min}^{-1}$ is the molar feed rate of A.
5. $$V = \frac{10 \times (10 - 5)}{0.5} = \frac{50}{0.5} = 100\ \text{L}$$
6. Check: space time $\tau = V/v_0 = 100/10 = 10\ \text{min}$, and $\tau(-r_A) = 10 \times 0.5 = 5\ \text{mol L}^{-1} = C_{A0} - C_A$, so the mole balance closes. The required volume is 100 L.

KEY IDEA

In an ideal mixed flow reactor the contents are uniform and identical to the outlet stream, so the whole volume reacts at the rate evaluated at the EXIT concentration: $V = v_0(C_{A0} - C_A)/(-r_A)_{\text{exit}}$. No integration is needed, even for a Michaelis-Menten rate law.

WATCH OUT FOR

Evaluating the rate at the feed concentration ($-r_A = 10/15 = 0.667$, giving 75 L) instead of at the exit concentration, or using the integrated plug-flow/batch expression $\tau = [K_m \ln(C_{A0}/C_A) + (C_{A0} - C_A)]/V_{max} = 5 \ln 2 + 5 \approx 8.47\ \text{min}$ (about 84.7 L), which applies to a PFR, not an MFR.

Q.60 NAT · 2 MARKS

Fundamentals of Biological Engineering › Bioreactor operation

Liquid-phase mass transfer coefficient (k_L) is measured in a stirred tank vessel using *steady-state method* by sparging air. Oxygen uptake by the microorganism is measured. The bulk concentration of O_2 is $10^{-4}\ \text{mol L}^{-1}$. Solubility of O_2 in water at $25\ ^\circ\text{C}$ is $10^{-3}\ \text{mol L}^{-1}$.

If the oxygen consumption rate is $9 \times 10^{-4}\ \text{mol L}^{-1}\ \text{s}^{-1}$, and interfacial area is $100\ \text{m}^2/\text{m}^3$, the value of k_L is _____ cm s^{-1}.

Official answer: **1**

SOLUTION

1. **Steady-state balance.** In the steady-state method the dissolved-oxygen level in the broth stops changing. Oxygen then enters the liquid exactly as fast as the cells use it, so the oxygen transfer rate (OTR) equals the oxygen uptake rate (OUR):
$$k_L a\,(C^* - C_L) = \text{OUR}$$
Here k_L is the liquid-film mass transfer coefficient, a is the gas-liquid interfacial area per unit liquid volume, C^* is the saturation (solubility) concentration of O_2, and C_L is the bulk dissolved O_2 concentration.
2. **Driving force.** $C^* - C_L = 10^{-3} - 10^{-4} = 9 \times 10^{-4}\ \text{mol L}^{-1}$.
3. **Volumetric coefficient.**
$$k_L a = \frac{\text{OUR}}{C^* - C_L} = \frac{9 \times 10^{-4}\ \text{mol L}^{-1}\,\text{s}^{-1}}{9 \times 10^{-4}\ \text{mol L}^{-1}} = 1\ \text{s}^{-1}$$
4. **Interfacial area in cm units.** $a = 100\ \text{m}^2/\text{m}^3 = 100\ \text{m}^{-1}$. Since $1\ \text{m} = 100\ \text{cm}$, $a = \dfrac{100}{100\ \text{cm}} = 1\ \text{cm}^{-1}$.
5. **Separate k_L.**
$$k_L = \frac{k_L a}{a} = \frac{1\ \text{s}^{-1}}{1\ \text{cm}^{-1}} = 1\ \text{cm s}^{-1}$$
This is the same as $0.01\ \text{m s}^{-1}$. The answer is $1\ \text{cm s}^{-1}$.

KEY IDEA

At steady state, oxygen transfer equals oxygen uptake: $k_L a\,(C^* - C_L) = \text{OUR}$. Divide the OUR by the driving force to get $k_L a$. Then divide by the specific interfacial area a to get k_L.

WATCH OUT FOR

There are three common slips. (1) Using C^* alone as the driving force instead of $C^* - C_L$, which gives $k_L a = 0.9\ \text{s}^{-1}$. (2) Leaving a as $100\ \text{m}^{-1}$, which gives $k_L = 0.01\ \text{m s}^{-1}$, then entering 0.01 even though the blank asks for cm s^{-1}. (3) Getting the m-to-cm conversion of a upside down, which gives $100\ \text{cm}^{-1}$.

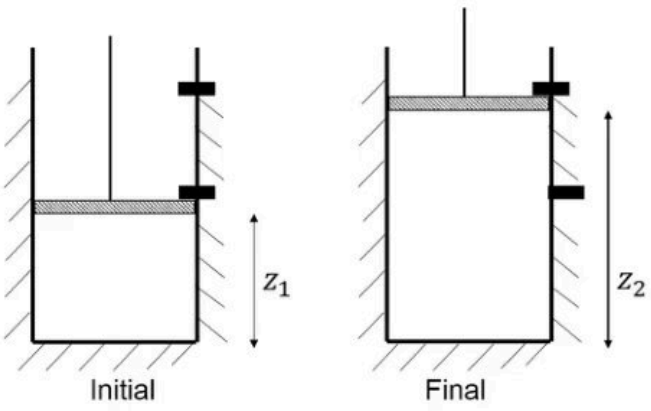
Q.61 NAT · 2 MARKS

Q.61

Consider a piston-cylinder assembly shown in the figure below. The walls of the cylinder are insulated. The cylinder contains 1 mole of an ideal gas at 300 K and the piston is held initially at the position z_1 using a stopper. After the stopper is removed, the piston *suddenly* rises against atmospheric pressure (1.013×10^5 Pa) to the new position z_2 where it is held by another stopper.

The heat capacity (C_v) of the gas is 12.5 J mol^{-1} K^{-1}. The cross-sectional area of the cylinder is 10^{-3} m^2. Assume the piston is weightless and frictionless.

If $z_2 - z_1 = 1$ m, the final temperature of the gas (rounded off to nearest integer) is _____ K.



BT

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Official answer: **291 to 293**

Q.62 NAT · 2 MARKS

Fundamentals of Biological Engineering › Growth kinetics

Consider the growth of *S. cerevisiae* under aerobic condition in a bioreactor and the specific growth rate of yeast is $0.5\ \text{h}^{-1}$. The overall reaction of the process is

$$2C_6H_{12}O_6 + 0.2NH_3 + 10.35O_2 \rightarrow CH_{1.8}O_{0.5}N_{0.2} + 0.2C_2H_6O + 10.6CO_2 + 10.8H_2O$$

The heat of combustion values for different compounds are tabulated below with the reference to CO_2, H_2O, O_2, and N_2 at standard conditions.

COMPOUND	HEAT OF COMBUSTION (KJ MOL^{-1})
$C_6H_{12}O_6$	2802
NH_3	383
$CH_{1.8}O_{0.5}N_{0.2}$	560
C_2H_6O	1366

The specific rate of heat production (rounded off to nearest integer) is _____ $\mathrm{kJ\ mol^{-1}\ h^{-1}}$.

Official answer: **2420 to 2430**

SOLUTION

1. Symbols used: μ is the specific growth rate of the yeast, $0.5\,\mathrm{h^{-1}}$. $Y_{Q/X}$ is the heat released per mol of biomass ($CH_{1.8}O_{0.5}N_{0.2}$) formed, in $\mathrm{kJ\ mol^{-1}}$. q_Q is the specific rate of heat production, meaning heat released per mol of biomass present per hour, in $\mathrm{kJ\ mol^{-1}\,h^{-1}}$.
2. Hess's law with heats of combustion. The heats are given relative to CO_2, H_2O, O_2 and N_2, so each of these four has a heat of combustion of zero. The heat released by the reaction is therefore
$$Q = \sum_{\text{reactants}} n_i(\Delta H_c)_i - \sum_{\text{products}} n_j(\Delta H_c)_j$$
3. Reactants:
$$2(2802) + 0.2(383) + 10.35(0) = 5604 + 76.6 = 5680.6\,\mathrm{kJ}$$
4. Products:
$$1(560) + 0.2(1366) + 10.6(0) + 10.8(0) = 560 + 273.2 = 833.2\,\mathrm{kJ}$$
5. Heat released: $Q = 5680.6 - 833.2 = 4847.4\,\mathrm{kJ}$, so the reaction is exothermic with $\Delta H_r = -4847.4\,\mathrm{kJ}$. The equation as written forms exactly 1 mol of biomass, so $Y_{Q/X} = 4847.4\,\mathrm{kJ}$ per mol of $CH_{1.8}O_{0.5}N_{0.2}$ formed.
6. The specific growth rate $\mu = \dfrac{1}{X}\dfrac{dX}{dt} = 0.5\,\mathrm{h^{-1}}$ means that each mol of biomass present forms 0.5 mol of new biomass per hour.
7. Specific rate of heat production:
$$q_Q = \frac{1}{X}\frac{dQ}{dt} = Y_{Q/X}\,\mu = 4847.4 \times 0.5 = 2423.7\,\mathrm{kJ\ mol^{-1}\,h^{-1}}$$
8. Rounded to the nearest integer: $q_Q \approx 2424\,\mathrm{kJ\ mol^{-1}\,h^{-1}}$.

KEY IDEA

When heats of combustion share one reference state (CO_2, H_2O, O_2, N_2 all zero), the heat a reaction releases is (sum over reactants of $n\,\Delta H_c$) minus (sum over products of $n\,\Delta H_c$). The equation forms 1 mol of biomass, so this difference is the heat yield $Y_{Q/X}$ per mol of biomass. Multiplying it by the specific growth rate μ gives the heat released per mol of biomass per hour: $q_Q = \mu\, Y_{Q/X}$.

WATCH OUT FOR

Three slips give answers outside the key. (1) Leaving out the ammonia term, which gives $0.5(5604 - 833.2) \approx 2385$. (2) Leaving out the ethanol by-product, which gives $0.5(5680.6 - 560) \approx 2560$. (3) Using glucose's heat of combustion once instead of twice. Two other errors are stopping at the heat yield (4847) without multiplying by μ, and getting the sign backwards by subtracting reactants from products. In that last case the magnitude is right but the reaction looks heat-absorbing, when it actually releases heat.

Q.63 NAT · 2 MARKS

Fundamentals of Biological Engineering › Upstream

A pilot sterilization was carried out in a vessel containing 100 m^3 medium with an initial spore concentration of 10^8 spores/ml. The accepted level of contamination after sterilization is 1 spore in the entire vessel. The specific death rate constant for the spore is 2 min^{-1} at 121 °C. Assuming no death takes place during the heating and cooling cycles, the holding time at 121 °C (rounded off to nearest integer) is _____ min.

Official answer: **17 to 19**

SOLUTION

1. Convert the vessel volume to millilitres: $V = 100\ \text{m}^3 = 100 \times 10^6\ \text{mL} = 10^8\ \text{mL}$ (since $1\ \text{m}^3 = 10^6\ \text{mL}$).
2. Initial number of spores in the whole vessel: $N_0 = (10^8\ \text{spores mL}^{-1})(10^8\ \text{mL}) = 10^{16}$ spores.
3. Final number allowed in the whole vessel: $N = 1$ spore.
4. Thermal death of spores is first order: $\frac{dN}{dt} = -k_d N$, which integrates at constant temperature to $\ln \frac{N_0}{N} = k_d t$. Here $k_d = 2\ \text{min}^{-1}$ is the specific death rate constant at $121\ ^\circ\text{C}$ and t is the time spent at that temperature.
5. Del factor needed: $\nabla = \ln \frac{N_0}{N} = \ln 10^{16} = 16 \times 2.3026 = 36.84$.
6. Since no death is credited to heating or cooling, the whole Del factor must come from holding:
$$t_{hold} = \frac{\ln(N_0/N)}{k_d} = \frac{36.84}{2\ \text{min}^{-1}} = 18.42\ \text{min}$$
7. Rounded to the nearest integer: $t_{hold} \approx 18\ \text{min}$.

KEY IDEA

Spore death is first order, so the Del factor you need is $\nabla = \ln(N_0/N)$, where N_0 and N are the spore counts in the WHOLE vessel. If heating and cooling kill nothing, all of it has to come from holding, so $t_{hold} = \nabla / k_d$.

WATCH OUT FOR

Using concentrations instead of total counts: taking $\ln(10^8/1)$ gives 9.2 min. The limit of 1 spore applies to the whole $100\ \text{m}^3$ vessel, so the volume must go into N_0 (10^8 mL, not 10^5 L mixed with a per-mL concentration). Another slip is using $\log_{10}$ instead of $\ln$, which gives $16/2 = 8$ min.

Q.64 NAT · 2 MARKS

Recombinant DNA Technology and Tools › Enzymes & vectors

A circular plasmid has three different but unique restriction sites for enzymes 'a', 'b' and 'c.' When enzymes 'a' and 'b' are used together, two fragments of equal size are generated. Enzyme 'c' creates fragments of equal size only from one of the fragments generated by those cleaved by 'a' and 'b'. The plasmid is treated with a mixture of 'a', 'b' and 'c' and analysed by agarose gel electrophoresis. The number of bands observed in the gel is _____.

Official answer: **2**

SOLUTION

1. Given: the plasmid is circular and has exactly one unique restriction site each for enzymes a, b and c (3 sites total, one copy of each).
2. Key rule: on a CIRCULAR DNA molecule, the number of linear fragments produced equals the number of cut sites used. (This differs from linear DNA, where n internal cuts give n+1 fragments; on a circle there are no free ends to begin with, so each additional cut simply adds one more piece to the ring you have already opened.)
3. Digesting with a + b (2 cuts on the circle) gives 2 fragments; the stem states these are of equal size, so let each fragment have size X (plasmid total size $= 2X$).

4. Since c has only ONE restriction site in total, and the stem says c produces equal-size fragments from only ONE of the two a+b fragments, c's single site must lie inside that one X-sized fragment (not the other).
5. Digesting with a + b + c together: 3 cuts on the circular plasmid $\Rightarrow$ 3 linear fragments in total.
6. The fragment that c does not cut stays intact at its original size, X.
7. The fragment that c does cut is split by c's one internal cut into two pieces; since the stem specifies these are of equal size, each piece is $X/2$.
8. So the three fragments produced are X, $X/2$, $X/2$: three fragments but only two distinct sizes.
9. On agarose gel electrophoresis, fragments of identical size co-migrate and appear as a single band, so the two $X/2$ fragments merge into one band.
10. Total distinct bands observed $= 2$ (one band at X, one band at $X/2$).

KEY IDEA
On a circular DNA molecule, the number of linear fragments produced equals the number of cut sites used (not sites + 1, as it is for linear DNA); co-migrating fragments of identical size appear as a single band on the gel.

WATCH OUT FOR
Applying the linear-DNA rule (fragments = sites + 1) to a circular plasmid, which would wrongly give 4 fragments instead of 3; or forgetting that two fragments of identical size run as one band, over-counting the bands as 3 instead of 2.

Q.65 NAT · 2 MARKS

Fundamentals of Biological Engineering › Growth kinetics

A bacterial strain is grown in nutrient medium at 37 °C under aerobic conditions. The medium is inoculated with 10^2 cells from a seed culture. If the number of cells in the culture is 10^5 after 10 hours of growth, the doubling time of the strain (rounded off to nearest integer) is _____ h.

Official answer: **1**

SOLUTION

1. Assume exponential growth over the whole 10 h, with no lag phase. Each doubling multiplies the cell count by 2, so $N = N_0\,2^n$, where N_0 is the inoculum, N is the final count and n is the number of generations.
2. Take the ratio of final to initial cells: $\dfrac{N}{N_0} = \dfrac{10^5}{10^2} = 10^3$.
3. Number of generations: $n = \log_2\left(10^3\right) = \dfrac{3\ln 10}{\ln 2} = \dfrac{3 \times 2.30259}{0.69315} \approx 9.966.$
4. Doubling time is the elapsed time divided by the number of generations:
$$t_d = \frac{t}{n} = \frac{10\ \text{h}}{9.966} \approx 1.003\ \text{h}$$
5. Check with the specific growth rate μ (in h^{-1}), defined by $\ln(N/N_0) = \mu t$: $\mu = \dfrac{\ln 1000}{10\ \text{h}} = 0.6908\ \text{h}^{-1}$, so $t_d = \dfrac{\ln 2}{\mu} = \dfrac{0.6931}{0.6908\ \text{h}^{-1}} \approx 1.003\ \text{h}.$
6. Rounded to the nearest integer, the doubling time is $1\ \text{h}$.

KEY IDEA

In exponential growth the cell count doubles once per doubling time, so the number of generations is $n = \log_2(N/N_0)$ and $t_d = t/n$. The same result comes from $t_d = \ln 2/\mu$, with $\mu = \ln(N/N_0)/t$. A 1000-fold rise is almost exactly 10 doublings, because $2^{10} = 1024$.

WATCH OUT FOR

Dividing by the wrong quantity. The common slips are using $\log_{10}$ in place of $\log_2$ (which gives 3 "generations" and $t_d \approx 3.3$ h), using the cell increase $10^5 - 10^2$ in place of the ratio, or reporting μ ($0.69\ \mathrm{h}^{-1}$) as the doubling time. The temperature and aerobic conditions are context only and do not enter the calculation.

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