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GATE BT · 2025

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GATE BT 2025 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 Roorkee

Online, with the questions linked to their topic notes: **iaeacademy.in/study/papers/bt-2025**

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About this paper

65 questions, 100 marks. Question types: 33 MCQ · 15 MSQ · 17 NAT.

Official answer key: IIT Roorkee · https://gate2025.iitr.ac.in/doc/2025/2025_Key/BT_Keys.pdf

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

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

Q	TYPE	MARKS	ANSWER
Q.1	MCQ	1	**D**
Q.2	MCQ	1	**D**
Q.3	MCQ	1	**C**
Q.4	MCQ	1	**A**
Q.5	MCQ	1	**B**
Q.6	MCQ	2	**B**
Q.7	MCQ	2	**C**
Q.8	MCQ	2	**A**
Q.9	MCQ	2	**B**
Q.10	MCQ	2	**B**
Q.11	MCQ	1	**B**
Q.12	MCQ	1	**A**
Q.13	MCQ	1	**A**
Q.14	MCQ	1	**D**
Q.15	MCQ	1	**A**
Q.16	MCQ	1	**A**
Q.17	MCQ	1	**A**
Q.18	MCQ	1	**A**
Q.19	MCQ	1	**D**
Q.20	MCQ	1	**D**
Q.21	MSQ	1	**B, D**
Q.22	MSQ	1	**A, D**
Q.23	MSQ	1	**A, C, D**
Q.24	MSQ	1	**B, D**
Q.25	MSQ	1	**A, D**
Q.26	MSQ	1	**A, B, C**
Q.27	MSQ	1	**B, D**
Q.28	NAT	1	**0.20 to 0.25**
Q.29	NAT	1	**15450 to 15750**
Q.30	NAT	1	**0.5**
Q.31	NAT	1	**300 to 310**
Q.32	NAT	1	**0.94 to 0.96**
Q.33	NAT	1	**0.72 to 0.75**
Q.34	NAT	1	**4**
Q.35	NAT	1	**0.16 to 0.18**
Q.36	MCQ	2	**A**
Q.37	MCQ	2	**A**
Q.38	MCQ	2	**A**
Q.39	MCQ	2	**C**
Q.40	MCQ	2	**A**
Q.41	MCQ	2	**A**
Q.42	MCQ	2	**C**
Q.43	MCQ	2	**A**
Q.44	MCQ	2	**C**
Q.45	MCQ	2	**B**
Q.46	MCQ	2	**C**
Q.47	MCQ	2	**B**
Q.48	MCQ	2	**A**
Q.49	MSQ	2	**A, B, D**
Q.50	MSQ	2	**A, C**
Q.51	MSQ	2	**A, D**
Q.52	MSQ	2	**B, C**
Q.53	MSQ	2	**A, C**
Q.54	MSQ	2	**A, B, C**
Q.55	MSQ	2	**A, B, C**
Q.56	MSQ	2	**B, C**
Q.57	NAT	2	**0.76 to 0.82**
Q.58	NAT	2	**3.30 to 3.60**
Q.59	NAT	2	**11**
Q.60	NAT	2	**1**
Q.61	NAT	2	**48000 to 49000**
Q.62	NAT	2	**3.4 to 3.8**
Q.63	NAT	2	**1**
Q.64	NAT	2	**23.2 to 23.8**
Q.65	NAT	2	**-32.00 to -30.00**

General Aptitude Q.1 to Q.10

Q.1 MCQ · 1 MARK

General Aptitude › Grammar & vocabulary

Is there any good show _____ television tonight?

Select the most appropriate option to complete the above sentence.

(A) in
(B) at
(C) within
(D) on

Official answer: **D**

SOLUTION

1. The blank comes between the noun "show" and "television", so we need the preposition that goes with a broadcast medium.
2. Programmes are described as being "on television", "on the radio" or "on air". A show that is broadcast is "on" the medium.
3. "in television" (A) refers to the industry or a career (for example, "a career in television"), not to a particular programme tonight.
4. "at television" (B) is not idiomatic. "At" marks a point or an event, as in "at the cinema" or "at 8 PM".
5. "within television" (C) means inside the field as a whole, which does not suit a specific show tonight.
6. So the sentence reads "Is there any good show on television tonight?" Answer: (D).

KEY IDEA
Broadcast programmes are said to be "on" a medium: on television, on the radio, on air.

WATCH OUT FOR
Choosing "in" because television feels like something you are "in". "In television" describes the industry or a career, not a programme being shown.

Q.2 MCQ · 1 MARK

General Aptitude › Grammar & vocabulary

As the police officer was found guilty of embezzlement, he was _____ dismissed from the service in accordance with the Service Rules.

Select the most appropriate option to complete the above sentence.

(A) sumptuously
(B) brazenly
(C) unintentionally
(D) summarily

Official answer: **D**

SOLUTION

1. The blank needs an adverb describing the manner in which the officer was dismissed after being found guilty of embezzlement, in accordance with the Service Rules.
2. (A) sumptuously means lavishly or luxuriously. It does not fit a dismissal.
3. (B) brazenly means boldly and shamelessly. It describes how an offender behaves, not the manner of an official dismissal.
4. (C) unintentionally means not on purpose. A dismissal by an authority is a deliberate act, so this is illogical.

5. (D) summarily means immediately and without a formal or lengthy procedure. 'Summarily dismissed' is the standard collocation and fits dismissal for proven misconduct.
6. Hence the correct option is (D).

KEY IDEA
Choose the adverb that suits the context and the standard collocation: 'summarily dismissed' means dismissed at once, without a lengthy formal process.

WATCH OUT FOR
Picking 'brazenly' because it sounds negative and so seems to match the crime. It describes how someone acts, not how an authority carries out a dismissal.

Q.3 MCQ · 1 MARK

General Aptitude › Numerical

The sum of the following infinite series is:

$$\frac{1}{1!}+\frac{1}{2!}+\frac{1}{3!}+\frac{1}{4!}+\frac{1}{5!}+\cdots$$

(A) π

(B) $1+e$

(C) $e-1$

(D) e

Official answer: **C**

SOLUTION

1. Recall the Maclaurin series of the exponential: $e^x = 1 + \frac{x}{1!} + \frac{x^2}{2!} + \frac{x^3}{3!} + \cdots$, valid for every real x.
2. Put $x = 1$: $e = 1 + \frac{1}{1!} + \frac{1}{2!} + \frac{1}{3!} + \cdots$.
3. The given series starts at $\frac{1}{1!}$, so it is the same series without the leading term 1 (which is $\frac{1}{0!}$).
4. Subtract 1 from both sides: $\frac{1}{1!} + \frac{1}{2!} + \frac{1}{3!} + \cdots = e - 1$.
5. Quick check: $1 + 0.5 + 0.1667 + 0.0417 + 0.0083 \approx 1.717$, close to $e - 1 \approx 1.718$. So the answer is option (C).

KEY IDEA
Compare the series with the Maclaurin series of e^x at $x = 1$. The given series is that series without its first term $\frac{1}{0!} = 1$.

WATCH OUT FOR
Forgetting that the series for e starts at $\frac{1}{0!} = 1$ and choosing e (option D). The given series starts at $\frac{1}{1!}$, so the leading 1 must be subtracted.

Q.4 MCQ · 1 MARK

General Aptitude › Spatial

A thin wire is used to construct all the edges of a cube of 1 m side by bending, cutting and soldering the wire. If the wire is 12 m long, what is the minimum number of cuts required to construct the wire frame to form the cube?

(A) 3

(B) 4

(C) 6

(D) 12

Official answer: **A**

SOLUTION

1. A cube has 12 edges of 1 m each, so the 12 m wire exactly covers all edges with nothing left over. Every edge must be made from wire, and no wire is wasted.

2. Think of the frame as a graph with 8 vertices (corners) and 12 edges. Exactly 3 edges meet at each corner, so every corner has odd degree.
3. Cutting the wire gives separate pieces. An uncut piece can be bent into a single continuous path that uses each edge at most once. For such a path, a corner it passes through uses 2 edges of that path (one in, one out), which is an even number. Only the two end points of the path use an odd number (1) of edges at their corner.
4. Each corner has 3 edges, an odd total. The contributions of the pieces at that corner add up to 3, so at least one piece must end at every corner. The 8 corners therefore need at least 8 piece ends in total.
5. Each piece has only 2 ends, so the number of pieces is at least $\frac{8}{2} = 4$.
6. Four pieces can be achieved. Label the bottom square ABCD and the top square EFGH, with vertical edges AE, BF, CG, DH. Piece 1 follows A-B-C-D-A-E-F-G-H-E, which uses 9 edges (9 m). Pieces 2, 3 and 4 are the single edges BF, CG and DH (1 m each). The lengths $9 + 1 + 1 + 1 = 12$ m use up all the wire and cover all 12 edges exactly once. The pieces are then soldered at the corners.
7. Cutting one wire into 4 pieces needs $4 - 1 = 3$ cuts. Fewer than 4 pieces is impossible by step 5, so fewer than 3 cuts is impossible.
8. Minimum number of cuts $= 3$, which is option (A).

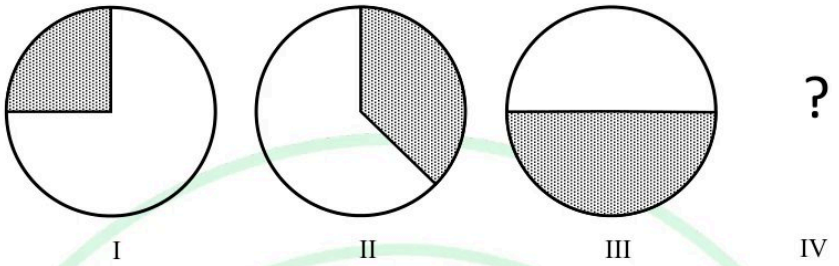
KEY IDEA
Every corner of a cube has 3 edges (odd). Each wire piece can end at only 2 corners, so 8 odd corners need at least 4 pieces, which means 3 cuts.

WATCH OUT FOR
Counting one cut per edge or per corner (answers 6 or 12), or forgetting that pieces are soldered back together, so only the number of pieces minus one matters.

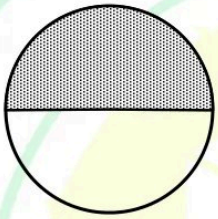
Q.5 MCQ · 1 MARK

General Aptitude › Spatial

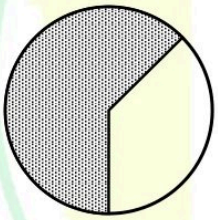
Q.5 The figures I, II and III are parts of a sequence. Which one of the following options comes next in the sequence at IV?



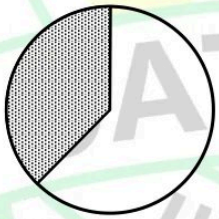
(A)



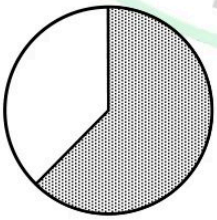
(B)



(C)



(D)



Official answer: **B**

SOLUTION

1. Measure the shaded sector of each figure. Figure I has 90° shaded (upper-left quarter), figure II has 135° (from 12 o'clock clockwise to about 4:30), and figure III has 180° (the lower half). The shaded angle grows by 45° each step, so figure IV must have 225° shaded. This rules out A (180°) and C (135°).
2. Measure both bounding radii clockwise from 12 o'clock. Figure I is shaded from 270° to 360°. Figure II is shaded from 0° to 135°. Figure III is shaded from 90° to 270°.

3. The starting radius turns clockwise by 90° each step: $270^\circ \to 360^\circ (= 0^\circ) \to 90^\circ$. The next start is 180°, a radius pointing straight down (6 o'clock).
4. The ending radius turns clockwise by 135° each step: $360^\circ \to 135^\circ \to 270^\circ$ (that is, $0^\circ \to 135^\circ \to 270^\circ$). The next end is $270^\circ + 135^\circ = 405^\circ$, which is 45°, a radius pointing up-right (about 1:30).
5. Figure IV is therefore shaded clockwise from 180° to 45° (through the left side and the top), which is 225°, consistent with step 1. The white wedge of 135° lies on the right, between 45° and 180°.
6. Option B matches: its radii point straight down and up-right, with the large 225° shaded part on the left. Option D has the right size but is shaded from 0° to 225° (right and bottom), so its position is wrong.

KEY IDEA

Follow the two bounding radii of the shaded sector separately. Each moves clockwise by a fixed amount per step, and the next figure is built from both positions.

WATCH OUT FOR

Matching only the size of the shaded sector. A and C have the wrong size, but D has the right 225° in the wrong position, so the position of the radii must be checked too.

Q.6 MCQ · 2 MARKS

General Aptitude › Reading

"Why do they pull down and do away with crooked streets, I wonder, which are my delight, and hurt no man living? Every day the wealthier nations are pulling down one or another in their capitals and their great towns: they do not know why they do it; neither do I. It ought to be enough, surely, to drive the great broad ways which commerce needs and which are the life-channels of a modern city, without destroying all history and all the humanity in between: the islands of the past." (From Hilaire Belloc's "The Crooked Streets")

Based only on the information provided in the above passage, which one of the following statements is true?

(A) The author of the passage takes delight in wondering.

(B) The wealthier nations are pulling down the crooked streets in their capitals.

(C) In the past, crooked streets were only built on islands.

(D) Great broad ways are needed to protect commerce and history.

Official answer: **B**

SOLUTION

1. The question asks which statement is true based only on the passage, so use only what the text says.
2. (A) The passage says the crooked streets are the author's delight. "I wonder" only reports that the author is puzzled. The passage never says the author delights in wondering. False.
3. (B) The passage says: "Every day the wealthier nations are pulling down one or another in their capitals and their great towns." Here "one or another" refers to crooked streets, which are the topic of the opening sentence. So the wealthier nations are pulling down crooked streets in their capitals. True.
4. (C) "The islands of the past" is a metaphor for the history and humanity between the broad ways. The passage does not say crooked streets were built only on islands. False.
5. (D) The passage says commerce needs the broad ways. It does not say the broad ways protect commerce or history. The author wants them driven without destroying history. False.
6. Only (B) is supported by the passage.

KEY IDEA
In a "which statement is true based only on the passage" question, pick the option that the text states or directly implies. Check each option against the exact words of the passage and ignore outside knowledge.

WATCH OUT FOR
Reading the metaphor "islands of the past" literally and choosing (C). Another slip is choosing (D) by mixing up "commerce needs broad ways" with "broad ways protect commerce and history". A third is choosing (A) by turning "I wonder" into "delights in wondering".

Q.7 MCQ · 2 MARKS

General Aptitude › Numerical

Rohit goes to a restaurant for lunch at about 1 PM. When he enters the restaurant, he notices that the hour and minute hands on the wall clock are exactly coinciding. After about an hour, when he leaves the restaurant, he notices that the clock hands are again exactly coinciding. How much time (in minutes) did Rohit spend at the restaurant?

(A) $64\frac{6}{11}$
(B) $66\frac{5}{13}$
(C) $65\frac{5}{11}$
(D) $66\frac{6}{13}$

Official answer: **C**

SOLUTION

1. The minute hand turns 6° per minute and the hour hand turns 0.5° per minute, so the minute hand gains 5.5° per minute on the hour hand.
2. The hands coincide, and then coincide again, when the minute hand has gained exactly one full turn, 360°, on the hour hand.
3. Time between two successive coincidences:
$$\frac{360}{5.5} = \frac{720}{11} = 65\frac{5}{11} \text{ minutes}$$
4. Check with the clock: after 12:00 the hands next coincide at about 1:05, which is 'about 1 PM'. The next coincidence is at about 2:10, which is 'about an hour' later.
5. Rohit entered at one coincidence and left at the next one, so he spent $65\frac{5}{11}$ minutes at the restaurant. This is option (C).

KEY IDEA
Successive coincidences of the hour and minute hands are $\frac{720}{11} = 65\frac{5}{11}$ minutes apart, because the minute hand must gain 360° at 5.5° per minute.

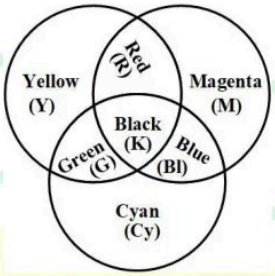
WATCH OUT FOR
Taking the time as exactly 60 minutes because the question says 'about an hour'. The hands do not coincide every hour, only every $65\frac{5}{11}$ minutes. Another slip is dividing 360 by 6 instead of by the relative speed 5.5.

Q.8 MCQ · 2 MARKS

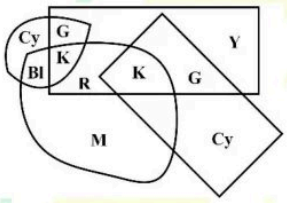
General Aptitude › Spatial

Q.8 A color model is shown in the figure with color codes: Yellow (Y), Magenta (M), Cyan (Cy), Red (R), Blue (Bl), Green (G), and Black (K).

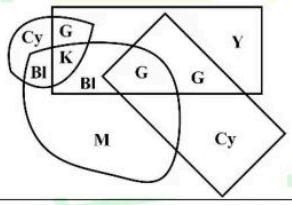
Which one of the following options displays the color codes that are consistent with the color model?



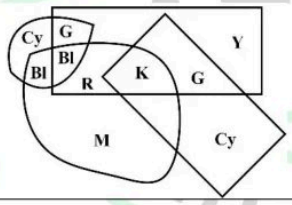
(A)



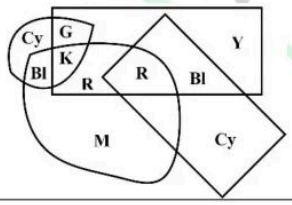
(B)



(C)



(D)



Official answer: **A**

SOLUTION

1. Read the colour model as overlaps of three circles. Y with M only is Red (R). Y with Cy only is Green (G). M with Cy only is Blue (Bl). All three together is Black (K).
2. In each option the rectangle is Y, the rounded blob is M and the rotated square is Cy. The small lens at the upper left is a second Cy region. It overlaps the rectangle and the blob and carries the same rule.

3. The region common to rectangle, blob and square must be K. Option B writes G there and option D writes R, so B and D are wrong.
4. The region common to rectangle and blob only (outside the square) must be R. Option B writes Bl there, which is another reason B is wrong.
5. The region common to rectangle and square only (outside the blob) must be G. Option D writes Bl there, which is another reason D is wrong.
6. In the left lens, the part inside the rectangle but outside the blob is Y with Cy, which is G. The part inside the rectangle and the blob is all three, which is K. Option C writes Bl in place of both G and K, so C is wrong.
7. Option A labels every overlap correctly: R for rectangle with blob, K for the triple overlap, G for rectangle with square, and G, K and Bl correctly in the lens. So A is consistent with the colour model.

KEY IDEA
Treat the colour model as a three-set Venn diagram: pair overlaps give R, G and Bl, and the triple overlap gives K. Then check each overlap region in every option against these labels.

WATCH OUT FOR
Checking only the pairwise overlaps and not the central triple overlap, or mixing up which colour belongs to which pair. For example, Y with Cy is Green, and Blue belongs to M with Cy.

Q.9 MCQ · 2 MARKS

General Aptitude › Geometry

A circle with center at $(x, y) = (0.5,\ 0)$ and radius = 0.5 intersects with another circle with center at $(x, y) = (1, 1)$ and radius = 1 at two points. One of the points of intersection (x, y) is:

(A) $(0, 0)$

(B) $(0.2, 0.4)$

(C) $(0.5, 0.5)$

(D) $(1, 2)$

Official answer: **B**

SOLUTION

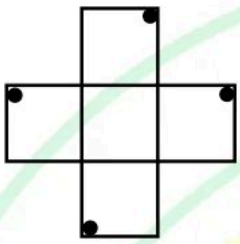
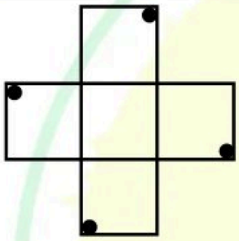
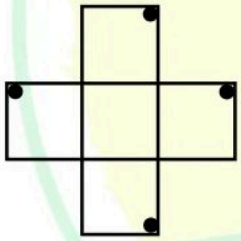
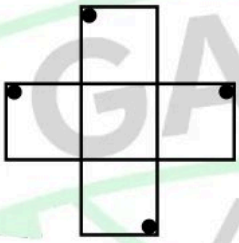
1. The first circle has centre $(0.5, 0)$ and radius 0.5: $(x - 0.5)^2 + y^2 = 0.25$. Expanding gives $x^2 - x + y^2 = 0$.
2. The second circle has centre $(1, 1)$ and radius 1: $(x - 1)^2 + (y - 1)^2 = 1$. Expanding gives $x^2 - 2x + y^2 - 2y + 1 = 0$.
3. A point of intersection satisfies both equations. Subtracting the second from the first cancels $x^2 + y^2$ and leaves the common chord: $x + 2y - 1 = 0$. Both intersection points lie on this line.
4. Test each option on the line. (A) $0 + 0 - 1 = -1 \neq 0$, so it fails. (C) $0.5 + 1 - 1 = 0.5 \neq 0$, so it fails. (D) $1 + 4 - 1 = 4 \neq 0$, so it fails. (B) $0.2 + 0.8 - 1 = 0$, so it passes.
5. Check (B) on circle 1: $x^2 - x + y^2 = 0.04 - 0.2 + 0.16 = 0$, so it lies on circle 1.
6. Check (B) on circle 2: $(0.2 - 1)^2 + (0.4 - 1)^2 = 0.64 + 0.36 = 1$, so it lies on circle 2.
7. So $(0.2, 0.4)$ lies on both circles. Option (A), $(0, 0)$, is on circle 1 but gives $(0 - 1)^2 + (0 - 1)^2 = 2 \neq 1$ on circle 2, so it is not an intersection point. The answer is (B).

KEY IDEA
Subtract the two circle equations to get the common chord, which is a line. Any intersection point lies on that line, so test the options on it. Then confirm the surviving option on both circles.

WATCH OUT FOR
Choosing $(0, 0)$ because it lies on the first circle, without checking the second. A point must satisfy both circle equations, and $(0, 0)$ fails the second ($1 + 1 = 2 \neq 1$).

Q.10 MCQ · 2 MARKS

General Aptitude › Spatial

Q.10	An object is said to have an n-fold rotational symmetry if the object, rotated by an angle of $\frac{2\pi}{n}$, is identical to the original. Which one of the following objects exhibits 4-fold rotational symmetry about an axis perpendicular to the plane of the screen? Note: The figures shown are representative.
(A)	
(B)	
(C)	
(D)	

Official answer: **B**

SOLUTION

1. The plain plus shape (four equal arms) already looks the same after a 90° turn ($\frac{2\pi}{4}$), so only the four dots decide the answer.
2. A 90° clockwise turn carries the top arm to the right arm, the right arm to the bottom arm, the bottom arm to the left arm and the left arm to the top arm.

3. Describe each dot by the side of its arm when you look outward from the centre along that arm: the clockwise (right-hand) side or the anticlockwise (left-hand) side. A rotation preserves this description.
4. So 4-fold symmetry needs all four dots on the same side (all clockwise or all anticlockwise).
5. (A) Top arm: dot on the right (clockwise). Right arm: dot at the top, which is the left-hand side when facing east (anticlockwise). Mixed, so not symmetric.
6. (B) Top arm, facing north: top-right dot is on the right-hand side. Left arm, facing west: top-left dot is on the right-hand side. Bottom arm, facing south: bottom-left dot is on the right-hand side. Right arm, facing east: bottom-right dot is on the right-hand side. All four are on the clockwise side, so each 90° turn maps the figure onto itself.
7. (C) Top and left dots are clockwise, but the right arm's top-right dot is anticlockwise. Not symmetric. (D) The top arm's top-left dot is anticlockwise, but the left arm's top-left dot is clockwise. Not symmetric.
8. Only (B) has the four dots in the same position relative to their arms, so it has 4-fold rotational symmetry.

KEY IDEA

For a figure whose outline is already 4-fold symmetric, check the markers. Each marker must sit in the same position relative to its own arm, for example always on the clockwise side when facing outward.

WATCH OUT FOR

Judging the dots by their absolute position (top-right, bottom-left, and so on) instead of their position relative to their own arm. Using an absolute position wrongly rules out (B) or accepts figures with mixed sides.

Biotechnology Q.11 to Q.65

Q.11 MCQ · 1 MARK

General Biology › Microbiology

Koch's postulate was established by Robert Koch while working on a disease caused by

(A) Mycobacterium tuberculosis

(B) Bacillus anthracis

(C) Streptococcus pneumoniae

(D) Bacillus subtilis

Official answer: **B**

SOLUTION

1. Koch's postulates link one specific microbe to one specific disease. The microbe must be present in every case of the disease, be isolated and grown in pure culture, cause the same disease when put into a healthy host, and be re-isolated from that host.
2. Koch's first demonstration of this chain came in 1876 with anthrax, a disease of cattle and sheep. He found rod-shaped bacteria in the blood of diseased animals, grew them in pure culture, and showed that the culture gave anthrax to healthy mice. The organism is *Bacillus anthracis*. This work is the origin of the postulates, so option (B) is correct.
3. Option (A): *Mycobacterium tuberculosis* was identified by Koch in 1882, six years after the anthrax work. The criteria were applied to tuberculosis and stated formally in the 1880s, but the disease on which the approach was first established was anthrax. So (A) is the tempting wrong option.
4. Option (C): *Streptococcus pneumoniae* was first isolated in 1881 by Pasteur and, independently, by Sternberg. It is not the organism with which Koch established his method.
5. Option (D): *Bacillus subtilis* is a harmless soil bacterium and not a pathogen, so no disease could be tied to it by the postulates.

KEY IDEA

Koch's 1876 work on anthrax was the first proof that one specific bacterium causes one specific disease, and it is the origin of the postulates. Tuberculosis (1882) came afterwards.

WATCH OUT FOR

Choosing Mycobacterium tuberculosis because Koch is best known for discovering the tuberculosis bacillus. That discovery came after the anthrax work.

Q.12 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Microbial genetics

Corynebacterium diphtheriae causes diphtheria in humans, only when this bacterium is infected by

(A) phage β

(B) epsilon phage

(C) T4 phage

(D) lambda phage

Official answer: **A**

SOLUTION

1. The question asks which bacteriophage must lysogenize Corynebacterium diphtheriae for it to become toxigenic (disease-causing), i.e., which phage carries the diphtheria toxin gene (tox).
2. Fact: the gene encoding diphtheria toxin (tox) is not part of the C. diphtheriae chromosome. It is carried on the genome of a temperate (lysogenic) bacteriophage, and toxin is expressed only in strains lysogenized by such a phage, a phenomenon called lysogenic (phage) conversion.

3. The phage responsible is corynephage β (and closely related tox+ corynephages); only C. diphtheriae strains lysogenized by phage β express diphtheria toxin and cause diphtheria.
4. Option (A) phage β: correct. This is the toxin-converting phage of C. diphtheriae.
5. Option (B) epsilon phage: incorrect. Epsilon toxin is associated with Clostridium perfringens, a different organism, not with C. diphtheriae toxin conversion.
6. Option (C) T4 phage: incorrect. T4 is a virulent (lytic) phage of E. coli; it has no lysogenic relationship with Corynebacterium and is unrelated to toxin production.
7. Option (D) lambda phage: incorrect. Lambda is a lysogenic phage of E. coli used as a classic molecular biology model, but it does not carry the diphtheria tox gene.
8. Hence, only lysogenic conversion by phage β makes C. diphtheriae toxigenic, giving answer (A).

KEY IDEA
Diphtheria toxin production by Corynebacterium diphtheriae is not encoded by the bacterial chromosome; it requires lysogenic conversion by the temperate corynephage β (bearing the tox gene), a classic textbook example of phage/lysogenic conversion in bacterial pathogenesis.

WATCH OUT FOR
Confusing this with other toxin-conversion systems (e.g., epsilon toxin of Clostridium perfringens) or with well-known model phages (T4, a lytic E. coli phage; lambda, a lysogenic E. coli phage) that have no role in C. diphtheriae toxigenicity.

Q.13 MCQ · 1 MARK

Engineering Mathematics › Differential equations

Let $y(t)$ be a bacterial population whose growth is given by $\frac{dy}{dt} = \lambda(y+2)$ where λ is the growth rate constant. If $y(0) = 1$ and $y(1) = 4$, then the value of λ is

(A) $\ln 2$
(B) $\ln 3$
(C) $\ln 4$
(D) $\ln 6$

Official answer: **A**

SOLUTION

1. The equation is separable: $\frac{dy}{y+2} = \lambda\, dt$.
2. Integrate both sides: $\ln|y+2| = \lambda t + C$, so $y + 2 = Ae^{\lambda t}$ with $A = \pm e^{C}$.
3. Use $y(0) = 1$: $1 + 2 = A$, so $A = 3$ and $y + 2 = 3e^{\lambda t}$.
4. Use $y(1) = 4$: $4 + 2 = 3e^{\lambda}$, so $e^{\lambda} = 2$.
5. Take the logarithm: $\lambda = \ln 2$, which is option (A).

KEY IDEA
Separate variables in $\frac{dy}{dt} = \lambda(y+2)$ to get $y + 2 = Ae^{\lambda t}$, then fix A and λ from the two given values of y.

WATCH OUT FOR
Using y instead of $y + 2$ in the exponential, i.e. writing $y = y_0 e^{\lambda t}$, which gives $e^{\lambda} = 4$ and $\lambda = \ln 4$ (option C).

Q.14 MCQ · 1 MARK

Engineering Mathematics › Calculus

The minimum value of the function $f(x) = x + \frac{4}{x}$ for $x > 0$ is

(A) 1
(B) 2

(C) 3

(D) 4

Official answer: **D**

SOLUTION

1. Differentiate: $f'(x) = 1 - \frac{4}{x^2}$.
2. Set $f'(x) = 0$: $x^2 = 4$, so $x = 2$ (only the positive root is allowed since $x > 0$).
3. Second derivative: $f''(x) = \frac{8}{x^3}$, so $f''(2) = 1 > 0$. Hence $x = 2$ is a local minimum, and it is the only critical point on $x > 0$.
4. Evaluate: $f(2) = 2 + \frac{4}{2} = 4$.
5. Check with AM-GM for positive numbers: $x + \frac{4}{x} \geq 2\sqrt{x \cdot \frac{4}{x}} = 4$, with equality when $x = \frac{4}{x}$, i.e. $x = 2$. The minimum value is 4, option (D).

KEY IDEA

Find the critical point with $f'(x) = 0$ and confirm it is a minimum with the second derivative. For a sum of the form $x + \frac{a}{x}$ with $x > 0$, AM-GM gives the minimum $2\sqrt{a}$ directly.

WATCH OUT FOR

Reading the critical point $x = 2$ as the minimum value, or answering 2 instead of evaluating $f(2) = 4$. Another slip is to include $x = -2$, which is excluded by $x > 0$ (there $f = -4$ is a local maximum).

Q.15 MCQ · 1 MARK

General Biology › Adaptive immunity

The diversity in T-cell receptors is generated by

(A) gene rearrangements

(B) somatic hypermutation of rearranged V region

(C) gene conversion

(D) class switching

Official answer: **A**

SOLUTION

1. T-cell receptor (TCR) chains are encoded by gene segments: V, D and J for the β and δ chains, and V and J for the α and γ chains. These segments are joined by V(D)J recombination in the developing thymocyte, catalysed by the RAG1/RAG2 recombinase.
2. Option A, gene rearrangements: correct. Random combinatorial choice of V, D and J segments, together with junctional diversity (random loss of nucleotides and addition of P and N nucleotides at the joints), produces a very large TCR repertoire.
3. Option B, somatic hypermutation of rearranged V region: wrong. This is AID-dependent and occurs in activated B cells in germinal centres, where it refines antibody affinity. Rearranged TCR genes are not hypermutated in this way.
4. Option C, gene conversion: wrong. It diversifies immunoglobulin genes in species such as chickens and rabbits. It is not the main source of TCR diversity.
5. Option D, class switching: wrong. It exchanges the heavy-chain constant region of an antibody (for example IgM to IgG, IgA or IgE) in B cells. TCRs have no isotypes to switch.
6. So TCR diversity is generated by gene rearrangements. The answer is (A).

KEY IDEA
TCR diversity comes from V(D)J gene rearrangement, with combinatorial and junctional diversity, by RAG1/RAG2 in the thymus. Somatic hypermutation, gene conversion and class switching are features of B-cell and immunoglobulin biology.

WATCH OUT FOR
Choosing somatic hypermutation because it is the best-known diversity mechanism in immunology. It acts only on rearranged immunoglobulin V regions in B cells, not on TCR genes.

Q.16 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Gene expression

Which one of the following is true for piRNAs?

(A) piRNAs silence transposable elements in germ cells

(B) piRNA is the abbreviation of P-element interacting RNA

(C) piRNAs modify the 2'-OH of ribose with methyl group

(D) piRNA is a long non-coding RNA

Official answer: **A**

SOLUTION

1. piRNAs (Piwi-interacting RNAs) are small non-coding RNAs of about 24-31 nucleotides, found predominantly in animal germline cells.
2. Option (A): piRNAs bind Piwi-clade Argonaute proteins and direct silencing of transposable elements in germ cells, protecting genome integrity during gametogenesis. This is the defining, well-established function of piRNAs. TRUE.
3. Option (B): The 'pi' in piRNA stands for Piwi-interacting, not 'P-element interacting.' P-elements are a specific class of DNA transposon (notably in Drosophila) that piRNAs can help silence, but this is not the origin of the name. FALSE.
4. Option (C): piRNAs themselves carry a 2'-O-methyl modification on the ribose of their 3' terminal nucleotide, added post-biogenesis by the methyltransferase Hen1 (Pimet in Drosophila); that is, piRNAs are the substrate that gets methylated, not the agent performing methylation on something else. The statement reverses this relationship. FALSE.
5. Option (D): piRNAs are small non-coding RNAs (~24-31 nt), a class distinct from long non-coding RNAs (lncRNAs, typically >200 nt). FALSE.
6. By elimination and direct knowledge of piRNA biology, only (A) is true.

KEY IDEA
piRNAs (Piwi-interacting RNAs) are small non-coding RNAs (~24-31 nt) found chiefly in germline cells, where they associate with Piwi-clade Argonaute proteins to silence transposable elements and protect genome integrity during gametogenesis.

WATCH OUT FOR
Confusing the "pi" in piRNA (Piwi-interacting) with "P-element interacting," or confusing which molecule methylates which: piRNAs themselves are 2'-O-methylated at their 3' end by the methyltransferase Hen1, they are not agents that methylate other molecules.

Q.17 MCQ · 1 MARK

General Biology › Enzymes

Which one of the following coenzymes is utilised by alanine racemase for the conversion of L-Alanine to D-Alanine?

(A) Pyridoxal phosphate

(B) Thiamine pyrophosphate

(C) Tetrahydrofolate

(D) Flavin mononucleotide

Official answer: **A**

SOLUTION

1. Alanine racemase interconverts L-alanine and D-alanine. This needs the alpha-hydrogen to be removed and put back on the opposite face, so the reaction happens at the alpha-carbon of an amino acid.
2. Reactions at the alpha-carbon of amino acids (racemisation, transamination, decarboxylation, beta-elimination) use **pyridoxal phosphate (PLP)**, the active form of vitamin B6.
3. Mechanism: the amino group of alanine forms a Schiff base (aldimine) with PLP. PLP acts as an electron sink, so the alpha-hydrogen is removed as a proton to give a resonance-stabilised quinonoid intermediate. Adding the proton back on the opposite face gives D-alanine.
4. (A) Pyridoxal phosphate: correct, for the reasons above.
5. (B) Thiamine pyrophosphate: carries active aldehyde groups (decarboxylation of alpha-keto acids, transketolase). It does not act on the alpha-carbon of amino acids, so it is wrong.
6. (C) Tetrahydrofolate: carries one-carbon units (formyl, methylene, methyl), so it is wrong.
7. (D) Flavin mononucleotide: a redox coenzyme for hydride or electron transfer. Racemisation involves no net oxidation or reduction, so it is wrong.

KEY IDEA

Pyridoxal phosphate (vitamin B6) is the coenzyme for reactions at the alpha-carbon of amino acids. It forms a Schiff base with the substrate and acts as an electron sink, which lets the alpha-proton leave and return on either face. This is how alanine racemase works.

WATCH OUT FOR

Picking a redox coenzyme such as flavin mononucleotide because the question mentions L- and D-forms, or picking thiamine pyrophosphate or tetrahydrofolate. Racemisation involves no net oxidation, and neither of those two acts on amino acid alpha-carbons.

Q.18 MCQ · 1 MARK

General Biology › Biomolecules

Q.18 Correctly match the following **Monosaccharides** with their respective **Epimers.**

Monosaccharide	Epimer
P. D-mannose	1. C-3 epimer of D-glucose
Q. D-allose	2. C-4 epimer of D-glucose
R. D-galactose	3. C-4 epimer of D-mannose
S. D-talose	4. C-2 epimer of D-glucose
	5. C-5 epimer of D-glucose

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

(B) P-5; Q-1; R-2; S-3

(C) P-4; Q-3; R-5; S-1

(D) P-1; Q-5; R-3; S-2

Official answer: **A**

SOLUTION

1. Epimers are sugars that differ in configuration at exactly one carbon. Compare each sugar with its reference sugar, one stereocentre at a time.
2. D-mannose differs from D-glucose only at C-2, so it is the C-2 epimer of D-glucose: P matches 4.
3. D-allose differs from D-glucose only at C-3, so it is the C-3 epimer of D-glucose: Q matches 1.
4. D-galactose differs from D-glucose only at C-4, so it is the C-4 epimer of D-glucose: R matches 2.
5. D-talose differs from D-mannose only at C-4 (it is also the C-2 epimer of D-galactose): S matches 3.
6. Entry 5, the C-5 epimer of D-glucose, would be L-idose, which is not in the list. It is the unused extra entry, so no sugar maps to it.
7. The matching P-4, Q-1, R-2, S-3 is option (A). Option (B) pairs mannose with 5, which is wrong. Options (C) and (D) pair allose, galactose or talose with the wrong carbon.

KEY IDEA

An epimer differs from its parent sugar at exactly one stereocentre. Among the D-aldohexoses, mannose is the C-2 epimer of glucose, allose the C-3 epimer, and galactose the C-4 epimer. Talose is the C-4 epimer of mannose.

WATCH OUT FOR

Pairing mannose with C-5 or confusing which carbon distinguishes allose and galactose from glucose. Entry 5 is the extra entry and matches none of the four sugars.

Q.19 MCQ · 1 MARK

Plant, Animal and Microbial Biotechnology › Microbial products

Q.19 Correctly match the following **Product classes** with their representative **Products.**

Product class	Product
P. Biofuel	1. Cellulase
Q. Bioplastic	2. Cephalosporin
R. Industrial enzyme	3. Butanol
S. Antibiotic	4. Poly-lactic acid
	5. Rituximab

(A) P-1; Q-5; R-3; S-2

(B) P-3; Q-4; R-5; S-2

(C) P-3; Q-2; R-1; S-5

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

Official answer: **D**

SOLUTION

1. Match each product class on its own, then compare with the four options.
2. Biofuel (P): butanol (3) is a fuel. Clostridium acetobutylicum makes it in acetone-butanol-ethanol (ABE) fermentation. So P-3. Cellulase (1) is an enzyme, not a fuel, so option A (P-1) is out.
3. Bioplastic (Q): poly-lactic acid (4) is a biodegradable polyester. It is made by polymerising lactic acid from microbial fermentation. So Q-4. Cephalosporin (2) and rituximab (5) are drugs, not plastics, so options A (Q-5) and C (Q-2) are out.
4. Industrial enzyme (R): cellulase (1) is a bulk industrial enzyme used in textiles, detergents, paper and biomass saccharification. So R-1. Rituximab is a therapeutic antibody, not an industrial enzyme, so option B (R-5) is out.
5. Antibiotic (S): cephalosporin (2) is a beta-lactam antibiotic originally obtained from the fungus Acremonium (Cephalosporium). So S-2. Rituximab (5) is an anti-CD20 monoclonal antibody used as a

drug, not an antibiotic, so option C (S-5) is out.

6. The full matching is P-3; Q-4; R-1; S-2. Item 5 (rituximab) is an extra item that matches none of the four classes. This is option D.

KEY IDEA

Classify each product by what it is. A fuel such as butanol is a biofuel, poly-lactic acid is a bioplastic, cellulase is an industrial enzyme, and cephalosporin is an antibiotic. Rituximab is a therapeutic monoclonal antibody and fits none of the four classes.

WATCH OUT FOR

Treating rituximab as an antibiotic because it is a drug made by a microbial or cell-culture process. It is an anti-CD20 monoclonal antibody, not an antibiotic. Another slip is placing cellulase under biofuel because it is used to make bioethanol. The enzyme is an industrial enzyme, and the fuel itself is butanol or ethanol.

Q.20 MCQ · 1 MARK

Recombinant DNA Technology and Tools › Libraries & cloning

Which one of the following hosts is used in mammalian cell culture for the production of glycosylated recombinant therapeutic proteins?

(A) Pichia pastoris

(B) Sf9 cells

(C) Escherichia coli

(D) Chinese hamster ovary cells

Official answer: **D**

SOLUTION

1. The question requires a host that is BOTH (i) a mammalian cell culture system AND (ii) used to produce glycosylated recombinant therapeutic proteins. Both conditions must hold.
2. (A) Pichia pastoris is a methylotrophic yeast (fungal), not a mammalian cell. It can glycosylate proteins, but with high-mannose, non-human-type glycans. Excluded on the mammalian criterion.
3. (B) Sf9 cells are insect cells (from Spodoptera frugiperda), used in the baculovirus expression vector system, not mammalian, so excluded.
4. (C) Escherichia coli is a prokaryotic bacterium with no endoplasmic reticulum/Golgi apparatus, so it cannot glycosylate proteins at all and is not a mammalian (or even eukaryotic) culture system. Excluded.
5. (D) Chinese hamster ovary (CHO) cells are a mammalian cell line and are the industry-standard host for producing glycosylated recombinant therapeutic proteins (e.g., monoclonal antibodies, EPO), because they carry out human-compatible N- and O-linked glycosylation and post-translational processing.
6. Only CHO cells satisfy both the mammalian-origin requirement and the correct-glycosylation requirement for a recombinant therapeutic protein, so the answer is (D).

KEY IDEA

CHO (Chinese hamster ovary) cells are the industry-standard mammalian host cell line for producing glycosylated recombinant therapeutic proteins (e.g., monoclonal antibodies, EPO) because they perform human-compatible N- and O-linked glycosylation and other post-translational modifications that non-mammalian systems cannot replicate.

WATCH OUT FOR

Confusing "can glycosylate proteins" with "is a mammalian host": Pichia pastoris (yeast) and Sf9 cells (insect, baculovirus system) both glycosylate proteins but produce non-human-type glycan patterns and are not mammalian cell lines, so they fail the question's explicit "mammalian cell culture" requirement even though they are valid non-mammalian expression hosts in other contexts.

Q.21 MSQ · 1 MARK

General Biology › Microbiology

Which of the following features is/are used to distinguish Archaea from Bacteria?

(A) Gram-staining

(B) Peptidoglycan in the cell wall

(C) Presence of N-acetylglucosamine

(D) 16S rRNA sequences

Official answer: **B, D**

SOLUTION

1. Archaea and Bacteria are both prokaryotes, so a distinguishing feature must separate the two domains and not merely describe prokaryotes in general.
2. (A) Gram-staining: not correct. Gram staining reflects wall thickness and structure, and archaea can stain either Gram-positive or Gram-negative. The stain does not mark the domain boundary.
3. (B) Peptidoglycan in the cell wall: correct. Bacterial walls contain peptidoglycan (murein), built from N-acetylglucosamine and N-acetylmuramic acid. Archaeal walls lack true peptidoglycan and have pseudomurein, S-layers or other polymers instead.
4. (C) Presence of N-acetylglucosamine: not correct. This sugar occurs in both domains. Bacterial peptidoglycan contains it, and archaeal pseudomurein also contains it, paired with N-acetyltalosaminuronic acid. Its presence does not separate the domains.
5. (D) 16S rRNA sequences: correct. The three-domain classification rests on 16S rRNA sequence signatures, and archaeal 16S rRNA sequences differ clearly from bacterial ones.
6. Correct options: (B) and (D).

KEY IDEA

Archaea lack true peptidoglycan (they have pseudomurein, S-layers or other polymers), and their 16S rRNA sequences form a separate lineage from bacterial ones. These two features separate the domains.

WATCH OUT FOR

Treating Gram-staining or the presence of N-acetylglucosamine as domain markers. Gram reaction varies within both domains, and N-acetylglucosamine is also found in archaeal pseudomurein, so neither one separates Archaea from Bacteria.

Q.22 MSQ · 1 MARK

Genetics, Cell and Molecular Biology › Gene expression

Which of the following enzymes is/are involved in the biogenesis of miRNA?

(A) Drosha

(B) Cas9

(C) XRCC4

(D) Dicer

Official answer: **A, D**

SOLUTION

1. Recall the miRNA biogenesis pathway: a long primary transcript (pri-miRNA) is processed by two sequential RNase III-family enzymes before it becomes a mature, functional miRNA.
2. Option A (Drosha): a nuclear RNase III enzyme that, with its partner DGCR8, cleaves pri-miRNA into pre-miRNA (a ~60-70 nt hairpin). This is the first, defining step of miRNA biogenesis. CORRECT.
3. Option B (Cas9): an RNA-guided DNA endonuclease from the bacterial CRISPR adaptive immune system, used for genome editing. It has no role in endogenous miRNA processing. INCORRECT.

4. Option C (XRCC4): a scaffold protein that partners with DNA Ligase IV in the non-homologous end joining (NHEJ) pathway of DNA double-strand break repair. It is unrelated to RNA processing. INCORRECT.
5. Option D (Dicer): a cytoplasmic RNase III enzyme that cleaves the pre-miRNA hairpin (exported from the nucleus via Exportin-5) into the mature miRNA duplex, which is then loaded onto Argonaute to form RISC. CORRECT.
6. Therefore the enzymes involved in miRNA biogenesis are Drosha (A) and Dicer (D).

KEY IDEA
miRNA biogenesis requires two sequential RNase III-family endonucleases: nuclear Drosha (with DGCR8) converts pri-miRNA to pre-miRNA, and cytoplasmic Dicer converts pre-miRNA to the mature miRNA duplex, which is then loaded into RISC (Argonaute).

WATCH OUT FOR
Confusing Cas9 (a CRISPR genome-editing nuclease with no role in endogenous miRNA processing) or XRCC4 (a DNA double-strand break repair protein) with the RNase III enzymes that actually process miRNA precursors.

Q.23 MSQ · 1 MARK

Fundamentals of Biological Engineering › Downstream

Which of the following separation processes is/are based on molecular size?

(A) Size-exclusion chromatography

(B) Ion exchange chromatography

(C) Membrane ultrafiltration

(D) Ultracentrifugation

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

SOLUTION

1. Take the options one at a time and ask which physical property each process uses to tell molecules apart.
2. (A) Size-exclusion (gel-filtration) chromatography: small molecules can enter the pores of the beads, so they travel a longer path and elute later. Large molecules are shut out of the pores and elute first. The elution volume V_e depends on hydrodynamic size, so A is **size-based**.
3. (B) Ion exchange chromatography: proteins bind to the charged resin by electrostatic attraction and come off when the salt concentration or pH is changed. What decides the separation is net surface charge, which depends on the protein's pI and the buffer pH, not on size. B is **not** size-based.
4. (C) Membrane ultrafiltration: a pressure-driven membrane with a molecular-weight cut-off (MWCO, typically 1 to $1000\ \mathrm{kDa}$) holds back molecules larger than its pores and lets smaller ones pass. This is sieving by molecular size, so C is **size-based**.
5. (D) Ultracentrifugation: in a centrifugal field, the settling velocity of a sphere follows Stokes' law,
$$v = \frac{d_p^2\,(\rho_p - \rho_f)\,\omega^2 r}{18\,\mu}$$
where d_p is the particle (molecule) diameter, ρ_p and ρ_f are the particle and fluid densities, ω is the angular speed, r is the radial distance from the axis and μ is the fluid viscosity.
6. Because $v \propto d_p^2$, larger molecules sediment faster. The sedimentation coefficient $S = v/(\omega^2 r)$ (in svedbergs) therefore rises with molecular size and mass. This is why differential and rate-zonal (sedimentation-velocity) ultracentrifugation separate macromolecules by size, so D is **size-based**. (Isopycnic density-gradient ultracentrifugation separates by buoyant density instead, but the standard sedimentation-velocity mode is size-based, and that is the sense the question uses.)
7. Only ion exchange works on a property other than size (charge). The correct options are **A, C and D**.

KEY IDEA

Name the physical property each process uses to tell molecules apart. Gel filtration uses pore exclusion, ultrafiltration uses a membrane MWCO, and ultracentrifugation uses sedimentation rate ($v \propto d_p^2$). All three are size-based. Ion exchange uses net charge.

WATCH OUT FOR

Leaving out ultracentrifugation on the grounds that centrifugation is 'density-based'. Only isopycnic (equilibrium density-gradient) runs separate by buoyant density. In differential and rate-zonal runs the sedimentation velocity scales with d_p^2, so the separation is by size and mass. The other common slip is to think ion exchange depends on size because larger proteins carry more charges, but the separation is set by net charge (pI relative to pH), not size.

Q.24 MSQ · 1 MARK

General Biology › Biomolecules

Which of the following show(s) optical activity at 100 mM concentration in water?

(A) Solution of NaCl

(B) Solution of D-Glucose

(C) Solution of Glycine

(D) Solution of L-Proline

Official answer: **B, D**

SOLUTION

1. Optical activity (rotation of plane-polarised light) needs chiral molecules present in a net excess of one enantiomer. An achiral compound, or a racemic mixture, gives no net rotation.
2. (A) NaCl dissociates into Na^+ and Cl^-. These are simple spherical ions with no chirality, so there is no optical activity. Wrong.
3. (B) D-Glucose has several chiral carbons (C2 to C5) and is a single enantiomer. Its solution rotates plane-polarised light (dextrorotatory, with the rotation settling at a fixed value after mutarotation). Correct.
4. (C) Glycine, $\mathrm{H_2N\text{-}CH_2\text{-}COOH}$, has two hydrogens on the alpha carbon. The alpha carbon is therefore not a stereocentre and the molecule is achiral, so there is no optical activity. Wrong.
5. (D) L-Proline has a chiral alpha carbon bearing four different groups (H, COO-, the ring nitrogen and the ring CH2), and it exists as a single enantiomer. Its solution is optically active (levorotatory). Correct.
6. Hence the optically active solutions are D-glucose and L-proline: options B and D.

KEY IDEA

A solution rotates plane-polarised light only if its solute is chiral and present as a single enantiomer (or an unequal mixture). Look for a stereocentre with four different groups.

WATCH OUT FOR

Treating every amino acid as optically active. Glycine has two hydrogens on its alpha carbon, so it is achiral and shows no rotation.

Q.25 MSQ · 1 MARK

Q.25	Which of the following fluids exhibit(s) non-Newtonian behaviour at 25 °C?
(A)	Toothpaste
(B)	Mercury
(C)	Brine
(D)	Blood plasma

Official answer: **A, D**

Q.26 MSQ · 1 MARK

Fundamentals of Biological Engineering › Growth kinetics

Which of the following compounds have the same degree of reduction per carbon-mole?

(A) Glucose

(B) Lactic acid

(C) Acetic acid

(D) Formic acid

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

SOLUTION

1. The degree of reduction per C-mole, γ, of an organic compound whose C-mole formula is $\mathrm{CH}_a\mathrm{O}_b\mathrm{N}_c$ is $\gamma = 4 + a - 2b - 3c$. It uses the valences C = 4, H = 1, O = -2, N = -3, with CO_2, $\mathrm{H}_2\mathrm{O}$ and NH_3 as the reference state.
2. Write each compound per carbon atom by dividing its molecular formula by its number of carbon atoms. None of the four contains nitrogen, so $c = 0$.
3. Glucose: $\mathrm{C}_6\mathrm{H}_{12}\mathrm{O}_6 \rightarrow \mathrm{CH}_2\mathrm{O}$, so $\gamma = 4 + 2 - 2(1) = 4$.
4. Lactic acid: $\mathrm{C}_3\mathrm{H}_6\mathrm{O}_3 \rightarrow \mathrm{CH}_2\mathrm{O}$, so $\gamma = 4 + 2 - 2(1) = 4$.
5. Acetic acid: $\mathrm{C}_2\mathrm{H}_4\mathrm{O}_2 \rightarrow \mathrm{CH}_2\mathrm{O}$, so $\gamma = 4 + 2 - 2(1) = 4$.
6. Formic acid: $\mathrm{CH}_2\mathrm{O}_2$ already has one carbon, so $\gamma = 4 + 2 - 2(2) = 2$.
7. Glucose, lactic acid and acetic acid all have the same C-mole formula, $\mathrm{CH}_2\mathrm{O}$, so all three have $\gamma = 4$. Formic acid is more oxidised ($\gamma = 2$) and does not match them. Correct options: A, B and C.

KEY IDEA

The degree of reduction per C-mole depends only on the C-mole formula, $\gamma = 4 + a - 2b - 3c$ for $\mathrm{CH}_a\mathrm{O}_b\mathrm{N}_c$. So any compounds that divide down to the same C-mole formula (here $\mathrm{CH}_2\mathrm{O}$) must have the same γ.

WATCH OUT FOR

Working out the degree of reduction per mole instead of per C-mole (glucose 24, lactic acid 12, acetic acid 8) and deciding the three are different. A second slip is to treat formic acid like the others and miss that it carries two oxygens on its single carbon, which gives $\gamma = 2$, not 4.

Q.27 MSQ · 1 MARK

Fundamentals of Biological Engineering › Downstream

A recombinant protein is secreted extracellularly in soluble form by an *E. coli* culture. Which of the following downstream processes is/are involved in the purification of the extracellular secreted protein?

(A) Cell disruption

(B) Membrane ultrafiltration

(C) Solubilisation of inclusion bodies

(D) Liquid chromatography

Official answer: **B, D**

SOLUTION

1. **Where the product is.** The protein is secreted into the culture medium. Once the cells are removed (by centrifugation or microfiltration), the product is in the clarified broth, not inside the cells.
2. **(A) Cell disruption: not needed.** Homogenisation or bead milling is only useful when the product is intracellular. Here it would release host proteins, nucleic acids and cell debris into the product stream and make purification harder.
3. **(C) Solubilisation of inclusion bodies: not needed.** Inclusion bodies are insoluble protein aggregates that form inside the cytoplasm. The question says the protein is secreted in soluble form, so there are no aggregates to dissolve (with urea or guanidine HCl) and refold.
4. **(B) Membrane ultrafiltration: involved.** An extracellular product is dilute, spread through a large volume of broth. Ultrafiltration through a membrane whose molecular-weight cut-off is below the protein's molecular weight keeps the protein back and lets water and small solutes through, which concentrates it. Diafiltration on the same membrane then exchanges the buffer before chromatography.
5. **(D) Liquid chromatography: involved.** High-resolution purification (ion-exchange, affinity, hydrophobic-interaction, size-exclusion) separates the target protein from other proteins in the broth, both secreted ones and any released by lysed cells.
6. Downstream train: cell removal → ultrafiltration/diafiltration → chromatography → polishing. So **(B) and (D)** are correct.

KEY IDEA

Where the product is decides the downstream train. An intracellular product needs cell disruption, and if it forms inclusion bodies it also needs solubilisation and refolding. A soluble extracellular product skips both: remove the cells, concentrate the dilute broth (ultrafiltration/diafiltration), then purify it by chromatography.

WATCH OUT FOR

Picking (C) because recombinant proteins made in E. coli often form inclusion bodies, or (A) because downstream processing is taught as starting with cell disruption. Both steps apply only to intracellular products. This question says outright that the protein is secreted and soluble.

Q.28 NAT · 1 MARK

Fundamentals of Biological Engineering › Growth kinetics

If the doubling time of a bacterial population is 3 hours, then its average specific growth rate during this period is _____ h^{-1}.

(Round off to two decimal places)

Official answer: **0.20 to 0.25**

SOLUTION

1. In exponential growth, $\frac{dX}{dt} = \mu X$, where X is the cell concentration and μ is the specific growth rate (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 for X to reach $2X_0$. So $2X_0 = X_0 e^{\mu t_d}$, which gives $e^{\mu t_d} = 2$ and $\mu = \dfrac{\ln 2}{t_d}$. Because the population exactly doubles over t_d, this μ is also the average specific growth rate over that interval, $\bar{\mu} = \dfrac{\ln(X/X_0)}{t}$.
3. Substitute $t_d = 3$ h:

$$\mu = \frac{\ln 2}{3\ \text{h}} = \frac{0.6931}{3}\ \text{h}^{-1} = 0.2310\ \text{h}^{-1}$$

4. Rounded to two decimal places, $\mu \approx 0.23\ \text{h}^{-1}$.

KEY IDEA

In exponential growth $X = X_0 e^{\mu t}$, so the specific growth rate and the doubling time are linked by $\mu\, t_d = \ln 2$. That gives $\mu = 0.693/t_d$.

WATCH OUT FOR

Taking $\mu = 1/t_d = 0.33\ \text{h}^{-1}$, which mixes up the specific growth rate with the number of doublings per hour. Using $\log_{10} 2$ instead of $\ln 2$, which gives $0.10\ \text{h}^{-1}$. Both answers fall outside the key. The natural log is needed because μ is defined through $e^{\mu t}$.

Q.29 NAT · 1 MARK

Q.29	For a mechanically reversible isobaric process taking place in a closed system involving 5 moles of an ideal gas, the temperature increases from an initial value of 300 K to a final value of 450 K. If the specific heat capacity at constant volume (C_v) is given as 12.5 J mol^{-1} K^{-1} and gas constant is 8.314 J mol^{-1} K^{-1}, the amount of heat transferred to the system will be _____ J. *(Round off to the nearest integer)*

Official answer: **15450 to 15750**

Q.30 NAT · 1 MARK

Genetics, Cell and Molecular Biology › Mendelian genetics

The allele associated with albinism in humans is recessive (c). The probability that an albino male (cc) and a carrier female (Cc) will have an offspring with normal skin pigmentation is _____ . (Round off to one decimal place)

Official answer: **0.5**

SOLUTION

1. Set up the cross: albino male (cc) × carrier female (Cc).
2. Determine gametes: the male, being homozygous recessive, produces only c gametes. The female, being heterozygous, produces C gametes with probability 1/2 and c gametes with probability 1/2.
3. Combine gametes to get offspring genotypes: c (from father) with C (from mother, prob 1/2) gives Cc; c (from father) with c (from mother, prob 1/2) gives cc. This is a standard test-cross, yielding a 1:1 genotypic ratio.
4. Assign phenotypes: since c is recessive, Cc offspring show normal skin pigmentation (C is dominant and masks c), while cc offspring are albino.
5. Probability of an offspring with normal pigmentation = P(Cc) = 1/2 = 0.5.

KEY IDEA
A test cross between a homozygous recessive individual (cc) and a heterozygous carrier (Cc) produces offspring in a 1:1 ratio of heterozygous (Cc, normal phenotype) to homozygous recessive (cc, albino) genotypes, since the recessive parent contributes only the c allele and the heterozygous parent contributes C or c with equal probability.

WATCH OUT FOR
Confusing this test cross with a standard Cc × Cc monohybrid cross (which gives a 3:1 phenotypic ratio) and answering 0.75 instead of recognizing that one parent is homozygous recessive, giving a 1:1 ratio and an answer of 0.5.

Q.31 NAT · 1 MARK

Genetics, Cell and Molecular Biology › Mutation & repair

The contour length of a B-DNA molecule that encodes a bacterial protein of 33 kDa is _____ nm.

Consider the average molecular weight of an amino acid as 110 Da and helix rise per base pair for B-DNA as 0.34 nm.

(Round off to the nearest integer)

Official answer: **300 to 310**

SOLUTION

1. Number of amino acid residues in the protein = protein mass ÷ average residue mass = 33{,}000\text{ Da} \div 110\text{ Da} = 300 residues.
2. The genetic code is triplet: each amino acid residue is specified by one codon of 3 nucleotides, i.e. 3 base pairs of the coding B-DNA. Number of coding base pairs = 300 \times 3 = 900\text{ bp}.
3. Contour length of B-DNA = (number of base pairs) \times (rise per base pair) = 900 \times 0.34\text{ nm} = 306\text{ nm}.
4. 306 is already an integer, so the rounded answer is 306 nm.

KEY IDEA
Convert protein mass to number of amino acid residues (mass ÷ average residue mass), use the triplet genetic code to get the number of coding base pairs (residues × 3), then multiply by the B-DNA rise per base pair (0.34 nm) to get contour length.

WATCH OUT FOR
Forgetting that each amino acid is encoded by a codon of 3 nucleotides (3 base pairs), and instead multiplying the number of amino acids directly by the rise per base pair (300 × 0.34 = 102 nm), which omits the triplet code entirely and gives a value far outside the key range.

Q.32 NAT · 1 MARK

Fundamentals of Biological Engineering › Enzyme kinetics

Within the Michaelis-Menten framework, the ratio of $v_0/V_{\max}$ when $[S] = 20 \times K_{\mathrm{m}}$ is _____. (Round off to two decimal places)

Official answer: **0.94 to 0.96**

SOLUTION

1. Symbols: v_0 is the initial reaction velocity, $V_{\max}$ is the maximum velocity, reached when the enzyme is fully saturated with substrate, K_m is the Michaelis constant (the substrate concentration at which $v_0 = V_{\max}/2$), and $[S]$ is the substrate concentration.
2. Michaelis-Menten equation: $v_0 = \dfrac{V_{\max}[S]}{K_m + [S]}$. Dividing both sides by $V_{\max}$ gives $\dfrac{v_0}{V_{\max}} = \dfrac{[S]}{K_m + [S]}$.
3. Substitute $[S] = 20K_m$:

$$\frac{v_0}{V_{\max}} = \frac{20K_m}{K_m + 20K_m} = \frac{20K_m}{21K_m} = \frac{20}{21}$$

4. K_m cancels, so the ratio depends only on how many multiples of K_m the substrate concentration is: $\frac{20}{21} = 0.9524$.
5. Rounded to two decimal places: $v_0/V_{\max} = 0.95$. At twenty times K_m the enzyme runs at about 95% of its maximum rate: close to saturation, but not fully saturated.

KEY IDEA

Divide the Michaelis-Menten equation by $V_{\max}$ to get the fractional saturation $v_0/V_{\max} = [S]/(K_m + [S])$. When $[S] = nK_m$, K_m cancels and the ratio is simply $n/(n+1)$. Here $n = 20$, so the ratio is $20/21$.

WATCH OUT FOR

Assuming the enzyme is fully saturated at $[S] \gg K_m$ and answering 1.00. At $20K_m$ the rate is still only $20/21$ of $V_{\max}$. The other common slip is dropping the K_m term from the denominator. Writing $20/20$ or $1/20$ instead of $20/21$ also gives an answer outside the key.

Q.33 NAT · 1 MARK

Engineering Mathematics › Numerical methods

Consider a nonlinear algebraic equation, $e^x - 2 = 0$. Using the Newton-Raphson method, with the initial guess of $x_0 = 1$, the approximated value of the root of the equation after one iteration is _____. (Round off to two decimal places)

Official answer: **0.72 to 0.75**

SOLUTION

1. Let $f(x) = e^x - 2$, so $f'(x) = e^x$.
2. Newton-Raphson formula: $x_1 = x_0 - \frac{f(x_0)}{f'(x_0)}$, with $x_0 = 1$ (one iteration).
3. At $x_0 = 1$: $f(1) = e - 2 \approx 0.71828$ and $f'(1) = e \approx 2.71828$.
4. $x_1 = 1 - \frac{e-2}{e} = \frac{2}{e}$.
5. $x_1 = \frac{2}{2.71828} \approx 0.7358$.
6. Rounded to two decimal places, $x_1 \approx 0.74$.

KEY IDEA

Apply $x_{n+1} = x_n - f(x_n)/f'(x_n)$ once. For $f(x) = e^x - 2$ the derivative equals e^x, so $x_1 = x_0 - 1 + 2e^{-x_0} = 2/e$ at $x_0 = 1$.

WATCH OUT FOR

Doing more than one iteration, or using $f'(x) = e^x - 2$ instead of e^x. Another slip is rounding e too early, which can shift the second decimal.

Q.34 NAT · 1 MARK

Engineering Mathematics › Linear algebra

The value of k, for which the linear equations $2x + 3y = 6$ and $4x + 6y = 3k$ have at least one solution, is _____. (Answer in integer)

Official answer: **4**

SOLUTION

1. Write the system as $A\mathbf{x} = \mathbf{b}$ with $A = \begin{bmatrix} 2 & 3 \\ 4 & 6 \end{bmatrix}$ and $\mathbf{b} = \begin{bmatrix} 6 \\ 3k \end{bmatrix}$.
2. The second row of A is twice the first, so $\det A = 12 - 12 = 0$ and $\text{rank}(A) = 1$.
3. A system has at least one solution exactly when $\text{rank}(A) = \text{rank}([A \mid \mathbf{b}])$ (consistency condition). So the augmented matrix must also have rank 1.
4. Row reduce: $R_2 \to R_2 - 2R_1$ gives $\begin{bmatrix} 2 & 3 & 6 \\ 0 & 0 & 3k - 12 \end{bmatrix}$.

5. For rank 1 we need $3k - 12 = 0$, so $k = 4$. For any other k the second row reads $0 = 3k - 12 \neq 0$, so the system has no solution.
6. Check: with $k = 4$ the second equation is $4x + 6y = 12$, which is twice the first, so the two equations coincide and have infinitely many solutions.

KEY IDEA
A linear system is consistent exactly when the coefficient matrix and the augmented matrix have the same rank. Here the coefficient rows are proportional, so the right-hand sides must be in the same ratio.

WATCH OUT FOR
Taking $\det A = 0$ to mean there is no solution. A zero determinant only rules out a unique solution. The system can still have infinitely many solutions when the equations are consistent, which happens here for $k = 4$.

Q.35 NAT · 1 MARK

Engineering Mathematics › Probability & statistics

Two fair six-sided dice, with sides numbered 1 to 6, are thrown once. The probability of getting 7 as the sum of the numbers on the top side of the dice is _____. (Round off to two decimal places)

Official answer: **0.16 to 0.18**

SOLUTION

1. Two fair dice give $6 \times 6 = 36$ equally likely ordered outcomes.
2. The outcomes with sum 7 are $(1,6), (2,5), (3,4), (4,3), (5,2), (6,1)$, which is 6 outcomes.
3. $P = \dfrac{\text{favourable}}{\text{total}} = \dfrac{6}{36} = \dfrac{1}{6}$.
4. $\dfrac{1}{6} \approx 0.1667$, which rounds to 0.17 to two decimal places.

KEY IDEA
With two fair dice all 36 ordered pairs are equally likely, so the probability of a sum is the number of ordered pairs giving that sum divided by 36.

WATCH OUT FOR
Counting $(1,6)$ and $(6,1)$ as one outcome, which gives 3 favourable cases out of 36 (or out of 21 unordered pairs). Ordered pairs are the equally likely outcomes, so all 6 must be counted.

Q.36 MCQ · 2 MARKS

General Biology › Microbiology

Q.36 Correctly match the **Microorganisms** with their respective **Nutrition and energy requirement.**

Microorganisms	Nutrition and energy requirement
P. Photolithoautotrophs	1. Use organic compounds as a source of energy, hydrogen, electron and carbon
Q. Chemoorganoheterotrophs	2. Use light energy and use CO_2 as their carbon source
R. Chemolithoautotrophs	3. Use light energy and use organic compounds as electron donor and carbon source
S. Photoorganoheterotrophs	4. Oxidise reduced-inorganic molecules as energy and electron source but derive carbon from organic sources

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

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

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

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

Official answer: **A**

SOLUTION

1. Split each name into its three prefixes. **Photo-** means the energy source is light and **chemo-** means chemical energy. **Litho-** means an inorganic electron donor and **organo-** means an organic one. **Auto-** means carbon comes from CO_2 and **hetero-** means carbon comes from organic compounds.
2. **P, photolithoautotrophs.** They use light energy and an inorganic electron donor, and they fix carbon from CO_2. This matches statement 2 (light energy, CO_2 as the carbon source), as in cyanobacteria and plants.
3. **Q, chemoorganoheterotrophs.** Organic compounds supply the energy, the electrons and hydrogen, and the carbon. This matches statement 1, as in E. coli and animals.
4. **S, photoorganoheterotrophs.** They use light energy, with organic compounds as the electron donor and carbon source. This matches statement 3, as in purple non-sulfur bacteria.

5. **R, chemolithoautotrophs.** They oxidise reduced inorganic molecules for energy and electrons. Of the four statements, only statement 4 describes inorganic oxidation, and statements 1, 2 and 3 are already used by P, Q and S. So R-4 is the intended pairing. Statement 4 ends with "carbon from organic sources", which is not true of a true autotroph, since chemolithoautotrophs fix CO_2. The match for R rests on the oxidation clause and on elimination.
6. **Check the options.** (B) pairs R with 3, a light-based statement, and S with 4, a chemical one, so both are wrong. (C) pairs P with 1 (organic energy) and Q with 2 (light), both wrong. (D) pairs P with 4 and R with 2, which swaps the chemical and light energy sources. Only (A), P-2; Q-1; R-4; S-3, is consistent with all four matches.

KEY IDEA

Decode the nutritional-type names from their prefixes: photo-/chemo- for the energy source, litho-/organo- for the electron donor, auto-/hetero- for the carbon source. Match the three unambiguous types first, then assign the remaining statement by elimination.

WATCH OUT FOR

Rejecting statement 4 for R because it says carbon comes from organic sources, when a chemolithoautotroph fixes CO_2. Statement 4 is loosely worded, but it is the only inorganic-oxidation statement left. Another slip is swapping the light and chemical energy sources, as options (C) and (D) do.

Q.37 MCQ · 2 MARKS

General Biology › Metabolism

Correctly match the Inhibitor with its respective Function in mitochondrial respiration.

Inhibitor | Function
P. FCCP | 1. Inhibits cytochrome c oxidase
Q. Cyanide | 2. Makes the membrane permeable to protons
R. Oligomycin A | 3. Blocks mitochondrial uptake of succinate
S. Butyl malonate | 4. Inhibits ATP synthase

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

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

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

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

Official answer: **A**

SOLUTION

1. FCCP is a protonophore (uncoupler). It carries protons across the inner mitochondrial membrane, so it makes the membrane permeable to protons and collapses the proton gradient. P matches 2. This removes option D, which gives P-3.
2. Cyanide binds the heme iron of cytochrome a_3 in Complex IV (cytochrome c oxidase) and blocks electron transfer to O_2. Q matches 1. This removes options B (Q-3) and C (Q-4).
3. Oligomycin A binds the F_0 part of F_0F_1 ATP synthase and blocks its proton channel, so it inhibits ATP synthase. R matches 4.
4. Butyl malonate is a malonate analogue that inhibits the dicarboxylate carrier of the inner membrane. It blocks mitochondrial uptake of succinate (and malate). S matches 3. Plain malonate would instead inhibit succinate dehydrogenase directly, but butyl malonate is the transport blocker.
5. The matching is P-2; Q-1; R-4; S-3, which is option A. Options B, C and D were already removed by steps 1 and 2.

KEY IDEA
Each inhibitor acts at a different point of mitochondrial respiration. FCCP is a protonophore and uncouples. Cyanide blocks Complex IV. Oligomycin blocks ATP synthase at F_0. Butyl malonate blocks the dicarboxylate carrier, so succinate cannot enter.

WATCH OUT FOR
Matching butyl malonate with inhibition of succinate dehydrogenase (that is plain malonate), or confusing the uncoupler FCCP with oligomycin. FCCP lets protons leak through, while oligomycin blocks the ATP synthase channel.

Q.38 MCQ · 2 MARKS

General Biology › Biomolecules

An octapeptide composed of these L-amino acids – Lys, Thr, Ser, Met, Arg, Trp, Tyr, Glu – was subjected to analyses with the following outcomes:
P. The N-terminal sequencing analysis by Sanger's method yielded 'Ser' at the N-terminus
Q. Chymotrypsin treatment gave a pentapeptide, a 'Tyr' containing dipeptide and a free 'Glu'
R. Cyanogen bromide treatment gave two tetrapeptides
S. Trypsin treatment gave two tripeptides and a dipeptide
Which one of the following is the correct octapeptide sequence?

(A) Ser-Tyr-Arg-Met-Lys-Thr-Trp-Glu
(B) Ser-Arg-Lys-Met-Tyr-Thr-Trp-Glu
(C) Ser-Met-Lys-Arg-Thr-Tyr-Trp-Glu
(D) Ser-Arg-Met-Lys-Trp-Thr-Tyr-Glu

Official answer: **A**

SOLUTION

1. Sanger's reagent (FDNB) labels the N-terminal residue, so Ser is residue 1. All four options begin with Ser, so clue P does not separate them.
2. Cyanogen bromide cleaves on the C-terminal side of Met. Two tetrapeptides means a single cut after residue 4, so Met must be residue 4. Option D has Met at position 3, which gives a tripeptide and a pentapeptide, so D is out. Option C has Met at position 2, which gives a dipeptide and a hexapeptide, so C is out.
3. Option B has Met at position 4 and passes the CNBr test. Chymotrypsin cuts after Tyr and Trp. In B, Tyr is at position 5 and Trp at position 7, giving Ser-Arg-Lys-Met-Tyr (pentapeptide), Thr-Trp (dipeptide) and free Glu. The dipeptide contains Trp, not Tyr, so B contradicts clue Q. Trypsin, which cuts after Arg and Lys, would also give Ser-Arg, Lys and Met-Tyr-Thr-Trp-Glu on B, which contradicts clue S. B is out.
4. Check A, Ser-Tyr-Arg-Met-Lys-Thr-Trp-Glu. Chymotrypsin cuts after Tyr(2) and Trp(7), giving Ser-Tyr (a Tyr-containing dipeptide), Arg-Met-Lys-Thr-Trp (a pentapeptide) and free Glu. This matches Q.
5. In A, CNBr cuts after Met(4), giving Ser-Tyr-Arg-Met and Lys-Thr-Trp-Glu, which are two tetrapeptides. This matches R.
6. In A, trypsin cuts after Arg(3) and Lys(5), giving Ser-Tyr-Arg (tripeptide), Met-Lys (dipeptide) and Thr-Trp-Glu (tripeptide). This matches S. Option A satisfies all four clues.

KEY IDEA
Use the specific cleavage sites. CNBr cuts after Met, trypsin after Lys and Arg, and chymotrypsin after Tyr, Trp and Phe. Start with the clue that fixes one position, here Met at residue 4, to eliminate options, then check the remaining clues on the survivor.

WATCH OUT FOR
Cutting on the wrong side of the residue, for example before Met instead of after it. Another mistake is forgetting that Trp is also cleaved by chymotrypsin, which makes B look acceptable.

Q.39 MCQ · 2 MARKS

General Biology › Adaptive immunity

Q.39 Correctly match the type of **Hypersensitivity reaction** with its respective **Example.**

Hypersensitivity reaction	Example
P. Type I	1. Tuberculin reaction
Q. Type II	2. Arthus reaction
R. Type III	3. Chronic urticaria
S. Type IV	4. Systemic anaphylaxis

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

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

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

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

Official answer: **C**

SOLUTION

1. Type I hypersensitivity is immediate and IgE-mediated: allergen cross-links IgE bound to mast cells, which release histamine. Its most severe form is systemic anaphylaxis, so **P matches 4**.
2. Type III hypersensitivity is caused by antigen-antibody (immune) complexes that deposit in tissue, fix complement and recruit neutrophils. The Arthus reaction is the classic local example, so **R matches 2**.
3. Type IV hypersensitivity is delayed-type and T-cell mediated, with no antibody involved. The tuberculin (Mantoux) reaction is the classic example, so **S matches 1**.
4. Type II hypersensitivity is antibody (IgG/IgM) mediated and acts against cell-surface or tissue antigens or receptors. Chronic urticaria is often autoimmune: IgG antibodies against the high-affinity IgE receptor on mast cells, or against IgE itself, trigger degranulation. Of the four listed examples this is the one that fits Type II, and it is also the only example left after P, R and S are matched, so **Q matches 3**.
5. The matching is P-4; Q-3; R-2; S-1, which is option C.
6. Option A is wrong because it puts chronic urticaria with Type I and anaphylaxis with Type II. Option B is wrong because it pairs Type III with the tuberculin reaction and Type IV with the Arthus reaction. Option D is wrong because it pairs Type I with the Arthus reaction and Type III with systemic anaphylaxis.

KEY IDEA

Type I is IgE and mast cells (anaphylaxis). Type II is antibody against cell or receptor targets (autoimmune chronic urticaria). Type III is immune complexes (Arthus reaction). Type IV is delayed and T-cell mediated (tuberculin reaction).

WATCH OUT FOR

Chronic urticaria looks like an allergy, so it gets matched with Type I. The cause here is autoantibody against the IgE receptor or IgE, which makes it Type II. Anaphylaxis is the Type I example.

Q.40 MCQ · 2 MARKS

Genetics, Cell and Molecular Biology › Mutation & repair

Q.40 Correctly match the **Enzyme** with its respective **Function**.

Enzyme	Function
P. Gyrase	1. Removes a damaged base by cleaving the bond between sugar and base
Q. Deadenylase	2. Provides a swivel allowing one DNA strand to rotate around the other
R. Glycosylase	3. Catalyses bond formation between 3′-OH and 5′-phosphate end of nucleotides in duplex DNA
S. DNA ligase	4. Is an exoribonuclease that removes the poly(A) tail

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

Official answer: **A**

SOLUTION

1. P. Gyrase is a bacterial type II topoisomerase whose physiological role during replication/transcription is to act as a swivel, allowing one DNA strand to rotate around the other and relieve torsional (supercoiling) stress ahead of the fork → matches function 2 (provides a swivel allowing one DNA strand to rotate around the other).
2. Q. Deadenylase (e.g., in the CCR4-NOT / PAN2-PAN3 complexes) is an exoribonuclease that removes the poly(A) tail from the 3' end of mRNA, the key first step initiating mRNA decay → matches function 4 (exoribonuclease that removes the poly(A) tail).

3. R. Glycosylase is the base-excision-repair enzyme that recognizes a damaged or inappropriate base and cleaves the N-glycosidic bond between that base and its deoxyribose sugar, creating an AP site, without removing the sugar-phosphate backbone → matches function 1 (removes a damaged base by cleaving the bond between sugar and base).
4. S. DNA ligase catalyses formation of a phosphodiester bond between a 3'-OH and a 5'-phosphate end of adjacent nucleotides in duplex DNA, sealing nicks (e.g., after Okazaki fragment processing or repair synthesis) → matches function 3 (catalyses bond formation between 3'-OH and 5'-phosphate end of nucleotides in duplex DNA).
5. Combining all four matches: P-2; Q-4; R-1; S-3.
6. Comparing with the options: this exactly matches option (A) P-2; Q-4; R-1; S-3.

KEY IDEA

Match each DNA/RNA-processing enzyme to its precise molecular function: gyrase relieves torsional strain by acting as a swivel, deadenylase is an exoribonuclease that removes the mRNA poly(A) tail, glycosylase excises a damaged base in base-excision repair, and DNA ligase seals nicks by joining a 3'-OH to a 5'-phosphate.

WATCH OUT FOR

Confusing glycosylase (removes only the damaged base, leaving an abasic site) with an endonuclease/exonuclease that removes nucleotides, or confusing gyrase's swivel/supercoiling-relief role with helicase's strand-unwinding role.

Q.41 MCQ · 2 MARKS

General Biology › Enzymes

Correctly match the Coenzyme with its respective involvement in a specific Reaction type. Coenzyme: P. Thiamine pyrophosphate; Q. Tetrahydrofolate; R. Flavin adenine dinucleotide; S. 5'-Deoxyadenosyl cobalamin. Reaction type: 1. Acyl group transfer; 2. Transfer of one carbon group; 3. Transfer of methyl group; 4. Oxidation-reduction; 5. Aldehyde transfer.

(A) P-5; Q-2; R-4; S-3

(B) P-5; Q-1; R-2; S-3

(C) P-1; Q-2; R-4; S-5

(D) P-5; Q-3; R-1; S-2

Official answer: **A**

SOLUTION

1. Thiamine pyrophosphate (TPP) carries an activated aldehyde (hydroxyalkyl) unit, as in transketolase and pyruvate decarboxylase. So P matches 5, aldehyde transfer. It is not an acyl group carrier in the sense of coenzyme A or lipoamide.
2. Tetrahydrofolate (THF) carries one-carbon units (formyl, methenyl, methylene, methyl). So Q matches 2, transfer of one carbon group.
3. Flavin adenine dinucleotide (FAD) accepts and donates electrons and hydrogen: $\mathrm{FAD} + 2\mathrm{H} \rightleftharpoons \mathrm{FADH_2}$. So R matches 4, oxidation-reduction.
4. 5'-Deoxyadenosyl cobalamin is a vitamin B12 coenzyme. Of the five reaction types listed, the only one that fits a cobalamin coenzyme is methyl group transfer, because the other four are taken by P, Q and R and acyl transfer belongs to none of the four coenzymes. So S matches 3. Strictly, the 5'-deoxyadenosyl form catalyses carbon-skeleton rearrangements, as in methylmalonyl-CoA mutase, which shifts a group between adjacent carbons. The methylcobalamin form is the one that transfers methyl groups. The question treats B12 as a methyl-group coenzyme, and this is the only reading consistent with a full set of matches.

5. Check each option against the three secure pairs P-5, Q-2 and R-4. Option B has Q-1, so THF is wrongly an acyl carrier. Option C has P-1, so TPP is wrongly an acyl carrier. Option D has Q-3 and R-1, so FAD is wrongly an acyl carrier. Option A is the only one with P-5, Q-2 and R-4, so it is the answer: P-5; Q-2; R-4; S-3.

KEY IDEA

Match each coenzyme to the group it carries: TPP carries an aldehyde unit, THF carries one-carbon units, FAD carries electrons and hydrogen in redox reactions, and cobalamin (vitamin B12) is the methyl and rearrangement coenzyme. Three firm matches (P, Q, R) leave only option A.

WATCH OUT FOR

Calling TPP an acyl carrier because it sits in the pyruvate dehydrogenase complex. In that complex TPP carries a hydroxyethyl (aldehyde-level) unit, and the acyl group is carried by lipoamide and coenzyme A. Another slip is assigning THF to methyl transfer alone, when it carries one-carbon units at several oxidation levels.

Q.42 MCQ · 2 MARKS

Fundamentals of Biological Engineering › Process control

A thermometer measuring body temperature follows a first-order response with a time constant of 40 seconds. The instrument will reach 95% of its steady-state output at _____ seconds.

(Round off to the nearest integer)

(A) 60

(B) 80

(C) 120

(D) 160

Official answer: **C**

SOLUTION

1. A first-order instrument has the transfer function $G(s) = \dfrac{K}{\tau s + 1}$, where K is the steady-state gain and τ is the time constant. Here $\tau = 40\ \text{s}$.
2. When the thermometer is exposed to a step change in temperature, its response in deviation form is $\dfrac{y(t)}{y_\infty} = 1 - e^{-t/\tau}$, where $y(t)$ is the change in reading at time t and y_∞ is the final (steady-state) change.
3. Set the response to 95% of steady state: $1 - e^{-t/\tau} = 0.95 \ \Rightarrow\ e^{-t/\tau} = 0.05$.
4. Take the natural logarithm and solve for t:
$$t = \tau \ln\left(\frac{1}{0.05}\right) = \tau \ln 20 = 2.9957\,\tau$$
5. Substitute $\tau = 40\ \text{s}$: $t = 2.9957 \times 40 = 119.83\ \text{s} \approx 120\ \text{s}$.
6. Check with the usual rule of thumb: a first-order system reaches 63.2% of its final change in 1τ, 86.5% in 2τ, 95.0% in 3τ and 98.2% in 4τ. So 95% takes about $3\tau = 120\ \text{s}$, which is option (C).

KEY IDEA

After a step change, a first-order instrument has covered the fraction $1 - e^{-t/\tau}$ of its final change by time t. Solving $1 - e^{-t/\tau} = 0.95$ gives $t = \tau \ln 20 \approx 3\tau$. So an instrument's 95% response time is about three time constants.

WATCH OUT FOR

Taking the time constant itself (40 s) as the settling time. One time constant only gets the instrument to 63.2% of its final value. Other mistakes are picking $2\tau = 80\ \text{s}$ (86.5%) or $4\tau = 160\ \text{s}$ (98.2%), or solving $e^{-t/\tau} = 0.95$ instead of 0.05, which gives about 2 s.

Q.43 MCQ · 2 MARKS

Fundamentals of Biological Engineering › Process control

The output $y(t)$ of a first-order process is governed by the following differential equation

$$\tau_p \frac{dy}{dt} + y = K_p f(t)$$

where τ_p is a non-zero time constant, K_p is the gain and $f(t)$ is the input with $f(0) = 0$.

Assume $y(0) = 0$. The transfer function for this process is (consider s as the independent variable in the Laplace domain)

(A) $\dfrac{K_p}{\tau_p s + 1}$

(B) $\dfrac{\tau_p}{K_p s + 1}$

(C) $\dfrac{\tau_p}{K_p(s+1)}$

(D) $\dfrac{K_p}{\tau_p(s+1)}$

Official answer: **A**

SOLUTION

1. Symbols: τ_p is the process time constant (units of time), K_p is the steady-state gain, $Y(s) = \mathcal{L}\{y(t)\}$ and $F(s) = \mathcal{L}\{f(t)\}$.
2. Laplace transform of a derivative: $\mathcal{L}\left\{\frac{dy}{dt}\right\} = sY(s) - y(0)$. Because $y(0) = 0$, this is just $sY(s)$. Since $y(0) = 0$ and $f(0) = 0$, both variables already start from zero, so they are already deviation variables.
3. Transform both sides of the model: $\tau_p\, sY(s) + Y(s) = K_p F(s)$.
4. Factor out $Y(s)$: $Y(s)\,(\tau_p s + 1) = K_p F(s)$.
5. The transfer function is output over input with zero initial conditions:
$$G(s) = \frac{Y(s)}{F(s)} = \frac{K_p}{\tau_p s + 1}$$
6. Check against the options. The steady-state gain must be $G(0) = K_p$ (by the final-value theorem, a unit step in f settles y at K_p), and the pole must be at $s = -1/\tau_p$. B gives $G(0) = \tau_p$ and C gives $G(0) = \tau_p/K_p$, so both are wrong. D, $\dfrac{K_p}{\tau_p(s+1)}$, gives $G(0) = K_p/\tau_p$ and a pole at $s = -1$. Only A meets both conditions, so the answer is (A).

KEY IDEA

With zero initial conditions, take the Laplace transform term by term ($dy/dt \to sY(s)$) and form $G(s) = Y(s)/F(s)$. A first-order process always has the standard form $K_p/(\tau_p s + 1)$: the gain is $G(0) = K_p$ and the single pole is at $s = -1/\tau_p$.

WATCH OUT FOR

Picking D, $K_p/[\tau_p(s+1)]$, by dividing the whole equation by τ_p and then factoring wrongly. That form changes the steady-state gain to K_p/τ_p and moves the pole to $s = -1$. It is also dimensionally inconsistent, because s has units of time^{-1} and cannot be added to a pure number 1 unless it is multiplied by τ_p.

Q.44 MCQ · 2 MARKS

Fundamentals of Biological Engineering › Bioreactor operation

For a specific bioreactor configuration, the power requirement for a Rushton-turbine impeller agitating an unaerated Newtonian fluid in the turbulent regime will be

(A) proportional to the stirring speed of the impeller

(B) proportional to the square of the stirring speed of the impeller

(C) proportional to the cube of the stirring speed of the impeller

(D) inversely proportional of the stirring speed of the impeller

Official answer: **C**

SOLUTION

1. Define the power number $N_P = \dfrac{P}{\rho N_i^3 D_i^5}$. Here P is the ungassed power input (W), ρ the fluid density ($\mathrm{kg\ m^{-3}}$), N_i the stirring speed ($\mathrm{s^{-1}}$) and D_i the impeller diameter (m).
2. The impeller Reynolds number is $Re_i = \dfrac{\rho N_i D_i^2}{\mu}$, where μ is the viscosity of the Newtonian fluid ($\mathrm{Pa\ s}$). The flow is fully turbulent above roughly $Re_i \approx 10^4$.
3. In the turbulent regime the power curve goes flat, so N_P no longer depends on Re_i. For one fixed geometry (a baffled vessel with a Rushton turbine) it settles at a constant value, $N_P \approx 5$ to 6.
4. Since N_P is constant, rearrange the definition:
$$P = N_P \, \rho \, N_i^3 D_i^5$$
5. For a specific configuration D_i is fixed, and for the same fluid ρ is fixed. So N_P, ρ and D_i^5 are all constants, and $P \propto N_i^3$.
6. For contrast, take the laminar regime ($Re_i < 10$). There $N_P = \dfrac{k_1}{Re_i}$, with k_1 a geometry constant, so $P = k_1 \mu N_i^2 D_i^3 \propto N_i^2$. That is the relation in option (B), and it does not hold in the turbulent regime.
7. So the power requirement is proportional to the cube of the stirring speed of the impeller. The answer is (C).

KEY IDEA

The power number $N_P = P/(\rho N_i^3 D_i^5)$ is constant in the turbulent regime (about 5 to 6 for a baffled Rushton turbine). So for a fixed impeller diameter and fluid density, ungassed power goes as N_i^3 (and as D_i^5). In the laminar regime $N_P \propto 1/Re_i$, so power goes as N_i^2 instead.

WATCH OUT FOR

Choosing (B) by carrying over the laminar result $P = k_1 \mu N_i^2 D_i^3 \propto N_i^2$ into the turbulent regime. Another mistake is treating N_P as if it still changes with speed in turbulent flow. Once Re_i is above about 10^4, N_P is flat, and all of the speed dependence sits in the N_i^3 of its definition.

Q.45 MCQ · 2 MARKS

Engineering Mathematics › Differential equations

Let m and n be fixed real numbers. If the function $y(t) = C_1 e^t + C_2 e^{-t}$ is a solution of $\dfrac{d^2y}{dt^2} + m\dfrac{dy}{dt} + ny = 0$ for any constants C_1 and C_2, then $m + n$ is equal to

(A) -2

(B) -1

(C) 0

(D) 1

Official answer: **B**

SOLUTION

1. The equation $y'' + my' + ny = 0$ is linear and homogeneous with constant coefficients. The function $y = C_1 e^t + C_2 e^{-t}$ must satisfy it for every choice of C_1 and C_2. Taking $(C_1, C_2) = (1, 0)$ and $(0, 1)$ shows that e^t and e^{-t} must each be a solution.
2. Substitute $y = e^{rt}$. Then $y' = re^{rt}$ and $y'' = r^2 e^{rt}$, so $(r^2 + mr + n)\, e^{rt} = 0$. Since $e^{rt} \neq 0$, the characteristic equation is $r^2 + mr + n = 0$.
3. Both $r = 1$ and $r = -1$ must be roots of this quadratic. A quadratic has at most two roots, so these are exactly its two roots.

4. Sum of roots: $1 + (-1) = 0 = -m$, so $m = 0$.
5. Product of roots: $(1)(-1) = -1 = n$, so $n = -1$.
6. Check: the equation becomes $y'' - y = 0$. For $y = e^t$ and for $y = e^{-t}$ we get $y'' = y$, so both satisfy it, and so does every combination $C_1 e^t + C_2 e^{-t}$.
7. Hence $m + n = 0 + (-1) = -1$, which is option (B).

KEY IDEA
If $C_1 e^t + C_2 e^{-t}$ solves a constant-coefficient linear homogeneous equation for all C_1, C_2, then $r = 1$ and $r = -1$ are the roots of its characteristic equation. Use the sum and product of roots to read off the coefficients.

WATCH OUT FOR
Mixing up the signs in Vieta's relations. The sum of roots is $-m$, not $+m$, and the product is $+n$. Another slip is to expect $n = +1$ by analogy with $y'' + y = 0$.

Q.46 MCQ · 2 MARKS

Engineering Mathematics › Calculus

If the function f(x) = { sin 2x, for x > 0; a + bx, for x ≤ 0 }, where a and b are constants, is differentiable at x = 0, then a + b is equal to

(A) 0
(B) 1
(C) 2
(D) 3

Official answer: **C**

SOLUTION

1. A function that is differentiable at $x = 0$ must first be continuous there, so $\lim_{x \to 0^+} f(x) = \lim_{x \to 0^-} f(x) = f(0)$.
2. Right-hand limit: $\lim_{x \to 0^+} \sin 2x = 0$. Since $0 \le 0$, $f(0) = a + b \cdot 0 = a$, and the left-hand limit is also a. Continuity gives $a = 0$.
3. Right-hand derivative: for $x > 0$, $f'(x) = 2\cos 2x$, so $f'(0^+) = 2\cos 0 = 2$. (Equivalently, $\lim_{h \to 0^+} \frac{\sin 2h - 0}{h} = 2$.)
4. Left-hand derivative: for $x < 0$, $f(x) = a + bx$, so $f'(0^-) = b$.
5. Differentiability at 0 requires $f'(0^-) = f'(0^+)$, so $b = 2$.
6. Hence $a + b = 0 + 2 = 2$, which is option (C).

KEY IDEA
For a piecewise function to be differentiable at the join, it must be continuous there and the one-sided derivatives must be equal. These two conditions give two equations for the two constants.

WATCH OUT FOR
Imposing only continuity, which gives $a = 0$ but leaves b undetermined. Another slip is to match the function values but not the slopes, or to take the derivative of $\sin 2x$ as $\cos 2x$ and so get $b = 1$ (option B).

Q.47 MCQ · 2 MARKS

Recombinant DNA Technology and Tools › Bioinformatics

Correctly match the following Bioinformatic tool/Database with its respective Utility.

Bioinformatic tool/Database:
P. BLAST
Q. Bowtie
R. AlphaFold
S. PDB

Utility:
1. Database for 3D protein structures
2. Tool to identify similarity of a query sequence to existing sequences available in databanks
3. Tool to align short read DNA sequences obtained from Next-generation sequencing to a reference genome
4. AI tool to predict protein structures

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

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

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

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

Official answer: **B**

SOLUTION

1. BLAST (Basic Local Alignment Search Tool) is a sequence-similarity search tool: given a query sequence, it searches sequence databanks and reports the most similar/homologous sequences. This matches Utility 2 ("Tool to identify similarity of a query sequence to existing sequences available in databanks"). So P-2.
2. Bowtie is a fast, memory-efficient short-read aligner built for next-generation sequencing data: it aligns short DNA reads to a reference genome. This matches Utility 3 ("Tool to align short read DNA sequences obtained from Next-generation sequencing to a reference genome"). So Q-3.
3. AlphaFold is DeepMind's deep-learning (AI) system that predicts a protein's 3D structure directly from its amino-acid sequence, without requiring experimental structure determination. This matches Utility 4 ("AI tool to predict protein structures"). So R-4.
4. PDB (Protein Data Bank) is the global repository that archives experimentally determined 3D structures of proteins and other biomolecules (solved by X-ray crystallography, NMR, cryo-EM, etc.). This matches Utility 1 ("Database for 3D protein structures"). So S-1.
5. Assembling the full mapping: P-2; Q-3; R-4; S-1.
6. Comparing against the options: (A) P-2;Q-3;R-1;S-4 wrongly swaps R and S (would make AlphaFold a structure database and PDB an AI predictor - the reverse of their real roles). (C) P-3;Q-2;R-4;S-1 wrongly swaps P and Q (BLAST is not a read-aligner; Bowtie is not a similarity-search tool). (D) P-4;Q-1;R-2;S-3 misassigns every pair. Only option (B) - P-2;Q-3;R-4;S-1 - correctly matches all four tools to their real functions.

KEY IDEA
Match each bioinformatics tool/database to its core function: BLAST = sequence similarity search; Bowtie = short-read genome alignment; AlphaFold = AI-based structure prediction; PDB = repository of solved 3D structures.

WATCH OUT FOR
Confusing BLAST (sequence similarity search against databanks) with a structure database, or confusing PDB (a repository of experimentally solved structures) with AlphaFold (a predictive AI tool); both concern protein structure but serve opposite roles (storage vs. prediction).

Q.48 MCQ · 2 MARKS

Plant, Animal and Microbial Biotechnology › Transgenic plants

Correctly match the herbicide with its mode of development of resistance in plants. Herbicide: P. Imidazolinones; Q. Bromoxynil; R. Glufosinate. Mode of development of resistance: 1. Transformation of bacterial nitrilase gene; 2. Transformation of resistant version of acetolactate synthetase; 3. Transformation of tfdA gene from Alcaligenes, which encodes a dioxygenase; 4. Transformation of bar gene from Streptomyces hygroscopicus which encodes phosphinothricin acetyltransferase.

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

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

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

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

Official answer: **A**

SOLUTION

1. Imidazolinones (such as imazapyr) inhibit acetolactate synthase (ALS), the first enzyme of branched-chain amino acid synthesis. Resistance is engineered by transforming a herbicide-insensitive version of ALS, so P matches 2.
2. Bromoxynil is a nitrile herbicide that blocks photosystem II. A bacterial nitrilase hydrolyses its nitrile group to a non-toxic carboxylic acid, so transforming the bacterial nitrilase gene gives resistance. Q matches 1.
3. Glufosinate (phosphinothricin) inhibits glutamine synthetase, so ammonia builds up and kills the plant. The bar gene from Streptomyces hygroscopicus encodes phosphinothricin acetyltransferase, which acetylates and inactivates the herbicide. R matches 4.
4. The tfdA gene from Alcaligenes encodes a dioxygenase that degrades the auxin-mimic herbicide 2,4-D. No herbicide in the list is 2,4-D, so item 3 is the unused extra item. Options B and D both pair R with 3, so both are wrong.
5. Option C pairs imidazolinones with the nitrilase gene (P-1) and bromoxynil with resistant ALS (Q-2), which is wrong. Only option A gives P-2, Q-1 and R-4.

KEY IDEA

Match each herbicide to its target or detoxifying enzyme. Imidazolinones target ALS, so the resistance gene is a resistant ALS. Bromoxynil is detoxified by bacterial nitrilase. Glufosinate is detoxified by the bar gene product, phosphinothricin acetyltransferase. The tfdA dioxygenase is the 2,4-D resistance route.

WATCH OUT FOR

Pairing glufosinate with tfdA, because both genes encode detoxifying enzymes. tfdA belongs to 2,4-D, which is not in the list. Another slip is to mix up the ALS-based and nitrilase-based routes for imidazolinones and bromoxynil.

Q.49 MSQ · 2 MARKS

General Biology › Metabolism

Which of the following statements is/are true regarding the effect of the concentration of metabolic intermediates on glycolysis in erythrocytes?

(A) Increased AMP levels stimulate glycolysis

(B) Increased citrate inhibits glycolysis

(C) Increased glucose 6-phosphate inhibits glycolysis

(D) Increased fructose 1,6-bisphosphate stimulates glycolysis

Official answer: **A, B, D**

Q.50 MSQ · 2 MARKS

Genetics, Cell and Molecular Biology › Gene expression

Which of the following statements about initiation of DNA replication in eukaryotes is/are true?

(A) DNA replication is initiated at the origin of replication licensed by loading of Mcm helicase complex

(B) Loading of Mcm helicase complex takes place in S phase

(C) Mcm helicase complex are activated by S-Cdks

(D) Mcm helicase complex is responsible for loading of origin recognition complex

Official answer: **A, C**

SOLUTION

1. Origin licensing: in late M/G1 phase, the Origin Recognition Complex (ORC), bound at the origin, recruits Cdc6 and Cdt1, which together load the Mcm2-7 helicase complex onto DNA as an inactive double hexamer. This loading event constitutes licensing of the origin for replication.
2. Evaluate (A): 'Replication is initiated at the origin licensed by loading of Mcm helicase complex': TRUE. Licensing is a precondition for firing; only licensed origins can initiate replication.
3. Evaluate (B): 'Loading of Mcm helicase complex takes place in S phase': FALSE. Mcm loading (licensing) occurs in G1 phase, before S phase begins, which keeps licensing and firing temporally separated so each origin fires only once per cell cycle.
4. Evaluate (C): 'Mcm helicase complex are activated by S-Cdks': TRUE. At the G1/S transition, DDK (Dbf4-dependent kinase) together with S-phase CDKs phosphorylates Mcm-associated firing factors (e.g., Sld2, Sld3/Treslin) and Mcm subunits, converting the loaded pre-RC into the active CMG helicase and triggering origin firing.
5. Evaluate (D): 'Mcm helicase complex is responsible for loading of origin recognition complex': FALSE. The order is reversed: ORC binds the origin first and recruits Cdc6/Cdt1 to load Mcm, not the other way around.
6. Therefore the true statements are (A) and (C).

KEY IDEA

Eukaryotic origin licensing (ORC → Cdc6/Cdt1 → Mcm2-7 double hexamer loading) occurs in late M/G1 phase; origin firing (activation of the loaded Mcm helicase into the active CMG complex) is triggered at the G1/S transition by DDK and S-phase Cdks. Licensing and firing are temporally separated so each origin fires only once per cycle.

WATCH OUT FOR

Confusing the order of events: thinking Mcm loading happens in S phase (it happens in G1, forming the pre-replication complex) or thinking Mcm loads/recruits ORC (it is the reverse: ORC binds first and recruits Cdc6/Cdt1 to load Mcm).

Q.51 MSQ · 2 MARKS

Genetics, Cell and Molecular Biology › Cell biology

Which of the following proteins is/are involved in intraflagellar transport?

(A) Microtubules

(B) Myosin

(C) Actin

(D) Kinesin

Official answer: **A, D**

SOLUTION

1. Intraflagellar transport (IFT) is the movement of particulate cargo (axonemal precursor proteins and signaling molecules) bidirectionally along the length of a cilium/flagellum, between the ciliary membrane and the underlying axoneme.
2. The axoneme, which also serves as the track for IFT, is built of microtubule doublets (polymers of the protein tubulin). Since microtubules form the structural track along which IFT particles move, Option (A) Microtubules is correct.
3. Anterograde IFT (movement from the base of the cilium to the tip) is driven by the motor protein kinesin-2, which walks along the microtubule doublets carrying IFT-B particle trains and their cargo. Hence Option (D) Kinesin is correct.

4. Retrograde IFT (tip to base) is driven by cytoplasmic dynein-2, not myosin. Myosin is a motor protein that moves along actin filaments (a distinct cytoskeletal system unrelated to ciliary/flagellar transport), so Option (B) Myosin is not involved in IFT.
5. Actin filaments are not components of the axoneme and do not participate in the IFT machinery, which is exclusively microtubule- and kinesin/dynein-based; so Option (C) Actin is not involved in IFT.
6. Therefore, the proteins involved in intraflagellar transport are Microtubules (the track) and Kinesin (the anterograde motor): Options (A) and (D).

KEY IDEA

Intraflagellar transport (IFT) is the bidirectional movement of protein cargo (axonemal precursors, signaling proteins) along the axoneme of a cilium/flagellum, between its base and tip. The axoneme itself (the transport track) is built of microtubule doublets. Anterograde (base→tip) movement of IFT trains is powered by kinesin-2 motors walking along these microtubules; retrograde (tip→base) movement uses cytoplasmic dynein-2. Actin and myosin belong to a separate cytoskeletal transport system and are not part of the ciliary/flagellar IFT machinery.

WATCH OUT FOR

Confusing the microtubule/kinesin-based IFT system (cilia/flagella) with the actin/myosin-based cytoskeletal transport system used elsewhere in the cell (e.g., cortical transport, melanosome movement); actin and myosin play no role inside the flagellum/IFT machinery.

Q.52 MSQ · 2 MARKS

Genetics, Cell and Molecular Biology › Gene expression

Which of the following statements is/are true about telomerase?

(A) Telomerase has 5'-3' DNA-dependent DNA polymerisation activity

(B) Telomerase has 5'-3' RNA-dependent DNA polymerisation activity

(C) Telomerase contains an RNA subunit

(D) Telomerase has 3'-5' DNA-dependent DNA polymerisation activity

Official answer: **B, C**

SOLUTION

1. Telomerase is a ribonucleoprotein enzyme composed of a catalytic protein subunit (TERT) and an integral RNA subunit (TERC/TR) that serves as the template for synthesising telomeric repeats. This makes statement (C) true.
2. Telomerase synthesises new telomeric DNA in the 5'\to3' direction using its own internal RNA (not a DNA template) as the template, i.e. it is a specialised reverse transcriptase with RNA-dependent DNA polymerase activity. This makes statement (B) true.
3. Statement (A) is false: telomerase does not copy a DNA template, so it has no DNA-dependent DNA polymerase activity.
4. Statement (D) is false on two counts: telomerase synthesises DNA only 5'\to3' (like every known polymerase, never 3'\to5'), and its template is RNA, not DNA.
5. Since the question is an MSQ, all true statements must be selected: (B) and (C).

KEY IDEA

Telomerase is a ribonucleoprotein reverse transcriptase: its RNA subunit (TERC) is the template it copies, and its protein subunit (TERT) extends chromosome ends 5'\to3' using that RNA template, i.e. RNA-dependent DNA polymerase activity.

WATCH OUT FOR

Confusing telomerase with a standard DNA-dependent DNA polymerase (choosing A) because both "make DNA", while missing that telomerase's template is its own RNA, not a DNA strand, and forgetting that all polymerases (including telomerase) synthesise only 5'\to3', which rules out D on direction alone even before considering the template type.

Q.53 MSQ · 2 MARKS

Genetics, Cell and Molecular Biology › Mendelian genetics

The blood group of the mother is A+ and that of the father is AB+. Which of the following statements is/are correct?

(A) Probability of the offspring with A+ blood group is 0.5

(B) Probability of the offspring with AB+ blood group is 0.125

(C) Probability of the offspring with B+ blood group is 0.125

(D) Probability of the offspring with O+ blood group is 0.375

Official answer: **A, C**

Q.54 MSQ · 2 MARKS

Fundamentals of Biological Engineering › Immobilisation

An enzyme immobilised in a porous spherical pellet, catalyses a strongly mass-transfer limited first-order reaction. The effectiveness factor for the immobilised enzyme reaction increases with the

(A) decrease in the size of the pellet

(B) increase in the pore diffusivity within the pellet

(C) decrease in the enzyme turnover number

(D) increase in the enzyme concentration within the pellet

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

SOLUTION

1. For a first-order enzyme reaction (substrate concentration well below K_m), the intrinsic rate per unit pellet volume is $v = k_1 S$, with $k_1 = \dfrac{V_{max}}{K_m} = \dfrac{k_{cat} E_0}{K_m}$. Here k_{cat} is the turnover number, E_0 the enzyme concentration inside the pellet, V_{max} the maximum rate and K_m the Michaelis constant.
2. Thiele modulus for a sphere of radius R with effective pore diffusivity D_e:
$$\phi = \frac{R}{3}\sqrt{\frac{k_1}{D_e}} = \frac{R}{3}\sqrt{\frac{k_{cat} E_0}{K_m D_e}}$$
3. Effectiveness factor for a first-order reaction in a sphere: $\eta = \dfrac{1}{\phi}\left(\dfrac{1}{\tanh 3\phi} - \dfrac{1}{3\phi}\right)$. This decreases steadily as ϕ increases. In the strongly diffusion-limited regime (ϕ large) it reduces to
$$\eta \approx \frac{1}{\phi} = \frac{3}{R}\sqrt{\frac{K_m D_e}{k_{cat} E_0}}$$
So η rises whenever ϕ falls.
4. (A) Smaller pellet: $\eta \propto 1/R$. A smaller R lowers ϕ and raises η. Correct.
5. (B) Higher pore diffusivity: $\eta \propto \sqrt{D_e}$. A larger D_e lowers ϕ and raises η. Correct.
6. (C) Lower turnover number: $\eta \propto 1/\sqrt{k_{cat}}$. A smaller k_{cat} lowers ϕ and raises η. The enzyme now reacts more slowly compared with how fast diffusion brings in substrate, so more of the pellet interior is used. The overall rate falls, but η is higher. Correct.

7. (D) More enzyme in the pellet: $\eta \propto 1/\sqrt{E_0}$. A larger E_0 raises ϕ and lowers η, because substrate is used up closer to the surface. Incorrect.
8. So the effectiveness factor increases for (A), (B) and (C).

KEY IDEA

The effectiveness factor depends only on the Thiele modulus $\phi = \frac{R}{3}\sqrt{\frac{k_{cat}E_0}{K_m D_e}}$, and it falls as ϕ rises (in the strongly diffusion-limited regime, $\eta \approx 1/\phi$). Anything that lowers R, k_{cat} or E_0, or raises D_e, increases η.

WATCH OUT FOR

Treating the effectiveness factor as if it were the reaction rate. More enzyme (D) raises the overall rate, but it lowers η because it raises ϕ. A lower turnover number (C) lowers the rate but raises η, so students often reject C and pick D.

Q.55 MSQ · 2 MARKS

Recombinant DNA Technology and Tools › Assays & electrophoresis

Which of the following methods is/are used for identifying histone modifications?

(A) ChIP-seq

(B) Mass spectrometry

(C) Immunofluorescence

(D) Patch-clamp electrophysiology

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

SOLUTION

1. This is an MSQ (one or more correct); evaluate each option on whether the named technique can detect/identify a chemical (post-translational) modification on a histone protein.
2. (A) ChIP-seq: a modification-specific antibody (e.g., anti-H3K27ac, anti-H3K4me3) immunoprecipitates chromatin bearing that mark, and sequencing the pulled-down DNA maps where the modification occurs genome-wide. This directly identifies histone modifications and their genomic location. CORRECT.
3. (B) Mass spectrometry: histone PTMs (acetylation, methylation, phosphorylation, etc.) each produce a characteristic, measurable mass shift on the modified residue. MS analysis of digested histone peptides identifies which residues carry which modification with high precision, and is the standard unbiased discovery method for histone PTMs. CORRECT.
4. (C) Immunofluorescence: modification-specific antibodies (e.g., anti-H3K9me3) conjugated to fluorophores visualize the presence and subcellular/chromatin localization of a histone modification directly in fixed cells. CORRECT.
5. (D) Patch-clamp electrophysiology measures ionic currents through membrane ion channels; it provides no biochemical or immunological readout for a covalent modification on a nuclear histone protein. INCORRECT.
6. Therefore the techniques that identify histone modifications are A, B and C.

KEY IDEA

Histone post-translational modifications (acetylation, methylation, phosphorylation, etc.) can be identified by antibody-based methods (ChIP-seq for genome-wide location, immunofluorescence for cellular localization) and by direct physical/chemical detection (mass spectrometry, which measures the mass shift the modification causes). Patch-clamp electrophysiology measures ion-channel currents across membranes and has no readout for a covalent chromatin modification.

WATCH OUT FOR

Confusing "identifying/detecting a modification" with "measuring gene expression": some students wrongly include RT-PCR/qPCR-type reasoning or wrongly exclude ChIP-seq thinking it only maps genomic location, not the modification itself, when the antibody step is precisely what identifies the modification.

Q.56 MSQ · 2 MARKS

Recombinant DNA Technology and Tools › Assays & electrophoresis

Which of the following amino acids contain(s) two chiral carbons?

(A) L-Leucine

(B) L-Threonine

(C) L-Isoleucine

(D) L-Asparagine

Official answer: **B, C**

SOLUTION

1. A chiral carbon is one bonded to four different substituents.
2. Every amino acid's α-carbon (bonded to -NH2, -COOH, -H and the side chain R) is chiral whenever R ≠ H, which is true for all four options, so each amino acid has at least one chiral carbon (Cα).
3. L-Leucine: side chain is -CH2-CH(CH3)2. The branched carbon bears two identical methyl groups, so it is not a stereocentre. Total chiral carbons = 1 (Cα only). Option A is incorrect.
4. L-Threonine: side chain is -CH(OH)-CH3. This β-carbon is bonded to -OH, -CH3, -H and the rest of the molecule (-CH(NH2)COOH): four different groups, so it is a second stereocentre. Total = 2 (Cα and Cβ). Option B is correct.
5. L-Isoleucine: side chain is -CH(CH3)-CH2-CH3. This β-carbon is bonded to -CH3, -CH2CH3, -H and the rest of the molecule: four different groups, so it is also a stereocentre. Total = 2 (Cα and Cβ). Option C is correct.
6. L-Asparagine: side chain is -CH2-CONH2. The -CH2- carbon has two identical hydrogens, and the amide carbon is sp2 (trigonal planar), so neither can be chiral. Total = 1 (Cα only). Option D is incorrect.
7. Hence only Threonine and Isoleucine have two chiral carbons each, consistent with each being known to have a diastereomeric 'allo' form (allo-threonine, allo-isoleucine) arising from the second stereocentre.

KEY IDEA

A carbon is chiral only if all four groups attached to it are different. In every amino acid the α-carbon (–NH2, –COOH, –H, side chain R) is chiral whenever R ≠ H; a second chiral centre exists only if some side-chain carbon also carries four distinct substituents.

WATCH OUT FOR

Forgetting to check the side-chain β-carbon for chirality and stopping after confirming only the α-carbon. This misses both Threonine and Isoleucine, or wrongly credits Leucine/Asparagine based on chain length alone rather than checking whether all four substituents on a given carbon are actually distinct.

Q.57 NAT · 2 MARKS

Q.57 A binary mixture of benzene and toluene under vapour-liquid equilibrium at 80 °C follows ideal Raoult's law. At this condition, the saturation pressures of benzene and toluene are 101 kPa and 40 kPa, respectively. If the mole fraction of benzene in the liquid phase is 0.6, the corresponding mole fraction of benzene in the vapour phase will be _____.

(Round off to two decimal places)

Official answer: **0.76 to 0.82**

Q.58 NAT · 2 MARKS

Fundamentals of Biological Engineering › Growth kinetics

In a fermentation process, each mole of glucose is converted to biomass ($CH_{1.8}O_{0.5}N_{0.2}$), with a biomass yield coefficient of 0.4 C-mol/C-mol, according to the unbalanced equation given below.

$$C_6H_{12}O_6 + NH_3 + O_2 \rightarrow CH_{1.8}O_{0.5}N_{0.2} + CO_2 + H_2O$$

The moles of oxygen consumption per mole of glucose consumed during fermentation is _____.

(*Round off to two decimal places*)

Official answer: **3.30 to 3.60**

SOLUTION

1. Work on a basis of 1 mol of glucose, which is 6 C-mol (six carbon atoms). The biomass yield coefficient on a carbon basis is $Y_{X/S} = 0.4\ \text{C-mol biomass per C-mol glucose}$, so the biomass formed is $0.4 \times 6 = 2.4\ \text{C-mol}$. One C-mol of $CH_{1.8}O_{0.5}N_{0.2}$ contains exactly one carbon atom.
2. Carbon balance: $6 = 2.4 + n_{CO_2}$, so $n_{CO_2} = 3.6\ \text{mol}$.
3. Degree of reduction γ (available electrons, counting C = 4, H = 1, O = −2, N = −3, with NH_3 as the nitrogen source). Glucose: $\gamma_S = 6(4) + 12(1) + 6(-2) = 24$ per mole (4 per C-mol). Biomass: $\gamma_X = 4 + 1.8 - 2(0.5) - 3(0.2) = 4.2$ per C-mol. NH_3, CO_2 and H_2O all have $\gamma = 0$, and each mole of O_2 accepts 4 electrons.
4. Available-electron balance: the electrons in the glucose end up either in the biomass or on oxygen, so $\gamma_S \times 1 = \gamma_X \times (\text{C-mol biomass}) + 4\,n_{O_2}$, i.e. $24 = 4.2 \times 2.4 + 4\,n_{O_2}$.
5. $$n_{O_2} = \frac{24 - 10.08}{4} = \frac{13.92}{4} = 3.48\ \text{mol } O_2 \text{ per mol glucose}$$
6. Check with a full element balance. Nitrogen: $NH_3 = 0.2 \times 2.4 = 0.48\ \text{mol}$. Hydrogen: $12 + 3(0.48) = 1.8(2.4) + 2w$, so $13.44 = 4.32 + 2w$ and $w = 4.56\ \text{mol } H_2O$. Oxygen: $6 + 2a = 0.5(2.4) + 2(3.6) + 4.56 = 12.96$, so $a = 3.48$. This agrees with the electron balance.
7. Oxygen consumed $= 3.48$ mol per mol of glucose.

KEY IDEA

Convert the carbon-basis yield to biomass C-mol (0.4 × 6 = 2.4). Then use the available-electron (degree of reduction) balance: the electrons in the glucose go either into the biomass or to oxygen. With NH3 as the nitrogen source, $\gamma_S = 24$ per mol glucose and $\gamma_X = 4.2$ per C-mol, so $4\,n_{O_2} = 24 - 4.2(2.4)$.

WATCH OUT FOR

Treating 0.4 as mol biomass per mol glucose instead of per C-mol, which gives 0.4 C-mol of biomass instead of 2.4. Using 4 as the degree of reduction for a whole mole of glucose (4 is per C-mol; per mole it is 24). Forgetting that N in NH3 counts as −3, which makes the biomass value 5.0 instead of 4.2.

Q.59 NAT · 2 MARKS

Engineering Mathematics › Calculus

Let $a_0 = 0$ and define $a_n = \frac{1}{2}(1 + a_{n-1})$ for all positive integers $n \geq 1$. The least value of n for which $|1 - a_n| < \frac{1}{2^{10}}$ is _____. (Answer in integer)

Official answer: **11**

SOLUTION

1. Let $e_n = 1 - a_n$. Since $a_0 = 0$, $e_0 = 1$.
2. Subtract the recurrence from 1: $1 - a_n = 1 - \frac{1}{2}(1 + a_{n-1}) = \frac{1}{2}(1 - a_{n-1})$, so $e_n = \frac{1}{2}e_{n-1}$.
3. This is a geometric sequence with ratio $\frac{1}{2}$ and first term $e_0 = 1$, so $e_n = \frac{1}{2^n}$. It is positive, so $|1 - a_n| = \frac{1}{2^n}$.
4. The condition $\frac{1}{2^n} < \frac{1}{2^{10}}$ means $2^n > 2^{10}$, so $n > 10$.
5. At $n = 10$ the error equals $\frac{1}{2^{10}}$ exactly, which is not strictly less. The least integer with $n > 10$ is $n = 11$.

KEY IDEA
Rewrite the recurrence for the error $1 - a_n$. The error halves at every step, so $|1 - a_n| = 2^{-n}$ exactly, and the inequality is strict.

WATCH OUT FOR
Answering $n = 10$. At $n = 10$ the error is exactly $\frac{1}{2^{10}}$, and the condition is strict ($<$), so $n = 10$ fails.

Q.60 NAT · 2 MARKS

Recombinant DNA Technology and Tools › Microscopy & spectroscopy

The percentage of light that would pass through a sample with an absorbance of 2 would be _____% . (Round off to the nearest integer)

Official answer: **1**

SOLUTION

1. Absorbance (A) and transmittance (T) are related by $A = -\log_{10}(T)$, where T is the fraction of incident light transmitted (0 to 1).
2. Rearranging: $T = 10^{-A}$.
3. Substitute $A = 2$: $T = 10^{-2} = 0.01$.
4. Percentage transmittance $= T \times 100 = 0.01 \times 100 = 1\%$.
5. Rounded to the nearest integer: 1%.

KEY IDEA
Absorbance and percentage transmittance are related by $A = -\log_{10}(T)$, where T is the fraction (0 to 1) of incident light transmitted; percentage transmittance is $T \times 100$.

WATCH OUT FOR
Confusing absorbance with percentage absorbed directly (e.g. assuming $A = 2$ means 2% or 98% transmittance), instead of using the logarithmic relation $T = 10^{-A}$.

Q.61 NAT · 2 MARKS

Q.61 A hot, freshly-sterilised fermentation medium is cooled in a double-pipe heat-exchanger. The medium enters the inner pipe of the exchanger at 95 °C and leaves the exchanger at 40 °C. Cooling water, flowing counter-currently to the medium, enters the annulus of the exchanger at 15 °C and leaves the exchanger at 45 °C. The overall heat transfer coefficient is 1350 W m^{-2} $°C^{-1}$. The rate of heat transfer per unit area will be _____ W/m^2.

(Round off to the nearest integer)

Official answer: **48000 to 49000**

Q.62 NAT · 2 MARKS

Fundamentals of Biological Engineering › Bioreactor operation

A 2 L bioreactor is being operated as a chemostat, at a flow rate of 0.8 L/h and sterile feed of 10 g/L substrate. The bacterial growth follows Monod kinetics at a maximum specific growth rate of 0.6 h^{-1} with a Monod constant of 0.5 g/L and a biomass yield coefficient of 0.4 g/g.

The exit biomass concentration is _____ g/L.

(*Round off to one decimal place*)

Official answer: **3.4 to 3.8**

SOLUTION

1. Dilution rate, where F is the volumetric flow rate and V the working volume: $D = \frac{F}{V} = \frac{0.8\ \text{L h}^{-1}}{2\ \text{L}} = 0.4\ \text{h}^{-1}$.
2. At steady state in a chemostat with sterile feed ($X_0 = 0$), and with no cell death or maintenance, the biomass balance $0 = -DX + \mu X$ with $X \neq 0$ gives specific growth rate = dilution rate: $\mu = D = 0.4\ \text{h}^{-1}$.
3. Monod kinetics: $\mu = \frac{\mu_{max} S}{K_s + S}$, where $\mu_{max} = 0.6\ \text{h}^{-1}$ is the maximum specific growth rate, $K_s = 0.5\ \text{g L}^{-1}$ is the Monod constant and S is the substrate concentration in the reactor (which equals the exit concentration in a well-mixed chemostat). Setting $\mu = D$ and solving for S:
$$S = \frac{K_s D}{\mu_{max} - D} = \frac{0.5 \times 0.4}{0.6 - 0.4} = 1.0\ \text{g L}^{-1}$$
4. Washout check, with $S_0 = 10\ \text{g L}^{-1}$ the feed substrate concentration: $D_{crit} = \frac{\mu_{max} S_0}{K_s + S_0} = \frac{0.6 \times 10}{0.5 + 10} = 0.571\ \text{h}^{-1}$. Since $D = 0.4\ \text{h}^{-1} < D_{crit}$, a steady state without washout exists.
5. Steady-state substrate balance, with $Y_{X/S} = 0.4\ \text{g g}^{-1}$ the biomass yield on substrate (grams of cells formed per gram of substrate consumed):
$$X = Y_{X/S}(S_0 - S) = 0.4 \times (10 - 1.0) = 3.6\ \text{g L}^{-1}$$
6. Exit biomass concentration $= 3.6\ \text{g L}^{-1}$.

KEY IDEA

At steady state in a chemostat with sterile feed, the specific growth rate equals the dilution rate ($\mu = D = F/V$). Putting that into the Monod equation gives the substrate concentration in the reactor, $S = K_s D/(\mu_{max} - D)$. The yield then gives the biomass, $X = Y_{X/S}(S_0 - S)$. Check first that D is below the washout dilution rate.

WATCH OUT FOR

Taking D as the flow rate itself (0.8 h^{-1}), which is above μ_{max} and so wrongly predicts washout. Another is using the feed concentration S_0 in place of $S_0 - S$ and getting $X = 0.4 \times 10 = 4.0$ g/L. It is also possible to swap K_s and μ_{max} when rearranging the Monod equation for S.

Q.63 NAT · 2 MARKS

Recombinant DNA Technology and Tools › Microscopy & spectroscopy

Let $A = \begin{pmatrix} 1 & 0 & 1 \\ 0 & k & 0 \\ 3 & 0 & -1 \end{pmatrix}$. If the eigenvalues of A are -2, 1, and 2, then the value of k is _____. (Answer in integer)

Official answer: **1**

SOLUTION

1. Given $A = \begin{bmatrix} 1 & 0 & 1 \\ 0 & k & 0 \\ 3 & 0 & -1 \end{bmatrix}$ with eigenvalues $-2, 1, 2$.
2. For any square matrix, trace(A) = sum of its eigenvalues. Here $\text{trace}(A) = 1 + k + (-1) = k$.
3. Sum of the given eigenvalues $= -2 + 1 + 2 = 1$, so $k = 1$.
4. Cross-check using $\det(A)$ = product of eigenvalues. Expanding along the second row (only the $(2,2)$ entry is nonzero there): $\det(A) = k \begin{vmatrix} 1 & 1 \\ 3 & -1 \end{vmatrix} = k(-1 - 3) = -4k$.

5. Product of the given eigenvalues $= (-2)(1)(2) = -4$, so $-4k = -4 \Rightarrow k = 1$, confirming the trace-based result.

KEY IDEA
For any square matrix, the trace equals the sum of its eigenvalues and the determinant equals the product of its eigenvalues: two independent checks on the same unknown.

WATCH OUT FOR
Forgetting that the trace–sum-of-eigenvalues relation holds for any square matrix (not just diagonalizable ones), or making a sign slip while expanding the determinant along the row/column containing k.

Q.64 NAT · 2 MARKS

Recombinant DNA Technology and Tools › Microscopy & spectroscopy

An NMR spectrometer operating at proton resonance frequency (v) of 1 GHz will have a magnetic field strength of _____ Tesla (T).

The gyromagnetic ratio for proton, γ = 2.675 × 10^8 T^-1 s^-1

(Round off to one decimal place)

Official answer: **23.2 to 23.8**

SOLUTION

1. Recognize the governing relation: the NMR resonance (Larmor) condition is $\omega = \gamma B_o$, where ω is the angular precession frequency of the proton in the magnetic field B_o and γ is the proton's gyromagnetic ratio.
2. Relate angular frequency to the given resonance frequency v: $\omega = 2\pi v$, so $v = \gamma B_o/(2\pi)$.
3. Solve for the field strength: $B_o = 2\pi v/\gamma$.
4. Convert the given frequency to SI units: v = 1 GHz = 1×10^9 Hz.
5. Substitute the given values: γ = 2.675×10^8 T^-1 s^-1, so $B_o = 2\pi(1\times10^9)/(2.675\times10^8)$.
6. Compute: 2π×10^9 = 6.283185307×10^9, and 6.283185307×10^9 / 2.675×10^8 ≈ 23.4885 T.
7. Round to one decimal place as instructed: $B_o \approx 23.5$ T.

KEY IDEA
The NMR resonance condition (Larmor equation) relates the applied magnetic field to the resonance (Larmor) frequency through the gyromagnetic ratio of the nucleus: the angular frequency $\omega = \gamma B_o$, and $\omega = 2\pi v$, so $v = \gamma B_o/(2\pi)$, giving $B_o = 2\pi v/\gamma$.

WATCH OUT FOR
Using v directly in the Larmor equation ω = γB0 without converting v to angular frequency (forgetting the factor of 2π), which gives a wrong field strength off by a factor of ~6.28.

Q.65 NAT · 2 MARKS

General Biology › Metabolism

For the coupled reactions given below

Glucose 6-phosphate + H2O → Glucose + Pi (Reaction 1)
ATP + Glucose → ADP + Glucose 6-phosphate (Reaction 2)

the standard free energy change of ATP hydrolysis at 25 °C is ___ kJ/mol.

The equilibrium constants for Reaction 1 and Reaction 2 are 360 and 800, respectively; Gas constant R = 8.314 J mol^-1 K^-1.

(Round off to two decimal places)

Official answer: **-32.00 to -30.00**

SOLUTION

1. Add the two reactions. Glucose 6-phosphate and glucose appear on both sides and cancel, leaving $\mathrm{ATP} + \mathrm{H_2O} \rightarrow \mathrm{ADP} + \mathrm{P}_i$, which is ATP hydrolysis.
2. Standard free energy changes of reactions that add together are added: $\Delta G^\circ_{\mathrm{hyd}} = \Delta G^\circ_1 + \Delta G^\circ_2$. Equivalently, the equilibrium constants multiply: $K_{\mathrm{hyd}} = K_1 K_2$.
3. Use $\Delta G^\circ = -RT \ln K$ with $T = 25 + 273.15 = 298.15$ K: $RT = 8.314 \times 298.15 \approx 2478.8$ J mol^{-1}.
4. $K_{\mathrm{hyd}} = 360 \times 800 = 2.88 \times 10^5$, so $\ln K_{\mathrm{hyd}} = \ln 2.88 + 5 \ln 10 \approx 1.0578 + 11.5129 = 12.5707$.
5. $\Delta G^\circ_{\mathrm{hyd}} = -2478.8 \times 12.5707 \approx -31160$ J mol^{-1} ≈ -31.16 kJ mol^{-1}.
6. Check by parts: $\Delta G^\circ_1 = -2478.8 \ln 360 = -2478.8 \times 5.8861 \approx -14.59$ kJ mol^{-1} and $\Delta G^\circ_2 = -2478.8 \ln 800 = -2478.8 \times 6.6846 \approx -16.57$ kJ mol^{-1}. Their sum is -31.16 kJ mol^{-1}, in agreement.

KEY IDEA

When reactions are coupled (added), their standard free energy changes add and their equilibrium constants multiply. Use $\Delta G^\circ = -RT \ln K$ with T in kelvin.

WATCH OUT FOR

Using $\log_{10}$ instead of $\ln$, using 25 K instead of 298.15 K, adding the equilibrium constants instead of multiplying them, or dropping the minus sign.

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