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GATE BT · 2023

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GATE BT 2023 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 Kanpur

Online, with the questions linked to their topic notes: **iaeacademy.in/study/papers/bt-2023**

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About this paper

65 questions, 100 marks. Question types: 32 MCQ · 7 MSQ · 26 NAT.

Official answer key: IIT Kanpur · https://gate.iitk.ac.in/GATE2023/doc/papers/2023/ANS/BT_ANS_GATE2023.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	**B**
Q.2	MCQ	1	**C**
Q.3	MCQ	1	**B**
Q.4	MCQ	1	**D**
Q.5	MCQ	1	**C**
Q.6	MCQ	2	**D**
Q.7	MCQ	2	**A**
Q.8	MCQ	2	**C**
Q.9	MCQ	2	**A**
Q.10	MCQ	2	**D**
Q.11	MCQ	1	**A**
Q.12	MCQ	1	**A**
Q.13	MCQ	1	**D**
Q.14	MCQ	1	**B**
Q.15	MCQ	1	**A**
Q.16	MCQ	1	**D**
Q.17	MCQ	1	**A**
Q.18	MCQ	1	**A**
Q.19	MCQ	1	**A**
Q.20	MCQ	1	**A**
Q.21	MCQ	1	**A**
Q.22	MCQ	1	**A**
Q.23	MCQ	1	**A**
Q.24	MCQ	1	**A**
Q.25	MCQ	1	**A**
Q.26	MCQ	1	**C**
Q.27	MCQ	1	**C**
Q.28	MCQ	1	**C**
Q.29	MCQ	1	**A**
Q.30	NAT	1	**25**
Q.31	NAT	1	**6**
Q.32	NAT	1	**2500**
Q.33	NAT	1	**0.10 to 0.12**
Q.34	NAT	1	**0.166 to 0.168**
Q.35	NAT	1	**1.40 to 1.42**
Q.36	MCQ	2	**A**
Q.37	MCQ	2	**A**
Q.38	MCQ	2	**A**
Q.39	MSQ	2	**B, C**
Q.40	MSQ	2	**A, B, C**
Q.41	MSQ	2	**A, B, D**
Q.42	MSQ	2	**A, C**
Q.43	MSQ	2	**A, B, C**
Q.44	MSQ	2	**A, B, C**
Q.45	MSQ	2	**A, B**
Q.46	NAT	2	**0.41 to 0.44**
Q.47	NAT	2	**2.24 to 2.26**
Q.48	NAT	2	**10**
Q.49	NAT	2	**94 to 96**
Q.50	NAT	2	**-2.74 to -2.71**
Q.51	NAT	2	**15**
Q.52	NAT	2	**945**
Q.53	NAT	2	**4.6 to 4.9**
Q.54	NAT	2	**20**
Q.55	NAT	2	**74**
Q.56	NAT	2	**1.0 to 1.2**
Q.57	NAT	2	**0.165 to 0.168**
Q.58	NAT	2	**10551**
Q.59	NAT	2	**-2**
Q.60	NAT	2	**5**
Q.61	NAT	2	**0.45**
Q.62	NAT	2	**1**
Q.63	NAT	2	**1437 to 1439**
Q.64	NAT	2	**4**
Q.65	NAT	2	**1600**

General Aptitude Q.1 to Q.10

Q.1 MCQ · 1 MARK

General Aptitude › Grammar & vocabulary

"You are delaying the completion of the task. Send _____ contributions at the earliest."

(A) you are

(B) your

(C) you're

(D) yore

Official answer: **B**

SOLUTION

1. The blank comes directly before the noun "contributions", so the missing word must modify a noun. That calls for a possessive determiner.
2. (A) "you are" is a subject plus a verb. It cannot modify a noun, and "Send you are contributions" is ungrammatical.
3. (C) "you're" is the contraction of "you are", so it fails for the same reason as (A).
4. (D) "yore" means "long ago" (as in "days of yore"). It is not a possessive and makes no sense here.
5. (B) "your" is the possessive determiner meaning "belonging to you". "Send your contributions at the earliest" is grammatical and fits the instruction to the person delaying the task.
6. Answer: (B).

KEY IDEA

A word placed before a noun to show ownership must be a possessive determiner (your). A subject plus verb, such as "you are" or "you're", cannot do that job.

WATCH OUT FOR

Confusing "your" (possessive) with "you're" (the contraction of "you are"). A quick test is to expand the contraction: "Send you are contributions" makes no sense.

Q.2 MCQ · 1 MARK

General Aptitude › Reasoning

References : _____ : : Guidelines : Implement
(By word meaning)

(A) Sight

(B) Site

(C) Cite

(D) Plagiarise

Official answer: **C**

SOLUTION

1. This is a verbal analogy (By word meaning): the blank must relate to "References" as "Implement" relates to "Guidelines".
2. Second pair: guidelines are put into practice, and "implement" is the action properly done to them.
3. So the blank must be the action properly done to references: one cites them, giving credit to the source.
4. Sight (vision) and Site (a place) are not actions done to references. They are only homophones of "cite".

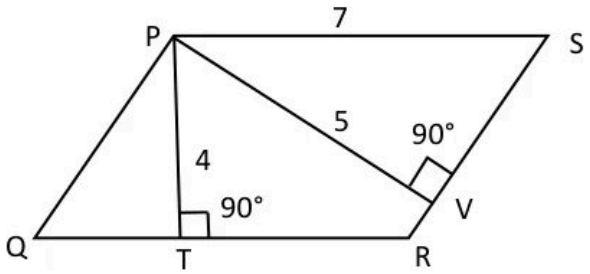
5. Plagiarise means to copy without credit. It is the improper treatment of references, so it does not match the proper action "Implement".
6. References : Cite :: Guidelines : Implement. The answer is (C).

KEY IDEA
In a verbal analogy, find the relation in the complete pair (Guidelines : Implement, the proper action done to the thing). Then choose the word that has that same relation to the first word.

WATCH OUT FOR
Choosing Plagiarise because it sounds connected to references, or picking Sight or Site because they sound like Cite. Plagiarise is the improper treatment, not the proper action, and Sight and Site are not actions done to references.

Q.3 MCQ · 1 MARK

General Aptitude › Geometry

Q.3	In the given figure, PQRS is a parallelogram with PS = 7 cm, PT = 4 cm and PV = 5 cm. What is the length of RS in cm? (The diagram is representative.)
	
(A)	$\frac{20}{7}$
(B)	$\frac{28}{5}$
(C)	$\frac{9}{2}$
(D)	$\frac{35}{4}$

Official answer: **B**

SOLUTION

1. Opposite sides of a parallelogram are equal, so $QR = PS = 7$ cm.
2. $PT \perp QR$ (right angle at T), so PT is the height on base QR. Area $= QR \times PT = 7 \times 4 = 28$ cm^2.
3. $PV \perp RS$ (right angle at V), so PV is the height on base RS. Area $= RS \times PV = 5\,RS$.
4. The area of a parallelogram is the same whichever side is taken as the base, so $5\,RS = 28$.

5. $$RS = \frac{28}{5}\ \text{cm}$$

6. This matches option (B).

KEY IDEA
A parallelogram's area equals base times the height perpendicular to that base, so the same area computed with two different base-and-height pairs gives an equation for the unknown side.

WATCH OUT FOR
Treating PV = 5 as a side length, or taking RS = PS = 7 or multiplying 7 by 5 and 4 without pairing each base with its own perpendicular height. Only the heights PT (on QR) and PV (on RS) pair with those bases.

Q.4 MCQ · 1 MARK

General Aptitude › Reasoning

In 2022, June Huh was awarded the Fields medal, which is the highest prize in Mathematics.

When he was younger, he was also a poet. He did not win any medals in the International Mathematics Olympiads. He dropped out of college.

Based only on the above information, which one of the following statements can be logically inferred with certainty?

(A) Every Fields medalist has won a medal in an International Mathematics Olympiad.

(B) Everyone who has dropped out of college has won the Fields medal.

(C) All Fields medalists are part-time poets.

(D) Some Fields medalists have dropped out of college.

Official answer: **D**

SOLUTION

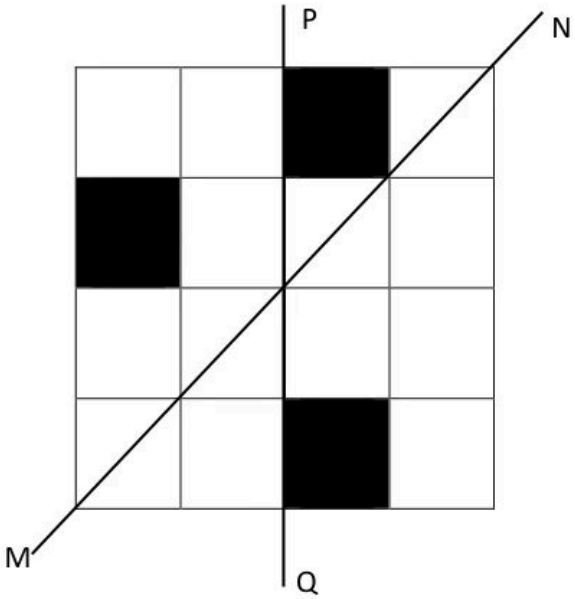
1. The facts given: June Huh won the Fields medal in 2022, was a poet when younger, won no medal in the International Mathematics Olympiads, and dropped out of college.
2. Option (A) says every Fields medalist has won an Olympiad medal. Huh is a Fields medalist who won none, so (A) is false.
3. Option (B) says everyone who has dropped out of college has won the Fields medal. Huh is one dropout who won it, but that does not show it for all dropouts, so (B) cannot be inferred.
4. Option (C) says all Fields medalists are part-time poets. Huh was a poet when younger, but the passage never says he was a part-time poet, and one person says nothing about all medalists, so (C) cannot be inferred.
5. Option (D) says some Fields medalists have dropped out of college. Huh is a Fields medalist and he dropped out of college, so at least one Fields medalist dropped out. (D) follows with certainty.
6. Rule: one example is enough to prove an existential ("some") statement, but never enough to prove a universal ("all" or "every") statement.

KEY IDEA
One named example proves a "some" statement. It cannot prove an "all" or "every" statement.

WATCH OUT FOR
Choosing (B) or (C) because Huh fits them. A single person who fits a universal claim does not establish it for everyone. Also, the passage says he was a poet, not a part-time poet.

Q.5 MCQ · 1 MARK

General Aptitude › Spatial

Q.5	A line of symmetry is defined as a line that divides a figure into two parts in a way such that each part is a mirror image of the other part about that line. The given figure consists of 16 unit squares arranged as shown. In addition to the three black squares, what is the minimum number of squares that must be coloured black, such that both PQ and MN form lines of symmetry? (The figure is representative)
	
(A)	3
(B)	4
(C)	5
(D)	6

Official answer: **C**

SOLUTION

1. Label each cell as (row, column), with rows counted from the top and columns from the left, in the 4 x 4 grid. The black cells are (1,3), (2,1) and (4,3). PQ is the vertical line between columns 2 and 3. MN is the diagonal from the bottom-left corner to the top-right corner. The two lines meet at the centre of the grid.
2. Reflecting in PQ sends column c to column $5 - c$, so $(r, c) \to (r, 5 - c)$. Reflecting in MN sends $(r, c) \to (5 - c,\ 5 - r)$. This fixes the bottom-left corner (4,1) and the top-right corner (1,4), which both

lie on MN.

3. The figure must look the same after both reflections. So whenever a cell is black, every cell reached from it by any chain of these two reflections must also be black. The two mirror lines meet at 45°, so their reflections together give the 8 symmetries of a square.
4. Follow the chain from the black cell (1,3). Reflect in PQ to get (1,2). Reflect in MN to get (3,4). Reflect in PQ to get (3,1). Reflect in MN to get (4,2)... Carrying on from the other cells gives the full set: (1,2), (1,3), (2,1), (2,4), (3,1), (3,4), (4,2), (4,3). That is 8 cells.
5. Check that the three given black cells are all in this set: (1,3) is in it. Under MN, (1,3) goes to (2,4), and under PQ, (2,4) goes to (2,1). Under MN, (2,1) goes to (4,3). So (2,1) and (4,3) are in the same set.
6. All 8 cells of this set must be black, and only these. The other 8 cells form sets of their own: (1,1), (1,4), (4,1), (4,4) and (2,2), (2,3), (3,2), (3,3). They are already white and form a symmetric pattern, so no more cells are needed.
7. Cells still to be coloured: $8 - 3 = 5$. The minimum number of extra squares is 5, which is option (C).

KEY IDEA

A figure with two lines of symmetry must be a union of whole sets of cells that the reflections swap among themselves. Find the set containing each black cell, colour the whole set, and count the cells that were not already black.

WATCH OUT FOR

Colouring only the mirror images of each black cell in one line, or in a single step, and stopping. The mirror images of the new cells in the other line must be coloured too, and so on until the set closes. This gives 3 or 4 instead of 5.

Q.6 MCQ · 2 MARKS

General Aptitude › Reasoning

Human beings are one among many creatures that inhabit an imagined world. In this imagined world, some creatures are cruel. If in this imagined world, it is given that the statement “Some human beings are not cruel creatures” is FALSE, then which of the following set of statement(s) can be logically inferred with certainty?

(i) All human beings are cruel creatures.
(ii) Some human beings are cruel creatures.
(iii) Some creatures that are cruel are human beings.
(iv) No human beings are cruel creatures.

(A) only (i)
(B) only (iii) and (iv)
(C) only (i) and (ii)
(D) (i), (ii) and (iii)

Official answer: **D**

SOLUTION

1. If "Some human beings are not cruel creatures" is FALSE, its contradictory must be TRUE. The contradictory of "Some H are not C" is "All H are C". So (i) "All human beings are cruel creatures" is true.
2. The passage says human beings inhabit this imagined world, so at least one human being exists. Every human being is cruel, so some human beings are cruel creatures. So (ii) is true.
3. "Some H are C" converts to "Some C are H". So some cruel creatures are human beings, and (iii) is true.
4. (iv) "No human beings are cruel creatures" contradicts (ii), which is true, so (iv) is false.
5. Exactly (i), (ii) and (iii) can be inferred with certainty. This is option (D).

KEY IDEA
The negation of "Some A are not B" is "All A are B". Check that the class is non-empty before concluding "Some", then convert "Some A are B" to "Some B are A".

WATCH OUT FOR
Choosing option (C) by forgetting that "Some human beings are cruel creatures" can be reversed to give (iii). Another slip is to doubt (ii) because "All" does not by itself imply "Some", when the passage does say that human beings exist.

Q.7 MCQ · 2 MARKS

General Aptitude › Numerical

To construct a wall, sand and cement are mixed in the ratio of 3:1. The cost of sand and that of cement are in the ratio of 1:2.

If the total cost of sand and cement to construct the wall is 1000 rupees, then what is the cost (in rupees) of cement used?

(A) 400
(B) 600
(C) 800
(D) 200

Official answer: **A**

SOLUTION

1. The quantities of sand and cement are in the ratio $3 : 1$, and the unit costs (per unit of material) are in the ratio $1 : 2$.
2. The money spent on each material is quantity $\times$ unit cost, so the ratio of money spent is the product of the two ratios.
3. Sand : cement cost $= 3 \times 1 : 1 \times 2 = 3 : 2$.
4. The total is $3 + 2 = 5$ parts, and these 5 parts make up Rs. 1000, so one part is Rs. 200.
5. Cement's share $= \frac{2}{5} \times 1000 = 400$ rupees.
6. Check: sand costs $3 \times 200 = 600$ and cement costs $2 \times 200 = 400$, and $600 + 400 = 1000$.

KEY IDEA
When a mixture is given by quantity ratio and unit-price ratio, the cost ratio of the components is the product of the two ratios. Then split the total in that cost ratio.

WATCH OUT FOR
Using the quantity ratio 3:1 directly as the cost ratio (giving cement 250 rupees, which is not an option), or using the price ratio 1:2 alone (giving cement 667 rupees). Both ratios must be multiplied.

Q.8 MCQ · 2 MARKS

General Aptitude › Reading

The World Bank has declared that it does not plan to offer new financing to Sri Lanka, which is battling its worst economic crisis in decades, until the country has an adequate macroeconomic policy framework in place. In a statement, the World Bank said Sri Lanka needed to adopt structural reforms that focus on economic stabilisation and tackle the root causes of its crisis. The latter has starved it of foreign exchange and led to shortages of food, fuel, and medicines. The bank is repurposing resources under existing loans to help alleviate shortages of essential items such as medicine, cooking gas, fertiliser, meals for children, and cash for vulnerable households.

Based only on the above passage, which one of the following statements can be inferred with *certainty*?

(A) According to the World Bank, the root cause of Sri Lanka's economic crisis is that it does not have enough foreign exchange.

(B) The World Bank has stated that it will advise the Sri Lankan government about how to tackle the root causes of its economic crisis.

(C) According to the World Bank, Sri Lanka does not yet have an adequate macroeconomic policy framework.

(D) The World Bank has stated that it will provide Sri Lanka with additional funds for essentials such as food, fuel, and medicines.

Official answer: **C**

SOLUTION

1. "Inferred with certainty" means the statement must follow from the passage alone. Reject any option that reverses a stated cause and effect, adds a promise the passage never makes, or states a fact the passage does not give.
2. Option (A): the passage says the root causes of the crisis "starved it of foreign exchange". The lack of foreign exchange is therefore an effect of the root causes, not the root cause itself. (A) reverses cause and effect.
3. Option (B): the passage says Sri Lanka needs to adopt structural reforms. It never says the World Bank will advise the government. (B) adds a promise that is not stated.
4. Option (D): the passage says the Bank is repurposing resources under existing loans, and that it does not plan new financing for now. Redirecting existing loan resources is not the same as providing additional funds, so (D) is not supported, and it conflicts with the refusal of new financing.
5. Option (C): the Bank will not offer new financing until the country has an adequate macroeconomic policy framework in place. Making that framework a condition for new financing means the Bank regards it as not yet in place. (C) follows directly.
6. Hence the answer is (C).

KEY IDEA

For "inferred with certainty" questions, accept only what the passage states or directly entails. A condition of the form "will not do X until Y" entails that Y does not yet hold.

WATCH OUT FOR

Choosing (A) because it sounds like the passage. The passage names foreign exchange shortage as a result of the root causes, not as the root cause. Choosing (D) because the Bank is helping with shortages overlooks that this uses existing loans and is not new funding.

Q.9 MCQ · 2 MARKS

General Aptitude › Numerical

The coefficient of x^4 in the polynomial $(x-1)^3(x-2)^3$ is equal to _____.

(A) 33

(B) -3

(C) 30

(D) 21

Official answer: **A**

SOLUTION

1. Combine the two cubes, since $a^3b^3 = (ab)^3$: $(x-1)^3(x-2)^3 = \big[(x-1)(x-2)\big]^3 = (x^2-3x+2)^3$.
2. The product has degree 6. Write it as three identical factors (x^2-3x+2). The x^4 term comes from picking one term from each factor so that the powers of x add to 4.
3. Case 1: pick x^2 from two factors and the constant 2 from the third. The powers are $2+2+0=4$. There are 3 ways to choose which factor gives the constant. Contribution: $3 \times (1)(1)(2) = 6$.

4. Case 2: pick x^2 from one factor and $-3x$ from the other two. The powers are $2+1+1=4$. There are 3 ways to choose which factor gives x^2. Contribution: $3 \times (1)(-3)(-3) = 27$.
5. No other selection gives total power 4. For example, three x^2 terms give 6, and x^2, $-3x$, 2 gives 3. Choices with no x^2 give at most $1+1+1=3$.
6. Add the contributions: $6 + 27 = 33$. The coefficient of x^4 is 33, option (A).

KEY IDEA

Rewrite $(x-1)^3(x-2)^3$ as $(x^2-3x+2)^3$. Then collect the x^4 term by listing which term each of the three factors contributes so the powers add to 4.

WATCH OUT FOR

Counting only the $x^2, x^2, 2$ case and forgetting the $x^2, -3x, -3x$ case, or leaving out the factor 3 for the arrangements. This gives 6 or 2 instead of 33.

Q.10 MCQ · 2 MARKS

General Aptitude › Spatial

Which one of the following shapes can be used to tile (completely cover by repeating) a flat plane, extending to infinity in all directions, without leaving any empty spaces in between them? The copies of the shape used to tile are identical and are not allowed to overlap.

(A) circle

(B) regular octagon

(C) regular pentagon

(D) rhombus

Official answer: **D**

SOLUTION

1. A shape tiles the plane with identical copies only if the copies can be fitted together with no gaps and no overlaps. At every meeting point (vertex) the angles must add up to 360°.
2. Circle: it has no corners and its edge is curved. Identical circles that touch always leave curved gaps between them, so a circle cannot tile the plane.
3. Regular octagon: each interior angle is $\frac{(8-2)\times 180^\circ}{8} = 135^\circ$. Two octagons meeting at a point use 270° and leave 90°, which an octagon corner (135°) cannot fill. Since $\frac{360^\circ}{135^\circ} = 2.67$ is not a whole number, the octagon alone cannot tile the plane.
4. Regular pentagon: each interior angle is $\frac{(5-2)\times 180^\circ}{5} = 108^\circ$. Since $\frac{360^\circ}{108^\circ} = 3.33$ is not a whole number, the pentagon alone cannot tile the plane.
5. Rhombus: it is a parallelogram, so its angles are α, $180^\circ - \alpha$, α, $180^\circ - \alpha$. At a vertex, put two corners of angle α and two corners of angle $180^\circ - \alpha$: the sum is $2\alpha + 2(180^\circ - \alpha) = 360^\circ$, so the copies close up exactly. Equivalently, every parallelogram tiles the plane by repeated translation.
6. So the rhombus is the only option that can tile the plane. Answer: (D).

KEY IDEA

For a shape to tile the plane, copies must fit around each vertex with angles summing to 360°. Every parallelogram, and so every rhombus, tiles by translation, because its four angles pair up to 360° at a vertex.

WATCH OUT FOR

Thinking that any regular-looking shape tiles. Only the regular triangle, square and hexagon tile the plane among regular polygons. The pentagon (angle 108°) and the octagon (angle 135°) do not divide 360° evenly, and the circle always leaves gaps.

Biotechnology Q.11 to Q.65

Q.11 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Gene expression

Eukaryotic transcription is carried out by

(A) DNA-dependent RNA polymerase

(B) DNA-dependent DNA polymerase

(C) RNA-dependent DNA polymerase

(D) RNA-dependent RNA polymerase

Official answer: **A**

SOLUTION

1. Transcription is defined as the synthesis of RNA using a DNA template, so the correct answer must describe an enzyme with DNA as template and RNA as product.
2. (A) DNA-dependent RNA polymerase: template = DNA, product = RNA: exactly matches transcription. In eukaryotes this activity is carried out by RNA polymerases I, II and III. Correct.
3. (B) DNA-dependent DNA polymerase: template = DNA, product = DNA. This is DNA replication, not transcription. Incorrect.
4. (C) RNA-dependent DNA polymerase: template = RNA, product = DNA. This is reverse transcriptase, used by retroviruses, not by eukaryotic cells for normal transcription. Incorrect.
5. (D) RNA-dependent RNA polymerase: template = RNA, product = RNA; used by RNA viruses to replicate their genomes, not used in eukaryotic transcription. Incorrect.
6. Hence eukaryotic transcription is carried out by DNA-dependent RNA polymerase, option (A).

KEY IDEA

Transcription is the DNA-templated synthesis of RNA; in eukaryotes this is carried out by DNA-dependent RNA polymerases (RNA Pol I, II and III), each transcribing a distinct class of genes (rRNA, mRNA/most genes, tRNA/5S rRNA respectively).

WATCH OUT FOR

Confusing the four polymerase/enzyme classes by template-versus-product: DNA-dependent DNA polymerase (B) performs replication, not transcription; RNA-dependent DNA polymerase (C) is reverse transcriptase, used by retroviruses to convert their RNA genome into DNA; RNA-dependent RNA polymerase (D) is used by RNA viruses to replicate RNA genomes; none of these describe normal eukaryotic transcription.

Q.12 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Cell signalling

Acetylcholine released by the parasympathetic nerves has which one of the following functions in the heart pacemaker cells?

(A) It binds to GPCR and activates G protein to slow the heart rate

(B) It stimulates GABA-activated ion-channel coupled receptor to increase the heart rate

(C) It binds to GPCR and inhibits G protein to slow the heart rate

(D) It inhibits GABA-activated ion-channel coupled receptor to increase the heart rate

Official answer: **A**

SOLUTION

1. Parasympathetic (vagal) acetylcholine acts on the M2 muscarinic acetylcholine receptor on SA-node pacemaker cells, a GPCR, not a ligand-gated ion channel.

2. Options B and D invoke a 'GABA-activated ion-channel coupled receptor', which is unrelated to cardiac pacemaker physiology (GABA-A receptors are neuronal ligand-gated Cl– channels) and both also wrongly claim an increase in heart rate; both are eliminated.
3. At the M2 receptor, ACh binding activates the coupled inhibitory G protein (Gi/Go); the G protein itself is turned ON, not inhibited.
4. The activated Gi/Go then inhibits adenylyl cyclase (lowering cAMP) and its Gβγ subunits open GIRK K+ channels, hyperpolarizing the SA node and slowing the pacemaker firing rate (negative chronotropy).
5. Option A ('binds to GPCR and activates G protein to slow the heart rate') matches this mechanism exactly.
6. Option C ('binds to GPCR and inhibits G protein to slow the heart rate') is wrong: ACh does not inhibit the G protein. It activates the inhibitory G protein; the inhibition occurs downstream, at adenylyl cyclase.
7. Correct answer: A.

KEY IDEA

In SA-node pacemaker cells, parasympathetic acetylcholine acts on M2 muscarinic receptors, GPCRs coupled to an inhibitory G protein (Gi/Go), not on any GABA-gated channel. Binding activates this Gi/Go protein, which then inhibits adenylyl cyclase (lowering cAMP) and opens GIRK K+ channels, hyperpolarizing the cell and slowing the pacemaker rate (negative chronotropy).

WATCH OUT FOR

Confusing "activates the inhibitory G protein" with "inhibits the G protein": the inhibition in this pathway happens downstream (Gi inhibits adenylyl cyclase), not at the G protein itself, which is what makes distractor (C) attractive but wrong.

Q.13 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Gene expression

Determine the correctness or otherwise of the following Assertion [a] and the Reason [r].

Assertion [a]: In multicellular organisms, cells of different lineages have different gene expression profiles.

Reason [r]: Alternative splicing is the only mechanism to generate protein diversity.

(A) Both [a] and [r] are false

(B) Both [a] and [r] are true and [r] is the correct reason for [a]

(C) Both [a] and [r] are true but [r] is not the correct reason for [a]

(D) [a] is true but [r] is false

Official answer: **D**

SOLUTION

1. Assertion [a]: In multicellular organisms, all cells share the same genome, but differentiated lineages (for example neurons versus hepatocytes) express distinct subsets of genes. This differential gene expression (driven by lineage-specific transcription factors, chromatin accessibility and epigenetic marks) is the well-established molecular basis of cell differentiation. Hence [a] is TRUE.
2. Reason [r]: The statement claims alternative splicing is 'the only mechanism' to generate protein diversity. Alternative splicing (producing multiple mRNA/protein isoforms from one pre-mRNA) is indeed a real and important source of protein diversity, but the claim of exclusivity must be checked against other known mechanisms.
3. Multiple other well-established mechanisms independently generate protein diversity: alternative promoter usage / alternative transcription start sites, alternative polyadenylation, RNA editing, and post-translational modifications (phosphorylation, glycosylation, proteolytic cleavage, etc.).

4. Because at least one other genuine mechanism exists (in fact several), the exclusivity claim 'the only mechanism' in [r] is factually incorrect. Hence [r] is FALSE.
5. With [a] true and [r] false, the correct match is option (D): '[a] is true but [r] is false'.
6. Elimination check: (A) requires both false, contradicted since [a] is true. (B) and (C) both require [r] to be true, contradicted since [r] is false. Only (D) is consistent with the analysis.

KEY IDEA

This is an Assertion-Reason question requiring two independent judgments: (1) is [a] true or false on its own biological merits, and (2) is [r] true or false on its own merits; only if both are true do you then ask whether [r] correctly explains [a]. Differential/lineage-specific gene expression (via differential transcription factor activity, chromatin state, epigenetic marks, etc.) is the well-established basis of cellular differentiation in multicellular organisms, making [a] true. Protein diversity, however, arises from multiple independent mechanisms: alternative splicing, alternative promoter usage/transcription start sites, alternative polyadenylation, RNA editing, and post-translational modifications (phosphorylation, glycosylation, proteolytic cleavage), so the absolute claim that alternative splicing is "the only" mechanism is false, regardless of alternative splicing's real importance.

WATCH OUT FOR

Treating alternative splicing as if it were "a" or "the main" source of protein diversity and conflating that with "the only" mechanism. Since alternative splicing genuinely does create isoform diversity, students may misread the exaggerated exclusivity claim in [r] as true and pick (B) or (C) instead of recognizing that "only" makes the reason factually false.

Q.14 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Population & evolution

Determine the correctness or otherwise of the following Assertion [a] and the Reason [r].

Assertion [a]: Chromosome mutations can change the structure of chromosomes.

Reason [r]: All chromosome mutations arise due to nondisjunction of chromosomes during mitosis or meiosis.

(A) Both [a] and [r] are false

(B) [a] is true but [r] is false

(C) Both [a] and [r] are true and [r] is the correct reason for [a]

(D) Both [a] and [r] are true but [r] is not the correct reason for [a]

Official answer: **B**

SOLUTION

1. Classify what each term describes. In standard cytogenetic classification, mutations affecting chromosomes fall into two distinct categories: (i) chromosomal (structural) mutations: deletions, duplications, inversions and translocations, which change the STRUCTURE/arrangement of a chromosome; and (ii) genomic (numerical) mutations: aneuploidy (e.g. trisomy, monosomy) and polyploidy, which change the NUMBER of chromosomes.
2. Evaluate Assertion [a]: 'Chromosome mutations can change the structure of chromosomes.' This is simply the definition of a structural chromosome mutation, so [a] is TRUE.
3. Evaluate Reason [r]: 'All chromosome mutations arise due to nondisjunction of chromosomes during mitosis or meiosis.' Nondisjunction is the failure of homologous chromosomes (meiosis I) or sister chromatids (meiosis II or mitosis) to separate properly; its consequence is a change in chromosome NUMBER in the daughter cells (aneuploidy), not a change in chromosome structure.

4. Structural chromosome mutations instead result from chromosome breakage (caused by radiation, mutagenic chemicals, or errors in recombination/replication) followed by incorrect rejoining, a mechanism unrelated to nondisjunction.
5. So [r] wrongly attributes structural chromosome mutations to nondisjunction, and its blanket claim 'All chromosome mutations arise due to nondisjunction' is also over-general even for numerical mutations. Hence [r] is FALSE.
6. Since [a] is true and [r] is false, options (A), (C) and (D), which all require [r] to be true, are eliminated, leaving option (B).

KEY IDEA

Chromosome (structural) mutations (deletions, duplications, inversions, translocations) change chromosome STRUCTURE and arise from breakage-and-faulty-rejoining; genomic (numerical) mutations (aneuploidy, polyploidy) change chromosome NUMBER and arise from nondisjunction. The two mechanisms and the two categories are distinct, so Reason [r] conflates them.

WATCH OUT FOR

Treating "chromosome mutation" as a blanket term covering any chromosome-related abnormality, and then assuming nondisjunction (the most commonly taught mutational mechanism) must be the cause, missing that nondisjunction specifically produces numerical (genomic), not structural, changes.

Q.15 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Mutation & repair

C-value paradox refers to

(A) the lack of correlation between genome size and genetic complexity of an organism

(B) the presence of genetic sequences that propagate themselves within a genome

(C) the coexistence of multiple alleles at a genetic locus

(D) the concept that two or more genes may have the same function

Official answer: **A**

SOLUTION

1. Recall the definition of "C-value": the amount of haploid DNA (genome size) contained in a cell of an organism.
2. The C-value paradox is the well-documented observation that genome size (C-value) does not correlate with the organism's morphological or genetic complexity; for example, some amoebae and lungfish have genomes far larger than the human genome despite not being more "complex," a discrepancy largely attributable to variable amounts of non-coding/repetitive DNA.
3. Option (A) states precisely this (lack of correlation between genome size and genetic complexity), so (A) is correct.
4. Option (B) describes the behaviour of selfish/transposable genetic elements, which is a proposed contributor to genome size expansion but is not itself the definition of the C-value paradox. Incorrect.
5. Option (C) describes the coexistence of multiple alleles at a locus, a population-genetics concept (related to heterozygosity), unrelated to genome size. Incorrect.
6. Option (D) describes functional redundancy among genes, unrelated to genome size or the paradox. Incorrect.
7. Hence only (A) correctly defines the C-value paradox.

KEY IDEA
The C-value paradox: an organism's haploid genome size (its C-value) does not correlate with its morphological or organismal complexity, e.g., some amoebae, lungfish, and even some plants have vastly larger genomes than humans, largely due to variable amounts of non-coding/repetitive DNA rather than a greater number of functional genes.

WATCH OUT FOR
Confusing the C-value paradox (genome size vs. complexity mismatch) with related but distinct concepts also tested as distractors: transposable/selfish DNA propagation (a proposed *cause* of genome size variation, not the paradox itself), multiple alleles at a locus (a population-genetics idea unrelated to genome size), or gene functional redundancy (unrelated to genome size).

Q.16 MCQ · 1 MARK

General Biology › Adaptive immunity

Which one of the following drugs is NOT an immune checkpoint inhibitor?

(A) Ipilimumab
(B) Pembrolizumab
(C) Nivolumab
(D) Trastuzumab

Official answer: **D**

SOLUTION

1. Immune checkpoint inhibitors are monoclonal antibodies that block inhibitory receptors on T cells, or their ligands, so the brake on T-cell activation against the tumour is released.
2. (A) Ipilimumab is an anti-CTLA-4 antibody. CTLA-4 competes with CD28 for B7 binding and dampens T-cell priming, so blocking it makes ipilimumab a checkpoint inhibitor.
3. (B) Pembrolizumab is an anti-PD-1 antibody. It blocks PD-1 from binding PD-L1 and PD-L2, so it is a checkpoint inhibitor.
4. (C) Nivolumab is also an anti-PD-1 antibody, so it is a checkpoint inhibitor.
5. (D) Trastuzumab is an antibody against the HER2/neu receptor on breast and gastric cancer cells. It acts by blocking HER2 signalling and by antibody-dependent cellular cytotoxicity. It does not target a T-cell checkpoint, so it is the one that is NOT a checkpoint inhibitor.
6. The answer is (D).

KEY IDEA
Checkpoint inhibitors target CTLA-4 (ipilimumab) or the PD-1/PD-L1 axis (pembrolizumab, nivolumab). Trastuzumab targets the HER2 receptor on tumour cells, which is a tumour-targeted therapy and not a checkpoint blocker.

WATCH OUT FOR
Treating every therapeutic antibody used in cancer as an immunotherapy checkpoint drug. All four names end in -mab, but only the first three act on T-cell checkpoints. Trastuzumab acts on HER2 on the cancer cell.

Q.17 MCQ · 1 MARK

General Biology › Adaptive immunity

Dendritic cells are involved in cross-presentation of antigens. Which of the following protein(s) is(are) required for cross-presentation?
P. Basic leucine zipper ATF-like transcription factor 3 (BATF3)
Q. Membrane associated ring-CH-type finger 1 (MARCH-1)
R. Solute carrier family 10 member 1 (SLC10A1)
S. Class II-associated invariant chain peptide (CLIP)

(A) P only
(B) P and R only

(C) P, Q and R only

(D) S only

Official answer: **A**

SOLUTION

1. Cross-presentation loads antigen taken up from outside the cell onto MHC class I, so that CD8 T cells are primed. In mice it is done mainly by the cDC1 subset of dendritic cells (CD8α+ and CD103+).
2. P, BATF3: this transcription factor is needed for cDC1 development. Batf3-deficient mice lack cDC1 cells and cross-present very poorly. So P is required.
3. Q, MARCH-1: this E3 ubiquitin ligase ubiquitinates MHC class II and CD86 and controls how long they stay on the cell surface. It acts on the MHC II pathway, not on cross-presentation. So Q is not required.
4. R, SLC10A1: this is the sodium taurocholate cotransporting polypeptide, a bile-acid transporter of hepatocytes that is also the hepatitis B virus entry receptor. It has no role in antigen processing. So R is not required.
5. S, CLIP: this is a fragment of the invariant chain that sits in the MHC II peptide groove until HLA-DM swaps it for an antigenic peptide. It belongs to MHC II loading, not to cross-presentation. So S is not required.
6. Only P is required, so the answer is (A) P only.

KEY IDEA

Cross-presentation depends on cDC1 dendritic cells, whose development needs BATF3. MARCH-1 and CLIP belong to the MHC II pathway. SLC10A1 is a liver bile-acid transporter.

WATCH OUT FOR

Picking MARCH-1 or CLIP because they sound like antigen-presentation proteins. Both act on MHC II, not on the MHC I route used in cross-presentation. SLC10A1 is also chosen by mistake because it is an unfamiliar name.

Q.18 MCQ · 1 MARK

General Biology › Adaptive immunity

Which one of the following is required for the development of B-cells in the bone marrow?

(A) Stromal cells

(B) Dendritic cells

(C) Kupffer cells

(D) NK cells

Official answer: **A**

SOLUTION

1. B-cells develop from hematopoietic stem cells in the bone marrow, passing through pro-B, pre-B and immature B-cell stages before they leave for the periphery.
2. Each stage depends on contact with bone marrow stromal cells (reticular cells, osteoblast-lineage cells and endothelial cells). These cells supply stem cell factor (SCF), the chemokine CXCL12, IL-7 and adhesion molecules such as VCAM-1.
3. (A) Stromal cells: correct. They form the niche that drives B-lymphopoiesis. Without IL-7 and CXCL12, development stalls at an early progenitor stage.
4. (B) Dendritic cells: wrong. They are antigen-presenting cells that activate T-cells in peripheral lymphoid organs. They are not part of the marrow niche for B-cell development.
5. (C) Kupffer cells: wrong. These are liver-resident macrophages that clear particles and pathogens from the blood. They are not part of the B-cell niche.

6. (D) NK cells: wrong. They are innate cytotoxic lymphocytes that kill virus-infected and tumour cells. B-cell maturation does not need them.
7. Hence the answer is (A).

KEY IDEA
B-lymphopoiesis in the bone marrow depends on the stromal cell niche, which supplies IL-7, CXCL12, SCF and adhesion molecules. Dendritic cells, Kupffer cells and NK cells play no part in it.

WATCH OUT FOR
Choosing dendritic cells because they are linked to antigen presentation and B-cell responses. That role is in peripheral lymphoid organs. It is not a requirement for B-cell development in the marrow.

Q.19 MCQ · 1 MARK

General Biology › Pathogens & antibiotics

Which one of the following statements is TRUE about leghemoglobin?

(A) It binds oxygen to protect nitrogenase
(B) It binds hemoglobin to protect oxygenase
(C) It binds oxygen to protect hydrogenase
(D) It binds oxygen to protect oxygenase

Official answer: **A**

SOLUTION

1. Leghemoglobin is a heme-containing, oxygen-binding protein made in the root nodules of legumes, where rhizobia (as bacteroids) fix nitrogen.
2. Nitrogenase, which reduces N_2 to NH_3, is irreversibly inactivated by free O_2, so the nodule interior must keep free O_2 very low.
3. The bacteroids still need O_2 for aerobic respiration, which supplies the large ATP demand of nitrogen fixation. Leghemoglobin binds O_2 with high affinity, so it holds free O_2 low and still delivers O_2 to the bacteroid respiratory chain.
4. Option (A) is correct: leghemoglobin binds oxygen and so protects nitrogenase.
5. Option (B) is wrong: leghemoglobin binds oxygen, not hemoglobin, and no oxygenase is the protected enzyme.
6. Option (C) is wrong: the enzyme protected is nitrogenase. Hydrogenase in the nodule only recycles the H_2 released by nitrogenase and is not what leghemoglobin protects.
7. Option (D) is wrong: oxygenases use O_2 as a substrate and are not damaged by it, so they need no protection.

KEY IDEA
Nitrogenase is destroyed by free oxygen, but the bacteroids still need oxygen to respire. Leghemoglobin buffers oxygen: it keeps free O_2 low and still delivers it to the bacteroids.

WATCH OUT FOR
Confusing leghemoglobin with ordinary hemoglobin, or thinking it protects an oxygenase or hydrogenase. The enzyme it protects is nitrogenase.

Q.20 MCQ · 1 MARK

General Biology › Pathogens & antibiotics

The correct sequence of events during bacteriophage infection of a bacterial cell is

(A) landing → attachment → tail contraction → penetration and unplugging → DNA ejection
(B) attachment → landing → penetration and unplugging → tail contraction → DNA ejection
(C) landing → tail contraction → attachment → DNA ejection → penetration and unplugging

(D) attachment → tail contraction → landing → penetration and unplugging → DNA ejection

Official answer: **A**

SOLUTION

1. For a contractile-tailed phage such as T4, infection follows a fixed order: landing, attachment, tail contraction, penetration and unplugging, then DNA ejection.
2. Landing comes first. The long tail fibres touch the cell surface and reversibly recognise receptors such as lipopolysaccharide or OmpC. Firm attachment cannot happen until the virion has landed.
3. Attachment follows. The short tail fibres and baseplate bind irreversibly, and this changes the baseplate shape and triggers the sheath.
4. Tail contraction comes next. The sheath shortens and drives the rigid inner tail tube forward. Contraction is triggered by a firmly attached baseplate, so it cannot come before attachment.
5. Penetration and unplugging follow. The tube crosses the outer membrane and peptidoglycan, and the plug at the tip is released, which opens the channel.
6. DNA ejection is last, because the genome can leave the head only through the open tube.
7. Option A gives exactly this order. B and D put attachment before landing. C puts contraction before attachment, and DNA ejection before penetration and unplugging. So only A is correct.

KEY IDEA
Phage infection proceeds from reversible landing to irreversible attachment, which triggers sheath contraction. The tube then penetrates and the plug opens, and only then is the DNA ejected.

WATCH OUT FOR
Swapping landing and attachment, or putting contraction before attachment. Contraction is the result of firm baseplate binding, not its cause. Another slip is to eject DNA before the channel is open.

Q.21 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Cell signalling

Intracellular proteins are targeted for proteolytic degradation in proteasomes upon conjugation with

(A) ubiquitin

(B) integrin

(C) peptidase

(D) calreticulin

Official answer: **A**

SOLUTION

1. Recall that intracellular protein turnover in eukaryotes proceeds mainly via the ubiquitin-proteasome system.
2. Option (A) ubiquitin: a 76-residue protein covalently conjugated to lysine residues of a target protein via the E1-E2-E3 enzyme cascade; polyubiquitination is the signal recognized by the 26S proteasome for degradation. Correct.
3. Option (B) integrin: a transmembrane cell-adhesion receptor linking the cytoskeleton to the extracellular matrix; not a degradation-targeting tag. Incorrect.
4. Option (C) peptidase: an enzyme class that hydrolyzes peptide bonds; a protein is not "conjugated with" a peptidase as a targeting signal (proteasome subunits themselves act as peptidases, but that is not the tagging event). Incorrect.
5. Option (D) calreticulin: an ER-lumen calcium-binding chaperone in the calnexin/calreticulin protein-folding quality-control cycle, not a proteasomal degradation tag. Incorrect.
6. Therefore the molecule whose conjugation targets proteins for proteasomal degradation is ubiquitin, giving answer (A).

KEY IDEA
Covalent tagging of a target protein with (poly)ubiquitin chains is the signal recognized by the 26S proteasome for ATP-dependent proteolytic degradation.

WATCH OUT FOR
Confusing peptidase (an enzyme that carries out proteolysis, including proteasomal subunits) with the actual conjugated targeting tag; peptidase is never itself covalently attached to a substrate as a degradation signal.

Q.22 MCQ · 1 MARK

Recombinant DNA Technology and Tools › Assays & electrophoresis

In ELISA, which of the following enzymes are conjugated to antibodies for detection of the analyte?

P. Alkaline phosphatase
Q. Trypsinase
R. Horseradish peroxidase
S. Amylase

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

Official answer: **A**

SOLUTION

1. The question asks which enzymes, when conjugated to antibodies in ELISA, produce a detectable signal for the analyte.
2. P. Alkaline phosphatase (ALP): a standard ELISA reporter enzyme; hydrolyzes chromogenic substrates such as p-nitrophenyl phosphate (pNPP) to give a measurable yellow product. Qualifies.
3. Q. Trypsinase (trypsin): a serine protease used for proteolytic digestion/cell dissociation; it has no chromogenic substrate reaction used for ELISA signal readout. Does not qualify.
4. R. Horseradish peroxidase (HRP): the other standard ELISA reporter enzyme; oxidizes substrates such as TMB or ABTS in an H_2O_2-dependent reaction to give a colored, highly sensitive signal. Qualifies.
5. S. Amylase: hydrolyzes starch; used in digestion/starch assays, not as an antibody-conjugated reporter in immunoassays. Does not qualify.
6. Only P (alkaline phosphatase) and R (horseradish peroxidase) are genuine ELISA reporter enzymes with established substrate-based detection chemistry.
7. This corresponds to option (A): P and R.

KEY IDEA
ELISA detection relies on antibody-enzyme conjugates whose enzyme activity produces a measurable colored/chemiluminescent signal upon substrate addition; only alkaline phosphatase and horseradish peroxidase are standard ELISA reporter enzymes among the four listed.

WATCH OUT FOR
Confusing any hydrolytic/digestive enzyme (trypsin, amylase) with a chromogenic reporter enzyme; only enzymes with a colorimetric/chemiluminescent substrate reaction (ALP, HRP) are used as ELISA labels.

Q.23 MCQ · 1 MARK

Plant, Animal and Microbial Biotechnology › Hybridomas & transgenics

In hybridoma technology, which one of the following enzymes is absent in the myeloma cells that are used for monoclonal antibody production?

(A) Hypoxanthine-guanine phosphoribosyltransferase

(B) Alanine aminotransferase

(C) Triose phosphate isomerase

(D) Glycosyltransferase

Official answer: **A**

SOLUTION

1. Hybridoma technology fuses antibody-secreting B cells, which die in culture after a short time, with immortal myeloma cells. The fused cells are grown in HAT medium (hypoxanthine, aminopterin, thymidine).
2. Aminopterin blocks the de novo pathway for purine and thymidylate synthesis, so a cell in HAT medium can survive only if the salvage pathway works.
3. The salvage pathway needs hypoxanthine-guanine phosphoribosyltransferase (HGPRT), which converts hypoxanthine and guanine into IMP and GMP. It also needs thymidine kinase for the thymidine route.
4. The myeloma cells chosen for fusion lack HGPRT. They are selected for resistance to 8-azaguanine, a toxic base analogue that only HGPRT-positive cells convert into a lethal nucleotide. Unfused myeloma cells therefore die in HAT medium.
5. A hybrid survives because the B-cell partner supplies HGPRT and the myeloma partner supplies immortality. HGPRT is therefore the enzyme absent from the myeloma cells, so option (A) is correct.
6. Option (B), alanine aminotransferase, is a general amino acid metabolism enzyme that every cell needs. Myeloma cells have it, so (B) is wrong.
7. Option (C), triose phosphate isomerase, is a glycolytic enzyme. Cells need it to make ATP from glucose, so myeloma cells have it and (C) is wrong.
8. Option (D), glycosyltransferase, is needed to add sugars to proteins. Myeloma cells carry out glycosylation, so they have it and (D) is wrong.

KEY IDEA

HAT selection depends on the myeloma partner lacking HGPRT. Aminopterin blocks the de novo nucleotide pathway, so unfused myeloma cells cannot use the salvage pathway and die. Only hybrids, which get HGPRT from the B cell, survive.

WATCH OUT FOR

Confusing the missing enzyme with the one aminopterin blocks. Aminopterin inhibits the de novo pathway (dihydrofolate reductase) in every cell. The myeloma cells are the ones missing the salvage enzyme HGPRT. Some students also pick a general metabolic enzyme, but a cell cannot live without those.

Q.24 MCQ · 1 MARK

Recombinant DNA Technology and Tools › PCR & sequencing

Which of the following methods are used for detection of DNA and RNA, respectively?

(A) Southern and Northern blotting

(B) Southern and Western blotting

(C) Northern and Southern blotting

(D) Northern and Western blotting

Official answer: **A**

SOLUTION

1. The question asks which technique detects DNA and which detects RNA, in that order (DNA first, RNA second, per "respectively").
2. Southern blotting (named after its inventor, Edwin M. Southern) is the standard technique for detecting specific DNA sequences: DNA is digested, size-separated by gel electrophoresis, transferred to a

membrane, and probed with a labeled complementary probe.

3. Northern blotting is the analogous technique for RNA (its name is a play on "Southern"), used to detect specific RNA transcripts by size-separation, blotting, and probing.
4. Western blotting detects proteins via antibodies, not nucleic acids, so any option pairing DNA/RNA detection with Western blotting (options B and D) is incorrect.
5. Since the required order is DNA then RNA, the correct pairing is Southern (for DNA) and Northern (for RNA): option (A).
6. Option (C), "Northern and Southern," reverses the required order and is therefore incorrect.
7. The correct choice is (A).

KEY IDEA

Southern blotting detects DNA (named after Edwin M. Southern); Northern blotting detects RNA (a naming pun on "Southern"); Western blotting detects proteins. The question asks in the order DNA, then RNA, so the pairing must be Southern, then Northern — option A.

WATCH OUT FOR

Confusing the mnemonic order: swapping Southern/Northern (option C) because the "Northern" name is a play on "Southern" and students misremember which technique targets DNA vs RNA, or wrongly pairing Western blotting (a protein-detection technique) with a nucleic acid.

Q.25 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Gene expression

Q.25 Match the types of RNA in Group I with their corresponding function in Group II.

Group I	Group II
P. mRNA	1. Serves as adaptors between mRNA and amino acids during protein synthesis
Q. rRNA	2. Regulates post-transcriptional gene expression
R. miRNA	3. Codes for proteins
S. tRNA	4. Forms the core of the ribosome structure and catalyzes protein synthesis

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

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

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

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

Official answer: **A**

SOLUTION

1. mRNA (P) is the messenger transcript that carries the protein-coding sequence and is translated by ribosomes: P → 3 ("codes for proteins").
2. rRNA (Q) is the structural scaffold of both ribosomal subunits, and its large-subunit rRNA catalyzes peptide bond formation (a ribozyme activity): Q → 4 ("forms the core of the ribosome structure and catalyzes protein synthesis").

3. miRNA (R) base-pairs with complementary mRNA after transcription to trigger degradation or block translation: R → 2 ("regulates post-transcriptional gene expression").
4. tRNA (S) uses its anticodon to read the mRNA codon while carrying the matching amino acid, linking codons to amino acids during translation: S → 1 ("serves as adaptor between mRNA and amino acids").
5. Combined mapping: P-3, Q-4, R-2, S-1.
6. Compare with options: (A) P-3, Q-4, R-2, S-1 matches exactly; (B) swaps R and S (R-1, S-2); (C) swaps P and Q (P-4, Q-3); (D) scrambles all four pairings. None of these match the derived mapping.
7. Hence the correct choice is (A).

KEY IDEA

Each RNA class has a distinct, non-overlapping functional role: mRNA carries coding sequence, rRNA is the ribosome's structural and catalytic (ribozyme) core, miRNA post-transcriptionally silences gene expression, and tRNA is the adaptor linking codons to amino acids.

WATCH OUT FOR

Confusing tRNA's adaptor role (item 1) with miRNA's regulatory role (item 2), as in distractor (B), since both are "small" non-coding RNAs, but only tRNA physically carries amino acids and reads codons via its anticodon; miRNA acts on mRNA stability/translation, not amino acid delivery.

Q.26 MCQ · 1 MARK

Recombinant DNA Technology and Tools › Bioinformatics

Which one of the following programs is used for finding distantly related (or remote) protein homologs?

(A) BLASTN

(B) BLASTX

(C) PSI-BLAST

(D) TBLASTX

Official answer: **C**

SOLUTION

1. BLASTN aligns a nucleotide query against a nucleotide database; it does not address protein homology at all, so it is not the tool sought here.
2. BLASTX translates a nucleotide query (all six reading frames) and searches it against a protein database in a single-pass alignment, useful for identifying a likely protein match but not specialized for remote/distant homology detection.
3. TBLASTX translates both the nucleotide query and a nucleotide database (six frames on each side) and compares the translated sequences, again a single, direct alignment pass; computationally heavy but not iterative, so it offers no special sensitivity boost for remote homologs.
4. PSI-BLAST (Position-Specific Iterated BLAST) runs an initial BLAST search, then builds a position-specific scoring matrix (profile) from the statistically significant hits, and repeats the profile search over multiple iterations.
5. This iterative, profile-based refinement is precisely what amplifies weak or distant sequence similarity signals that a single-pass alignment (as in A, B, D) would miss, making PSI-BLAST the standard choice for detecting distantly related (remote) protein homologs.
6. Therefore option (C) PSI-BLAST is correct; options (A) BLASTN, (B) BLASTX, and (D) TBLASTX are each single-pass tools not designed for remote homology detection.

KEY IDEA

PSI-BLAST (Position-Specific Iterated BLAST) builds and iteratively refines a position-specific scoring matrix (profile) from initial hits, which amplifies weak, distant sequence similarity, making it the standard BLAST variant for detecting remote protein homologs, unlike the single-pass BLASTN/BLASTX/TBLASTX searches.

WATCH OUT FOR

Picking BLASTX or TBLASTX because they sound more "thorough" (translated searches), while missing that PSI-BLAST's iterative profile refinement, not translation of nucleotide frames, is what specifically boosts sensitivity to distant/remote homologs.

Q.27 MCQ · 1 MARK

Recombinant DNA Technology and Tools › Bioinformatics

Which one of the following is used for global alignment of two protein sequences?

(A) Chou-Fasman method

(B) Garnier-Osguthorpe-Robson (GOR) method

(C) Needleman-Wunsch algorithm

(D) Smith-Waterman algorithm

Official answer: **C**

SOLUTION

1. Chou-Fasman method (A): an empirical statistical method that predicts protein secondary structure (helix/sheet/turn propensities) from the amino acid sequence. It is a structure-prediction tool, not a sequence alignment method. Eliminated.
2. Garnier-Osguthorpe-Robson (GOR) method (B): another secondary-structure prediction method, based on information theory applied to sequence windows. Also not an alignment algorithm. Eliminated.
3. Needleman-Wunsch algorithm (C): a dynamic-programming algorithm that aligns the entire length of both input sequences end-to-end, inserting gaps as needed to maximize the overall alignment score. This is precisely the definition of global alignment.
4. Smith-Waterman algorithm (D): a dynamic-programming algorithm that finds the highest-scoring local region of similarity between two sequences; the alignment can start and end anywhere and excludes poorly matching regions. This is local alignment, not global. Eliminated despite also being a well-known alignment tool.
5. Since the question asks specifically for the algorithm used for global alignment of two protein sequences, and Needleman-Wunsch is the standard global-alignment algorithm (paired conceptually with Smith-Waterman for local alignment), option (C) is correct.

KEY IDEA

Needleman-Wunsch is the classic dynamic-programming algorithm for global sequence alignment (aligns full length, end to end); Smith-Waterman is its local-alignment counterpart (best-scoring subregion only). Chou-Fasman and GOR are unrelated secondary-structure prediction methods, not alignment algorithms.

WATCH OUT FOR

Confusing Needleman-Wunsch (global) with Smith-Waterman (local) since both are DP-based pairwise alignment algorithms. Remembering "N for 'k(N)ow the whole thing' = global" or simply memorizing the pairing (Needleman-Wunsch = Global, Smith-Waterman = Local) avoids the mix-up. A secondary mistake is confusing alignment algorithms with secondary-structure prediction methods (Chou-Fasman, GOR), which solve a completely different problem.

Q.28 MCQ · 1 MARK

Recombinant DNA Technology and Tools › Microscopy & spectroscopy

Which one of the following methods CANNOT be used to determine the secondary structure content of a protein?

(A) Circular dichroism spectroscopy

(B) Fourier transform infrared spectroscopy

(C) Mass spectrometry

(D) X-ray crystallography

Official answer: **C**

SOLUTION

1. The question asks which technique CANNOT determine the secondary structure content (percentage α-helix, β-sheet, random coil) of a protein.
2. (A) Circular dichroism (CD) spectroscopy: the far-UV CD spectrum (190–250 nm) shows characteristic signatures for α-helix (double minima near 208 nm and 222 nm), β-sheet (minimum near 218 nm) and random coil, and is routinely deconvoluted to estimate % secondary structure, so CD CAN determine it.
3. (B) FTIR spectroscopy: the amide I band (about 1600–1700 cm^{-1}) position and its sub-band deconvolution directly reflect the fractions of α-helix, β-sheet, turns and unordered structure, so FTIR CAN determine it.
4. (D) X-ray crystallography: gives the atomic-resolution three-dimensional structure of the folded protein, from which secondary structure elements (helices, strands) are read out directly, so X-ray crystallography CAN determine it.
5. (C) Mass spectrometry: measures the mass-to-charge ratio of ionized peptides/proteins, giving molecular mass, amino-acid composition, sequence and post-translational modifications. It does not probe backbone dihedral angles or hydrogen-bonding patterns, so it CANNOT report secondary structure content.
6. Hence the technique that cannot determine secondary structure content is (C) Mass spectrometry.

KEY IDEA

Secondary structure content (%α-helix, %β-sheet, %random coil) of a protein is determined by spectroscopic/structural methods that probe backbone conformation and H-bonding: CD (far-UV signature bands), FTIR (amide I band deconvolution), and X-ray crystallography (atomic-resolution structure). Mass spectrometry measures mass-to-charge ratio and reports mass, composition, sequence and PTMs, not backbone conformation, so it cannot determine secondary structure content.

WATCH OUT FOR

Students sometimes assume any advanced structural/analytical technique (including MS) can report "structure" in a general sense, without distinguishing between primary-structure/mass information (MS) and conformational/secondary-structure information (CD, FTIR, X-ray).

Q.29 MCQ · 1 MARK

Plant, Animal and Microbial Biotechnology › Plant tissue culture

Which one of the following plant growth regulators facilitate adventitious root formation?

(A) Auxin

(B) Zeatin

(C) Dihydrozeatin

(D) Kinetin

Official answer: **A**

SOLUTION

1. Adventitious roots (roots arising from stems, leaves or callus rather than from the primary root) are induced by the auxin to cytokinin balance: a high auxin to cytokinin ratio favours root formation, and a high cytokinin to auxin ratio favours shoot formation.
2. (A) Auxin (for example IAA, IBA, NAA) stimulates cells near the vascular tissue to divide and form root primordia, so it promotes adventitious root formation. Correct.
3. (B) Zeatin is a naturally occurring cytokinin. Cytokinins promote shoot bud formation and tend to inhibit root initiation. Wrong.
4. (C) Dihydrozeatin is a reduced derivative of zeatin and is also a cytokinin, so it does not promote rooting. Wrong.
5. (D) Kinetin is a synthetic cytokinin (a furfuryl adenine derivative) that promotes cell division and shoot formation, not rooting. Wrong.
6. Options B, C and D are all cytokinins and only option A is an auxin, so the answer is (A).

KEY IDEA
Rooting versus shooting in plant tissue culture is set by the auxin to cytokinin ratio. High auxin gives roots, and high cytokinin gives shoots. Zeatin, dihydrozeatin and kinetin are all cytokinins.

WATCH OUT FOR
Picking a cytokinin because it sounds like a general growth promoter. Cytokinins drive cell division and shoot buds, and they tend to suppress root initiation.

Q.30 NAT · 1 MARK

Genetics, Cell and Molecular Biology › Population & evolution

Fabry disease in humans is a X-linked disease. The probability (in percentage) for a phenotypically normal father and a carrier mother to have a son with Fabry disease is _____.

Official answer: **25**

SOLUTION

1. Fabry disease is X-linked recessive. Let A = normal (dominant) allele and a = Fabry-disease (recessive) allele on the X chromosome.
2. A phenotypically normal father has only one X chromosome and is unaffected, so his genotype must be X^AY.
3. A carrier mother is heterozygous (unaffected herself but carrying one copy of the disease allele), so her genotype is X^AX^a.
4. Cross $X^AY \times X^AX^a$: the father passes X^A or Y (each with probability $\frac{1}{2}$), and the mother passes X^A or X^a (each with probability $\frac{1}{2}$), giving four equally likely offspring: X^AX^A (normal daughter), X^AX^a (carrier daughter), X^AY (normal son), X^aY (affected son).
5. Exactly one of these four equally likely outcomes (X^aY) is a son affected with Fabry disease.
6. Probability of an affected son $= \frac{1}{4} = 25\%$.

KEY IDEA

Fabry disease is X-linked recessive. A normal father (X^AY) crossed with a carrier mother (X^AX^a) produces four equally likely offspring classes; only one of the four (X^aY, an affected son) has the disease, giving a probability of $\frac{1}{4} = 25\%$ among all offspring.

WATCH OUT FOR

Confusing "probability among all offspring" (1/4) with "probability among sons only" (1/2); the question asks for the former.

Q.31 NAT · 1 MARK

Engineering Mathematics › Calculus

The value of $\lim_{x\to 0}\left[\dfrac{\cos 2x - \cos 4x}{x^2}\right]$ is _____.

Official answer: **6**

SOLUTION

1. At $x = 0$ the numerator is $\cos 0 - \cos 0 = 1 - 1 = 0$ and the denominator is $0^2 = 0$, so the limit has the form $\frac{0}{0}$ and L'Hopital's rule (or a series expansion) applies.
2. Differentiate numerator and denominator: $\lim_{x\to 0}\dfrac{-2\sin 2x + 4\sin 4x}{2x}$. At $x = 0$ this is again $\frac{0}{0}$.
3. Apply the rule a second time: $\lim_{x\to 0}\dfrac{-4\cos 2x + 16\cos 4x}{2}$.
4. Put $x = 0$: $\dfrac{-4 + 16}{2} = 6$.
5. Check with the Maclaurin series $\cos ax \approx 1 - \dfrac{a^2x^2}{2}$: the numerator is $\left(1 - 2x^2\right) - \left(1 - 8x^2\right) = 6x^2$ up to terms of order x^4, so the ratio tends to 6.

KEY IDEA

The limit has the form 0/0, so apply L'Hopital's rule twice, or expand cos ax as 1 - a^2 x^2/2 and compare the x^2 terms: the coefficient of x^2 in cos 2x - cos 4x is -2 + 8 = 6.

WATCH OUT FOR

Stopping after one application of L'Hopital's rule, when the form is still 0/0. Another slip is forgetting the chain-rule factors 2 and 4, which turns -2 sin 2x + 4 sin 4x into a wrong coefficient. A sign slip on the cosine derivative gives -6 instead of 6.

Q.32 NAT · 1 MARK

Engineering Mathematics › Calculus

A series (S) is given as S = 1 + 3 + 5 + 7 + 9 + ... The sum of the first 50 terms of S is _____.

Official answer: **2500**

SOLUTION

1. The series $1 + 3 + 5 + 7 + 9 + \ldots$ is an arithmetic progression with first term $a = 1$ and common difference $d = 2$.
2. The sum of the first n terms of an AP is $S_n = \dfrac{n}{2}\left[2a + (n-1)d\right]$.
3. For $n = 50$: $S_{50} = \dfrac{50}{2}\left[2(1) + 49(2)\right]$.
4. $S_{50} = 25\left[2 + 98\right] = 25 \times 100 = 2500$.
5. Check: the sum of the first n odd numbers is n^2, so $S_{50} = 50^2 = 2500$.

KEY IDEA
The terms are consecutive odd numbers, an AP with a=1 and d=2, so the sum of the first n terms is n^2.

WATCH OUT FOR
Summing 50 terms but using the last term as 50 or 99 in the wrong formula, or taking the 50th odd number as 100 instead of 99 (the nth odd number is 2n-1).

Q.33 NAT · 1 MARK

Engineering Mathematics › Probability & statistics

Two fair six-sided dice are thrown. The probability of getting 12 as the product of the numbers on the dice (rounded off to two decimal places) is _____.

Official answer: **0.10 to 0.12**

SOLUTION

1. Two fair dice give $6 \times 6 = 36$ equally likely ordered outcomes (a, b) with $1 \le a, b \le 6$.
2. We need $a \cdot b = 12$. The factor pairs of 12 are $(1, 12)$, $(2, 6)$, $(3, 4)$, $(4, 3)$, $(6, 2)$ and $(12, 1)$. A die shows at most 6, so $(1, 12)$ and $(12, 1)$ are impossible.
3. The favourable outcomes are $(2, 6)$, $(6, 2)$, $(3, 4)$ and $(4, 3)$, so there are 4 of them.
4. $$P = \frac{4}{36} = \frac{1}{9} \approx 0.111$$
5. Rounded to two decimal places, $P = 0.11$.

KEY IDEA
List the ordered pairs on the two dice whose product is 12, count them, and divide by the 36 equally likely outcomes.

WATCH OUT FOR
Counting (2,6) and (3,4) only once each, which gives 2/36 = 0.06. The dice are distinct, so (6,2) and (4,3) are separate outcomes.

Q.34 NAT · 1 MARK

Q.34	If $7^{3x} = 216$, the value of 7^{-x} (rounded off to three decimal places) is .

Official answer: **0.166 to 0.168**

Q.35 NAT · 1 MARK

Q.35	The distance between the two points of intersection of $x^2 + y = 7$ and $x + y = 7$ (rounded off to two decimal places) is _____.

Official answer: **1.40 to 1.42**

Q.36 MCQ · 2 MARKS

General Biology › Adaptive immunity

Match the immune tolerance mechanisms in Group I with their respective outcomes in Group II.

Group I: P. Anergy; Q. Activation-induced cell death; R. Receptor editing; S. Regulatory T-cells.
Group II: 1. Elimination of activated T-cells after antigen clearance; 2. Inhibition of auto-reactive T-cells at periphery; 3. Unresponsiveness to antigens due to lack of co-stimulatory molecules; 4. Elimination of auto-reactive B-cells.

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

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

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

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

Official answer: **A**

SOLUTION

1. **Anergy (P):** a T-cell that meets antigen without co-stimulation (no CD28 signal from B7 on the antigen-presenting cell) becomes functionally unresponsive. So P matches 3.
2. **Activation-induced cell death (Q):** repeated or prolonged stimulation of activated T-cells raises Fas and FasL, and the cells die by apoptosis. This removes the expanded T-cell pool once the antigen has been cleared. So Q matches 1.
3. **Receptor editing (R):** a developing B-cell in the bone marrow whose receptor binds self-antigen re-expresses RAG and rearranges a new light chain. If editing fails, the B-cell is deleted. This is tolerance of auto-reactive B-cells, so R matches 4.
4. **Regulatory T-cells (S):** Foxp3-positive Tregs suppress auto-reactive T-cells in the periphery, using IL-10, TGF-β and CTLA-4. So S matches 2.
5. The full matching is P-3, Q-1, R-4, S-2.
6. Option B pairs anergy with 4 and receptor editing with 1, which is wrong. Option C pairs Q with 4 and R with 2, which is wrong. Option D pairs Q with 2 and S with 1, which is wrong. Only option A fits all four pairs.

KEY IDEA

Match each tolerance mechanism to the cell type and the stage it acts at. Anergy is a T-cell left unresponsive for lack of co-stimulation. Activation-induced cell death removes spent activated T-cells through Fas and FasL. Receptor editing acts on B-cells in the bone marrow (central tolerance). Regulatory T-cells suppress auto-reactive T-cells in the periphery.

WATCH OUT FOR

Confusing activation-induced cell death with regulatory T-cell suppression, because both limit T-cell responses in the periphery. One kills activated T-cells after the antigen is cleared. The other suppresses auto-reactive T-cells. Another slip is pairing receptor editing with a T-cell outcome, when it acts only on B-cells.

Q.37 MCQ · 2 MARKS

General Biology › Microbiology

Q.37 Match the type of bacteria in Group I with their respective growth properties in Group II.

Group I	Group II
P. Halophile	1. Grows optimally between 20 °C and 45 °C
Q. Piezophile	2. Grows best at low water activity
R. Mesophile	3. Grows at high level of salt
S. Xerophile	4. Grows optimally at high hydrostatic pressure

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

Official answer: **A**

SOLUTION

1. Halophile: the name means salt-loving. It needs and grows at a high level of salt, so P matches 3.
2. Piezophile (barophile): the name comes from the Greek for pressure. It grows best at high hydrostatic pressure, as in deep-sea trenches, so Q matches 4.
3. Mesophile: grows at moderate temperature, with an optimum between about 20 °C and 45 °C. Many human-associated bacteria, such as E. coli, are mesophiles. So R matches 1.

4. Xerophile: the name means dry-loving. It tolerates or prefers very low water activity (a_w), as in dry or sugary habitats, so S matches 2.
5. The full matching is P-3, Q-4, R-1, S-2.
6. Check the options. B puts P with 2 and R with 4, which is wrong. C puts Q with 1 and R with 2, which is wrong. D puts P with 4 and Q with 3, which swaps salt and pressure. Only A is consistent.

KEY IDEA
The name of each group of microbes tells you its preferred condition: halo means salt, piezo means pressure, meso means moderate temperature (about 20 to 45 °C), and xero means dry (low water activity).

WATCH OUT FOR
Confusing a halophile (high salt) with a xerophile (low water activity). Both live in water-poor settings, but a halophile is defined by salt and a xerophile by dryness. Another slip is swapping salt and pressure for halophile and piezophile.

Q.38 MCQ · 2 MARKS

General Biology › Pathogens & antibiotics

Match the virus in Group I with the type of genome it contains in Group II.

Group I: P. T4 bacteriophage; Q. SARS-CoV-2; R. Pseudomonas phage φ6; S. φX174 bacteriophage.
Group II: 1. dsRNA; 2. ssDNA; 3. dsDNA; 4. ssRNA.

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

Official answer: **A**

SOLUTION

1. T4 bacteriophage is a large tailed phage of $E.\ coli$ with a linear double-stranded DNA genome, so P matches 3 (dsDNA).
2. SARS-CoV-2 is a coronavirus. Its genome is one positive-sense single-stranded RNA molecule of about 30 kb that acts directly as mRNA, so Q matches 4 (ssRNA).
3. Pseudomonas phage $\phi 6$ is an enveloped phage of the family Cystoviridae. Its genome is three segments of double-stranded RNA, so R matches 1 (dsRNA).
4. $\phi X174$ is a small icosahedral phage with a circular single-stranded DNA genome of about 5.4 kb, so S matches 2 (ssDNA).
5. The combination is P-3, Q-4, R-1, S-2, which is option (A).
6. Option (B) gives T4 ssDNA, which is wrong. Option (C) gives SARS-CoV-2 dsDNA, which is wrong. Option (D) gives T4 dsRNA, which is wrong. Each of these fails on at least one of the facts above.

KEY IDEA
Know the genome type of the standard model viruses. T4 is dsDNA, φX174 is ssDNA, SARS-CoV-2 is ssRNA (positive sense), and φ6 is the classic dsRNA phage with a three-segment genome.

WATCH OUT FOR
Assuming every phage has a DNA genome and overlooking that φ6 is a dsRNA phage. Another slip is mixing up T4 (dsDNA) and φX174 (ssDNA), which are both well-known E. coli phages.

Q.39 MSQ · 2 MARKS

Genetics, Cell and Molecular Biology › Population & evolution

The event(s) that lead(s) to inactivation of tumor suppressor genes in cancer cells is(are)

(A) gene amplification
(B) promoter methylation

(C) loss of heterozygosity

(D) histone acetylation

Official answer: **B, C**

SOLUTION

1. Apply Knudson's two-hit hypothesis: a tumor suppressor gene must lose function on BOTH alleles to be fully inactivated in a cell.
2. (A) Gene amplification raises a gene's copy number and expression; this is the standard mechanism of ONCOGENE activation (e.g., HER2, MYC), not tumor suppressor inactivation. Eliminate A.
3. (B) Promoter methylation: hypermethylation of CpG islands in a tumor suppressor's promoter recruits repressive methyl-binding complexes and silences transcription of that allele, a recognized 'second hit' mechanism (e.g., BRCA1, MLH1, p16); include B.
4. (C) Loss of heterozygosity: after one allele is already mutated, loss of the remaining wild-type allele (via deletion, mitotic recombination, or chromosome loss) removes the last functional copy, the classic second hit in the Knudson model (e.g., RB1); include C.
5. (D) Histone acetylation neutralizes histone charge, opens chromatin, and generally ACTIVATES transcription, the opposite of gene silencing; silencing is instead associated with histone DEacetylation (HDACs). Eliminate D.
6. Therefore the events leading to tumor suppressor gene inactivation are promoter methylation and loss of heterozygosity: options B and C.

KEY IDEA

Tumor suppressor genes are inactivated by loss-of-function events on both alleles (Knudson's two-hit hypothesis): genetic hits such as loss of heterozygosity (deletion, mitotic recombination, or chromosome loss of the remaining wild-type allele) and epigenetic hits such as promoter hypermethylation, which silences transcription. Oncogenes, by contrast, are activated (not tumor suppressors inactivated) by gene amplification, and gene silencing is generally associated with histone deacetylation, not acetylation.

WATCH OUT FOR

Confusing gene amplification (an oncogene-activation mechanism, e.g. HER2/MYC copy number gain) with tumor suppressor inactivation, or confusing histone acetylation (which opens chromatin and activates transcription) with histone deacetylation (which is the actual silencing mechanism associated with HDACs).

Q.40 MSQ · 2 MARKS

Genetics, Cell and Molecular Biology › Gene expression

Methylation of CpG islands near the promoter of a gene can inhibit transcription by

(A) preventing RNA polymerase binding

(B) facilitating repressor binding

(C) facilitating heterochromatin formation

(D) inducing euchromatin formation

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

Q.41 MSQ · 2 MARKS

Genetics, Cell and Molecular Biology › Cell biology

Which of the following statement(s) is(are) TRUE about induced pluripotent stem cells?

(A) They can self-renew

(B) They require specific signals to maintain their stemness

(C) They cannot be genetically manipulated

(D) They can form organoids in vitro

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

SOLUTION

1. Recall that pluripotent stem cells (embryonic stem cells and iPSCs alike) are defined by two coupled properties: pluripotency (ability to give rise to derivatives of all three germ layers) and self-renewal (indefinite division while remaining undifferentiated).
2. (A) Self-renewal is a core defining property of iPSCs, so this statement is TRUE.
3. (B) The undifferentiated, self-renewing state of iPSCs is actively maintained, not automatic: culture requires specific signalling inputs (defined growth-factor/cytokine cocktails and supportive niche/matrix conditions). Withdrawing these signals causes spontaneous differentiation, so maintenance of stemness does require specific signals. This statement is TRUE.
4. (C) iPSCs are themselves produced by a genetic/molecular reprogramming procedure (forced expression of transcription factors such as Oct4, Sox2, Klf4, c-Myc), and established iPSC lines are routinely further genetically engineered (CRISPR editing, reporter knock-ins, correction of mutations). So the claim that they 'cannot be genetically manipulated' is FALSE.
5. (D) iPSCs are a standard source for generating three-dimensional organoids in culture (e.g., brain, intestinal, kidney, cardiac organoids), so this statement is TRUE.
6. Collecting the TRUE statements: A, B, and D are true; C is false.

KEY IDEA

Induced pluripotent stem cells (iPSCs) are self-renewing, pluripotent cells generated from somatic cells by forced expression of reprogramming transcription factors. Like other pluripotent stem cells, their undifferentiated, self-renewing state is not a passive default: it must be actively maintained by specific extrinsic signals/culture conditions, and withdrawing these signals triggers spontaneous differentiation. Because iPSCs arise from a genetic reprogramming procedure in the first place, they are inherently amenable to further genetic manipulation (e.g., CRISPR editing, reporter knock-ins, gene correction) and are widely used to derive three-dimensional organoids (e.g., brain, intestinal, kidney, cardiac organoids) in culture.

WATCH OUT FOR

Confusing "genetically manipulated" with "genetically abnormal" or assuming pluripotent cells are somehow protected from manipulation because they are so tightly regulated; in fact iPSCs are created BY genetic manipulation (forced expression of reprogramming factors such as Oct4, Sox2, Klf4, c-Myc) and are routinely further engineered (e.g. CRISPR gene editing, reporter knock-ins), so (C) is clearly false. A second common error is treating "self-renewal" as needing no external input, which would wrongly make (B) look false or contradictory to (A). Self-renewal of pluripotent stem cells is not spontaneous/unconditional; it is actively maintained by specific signalling inputs, so (A) and (B) are both true and not in conflict.

Q.42 MSQ · 2 MARKS

General Biology › Pathogens & antibiotics

Which of the following statement(s) is(are) TRUE about fluoroquinolone drugs?

(A) They contain quinolone ring(s)

(B) They inhibit RNA polymerase

(C) They bind to bacterial topoisomerase

(D) They bind to 23S rRNA within the 50S ribosome subunit

Official answer: **A, C**

SOLUTION

1. Fluoroquinolones (ciprofloxacin, levofloxacin, norfloxacin) are synthetic antibiotics built on the quinolone core, a 4-oxo-quinoline-3-carboxylic acid, with a fluorine atom at C-6. So (A) is true.

2. Their targets are the bacterial type II topoisomerases, DNA gyrase and topoisomerase IV. The drug traps the enzyme-DNA cleavage complex, so double-strand breaks build up and DNA replication stops. So (C) is true.
3. (B) is false. Inhibition of RNA polymerase is the action of rifampicin and the other rifamycins, not of fluoroquinolones.
4. (D) is false. Binding to 23S rRNA in the 50S subunit is how macrolides, lincosamides, chloramphenicol and oxazolidinones block protein synthesis. Fluoroquinolones act on DNA replication.
5. The true statements are (A) and (C).

KEY IDEA
Match each antibiotic class to its target. Fluoroquinolones have a quinolone ring and inhibit bacterial DNA gyrase and topoisomerase IV, so they block DNA replication. Rifamycins inhibit RNA polymerase. Macrolides and related drugs bind 23S rRNA in the 50S subunit.

WATCH OUT FOR
Mixing up the targets of different antibiotic classes, for example choosing (B) because of rifampicin or (D) because of macrolides, when fluoroquinolones act on DNA topoisomerases.

Q.43 MSQ · 2 MARKS

Plant, Animal and Microbial Biotechnology › Transgenic plants

Which of the following is(are) plant protoplast fusogenic agent(s)?

(A) Sodium nitrate

(B) Polyvinyl alcohol

(C) Polyethylene glycol

(D) Bromoxynil

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

SOLUTION

1. Protoplast fusion needs a fusogen: an agent that makes the plasma membranes of adjacent protoplasts stick together and merge.
2. (A) Sodium nitrate is correct. It was one of the earliest chemical fusogens used for plant protoplasts, and it induces fusion.
3. (B) Polyvinyl alcohol is correct. It is a polymer that promotes protoplast agglutination and fusion, and has been used as a fusogen in plant protoplast work.
4. (C) Polyethylene glycol is correct. PEG at about 25-30% dehydrates the membranes and bridges adjacent protoplasts, causing fusion. It is the most widely used chemical fusogen, often followed by a high-pH, high-Ca^{2+} wash.
5. (D) Bromoxynil is wrong. It is a herbicide that inhibits photosystem II, and it is the basis of the bxn transgene resistance marker. It is not a fusogen.
6. So the fusogens are sodium nitrate, polyvinyl alcohol and polyethylene glycol: A, B and C.

KEY IDEA
Chemical fusogens for plant protoplasts include sodium nitrate, polyvinyl alcohol, PEG and high-pH, high-Ca2+ solutions. A herbicide used as a selection marker is not a fusogen.

WATCH OUT FOR
Picking only PEG because it is the best known fusogen, or choosing bromoxynil because it appears in plant biotechnology as a herbicide-resistance marker.

Q.44 MSQ · 2 MARKS

Recombinant DNA Technology and Tools › Enzymes & vectors

Direct DNA transfer method(s) used for plant genetic engineering is(are)

(A) microparticle bombardment

(B) electroporation

(C) polyethylene glycol treatment

(D) Agrobacterium-mediated transformation

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

SOLUTION

1. Criterion: classify each option as a 'direct' (physical/chemical, vector-free) DNA delivery method versus a 'vector-mediated' (biological, indirect) method.
2. (A) Microparticle bombardment (biolistics/gene gun): DNA-coated metal particles are physically accelerated into cells; no biological vector is involved. Direct method. Correct option.
3. (B) Electroporation: an electric pulse transiently permeabilizes the plasma membrane (usually of protoplasts), letting naked DNA enter directly; no biological vector. Direct method. Correct option.
4. (C) Polyethylene glycol (PEG) treatment: PEG destabilizes the protoplast plasma membrane, enabling direct chemical-mediated uptake of naked DNA; no biological vector. Direct method. Correct option.
5. (D) Agrobacterium-mediated transformation: uses the bacterium's own Ti-plasmid T-DNA transfer machinery as a biological vector to deliver DNA into the plant genome; an indirect (vector-mediated), not direct, method. Incorrect option.
6. Therefore the direct DNA transfer methods used for plant genetic engineering are (A), (B), and (C) only.

KEY IDEA

Direct (physical/chemical, vector-independent) DNA delivery methods for plants include microparticle bombardment (biolistics/gene gun), electroporation, and PEG-mediated uptake (typically into protoplasts); Agrobacterium-mediated transformation is an indirect, biological-vector method relying on the natural Ti-plasmid T-DNA transfer machinery.

WATCH OUT FOR

Students sometimes misclassify Agrobacterium-mediated transformation as a "direct" method because it is the most common and efficient transformation technique taught, forgetting that "direct" specifically means vector-independent (no biological carrier); Agrobacterium's Ti-plasmid T-DNA system makes it a vector-mediated (indirect) method regardless of its ubiquity.

Q.45 MSQ · 2 MARKS

Recombinant DNA Technology and Tools › Enzymes & vectors

Which of the following vector(s) is(are) used to clone a DNA fragment of size 220 kb?

(A) Bacterial artificial chromosome

(B) Yeast artificial chromosome

(C) Cosmids

(D) pUC19 plasmid

Official answer: **A, B**

SOLUTION

1. Recall typical insert-capacity ranges for cloning vectors: plasmids (e.g. pUC19): up to about 10 kb; cosmids: about 30-45 kb, limited by the lambda phage head packaging constraint (total packaged DNA of 37-52 kb including the cos sites); BACs: about 100-300 kb, based on the single-copy F-plasmid replicon; YACs: about 100 kb up to 1-2 Mb, a linear vector with yeast telomeres and a centromere.
2. Option (D) pUC19 plasmid: capacity of only a few kb, far too small to carry a 220 kb insert. Reject.
3. Option (C) Cosmids: capacity capped at ~30-45 kb by the phage-packaging limit; 220 kb greatly exceeds this. Reject.

4. Option (A) Bacterial artificial chromosome (BAC): F-plasmid based, routinely carries 100-300 kb inserts; 220 kb fits comfortably. Accept.
5. Option (B) Yeast artificial chromosome (YAC): linear vector with telomeres and centromere, carries inserts from ~100 kb to several Mb; 220 kb fits easily. Accept.
6. Therefore the vectors capable of cloning a 220 kb fragment are the BAC and the YAC (options A and B).

KEY IDEA
Cloning vector choice depends on insert-capacity range: plasmids (e.g. pUC19) hold only a few kb, cosmids are capped by lambda phage packaging at ~30-45 kb, while BACs (F-plasmid based, 100-300 kb) and YACs (linear yeast chromosome with telomeres/centromere, 100 kb to several Mb) are the vectors built for large (>100 kb) inserts such as 220 kb.

WATCH OUT FOR
Confusing cosmids (packaging-limited by the lambda phage head to ~30-45 kb total) with BACs, or assuming any "artificial chromosome" vector name alone (without checking insert-capacity range) is enough. Some students pick cosmids because they associate "large insert" loosely with cosmids rather than knowing the phage-packaging ceiling.

Q.46 NAT · 2 MARKS

Fundamentals of Biological Engineering › Growth kinetics

The following reaction represents biomass synthesis from hexadecane

$$C_{16}H_{34} + 12.5O_2 + 2.13NH_3 \rightarrow 10.6CH_{1.66}O_{0.27}N_{0.27} + 5.37CO_2 + 11.4H_2O$$

where $CH_{1.66}O_{0.27}N_{0.27}$ represents the biomass. The value of respiratory quotient (rounded off to two decimal places) is _____.

Official answer: **0.41 to 0.44**

SOLUTION

1. Definition of respiratory quotient:
$$\mathrm{RQ} = \frac{\text{moles of } \mathrm{CO_2} \text{ evolved}}{\text{moles of } \mathrm{O_2} \text{ consumed}}$$
Both are taken per mole of substrate, so RQ is a ratio in $\mathrm{mol\ mol^{-1}}$ and has no units. Here the substrate is hexadecane, $C_{16}H_{34}$.
2. Read the two coefficients from the stoichiometric equation. Per mole of $C_{16}H_{34}$: $\mathrm{O_2}$ consumed $= 12.5\ \mathrm{mol}$ and $\mathrm{CO_2}$ evolved $= 5.37\ \mathrm{mol}$.
3. Check the carbon balance to confirm the coefficients are consistent: $16 = 10.6\ (\text{biomass, 1 C each}) + 5.37\ (\mathrm{CO_2}) = 15.97 \approx 16$.
4. Compute:
$$\mathrm{RQ} = \frac{5.37}{12.5} = 0.4296 \approx 0.43$$
5. Why it is so low: hexadecane is a highly reduced substrate. It has no oxygen and $\mathrm{H/C} = 34/16 = 2.125$. A large share of the $\mathrm{O_2}$ goes into oxidising hydrogen to water ($11.4\ \mathrm{mol\ H_2O}$), and about two-thirds of the carbon ($10.6/16 \approx 0.66$) ends up in biomass instead of $\mathrm{CO_2}$. Both effects push RQ well below 1, which is typical of growth on alkanes.

KEY IDEA
Respiratory quotient is moles of CO2 evolved divided by moles of O2 consumed. Both numbers can be read straight off the growth stoichiometry, so no elemental balancing is needed. Very reduced substrates such as alkanes give RQ well below 1.

WATCH OUT FOR
Inverting the ratio (O2/CO2 = 12.5/5.37 = 2.33). Another is dividing by the moles of biomass or NH3 instead of O2. A third is assuming RQ is about 1, as it is for glucose. For a highly reduced substrate like hexadecane most of the oxygen goes to water and biomass, so RQ is far below 1.

Q.47 NAT · 2 MARKS

Fundamentals of Biological Engineering › Enzyme kinetics

Temperature of a reaction with an activation energy value of $15\ \text{kcal mol}^{-1}$ is increased from $300\ \text{K}$ to $310\ \text{K}$. If the value of the ideal gas constant (R) is $1.9872\ \text{cal mol}^{-1}\,\text{K}^{-1}$, the ratio of the reaction rate constants (k_{310}/k_{300}) (rounded off to two decimal places) is _____.

Official answer: **2.24 to 2.26**

SOLUTION

1. Arrhenius equation: $k = A\,e^{-E_a/RT}$, where k is the rate constant, A the pre-exponential factor, E_a the activation energy, R the gas constant and T the absolute temperature. Write it at $T_1 = 300\ \text{K}$ and $T_2 = 310\ \text{K}$ and divide one by the other. A cancels (it is taken as independent of temperature):
$$\ln\frac{k_{310}}{k_{300}} = \frac{E_a}{R}\left(\frac{1}{T_1} - \frac{1}{T_2}\right)$$
2. Put E_a and R in the same energy unit: $E_a = 15\ \text{kcal mol}^{-1} = 15000\ \text{cal mol}^{-1}$, so $\dfrac{E_a}{R} = \dfrac{15000\ \text{cal mol}^{-1}}{1.9872\ \text{cal mol}^{-1}\,\text{K}^{-1}} = 7548.31\ \text{K}$.
3. Temperature term: $\dfrac{1}{300} - \dfrac{1}{310} = \dfrac{310-300}{300\times310} = \dfrac{10}{93000} = 1.0753\times10^{-4}\ \text{K}^{-1}$.
4. Multiply: $\ln\dfrac{k_{310}}{k_{300}} = 7548.31\ \text{K}\times1.0753\times10^{-4}\ \text{K}^{-1} = 0.8116$. The result has no units, as it must.
5. Take the exponential: $\dfrac{k_{310}}{k_{300}} = e^{0.8116} = 2.2516 \approx 2.25$.

KEY IDEA

Divide the Arrhenius equation at one temperature by the same equation at the other. The pre-exponential factor cancels, leaving $\ln(k_2/k_1) = \dfrac{E_a}{R}\left(\dfrac{1}{T_1} - \dfrac{1}{T_2}\right)$. Only E_a, R and the two absolute temperatures are needed, provided E_a and R use the same energy unit.

WATCH OUT FOR

Mixing kcal and cal. Putting $E_a = 15$ over $R = 1.9872$ gives a ratio of about 1.00. Also watch the sign and order of $\left(\dfrac{1}{T_1} - \dfrac{1}{T_2}\right)$: reversing it gives the inverse ratio, about 0.44. Approximating the bracket as $\Delta T/T^2$ with $T = 300\ \text{K}$ inflates the answer to about 2.31. Finally, rounding R to 2 gives 2.2400, which only just sits on the edge of the key, so keep $R = 1.9872$ as printed.

Q.48 NAT · 2 MARKS

Fundamentals of Biological Engineering › Bioreactor operation

E. coli is cultivated in a chemostat operated at a dilution rate of $0.2\ \text{h}^{-1}$. The values of biomass yield due to oxygen consumption and the steady state biomass concentration are $0.2\ \text{g.g}^{-1}$ and $10\ \text{g.L}^{-1}$, respectively. The oxygen transfer rate (in $\text{g.L}^{-1}\text{.h}^{-1}$) is _____.

Official answer: **10**

SOLUTION

1. At chemostat steady state (sterile feed, negligible cell death) the biomass balance gives $\mu = D = 0.2\ \text{h}^{-1}$. Here μ is the specific growth rate and D is the dilution rate.
2. Volumetric biomass production rate: $r_X = \mu X = DX = 0.2\times10 = 2\ \text{g L}^{-1}\text{h}^{-1}$, where $X = 10\ \text{g L}^{-1}$ is the steady-state biomass concentration.
3. The biomass yield on oxygen, $Y_{X/O} = 0.2\ \text{g biomass per g O}_2$, links growth to oxygen use: $\text{OUR} = \dfrac{\mu X}{Y_{X/O}}$, where OUR is the volumetric oxygen uptake rate. The specific uptake rate is $q_{O_2} = \mu/Y_{X/O} = 0.2/0.2 = 1\ \text{g O}_2\ \text{g}^{-1}\text{h}^{-1}$.

4. $$\text{OUR} = \frac{2\ \text{g L}^{-1}\text{h}^{-1}}{0.2\ \text{g g}^{-1}} = 10\ \text{g O}_2\ \text{L}^{-1}\text{h}^{-1}$$

5. At steady state dissolved oxygen does not accumulate, and the O_2 carried out dissolved in the outflow is negligible. So the oxygen transfer rate equals the oxygen uptake rate: $\text{OTR} = \text{OUR} = 10\ \text{g L}^{-1}\text{h}^{-1}$.

KEY IDEA

In a chemostat at steady state, $\mu = D$. The oxygen supplied must equal the oxygen the cells consume, so $\text{OTR} = \text{OUR} = \frac{DX}{Y_{X/O}}$.

WATCH OUT FOR

Multiplying by the yield instead of dividing, which gives $DXY_{X/O} = 0.4$. Another is reporting the specific uptake rate $q_{O_2} = \mu/Y_{X/O} = 1\ \text{h}^{-1}$ without multiplying by the biomass concentration X. A yield is biomass made per unit of oxygen used, so the oxygen needed is biomass made divided by the yield.

Q.49 NAT · 2 MARKS

Fundamentals of Biological Engineering › Downstream

Aqueous two-phase extraction is used to recover α-amylase from a solution. A polypropylene glycol-dextran mixture is added and the solution separates into upper and lower phases. The partition coefficient is 4.0 and the ratio of upper to lower phase volume is 5.0. The enzyme recovery or yield (in percentage, rounded off to the nearest integer) is _____.

Official answer: **94 to 96**

SOLUTION

1. Define the symbols. The partition coefficient is $K = \frac{C_U}{C_L} = 4.0$, where C_U and C_L are the enzyme concentrations in the upper and lower phases. The volume ratio is $R = \frac{V_U}{V_L} = 5.0$, where V_U and V_L are the upper- and lower-phase volumes. By the usual convention K is written upper-over-lower, and $K > 1$ means the enzyme favours the upper phase, so the product is recovered from the upper phase.
2. Mass balance on the enzyme. The total enzyme is shared between the two phases: $\text{total} = C_U V_U + C_L V_L$.
3. Fraction of the enzyme recovered in the upper phase:
$$Y_U = \frac{C_U V_U}{C_U V_U + C_L V_L} = \frac{KR}{1 + KR}$$
(divide the numerator and the denominator by $C_L V_L$, using $\frac{C_U}{C_L} = K$ and $\frac{V_U}{V_L} = R$).
4. Substitute: $KR = 4.0 \times 5.0 = 20$.
5. $$Y_U = \frac{20}{1 + 20} = \frac{20}{21} = 0.9524$$
6. Yield $= 95.24\% \approx 95\%$ (rounded to the nearest integer).

KEY IDEA

In a two-phase partition, the fraction of solute in the upper phase depends only on the product KR (partition coefficient times the upper-to-lower volume ratio): $Y_U = \frac{KR}{1 + KR}$. A large upper-phase volume raises the yield even when K is modest. Here $KR = 20$, so only $1/21$ of the enzyme stays in the lower phase.

WATCH OUT FOR

Using K alone and writing $\frac{K}{1+K} = 80\%$, which ignores the volume ratio. Another slip is inverting R ($V_L/V_U = 0.2$), which gives $\frac{0.8}{1.8} = 44\%$. A third is reporting the lower-phase fraction, $\frac{1}{1+KR} = 4.76\%$, as the yield.

Q.50 NAT · 2 MARKS

General Biology › Biomolecules

E. coli cultivated at 298 K uptakes an uncharged compound (A) by passive diffusion. The intracellular and extracellular concentrations of A are 0.001 M and 0.1 M, respectively. If the value of the ideal gas constant R is 1.9872 cal.mol^-1.K^-1, the free-energy change (in kcal.mol^-1) for this passive diffusion of A (rounded off to two decimal places) is _____.

Official answer: **-2.74 to -2.71**

SOLUTION

1. Passive diffusion of an uncharged solute is movement down its concentration gradient, so the free-energy change has only the concentration term: $\Delta G = RT \ln \dfrac{C_{in}}{C_{out}}$. There is no membrane-potential term because A is uncharged.
2. Concentration ratio: $\dfrac{C_{in}}{C_{out}} = \dfrac{0.001}{0.1} = 0.01$, so $\ln 0.01 = -4.6052$.
3. $RT = 1.9872 \times 298 = 592.19 \text{ cal mol}^{-1} = 0.59219 \text{ kcal mol}^{-1}$.
4. $\Delta G = 0.59219 \times (-4.6052) \approx -2.727 \text{ kcal mol}^{-1}$.
5. The sign is negative, so the process is spontaneous. This fits movement from the high (outside) concentration to the low (inside) concentration.
6. Rounded to two decimal places: $\Delta G \approx -2.73 \text{ kcal mol}^{-1}$.

KEY IDEA

For an uncharged solute, the free-energy change of transport is $\Delta G = RT \ln(C_{in}/C_{out})$. Take the ratio as destination over source and convert the units of R to kcal before multiplying.

WATCH OUT FOR

Using C_{out}/C_{in} gives $+2.73$, the wrong sign. Forgetting to convert cal to kcal gives -2727. Using $\log_{10}$ in place of $\ln$ gives a value about 2.3 times too small.

Q.51 NAT · 2 MARKS

Recombinant DNA Technology and Tools › Bioinformatics

If there are three unrooted trees for four protein sequences, the number of rooted trees for the same number of sequences is _____.

Official answer: **15**

SOLUTION

1. An unrooted bifurcating (binary) tree for n taxa has $(2n - 3)$ branches (edges). For $n = 4$ leaves: internal nodes $= n - 2 = 2$, total nodes $= 6$, so total edges $=$ nodes $-1 = 5 = 2(4) - 3$.
2. The number of distinct unrooted binary trees for $n = 4$ taxa is $(2n - 5)!! = 3!! = 3$, matching the value given in the question stem (this is a consistency check on the standard formula, not something to be computed from scratch).
3. A root can be inserted at any point along any one of the $2n - 3 = 5$ branches of a given unrooted tree, and each distinct branch placement produces a distinct rooted tree. Hence (number of rooted trees) $=$ (number of unrooted trees) $\times (2n - 3)$.
4. Substituting: rooted trees $= 3 \times 5 = 15$.
5. Cross-check using the direct closed-form for rooted binary trees, $(2n - 3)!!$: for $n = 4$, $(2 \cdot 4 - 3)!! = 5!! = 5 \times 3 \times 1 = 15$, consistent with the step-by-step result.

KEY IDEA

An unrooted bifurcating tree for n taxa has $(2n-3)$ branches, and placing a root on any one of these branches produces a distinct rooted tree. So rooted trees = (number of unrooted trees) $\times(2n-3)$.

WATCH OUT FOR

Confusing the two standard counting formulas: using $(2n-3)!!$ (rooted count) as if it directly gave the unrooted count, or forgetting that the multiplier linking unrooted to rooted trees is the number of branches ($2n-3$), not the number of taxa (n) or internal nodes.

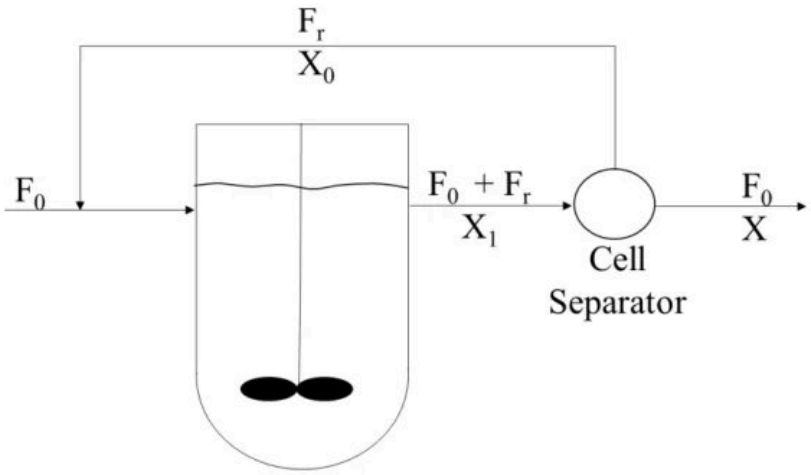
Q.52 NAT · 2 MARKS

Q.52	The number of different possible ways of forming five intramolecular disulfide bonds with ten cysteine residues of a protein is _____.

Official answer: **945**

Q.53 NAT · 2 MARKS

Q.53 The following schematic diagram shows a chemostat with cell recycle



where F_0 and F_r are the volumetric flow rates (in $L.h^{-1}$) of feed and recycle streams, respectively. X_1, X_0 and X are the cell concentrations (in $g.L^{-1}$) in the reactor, recycle-stream and product-stream, respectively. If $\frac{X_0}{X_1}=1.5, \frac{F_r}{F_0}=0.7$ and X_1 is $7.3\,g.L^{-1}$, the value of X (in $g.L^{-1}$, rounded off to one decimal place) is .

Official answer: **4.6 to 4.9**

SOLUTION

1. Symbols: F_0 = feed flow rate, which is also the product flow rate ($\mathrm{L\,h^{-1}}$). F_r = recycle flow rate ($\mathrm{L\,h^{-1}}$). X_1 = cell concentration in the reactor ($\mathrm{g\,L^{-1}}$). X_0 = cell concentration in the recycle stream. X = cell concentration in the product stream. Define the recycle ratio $\alpha = F_r/F_0 = 0.7$ and the concentration factor $C = X_0/X_1 = 1.5$.
2. The reactor is well mixed, so the stream leaving it, $F_0 + F_r$, carries cells at the reactor concentration X_1. That stream enters the cell separator. Two streams leave the separator: the recycle, F_r at X_0, and the product, F_0 at X. The flows balance: $F_0 + F_r$ in, $F_r + F_0$ out.
3. Take a steady-state cell balance on the separator alone. Cells do not grow or die in the separator, so cells in = cells out:
$$(F_0 + F_r)X_1 = F_r X_0 + F_0 X$$
4. Divide by F_0 and substitute $X_0 = CX_1$:
$$(1+\alpha)X_1 = \alpha C X_1 + X \;\Rightarrow\; X = X_1\,(1 + \alpha - \alpha C)$$
5. Substitute the numbers: $1 + \alpha - \alpha C = 1 + 0.7 - 0.7 \times 1.5 = 1.7 - 1.05 = 0.65$.
6. $X = 0.65 \times 7.3 = 4.745\ \mathrm{g\,L^{-1}} \approx 4.7\ \mathrm{g\,L^{-1}}$ (to one decimal place). As a check, X is less than X_1, which is what we expect: the separator sends concentrated cells ($X_0 > X_1$) back to the reactor, so the product stream leaving it is thinner.

KEY IDEA

All you need is a cell balance around the cell separator. Nothing grows there, so at steady state the cells coming in with the reactor outflow, $(F_0 + F_r)X_1$, must equal the cells leaving in the recycle, $F_r X_0$, plus those leaving in the product, $F_0 X$. No growth kinetics (μ, D, K_s) are needed. Dividing by F_0 gives $X = X_1(1 + \alpha - \alpha C)$, with $\alpha = F_r/F_0$ and $C = X_0/X_1$.

WATCH OUT FOR

Three mistakes come up often. (1) Giving the stream into the separator a flow of F_0 instead of $F_0 + F_r$. That gives $X = X_1(1 - \alpha C) = -0.37\,X_1$, a negative concentration, which is impossible. (2) Writing the balance over the reactor instead. That brings in growth and needs μ, which the question does not give. (3) Getting the sign wrong on the recycle term, e.g. $X = X_1(1 + \alpha + \alpha C) = 2.75\,X_1$. With recycle concentrated at the separator, the product concentration must come out below X_1, not above it.

Q.54 NAT · 2 MARKS

Fundamentals of Biological Engineering › Enzyme kinetics

An enzyme (E) catalyzes the biochemical reaction $A \rightarrow B$ with k_{cat} equal to $500\ \mathrm{s}^{-1}$. If the initial reaction velocity (V_0) is $10\ \mu\mathrm{M.s}^{-1}$ at the total enzyme concentration $[E_t]$ of $30\ \mathrm{nM}$ and substrate concentration [A] of $40\ \mu\mathrm{M}$, the value of K_m (in $\mu\mathrm{M}$) is _____.

Official answer: **20**

SOLUTION

1. Symbols: k_{cat} is the turnover number, $[E_t]$ the total enzyme concentration, V_{max} the maximum rate, V_0 the initial rate and K_m the Michaelis constant.
2. Maximum rate: $V_{max} = k_{cat}[E_t]$. Put the concentrations in the same units first: $[E_t] = 30\ \mathrm{nM} = 0.030\ \mu\mathrm{M}$.
3. $$V_{max} = 500\ \mathrm{s}^{-1} \times 0.030\ \mu\mathrm{M} = 15\ \mu\mathrm{M\,s}^{-1}$$
4. Michaelis-Menten: $V_0 = \dfrac{V_{max}[A]}{K_m + [A]}$. Rearranging gives $K_m = [A]\left(\dfrac{V_{max}}{V_0} - 1\right)$.
5. $$K_m = 40\left(\frac{15}{10} - 1\right) = 40 \times 0.5 = 20\ \mu\mathrm{M}$$
6. Check: $V_0 = \dfrac{15 \times 40}{20 + 40} = 10\ \mu\mathrm{M\,s}^{-1}$, which matches the given rate. It also fits the rule that $V_0 = \frac{2}{3}V_{max}$ when $[A] = 2K_m$.

KEY IDEA

$V_{max} = k_{cat}[E_t]$, then solve Michaelis-Menten for K_m: $K_m = [A]\left(\dfrac{V_{max}}{V_0} - 1\right)$.

WATCH OUT FOR

Forgetting to convert $[E_t]$ from nM to μM. Using 30 directly gives $V_{max} = 15000\ \mu\mathrm{M\,s}^{-1}$ and a K_m that is wrong by orders of magnitude. The other slip is treating V_0 as V_{max}.

Q.55 NAT · 2 MARKS

Genetics, Cell and Molecular Biology › Mutation & repair

DNA sample collected from an unidentified bacterial species (Y) contains 13% of adenine. The G+C content (in percentage) of Y is _____.

Official answer: **74**

SOLUTION

1. Chargaff's rule for double-stranded DNA: the percentage of Adenine (A) equals the percentage of Thymine (T), and the percentage of Guanine (G) equals the percentage of Cytosine (C), because A pairs with T and G pairs with C across the two strands.
2. Given %A = 13%. By Chargaff's rule, %T = 13% as well.

3. So %A + %T = 13% + 13% = 26%.
4. Since the four bases together account for 100% of the DNA, $\%G + \%C = 100\% - (\%A + \%T) = 100\% - 26\% = 74\%$.

KEY IDEA
In double-stranded DNA, Chargaff's rule gives %A = %T and %G = %C, and all four bases sum to 100%, so %G + %C = 100% − 2(%A).

WATCH OUT FOR
Assuming A = G = C = T = 25% by default instead of applying Chargaff's pairing rule to the given 13% adenine value, or forgetting to double the adenine percentage before subtracting from 100%.

Q.56 NAT · 2 MARKS

Genetics, Cell and Molecular Biology › Mutation & repair

If 1000 bp of a double-helical DNA weighs 1×10^{-18} gm and distance between two bp is 0.34 nm, the total amount of DNA (in mg, rounded off to one decimal place) required to stretch from Earth to Moon (assuming the distance between Earth and Moon to be 3,74,000 km) is _____.

Official answer: **1.0 to 1.2**

SOLUTION

1. Convert the Earth–Moon distance into nanometres, the same unit as the base-pair rise: $3{,}74{,}000\ \text{km} = 3.74 \times 10^5\ \text{km} = 3.74 \times 10^8\ \text{m} = 3.74 \times 10^{17}\ \text{nm}$ (using $1\ \text{m} = 10^9\ \text{nm}$).
2. The distance between two base pairs, 0.34 nm, is the rise per base pair along the double helix. So the number of base pairs needed to span a given length is $\dfrac{\text{length}}{\text{rise per bp}}$.
3. Number of bp $= \dfrac{3.74 \times 10^{17}\ \text{nm}}{0.34\ \text{nm/bp}} = \dfrac{3.74}{0.34} \times 10^{17}\ \text{bp} = 11 \times 10^{17}\ \text{bp} = 1.1 \times 10^{18}\ \text{bp}$ (since $3.74/0.34 = 11$).
4. Convert the given mass per 1000 bp to mass per single bp: $\dfrac{1 \times 10^{-18}\ \text{gm}}{1000\ \text{bp}} = 1 \times 10^{-21}\ \text{gm/bp}$.
5. Total mass $= 1 \times 10^{-21}\ \text{gm/bp} \times 1.1 \times 10^{18}\ \text{bp} = 1.1 \times 10^{-3}\ \text{gm}$.
6. Convert grams to milligrams ($1\ \text{gm} = 10^3\ \text{mg}$): $1.1 \times 10^{-3}\ \text{gm} = 1.1\ \text{mg}$.
7. Rounded to one decimal place, the total amount of DNA required is $1.1\ \text{mg}$.

KEY IDEA
Convert the Earth–Moon distance to nanometres, divide by the 0.34 nm rise per base pair to get the total number of base pairs needed, then multiply by the mass per base pair (derived from the given 1×10^{-18} g per 1000 bp) to get the total mass, converting grams to milligrams at the end.

WATCH OUT FOR
Forgetting to convert km to nm before dividing by the 0.34 nm rise (mixing units gives a wildly wrong bp count), or dividing by 1000 bp instead of multiplying back up when converting mass-per-1000-bp to mass-per-bp, or missing the final g-to-mg conversion (leaving the answer as 0.0011 instead of 1.1).

Q.57 NAT · 2 MARKS

Recombinant DNA Technology and Tools › Editing & interactions

A protein has three identical sites arranged at the vertices of an equilateral triangle. If one site is filled with a dye (donor), the measured quantum yield (ϕ_D) is 0.5. Filling one site with a donor dye and a second site

with an acceptor dye results in ϕ_D of 0.25. The measured ϕ_D of one site filled with donor and the other two sites filled with acceptor dye (rounded off to three decimal places) is ___.

Official answer: **0.165 to 0.168**

SOLUTION

1. Let $k_0 = k_r + k_{nr}$ be the donor's total decay rate with no acceptor present, where k_r is the radiative rate. Donor-alone quantum yield: $\phi_{D0} = \dfrac{k_r}{k_0} = 0.5 \Rightarrow k_r = 0.5\,k_0$.
2. With one acceptor at a second vertex, energy transfer (FRET) opens one additional non-radiative decay channel with rate k_T:
$$\phi_{D1} = \frac{k_r}{k_0 + k_T} = 0.25$$
3. Substitute $k_r = 0.5k_0$:
$$\frac{0.5k_0}{k_0 + k_T} = 0.25 \;\Rightarrow\; 0.5k_0 = 0.25k_0 + 0.25k_T \;\Rightarrow\; k_T = k_0$$
4. Since the three sites form an equilateral triangle, the donor is equidistant from both remaining vertices. Förster transfer to two independent, non-interacting acceptors is additive, so filling both remaining sites with acceptor gives a total transfer rate of $2k_T$.
5. New quantum yield:
$$\phi_{D2} = \frac{k_r}{k_0 + 2k_T} = \frac{0.5k_0}{k_0 + 2k_0} = \frac{0.5k_0}{3k_0} = \frac{1}{6}$$
6. $\dfrac{1}{6} = 0.1\overline{6}$, which rounds to 0.167 at three decimal places.

KEY IDEA

In a FRET (Förster resonance energy transfer) system, the donor's total decay rate is $k_0 = k_r + k_{nr}$ without any acceptor. Each acceptor nearby opens one additional non-radiative decay pathway (energy transfer) with rate k_T. Since all three sites sit at the vertices of an equilateral triangle, the donor is equidistant from both other vertices, so the transfer rate to two independent acceptors adds: total transfer rate becomes $2k_T$, not some geometry-dependent combination.

WATCH OUT FOR

Assuming energy transfer to two acceptors combines non-additively (e.g., only the nearer acceptor matters, or the rates combine as some average) instead of simply summing the two independent FRET pathways, since Förster transfer rates from a single donor to multiple non-interacting acceptors are additive.

Q.58 NAT · 2 MARKS

Engineering Mathematics › Linear algebra

If $A = \begin{pmatrix} 1 & 2 \\ 3 & 5 \end{pmatrix}$, the value of $\left|A^4 + 3A^2 - 5A + 6I\right|$ is _____.

Official answer: **10551**

SOLUTION

1. For $A = \begin{bmatrix} 1 & 2 \\ 3 & 5 \end{bmatrix}$, the trace is $1 + 5 = 6$ and $\det A = 5 - 6 = -1$. The eigenvalues satisfy $\lambda^2 - 6\lambda - 1 = 0$, so $\lambda_1 + \lambda_2 = 6$ and $\lambda_1\lambda_2 = -1$.
2. Let $p(x) = x^4 + 3x^2 - 5x + 6$. The eigenvalues of $p(A) = A^4 + 3A^2 - 5A + 6I$ are $p(\lambda_1)$ and $p(\lambda_2)$. The determinant is their product, so $|p(A)| = p(\lambda_1)\,p(\lambda_2)$.
3. Reduce the powers using $\lambda^2 = 6\lambda + 1$:
$$\lambda^4 = (6\lambda + 1)^2 = 36\lambda^2 + 12\lambda + 1 = 36(6\lambda + 1) + 12\lambda + 1 = 228\lambda + 37.$$
4. Then

$$p(\lambda) = (228\lambda + 37) + 3(6\lambda + 1) - 5\lambda + 6 = 241\lambda + 46.$$

5. The determinant is

$$|p(A)| = (241\lambda_1 + 46)(241\lambda_2 + 46) = 241^2\lambda_1\lambda_2 + 241 \cdot 46\,(\lambda_1 + \lambda_2) + 46^2.$$

6. Substitute:

$$-58081 + 11086 \cdot 6 + 2116 = -58081 + 66516 + 2116 = 10551.$$

KEY IDEA

The determinant of a polynomial in A equals the product of the polynomial evaluated at the eigenvalues. Reduce high powers with the characteristic equation $\lambda^2 = 6\lambda + 1$ to get a linear expression in λ. Then use the sum and product of the eigenvalues.

WATCH OUT FOR

Taking the determinant term by term, for example $|A|^4 + 3|A|^2 - \ldots$. The determinant is not additive. Another slip is a sign error in $\lambda_1\lambda_2 = \det A = -1$.

Q.59 NAT · 2 MARKS

Engineering Mathematics › Calculus

If $f(x) = \dfrac{\sin x + \cos x}{\sin x - \cos x}$, the value of $f'(x)$ at $x = 0$ is _____.

Official answer: **-2**

SOLUTION

1. Write $f = \dfrac{u}{v}$ with $u = \sin x + \cos x$ and $v = \sin x - \cos x$.
2. Differentiate: $u' = \cos x - \sin x = -v$ and $v' = \cos x + \sin x = u$.
3. Quotient rule: $f' = \dfrac{u'v - uv'}{v^2} = \dfrac{-v^2 - u^2}{v^2} = -\dfrac{u^2 + v^2}{v^2}$.
4. Add the squares: $u^2 + v^2 = 2(\sin^2 x + \cos^2 x) = 2$, so $f'(x) = -\dfrac{2}{(\sin x - \cos x)^2}$.
5. At $x = 0$: $\sin 0 - \cos 0 = -1$, so $(\sin x - \cos x)^2 = 1$.
6. Hence $f'(0) = -\dfrac{2}{1} = -2$.

KEY IDEA

In the quotient rule, the derivative of each of the numerator and denominator is plus or minus the other, so the numerator of f' collapses to $-(u^2 + v^2) = -2$.

WATCH OUT FOR

Slipping on the sign of the quotient rule numerator, or mis-evaluating $\sin 0 - \cos 0$ as $+1$. Neither changes the squared denominator, but the sign of the numerator decides whether the answer is -2 or $+2$.

Q.60 NAT · 2 MARKS

Q.60	If $f(2) = 5$ and $(f(x))(f(x+1)) = 3$ for all real values of x, the value of $f(10)$ is _____.

Official answer: **5**

Q.61 NAT · 2 MARKS

Engineering Mathematics › Probability & statistics

Ten playing cards numbered 1, 2, 3, ..., 10 are placed face down on a table. One card is drawn at random, its number recorded, and then replaced face down. A card is drawn again at random. The probability that

the number on the second draw is greater than the number on the first draw (rounded off to two decimal places) is _____.

Official answer: **0.45**

SOLUTION

1. Because the first card is replaced, the two draws are independent. There are $10 \times 10 = 100$ equally likely ordered pairs (a, b), where a is the first number and b the second.
2. Exactly one of three things happens: $b > a$, $b < a$ or $b = a$. So $P(b > a) + P(b < a) + P(b = a) = 1$.
3. Both draws follow the same distribution and are independent, so swapping the two draws maps pairs with $b > a$ one-to-one onto pairs with $b < a$. Hence $P(b > a) = P(b < a)$.
4. Equal numbers occur in exactly 10 pairs, $(1, 1), (2, 2), \ldots, (10, 10)$. So $P(b = a) = \dfrac{10}{100} = 0.1$.
5. Therefore $P(b > a) = \dfrac{1 - 0.1}{2} = 0.45$.
6. Check by counting: if the first number is a, there are $10 - a$ larger values for the second draw. The number of favourable pairs is $\sum_{a=1}^{10}(10 - a) = 9 + 8 + \cdots + 0 = 45$, so the probability is $\dfrac{45}{100} = 0.45$.

KEY IDEA

With replacement the draws are independent and identically distributed. Split the outcomes into greater, less and equal, then use symmetry between the first two: $P(b > a) = \dfrac{1 - P(b = a)}{2}$.

WATCH OUT FOR

Forgetting that a tie is possible, which gives $\dfrac{1}{2}$ instead of 0.45. Another slip is to count pairs as if the card were not replaced, so that the tie case disappears and the total becomes 90.

Q.62 NAT · 2 MARKS

Q.62 The values of the consistency index 'K' and the flow behavior index 'n' of a dilatant fluid are 0.415 (in CGS units) and 1.23, respectively. The value of the apparent viscosity (in $g.cm^{-1}.s^{-1}$) of this fluid at a shear rate of $60\,s^{-1}$ (rounded off to the nearest integer) is _____.

Official answer: **1**

Q.63 NAT · 2 MARKS

Q.63 An evaporator is insulated using glass wool material of 0.15 m thickness. The inner most surface and the outer surface of the insulation are at 700 °C and 80 °C, respectively. The mean thermal conductivity of the glass wool under these conditions is $0.29\ W.m^{-1}.K^{-1}$. The rate of heat loss (in W) through $1.2\ m^2$ of the evaporator wall surface (rounded off to the nearest integer) is _____.

Official answer: **1437 to 1439**

Q.64 NAT · 2 MARKS

Fundamentals of Biological Engineering › Process control

A proportional controller is used to control the temperature of an autoclave from $60\,^{\circ}\mathrm{C}$ to $130\,^{\circ}\mathrm{C}$. If the proportional band setting of the controller is 25%, the proportional gain value is _____.

Official answer: **4**

SOLUTION

1. A proportional controller gives output $p = \bar{p} + K_c\,\varepsilon$. Here p is the controller output, $\bar{p}$ is the output when the error is zero (the bias), K_c is the proportional gain and ε is the error. When the input and the output are both written as a percentage of their spans, K_c has no units.
2. The proportional band (PB) is the percentage of the measured-variable span that drives the controller output through its full range (0 to 100%).
3. Span of the measured temperature: $130 - 60 = 70\,^{\circ}\mathrm{C}$.
4. With PB = 25%, a temperature change of $0.25 \times 70 = 17.5\,^{\circ}\mathrm{C}$ drives the output through 100% of its range.
5. As a percentage of the input span, that change is $\dfrac{17.5}{70} \times 100\% = 25\%$. So the gain is
$$K_c = \frac{\Delta(\text{output},\,\%)}{\Delta(\text{input},\,\%)} = \frac{100\%}{25\%} = 4$$
6. This is the standard relation $K_c = \dfrac{100}{\mathrm{PB}\,(\%)} = \dfrac{100}{25} = 4$. The $70\,^{\circ}\mathrm{C}$ span cancels, so the temperature range does not affect the dimensionless gain. It only fixes how many degrees the 25% band covers ($17.5\,^{\circ}\mathrm{C}$).

KEY IDEA

Proportional band and gain are reciprocals when both are expressed in percent of span: $K_c = 100/\mathrm{PB}(\%)$. A 25% band means a quarter of the input span swings the output through its full range, so the gain is 4. The span of the measured variable cancels out.

WATCH OUT FOR

Using the temperature range directly. For example, $100\%/17.5\,^{\circ}\mathrm{C} \approx 5.71\,\%/^{\circ}\mathrm{C}$ is a gain with units, not the dimensionless gain the question asks for. Other slips are $70/25 = 2.8$, or reading PB = 25% as $K_c = 0.25$ (confusing the band with the gain, which is its reciprocal).

Q.65 NAT · 2 MARKS

Recombinant DNA Technology and Tools › PCR & sequencing

A dNTP master-mix is prepared by combining 40 µL of each 20 mM dNTP stock (dATP, dCTP, dGTP and dTTP). 4 µL of this dNTP master-mix is added to a PCR mix and the final volume is adjusted to 50 µL. The concentration (in µM) of total dNTPs in the PCR mix is _____.

Official answer: **1600**

SOLUTION

1. Total master-mix volume after combining the four stocks = 40 µL × 4 = 160 µL.
2. Each dNTP is diluted from its 20 mM stock (40 µL) into the 160 µL master-mix: using $C_1V_1 = C_2V_2$, $C = \dfrac{20\ \mathrm{mM} \times 40\ \mu\mathrm{L}}{160\ \mu\mathrm{L}} = 5\ \mathrm{mM}$ for each of dATP, dCTP, dGTP and dTTP.
3. Total dNTP concentration in the master-mix (sum of the four species) = $4 \times 5\ \mathrm{mM} = 20\ \mathrm{mM}$.
4. This master-mix is diluted into the PCR reaction: 4 µL of the 20 mM (total) master-mix is added to a final volume of 50 µL.
5. Applying $C_1V_1 = C_2V_2$ to the total dNTP concentration: $C_2 = \dfrac{20\ \mathrm{mM} \times 4\ \mu\mathrm{L}}{50\ \mu\mathrm{L}} = 1.6\ \mathrm{mM}$.
6. Converting to µM: $1.6\ \mathrm{mM} = 1600\ \mu\mathrm{M}$.

KEY IDEA

Track dilution in two stages using $C_1V_1 = C_2V_2$ separately: (1) each 20 mM dNTP stock is diluted from 40 µL into the pooled 160 µL master-mix, giving each species a concentration of 5 mM, so the four species sum to a total dNTP concentration of 20 mM in the master-mix; (2) this master-mix is itself diluted 4 µL into a 50 µL PCR reaction, scaling the total 20 mM down by the factor 4/50.

WATCH OUT FOR

Confusing "total dNTPs" with a single dNTP's concentration: some solvers compute only 400 µM (one species) and forget to multiply by 4 for the sum of dATP+dCTP+dGTP+dTTP, or forget the mM→µM conversion factor of 1000.

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