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GATE BT · 2019

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GATE BT 2019 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 Madras

Online, with the questions linked to their topic notes: **iaeacademy.in/study/papers/bt-2019**

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About this paper

65 questions, 100 marks. Question types: 47 MCQ · 18 NAT.

Official answer key: IIT Madras · https://web.archive.org/web/20190727212246/http://gate.iitm.ac.in/gate2019/pdfs/Anskey/BT_key_Published.pdf

This paper numbers General Aptitude GA Q.1 to GA Q.10 and the subject questions Q.1 to Q.55: 65 questions in all.

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: **iaeacademy.in/study/papers/bt-2019**

Answer key

Q	TYPE	MARKS	ANSWER
GA Q.1	MCQ	1	**C**
GA Q.2	MCQ	1	**C**
GA Q.3	MCQ	1	**C**
GA Q.4	MCQ	1	**C**
GA Q.5	MCQ	1	**A**
GA Q.6	MCQ	2	**C**
GA Q.7	MCQ	2	**A**
GA Q.8	MCQ	2	**C**
GA Q.9	MCQ	2	**B**
GA Q.10	MCQ	2	**D**
Q.1	MCQ	1	**A**
Q.2	MCQ	1	**B**
Q.3	MCQ	1	**D**
Q.4	MCQ	1	**A**
Q.5	MCQ	1	**A**
Q.6	MCQ	1	**C**
Q.7	MCQ	1	**C**
Q.8	MCQ	1	**B**
Q.9	MCQ	1	**C or B**
Q.10	MCQ	1	**D**
Q.11	MCQ	1	**B**
Q.12	MCQ	1	**B**
Q.13	MCQ	1	**B**
Q.14	MCQ	1	**D**
Q.15	MCQ	1	**D**
Q.16	MCQ	1	**C**
Q.17	MCQ	1	**A**
Q.18	MCQ	1	**B**
Q.19	NAT	1	**3**
Q.20	NAT	1	**-6**
Q.21	NAT	1	**16**
Q.22	NAT	1	**20**
Q.23	NAT	1	**4**
Q.24	NAT	1	**31800 to 32000**
Q.25	NAT	1	**50**
Q.26	MCQ	2	**C**
Q.27	MCQ	2	**B**
Q.28	MCQ	2	**A**
Q.29	MCQ	2	**B**
Q.30	MCQ	2	**B**
Q.31	MCQ	2	**A**
Q.32	MCQ	2	**C**
Q.33	MCQ	2	**A**
Q.34	MCQ	2	**B**
Q.35	MCQ	2	**C**
Q.36	MCQ	2	**C**
Q.37	MCQ	2	**A**
Q.38	MCQ	2	**B**
Q.39	MCQ	2	**D**
Q.40	MCQ	2	**D**
Q.41	MCQ	2	**B**
Q.42	MCQ	2	**C**
Q.43	MCQ	2	**D**
Q.44	MCQ	2	**B**
Q.45	NAT	2	**2**
Q.46	NAT	2	**280 to 295**
Q.47	NAT	2	**0.75**
Q.48	NAT	2	**0.6**
Q.49	NAT	2	**128 to 130**
Q.50	NAT	2	**2.20 to 2.50**
Q.51	NAT	2	**12500 to 14500**
Q.52	NAT	2	**970 to 1010**
Q.53	NAT	2	**1**
Q.54	NAT	2	**9 to 10**
Q.55	NAT	2	**30**

General Aptitude GA Q.1 to Q.10

GA Q.1 MCQ · 1 MARK

General Aptitude › Grammar & vocabulary

The fishermen, _____ the flood victims owed their lives, were rewarded by the government.

(A) whom

(B) to which

(C) to whom

(D) that

Official answer: **C**

SOLUTION

1. The blank opens a relative clause about 'the fishermen': the flood victims owed their lives _____ the fishermen.
2. The verb 'owe' takes the person owed after 'to': one owes something to someone. So the relative pronoun must come with 'to'.
3. The fishermen are people, so the pronoun is 'whom' (not 'which'). It is the object of the preposition 'to', so the object form 'whom' is needed. This gives 'to whom'.
4. (A) 'whom' alone leaves 'owed their lives' with no 'to' marking the person owed, so the clause is incomplete.
5. (D) 'that' cannot follow a preposition. It also cannot introduce a non-restrictive clause set off by a comma.
6. (B) 'to which' is wrong because 'which' refers to things, not people.
7. Completed sentence: 'The fishermen, to whom the flood victims owed their lives, were rewarded by the government.'

KEY IDEA

'Owe' takes 'to' before the person owed. When the relative pronoun stands for a person after a preposition, use 'preposition + whom' ('to whom').

WATCH OUT FOR

Choosing 'whom' alone (A) because the antecedent is a person, and forgetting that 'owed ... to' needs the preposition. Another slip is picking 'that' (D), which cannot follow a preposition or a comma-set clause.

GA Q.2 MCQ · 1 MARK

General Aptitude › Reasoning

Some students were not involved in the strike.

If the above statement is true, which of the following conclusions is/are logically necessary?

1. Some who were involved in the strike were students.
2. No student was involved in the strike.
3. At least one student was involved in the strike.
4. Some who were not involved in the strike were students.

(A) 1 and 2

(B) 3

(C) 4

(D) 2 and 3

Official answer: **C**

SOLUTION

1. The given statement is a particular negative: "Some students were not involved in the strike." It says that at least one student exists, and that this student was not involved in the strike.
2. Test conclusion 4, "Some who were not involved in the strike were students": this says there is at least one student outside the strike. That is the given statement turned around, so it is logically necessary.
3. Test conclusion 1, "Some who were involved in the strike were students": the statement says nothing about students who were involved. Every other student could have been uninvolved, so this need not hold.
4. Test conclusion 2, "No student was involved in the strike": this is stronger than the statement. One student being uninvolved does not rule out other students being involved, so this need not hold.
5. Test conclusion 3, "At least one student was involved in the strike": this has the same meaning as conclusion 1 and is not forced. A particular negative does not imply a particular affirmative.
6. Only conclusion 4 is logically necessary, so the answer is (C).

KEY IDEA
"Some A are not B" is the same claim as "Some non-B are A". It guarantees that a student outside the strike exists. It says nothing about whether any student took part.

WATCH OUT FOR
Reading "some students were not involved" as implying that the other students were involved, and so picking conclusion 3 or 1. A particular negative does not imply a particular affirmative. Another slip is jumping to "no student was involved" (conclusion 2), which is far stronger than the statement.

GA Q.3 MCQ · 1 MARK

General Aptitude › Geometry

The radius as well as the height of a circular cone increases by 10%. The percentage increase in its volume is _____.

(A) 17.1

(B) 21.0

(C) 33.1

(D) 72.8

Official answer: **C**

SOLUTION

1. The volume of a cone is $V = \frac{1}{3}\pi r^2 h$, so $V \propto r^2 h$.
2. A 10% increase multiplies both r and h by 1.1.
3. The new volume is $V' = \frac{1}{3}\pi(1.1r)^2(1.1h) = (1.1)^3\, V$.
4. $(1.1)^3 = 1.331$.
5. Percentage increase $= (1.331 - 1) \times 100\% = 33.1\%$.
6. This matches option (C).

KEY IDEA
Volume goes as $r^2 h$, so raising both r and h by 10% multiplies the volume by $1.1^3 = 1.331$.

WATCH OUT FOR
Adding the two percentage increases (10% + 10% = 20%), or counting r^2 as a single 10% factor to get $1.1^2 = 1.21$, which gives 21.0%. The volume depends on r squared and on h, so the multiplier is 1.1^3.

GA Q.4 MCQ · 1 MARK

General Aptitude › Reasoning

Five numbers 10, 7, 5, 4 and 2 are to be arranged in a sequence from left to right following the directions given below:
1. No two odd or even numbers are next to each other.
2. The second number from the left is exactly half of the left-most number.
3. The middle number is exactly twice the right-most number.

Which is the second number from the right?

(A) 2
(B) 4
(C) 7
(D) 10

Official answer: **C**

SOLUTION

1. Of the numbers 10, 7, 5, 4, 2, three are even (10, 4, 2) and two are odd (7, 5). Rule 1 says no two odd numbers and no two even numbers are next to each other, so the parities must alternate. With 3 evens and 2 odds, the only possible pattern is even, odd, even, odd, even. So positions 1, 3, 5 hold even numbers and positions 2, 4 hold odd numbers.
2. Rule 2: the number in position 2 is half the number in position 1. Position 2 is odd, so it is 7 or 5. That would make position 1 equal to 14 or 10. Only 10 is available, so position 1 is 10 and position 2 is 5.
3. Rule 3: the middle number (position 3) is twice the right-most number (position 5). The even numbers left are 4 and 2. Since $4 = 2 \times 2$, position 3 is 4 and position 5 is 2. The other choice fails, because $2 \neq 2 \times 4$.
4. The only number left is 7, and it goes to position 4.
5. The sequence is $10,\ 5,\ 4,\ 7,\ 2$. It satisfies all three rules. The second number from the right is 7, which is option (C).

KEY IDEA
Fix the parity pattern first (3 evens and 2 odds can only alternate as even, odd, even, odd, even). Then use the half and double relations to pin down the numbers.

WATCH OUT FOR
Skipping the parity step and trying orderings by trial. Another slip is reading "second number from the right" as position 2 from the left.

GA Q.5 MCQ · 1 MARK

General Aptitude › Grammar & vocabulary

Until Iran came along, India had never been _____ in kabaddi.

(A) defeated
(B) defeating
(C) defeat
(D) defeatist

Official answer: **A**

SOLUTION

1. The sentence reads: "Until Iran came along, India had never been _____ in kabaddi." The blank follows "had never been", so we need a word that fits after "been".
2. The meaning is that before Iran appeared, India had never lost a kabaddi match. India is the one on the receiving end of the defeat, so the verb must be passive: "been defeated" (a past participle after

"been").

3. (B) "been defeating" is the progressive form and would mean India was doing the defeating. That reverses the sense of the sentence, because Iran is the side that finally beat India.
4. (C) "been defeat" is ungrammatical. "Defeat" is a noun or a bare verb, and a noun here would need an article, as in "been a defeat".
5. (D) "been defeatist" is grammatical, but "defeatist" describes an attitude of expecting to lose. It does not fit "in kabaddi" and does not match the "Until Iran came along" contrast.
6. So the passive participle fits: "India had never been defeated in kabaddi." The answer is (A).

KEY IDEA

After "had never been", a transitive verb such as "defeat" needs its past participle to form the passive. Here India receives the action, so "been defeated" is the form that fits.

WATCH OUT FOR

Picking "defeating" because "been" can be followed by an -ing form. That is the progressive, and it would make India the one doing the defeating. Another slip is picking "defeatist" because it looks like a word that could follow "been". It describes an attitude, not the result of losing a match.

GA Q.6 MCQ · 2 MARKS

General Aptitude › Reading

Since the last one year, after a 125 basis point reduction in repo rate by the Reserve Bank of India, banking institutions have been making a demand to reduce interest rates on small saving schemes. Finally, the government announced yesterday a reduction in interest rates on small saving schemes to bring them on par with fixed deposit interest rates.

Which one of the following statements can be inferred from the given passage?

(A) Whenever the Reserve Bank of India reduces the repo rate, the interest rates on small saving schemes are also reduced

(B) Interest rates on small saving schemes are always maintained on par with fixed deposit interest rates

(C) The government sometimes takes into consideration the demands of banking institutions before reducing the interest rates on small saving schemes

(D) A reduction in interest rates on small saving schemes follow only after a reduction in repo rate by the Reserve Bank of India

Official answer: **C**

SOLUTION

1. An inference question asks which statement must follow from the passage alone. A statement using a universal word such as "whenever", "always" or "only after" needs support for every case, and a single episode cannot give that.
2. The passage describes one episode. The repo rate was cut by 125 basis points. Banks then demanded a cut in small-savings rates. The government announced a cut to bring those rates on par with fixed deposit rates.
3. (A) says that whenever the repo rate falls, small-savings rates fall too. The passage gives one case and says nothing about a general rule. It cannot be inferred.
4. (B) says small-savings rates are always on par with fixed deposit rates. The passage says this cut was made to bring them on par. That suggests they had not been on par before, so "always" is not supported and is contradicted if anything. It cannot be inferred.
5. (D) says a cut follows only after a repo-rate cut. The passage gives one case of a cut after a repo cut. It does not say a repo cut is the only possible trigger. It cannot be inferred.

6. (C) says the government sometimes takes into account the demands of banking institutions before reducing small-savings rates. The banks demanded a cut and the government then cut the rates. The government therefore acted in line with the banks' demand in at least this one instance. "Sometimes" claims only that much, so it is supported.
7. Answer: (C).

KEY IDEA
In an inference question, choose the statement that the passage alone makes certain. A modest claim such as "sometimes" is supported by a single example. A universal claim such as "whenever", "always" or "only after" is not.

WATCH OUT FOR
Picking (A) or (D) because the repo-rate cut and the small-savings cut appear linked in the passage. One episode does not establish a rule that holds every time, or that a repo cut is the only trigger. Another slip is choosing (B) without noticing that the passage implies the rates were not on par before.

GA Q.7 MCQ · 2 MARKS

General Aptitude › Numerical

In a country of 1400 million population, 70% own mobile phones. Among the mobile phone owners, only 294 million access the Internet. Among these Internet users, only half buy goods from e-commerce portals. What is the percentage of these buyers in the country?

(A) 10.50
(B) 14.70
(C) 15.00
(D) 50.00

Official answer: **A**

SOLUTION

1. Population of the country: 1400 million. Mobile phone owners: 70% of $1400 = 980$ million.
2. The number of Internet users among them is given directly: 294 million (this is 30% of the 980 million owners, so no further percentage needs to be applied).
3. Buyers from e-commerce portals are half of the Internet users: $\frac{294}{2} = 147$ million.
4. The question asks for the percentage of buyers in the whole country, so divide by the total population of 1400 million.
5. $$\frac{147}{1400} \times 100 = 10.5\%$$
6. The answer is option (A) 10.50.

KEY IDEA
Percentage of the country means the count divided by the whole population (1400 million), not by an intermediate group. Use the 294 million figure as given.

WATCH OUT FOR
Taking 30% or 70% again of the phone owners or Internet users, or dividing 147 million by 980 million (giving 15%) or by 294 million (giving 50%), instead of dividing by the total population.

GA Q.8 MCQ · 2 MARKS

General Aptitude › Reading

The nomenclature of Hindustani music has changed over the centuries. Since the medieval period *dhrupad* styles were identified as *baanis*. Terms like *gayaki* and *baaj* were used to refer to vocal and instrumental styles, respectively. With the institutionalization of music education the term *gharana* became acceptable. *Gharana* originally referred to hereditary musicians from a particular lineage, including disciples and grand disciples.

Which one of the following pairings is NOT correct?

(A) *dhrupad*, *baani*

(B) *gayaki*, vocal

(C) *baaj*, institution

(D) *gharana*, lineage

Official answer: **C**

SOLUTION

1. The question asks which pairing is NOT supported by the passage, so check each pair against the text.
2. (A) The passage says *dhrupad* styles were identified as *baanis*. The pairing *dhrupad*, *baani* is correct.
3. (B) The passage says *gayaki* and *baaj* refer to vocal and instrumental styles, respectively. So *gayaki* matches vocal. Correct.
4. (C) By the same sentence, *baaj* refers to instrumental styles. The passage does not link it to an institution. The word institutionalization appears only in connection with the term *gharana*. This pairing is NOT correct.
5. (D) The passage says *gharana* referred to hereditary musicians from a particular lineage. The pairing *gharana*, lineage is correct.
6. Only (C) contradicts the passage, so the answer is (C).

KEY IDEA

In a NOT-correct question, test each option against the exact words of the passage. The respective order of the terms (gayaki and baaj, vocal and instrumental) fixes which term goes with which style.

WATCH OUT FOR

Picking (C) is easy to miss because the word institutionalization is in the passage. It attaches to gharana, not to baaj, so a reader who matches words loosely may skip (C) or wrongly doubt (B).

GA Q.9 MCQ · 2 MARKS

General Aptitude › Numerical

Two trains started at 7AM from the same point. The first train travelled north at a speed of 80km/h and the second train travelled south at a speed of 100 km/h. The time at which they were 540 km apart is _____ AM.

(A) 9

(B) 10

(C) 11

(D) 11.30

Official answer: **B**

SOLUTION

1. The trains start from the same point at 7 AM and travel in opposite directions (north and south), so the distance between them grows at the sum of their speeds.
2. Separation rate: $80 + 100 = 180\ \mathrm{km/h}$.
3. Time needed to be 540 km apart: $t = \dfrac{540}{180} = 3\ \mathrm{h}$.
4. Clock time: $7\ \mathrm{AM} + 3\ \mathrm{h} = 10\ \mathrm{AM}$.
5. The answer is option (B).

KEY IDEA
When two objects leave the same point in opposite directions, the gap between them grows at the sum of their speeds. Divide the distance by that sum to get the time, then add it to the start time.

WATCH OUT FOR
Subtracting the speeds ($100 - 80 = 20$ km/h), which applies to travel in the same direction, or giving the elapsed time (3 h) instead of the clock time (10 AM).

GA Q.10 MCQ · 2 MARKS

General Aptitude › Reading

"I read somewhere that in ancient times the prestige of a kingdom depended upon the number of taxes that it was able to levy on its people. It was very much like the prestige of a head-hunter in his own community."

Based on the paragraph above, the prestige of a head-hunter depended upon _____

(A) the prestige of the kingdom

(B) the prestige of the heads

(C) the number of taxes he could levy

(D) the number of heads he could gather

Official answer: **D**

SOLUTION

1. Reading comprehension (analogy in the passage): the passage compares two things, the kingdom's prestige and the head-hunter's prestige, joined by the words "very much like".
2. The kingdom's prestige depended on the number of taxes it could levy on its people. So the kingdom's prestige rests on a countable quantity it collects.
3. A head-hunter collects heads, so the matching quantity for him is the number of heads he could gather.
4. Option A: the passage says the head-hunter's prestige is like the kingdom's prestige. It does not say it depends on it. Eliminate.
5. Option B: the passage never mentions the prestige of the heads, and it is not a quantity he collects. Eliminate.
6. Option C: taxes belong to the kingdom half of the comparison, and a head-hunter levies none. Eliminate.
7. Option D: the number of heads he could gather mirrors the number of taxes a kingdom could levy. Correct.

KEY IDEA
In an analogy passage, match the parts. The kingdom's prestige depends on the number of taxes it collects, so the head-hunter's prestige depends on the number of heads he collects.

WATCH OUT FOR
Picking (A) or (C) because they repeat words from the passage ('prestige of the kingdom', 'taxes'). These belong to the kingdom side of the comparison, not the head-hunter's.

Biotechnology Q.1 to Q.55

Q.1 MCQ · 1 MARK

Plant, Animal and Microbial Biotechnology › Transgenic plants

The Bt toxin gene from Bacillus thuringiensis used to generate genetically modified crops is

(A) cry

(B) cro

(C) cdc

(D) cre

Official answer: **A**

SOLUTION

1. The Bt toxin is the crystal (Cry) protein, a delta-endotoxin made by Bacillus thuringiensis as parasporal crystals. The gene that encodes it is named cry.
2. Option (A) cry: correct. The cry gene is expressed in plants such as Bt cotton and Bt brinjal. It gives insect resistance because the protoxin is activated in the alkaline insect midgut and the active toxin binds gut receptors.
3. Option (B) cro: wrong. cro encodes the Cro repressor of bacteriophage lambda, which acts in the lytic-lysogenic switch.
4. Option (C) cdc: wrong. The cdc genes are cell division cycle genes of yeast and other eukaryotes. They control cell-cycle progression.
5. Option (D) cre: wrong. cre encodes Cre recombinase of bacteriophage P1, which acts at loxP sites. It is used in genetic engineering to excise or invert DNA, not to confer insect resistance.

KEY IDEA

Bt toxin is the Cry (crystal) protein, a delta-endotoxin of Bacillus thuringiensis, and its gene is cry. Expressed in crops, it protects them against certain insects.

WATCH OUT FOR

Picking cre or cro because the three-letter names look alike. cre is the P1 recombinase gene and cro is a lambda phage repressor gene. Neither has anything to do with insect toxins.

Q.2 MCQ · 1 MARK

Plant, Animal and Microbial Biotechnology › Animal cell culture

Which one of the following is used as a pH indicator in animal cell culture medium?

(A) Acridine orange

(B) Phenol red

(C) Bromophenol blue

(D) Coomassie blue

Official answer: **B**

SOLUTION

1. Animal cell culture media are buffered near pH 7.2 to 7.4. Cell metabolism produces acids (lactic acid, CO_2), so the pH of the medium must be easy to monitor.
2. Phenol red is a weak-acid dye added to culture media. It is red at physiological pH, yellow when the medium turns acidic and purple-pink when it turns alkaline, so the colour of the medium shows its pH at a glance. Option B is correct.
3. Acridine orange is a fluorescent nucleic acid stain, used for DNA/RNA staining and for viability and apoptosis assays. It is not a pH indicator for the medium. Option A is wrong.

4. Bromophenol blue is mainly a tracking dye in gel electrophoresis loading buffers. As a pH indicator it changes colour only at about pH 3.0 to 4.6, far from the physiological range, so it is not used in culture media. Option C is wrong.
5. Coomassie blue is a protein stain for gels and protein assays, not a pH indicator. Option D is wrong.

KEY IDEA
Phenol red is the pH indicator built into most animal cell culture media. It changes colour (red at about pH 7.4, yellow when acidic, purple-pink when alkaline) in the range where cells grow, so you can judge the medium's pH by eye.

WATCH OUT FOR
Picking bromophenol blue because it is also a pH-sensitive dye. Its colour change is at about pH 3.0 to 4.6, nowhere near the neutral range of culture media. Acridine orange and Coomassie blue are stains, not indicators.

Q.3 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Gene expression

Tetracycline inhibits the

(A) interaction between tRNA and mRNA
(B) translocation of mRNA through ribosome
(C) peptidyl transferase activity
(D) binding of amino-acyl tRNA to ribosome

Official answer: **D**

SOLUTION

1. Tetracycline is a well-known bacterial translation inhibitor that binds the 30S ribosomal subunit.
2. Its specific mechanism is steric blockage of the A site on the 30S subunit, which prevents the aminoacyl-tRNA-EF-Tu-GTP ternary complex from docking there.
3. Option A (interaction/pairing between tRNA and mRNA) is not tetracycline's target: codon-anticodon pairing proceeds once a tRNA is positioned; this is not tetracycline's described mechanism.
4. Option B (translocation of mRNA/tRNA through the ribosome) is the EF-G-dependent step, blocked by drugs such as fusidic acid, not tetracycline.
5. Option C (peptidyl transferase activity, the 50S ribozyme reaction) is inhibited by chloramphenicol, not tetracycline.
6. Option D (binding of amino-acyl tRNA to the ribosome) matches tetracycline's textbook mechanism exactly: it blocks the A site so aminoacyl-tRNA cannot bind.
7. Therefore the correct answer is D.

KEY IDEA
Tetracycline is a bacteriostatic protein-synthesis inhibitor that binds the 30S ribosomal subunit and sterically blocks the A site, preventing the aminoacyl-tRNA-EF-Tu-GTP ternary complex from docking; it stops aminoacyl-tRNA from binding to the ribosome.

WATCH OUT FOR
Confusing tetracycline (blocks aminoacyl-tRNA binding at the A site) with chloramphenicol (blocks peptidyl transferase) or fusidic acid (blocks translocation/EF-G recycling).

Q.4 MCQ · 1 MARK

Recombinant DNA Technology and Tools › Bioinformatics

Which one of the following is a database of protein sequence motifs?

(A) PROSITE
(B) TrEMBL
(C) SWISSPROT

(D) PDB

Official answer: **A**

SOLUTION

1. A protein sequence motif database stores conserved patterns/signatures (regular-expression-like patterns and profiles) associated with protein families, domains and functional sites.
2. (A) PROSITE is exactly this: a curated database of protein domains, families and functional sites, represented as patterns and profiles derived from conserved motifs in multiple sequence alignments. Correct.
3. (B) TrEMBL is the unreviewed, computationally annotated section of UniProt. It stores full protein sequences with automatic annotation, not a motif/pattern collection. Incorrect.
4. (C) SWISS-PROT is the manually curated, reviewed section of UniProt, again full annotated sequences, not a motif database. Incorrect.
5. (D) PDB (Protein Data Bank) stores experimentally determined 3D structures of proteins and nucleic acids, not sequence motifs. Incorrect.
6. Hence the correct answer is PROSITE.

KEY IDEA
PROSITE is a curated database of protein domains, families and functional sites, represented as sequence patterns (regular-expression-like signatures) and profiles derived from conserved motifs, as opposed to UniProt/TrEMBL/Swiss-Prot (full sequence records) or PDB (3D structures).

WATCH OUT FOR
Confusing any UniProt-family database (TrEMBL, SWISS-PROT) with a motif database just because they are also "protein sequence" resources. They store full annotated sequences, not curated pattern/profile signatures of motifs.

Q.5 MCQ · 1 MARK

General Biology › Pathogens & antibiotics

Which one of the following enzymes is encoded by human immunodeficiency virus (HIV) genome?

(A) Reverse transcriptase

(B) Phospholipase

(C) Phosphatase

(D) ATP synthase

Official answer: **A**

SOLUTION

1. HIV is a retrovirus with a single-stranded RNA genome. Its genome carries three major genes: gag (structural proteins), pol (enzymes) and env (envelope glycoproteins), plus regulatory and accessory genes.
2. The pol gene encodes the viral enzymes reverse transcriptase, integrase and protease. Reverse transcriptase copies the viral RNA into DNA, which integrase inserts into the host genome. So (A) is encoded by the HIV genome.
3. (B) Phospholipase is a lipid-hydrolysing enzyme made by host cells and some bacteria. The HIV genome has no gene for it, so it is wrong.
4. (C) Phosphatase removes phosphate groups and is a host cell enzyme. The HIV genome has no gene for it, so it is wrong.
5. (D) ATP synthase is a membrane enzyme of mitochondria, chloroplasts and bacteria. A virus has no energy-generating machinery and does not encode it, so it is wrong.
6. Only reverse transcriptase is encoded by HIV, so the answer is (A).

KEY IDEA
HIV is a retrovirus. Its pol gene encodes reverse transcriptase, integrase and protease, and these are the enzymes the virus brings with it.

WATCH OUT FOR
Choosing a familiar host enzyme such as phosphatase or phospholipase. Viruses encode very few enzymes, and only those needed for their own replication cycle.

Q.6 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Cell biology

DNA synthesis in eukaryotes occurs during which phase of the mitotic cell cycle?

(A) M
(B) G_1
(C) S
(D) G_0

Official answer: **C**

SOLUTION

1. The eukaryotic mitotic cell cycle consists of Interphase (G1, S, G2) followed by M phase (mitosis).
2. G1 (Gap 1) phase: the cell grows and synthesizes the enzymes and proteins required for replication, but DNA itself is not yet replicated.
3. S (Synthesis) phase: this is, by definition, the phase in which the entire genome is replicated, so DNA content rises from 2C to 4C. This is where DNA synthesis occurs.
4. G2 (Gap 2) phase: the cell grows further and checks for replication errors before mitosis; DNA synthesis is already complete by this stage.
5. M (Mitotic) phase: replicated chromosomes condense and segregate into two daughter cells; no new DNA synthesis occurs here.
6. G0 is a quiescent/resting state outside the active division cycle, not a phase of DNA replication.
7. Hence DNA synthesis occurs specifically in S phase: option (C).

KEY IDEA
The eukaryotic mitotic cell cycle is Interphase (G1 → S → G2) followed by M phase; DNA replication (synthesis of new DNA, doubling content from 2C to 4C) is confined to S phase, giving it its name ("Synthesis").

WATCH OUT FOR
Confusing G1 and G2 (both non-synthetic growth phases) with S phase, or assuming G0 (quiescence) is simply "before M phase" and therefore synthetic.

Q.7 MCQ · 1 MARK

General Biology › Pathogens & antibiotics

Match the human diseases in Group I with the causative agents in Group II.

Group I: P. Amoebiasis; Q. African sleeping sickness; R. Kala azar; S. Chagas' disease
Group II: 1. Leishmania donovani; 2. Trypanosoma cruzi; 3. Entamoeba histolytica; 4. Trypanosoma gambiense

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

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

Official answer: **C**

SOLUTION

1. Amoebiasis (amoebic dysentery) is caused by the protozoan *Entamoeba histolytica*, so P-3. This rules out option D (P-4).
2. African sleeping sickness (trypanosomiasis) is caused by *Trypanosoma brucei*, which occurs as the subspecies *T. b. gambiense* (West and Central Africa) and *T. b. rhodesiense* (East Africa), both spread by the tsetse fly. Of the agents listed, only *Trypanosoma gambiense* fits, so Q-4. This rules out option B (Q-2).
3. Kala azar (visceral leishmaniasis) is caused by *Leishmania donovani* and spread by the sandfly, so R-1. This rules out option A (R-2).
4. Chagas' disease (American trypanosomiasis) is caused by *Trypanosoma cruzi* and spread by the reduviid (kissing) bug in Central and South America, so S-2.
5. The full matching is P-3, Q-4, R-1, S-2, which is option (C).

KEY IDEA

Match each protozoan disease to its parasite: amoebiasis with Entamoeba histolytica, African sleeping sickness with Trypanosoma brucei (gambiense), kala azar with Leishmania donovani, and Chagas' disease with Trypanosoma cruzi. Remember the vector and the region: tsetse fly and Africa, sandfly, reduviid bug and the Americas.

WATCH OUT FOR

Swapping the two trypanosomes. Trypanosoma cruzi causes Chagas' disease in the Americas, not African sleeping sickness. Another slip is pairing kala azar with a Trypanosoma species, when it is caused by Leishmania.

Q.8 MCQ · 1 MARK

Recombinant DNA Technology and Tools › Assays & electrophoresis

Which one of the following techniques can be used to compare the expression of a large number of genes in two biological samples in a single experiment?

(A) Polymerase chain reaction

(B) DNA microarray

(C) Northern hybridization

(D) Southern hybridization

Official answer: **B**

SOLUTION

1. The question requires a technique that: (1) measures gene expression (RNA transcript levels), (2) for a large number of genes, (3) comparing two biological samples, (4) in a single experiment.
2. Option (A) PCR: amplifies/quantifies one or a small targeted set of specific DNA/cDNA sequences per run; not designed for large-scale, genome-wide comparison in a single experiment. Eliminated.
3. Option (B) DNA microarray: a chip carrying thousands to tens of thousands of gene-specific probe spots. cDNA from two samples (commonly labelled with two different fluorophores, e.g. Cy3/Cy5) is hybridized to the chip simultaneously, and the relative fluorescence at each spot reflects the relative expression of that gene between the two samples. This is exactly a large-scale, two-sample, single-experiment comparison. Matches all requirements.
4. Option (C) Northern hybridization: detects and semi-quantifies one specific RNA species per blot using a single labelled probe; not suited to comparing large numbers of genes at once. Eliminated.

5. Option (D) Southern hybridization: probes for specific genomic DNA sequences, not gene expression (RNA) at all, and again targets only one or a few sequences per blot. Eliminated.
6. Only DNA microarray satisfies both the 'large number of genes' and the 'simultaneous two-sample, single-experiment' requirements.

KEY IDEA

A DNA microarray carries thousands of gene-specific probe spots on a single chip; fluorescently labelled cDNA from two samples is hybridized to it simultaneously, so the relative signal at each spot gives a genome-scale, single-experiment comparison of gene expression between the two samples, something PCR, Northern and Southern hybridization each do only one (or a few) targets at a time.

WATCH OUT FOR

Confusing DNA microarray (measures RNA/gene expression via labelled cDNA hybridized to probe spots) with Southern hybridization (detects specific DNA sequences, not expression). The word "DNA" in "DNA microarray" misleads some students into picking a genomic-DNA technique like (D) instead.

Q.9 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Microbial genetics

Which of the following processes can increase genetic diversity of bacteria in nature?
P. Conjugation
Q. Transformation
R. Transduction
S. Transfection

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

Official answer: **C or B**

SOLUTION

1. P. Conjugation: direct cell-to-cell transfer of plasmid/chromosomal DNA through a pilus. This occurs naturally among bacteria in the environment (e.g., spread of antibiotic-resistance plasmids) and increases genetic diversity. Include.
2. Q. Transformation: uptake of free (naked) DNA released from lysed cells by naturally competent bacteria such as Streptococcus pneumoniae, Bacillus subtilis and Neisseria species. This is a spontaneous natural process and increases genetic diversity. Include.
3. R. Transduction: bacteriophages package host bacterial DNA (generalized transduction) or adjacent genes (specialized transduction) and inject it into a new host cell during their normal infection cycle in nature. This increases genetic diversity. Include.
4. S. Transfection: the deliberate, artificial introduction of naked DNA or viral nucleic acid into cells using laboratory methods (chemical reagents, electroporation, etc.). It is a technique performed by experimenters, not a process bacteria undergo spontaneously in nature. Exclude.
5. Since only conjugation, transformation and transduction are natural mechanisms that increase genetic diversity of bacteria in nature, the correct option is (C) P, Q and R only.

KEY IDEA
Bacteria acquire new genetic material through three natural horizontal gene transfer mechanisms: conjugation (direct transfer via pilus), transformation (uptake of free environmental DNA), and transduction (phage-mediated DNA transfer). Transfection is a laboratory technique for artificially introducing nucleic acid into cells and is not a process that occurs on its own in nature.

WATCH OUT FOR
Confusing transfection (lab-mediated artificial introduction of naked DNA/RNA into cells) with transformation (natural uptake of free DNA by competent bacteria); both involve "naked" nucleic acid entering a cell, but only transformation is a process bacteria undergo spontaneously in nature.

Q.10 MCQ · 1 MARK

General Biology › Immune system

Which one of the following is NOT a part of the human nonspecific defense system?

(A) Interferon

(B) Mucous

(C) Saliva

(D) Antibody

Official answer: **D**

SOLUTION

1. Nonspecific (innate) defence acts the same way against any pathogen and needs no prior exposure. It includes physical and chemical barriers, phagocytes, natural killer cells, inflammation and interferons.
2. (A) Interferon: antiviral proteins released by infected cells that put neighbouring cells into an antiviral state against any virus. This is innate, so it is part of the nonspecific system.
3. (B) Mucous: mucus membranes trap microbes and carry them away by ciliary action. This is a physical barrier, so it is nonspecific.
4. (C) Saliva: it contains lysozyme, which breaks down bacterial peptidoglycan, and it washes microbes away. This is a chemical barrier, so it is nonspecific.
5. (D) Antibody: immunoglobulins are made by plasma cells (activated B cells) and bind one particular antigen. This is the adaptive, specific response, so it is NOT part of the nonspecific system.
6. Hence the answer is (D).

KEY IDEA
Innate (nonspecific) defences work the same against any pathogen without prior exposure: barriers such as mucus and saliva, phagocytes, NK cells, inflammation and interferons. Antibodies are made against one particular antigen, so they belong to the adaptive response.

WATCH OUT FOR
Counting interferon as specific because it acts against viruses. It protects against any virus and needs no prior exposure, so it is innate. Antibodies are the only option that recognises one particular antigen.

Q.11 MCQ · 1 MARK

Genetics, Cell and Molecular Biology › Mutation & repair

A mutation in a gene that codes for a polypeptide results in a variant polypeptide that lacks the last three amino acids. What type of mutation is this?

(A) Synonymous mutation

(B) Nonsense mutation

(C) Missense mutation

(D) Silent mutation

Official answer: **B**

SOLUTION

1. A mutation in a gene produces a variant polypeptide that is shorter by exactly the last three amino acids; nothing else about the protein (reading frame, downstream identity) is stated to differ, since translation simply stops earlier than normal.
2. This pattern (reading frame preserved, chain ending early at a fixed point) is the signature of a premature stop (termination) codon appearing in place of what was originally a sense codon three residues before the natural end.
3. Check each option against this fact: (A) A synonymous mutation changes a codon to a different codon for the SAME amino acid, so the protein sequence does not change at all; it cannot shorten the polypeptide. Eliminated.
4. (B) A nonsense mutation changes a sense codon into a stop codon, causing translation to terminate at that point and truncating the polypeptide downstream of the mutation; this exactly matches losing the last three amino acids. Fits.
5. (C) A missense mutation changes a codon so that it codes for a DIFFERENT amino acid, giving a full-length polypeptide with one substituted residue, not a shortened one. Eliminated.
6. (D) A silent mutation has no effect on the amino acid sequence (most commonly synonymous, sometimes in a non-coding/regulatory region); again, no truncation is possible. Eliminated.
7. Only a nonsense mutation explains a variant polypeptide that terminates prematurely, precisely removing the terminal three residues.

KEY IDEA

A polypeptide that is simply shortened (truncated) at a fixed point, with nothing else about it changed, points to a stop codon appearing where a sense codon used to be: a nonsense mutation.

WATCH OUT FOR

Confusing "nonsense" (produces a premature STOP codon, truncating the protein) with "missense" (changes to a DIFFERENT amino acid, full length) or "silent"/"synonymous" (no change to the protein at all).

Q.12 MCQ · 1 MARK

Engineering Mathematics › Differential equations

Which one of the following equations represents a one-dimensional wave equation?

(A) ∂u/∂t = c² ∂²u/∂x²

(B) ∂²u/∂t² = c² ∂²u/∂x²

(C) ∂²u/∂t² = c² ∂u/∂x

(D) ∂²u/∂t² + ∂²u/∂x² = 0

Official answer: **B**

SOLUTION

1. The one-dimensional wave equation describes a disturbance travelling at speed c along x. It is second order in both time and space: $\frac{\partial^2 u}{\partial t^2} = c^2 \frac{\partial^2 u}{\partial x^2}$.
2. Check with d'Alembert's solution $u = f(x - ct) + g(x + ct)$. Differentiating twice in t gives $u_{tt} = c^2 f'' + c^2 g''$. Differentiating twice in x gives $u_{xx} = f'' + g''$. Hence $u_{tt} = c^2 u_{xx}$.
3. Option (A) has a first derivative in time and a second in space: $u_t = c^2 u_{xx}$. This is the heat (diffusion) equation, not the wave equation.

4. Option (C) has a second time derivative and a first space derivative. It is not the wave equation. Try $u = f(x - ct)$ in it: $c^2 f'' = c^2 f'$, so $f'' = f'$, which holds only for $f = Ae^s + B$ with $s = x - ct$. Travelling waves of arbitrary shape are therefore not solutions.
5. Option (D) has a plus sign between the second derivatives: $u_{tt} + u_{xx} = 0$. This is Laplace's equation in (x, t), which is elliptic. It has no wave-like solutions.
6. Only option (B) has the form $u_{tt} = c^2 u_{xx}$, so (B) is the one-dimensional wave equation.

KEY IDEA
The wave equation is second order in both time and space with a positive coefficient, $u_{tt} = c^2 u_{xx}$. It is hyperbolic and has solutions $f(x - ct) + g(x + ct)$. The heat equation is first order in time, and Laplace's equation has the same sign on both second derivatives.

WATCH OUT FOR
Confusing the wave equation with the heat equation (option A) because both have c^2 and $\partial^2/\partial x^2$. The deciding factor is whether the time derivative is first order (heat) or second order (wave).

Q.13 MCQ · 1 MARK

Engineering Mathematics › Calculus

Which of the following are geometric series?
P. 1, 6, 11, 16, 21, 26, ...
Q. 9, 6, 3, 0, -3, -6, ...
R. 1, 3, 9, 27, 81, ...
S. 4, -8, 16, -32, 64, ...

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

Official answer: **B**

SOLUTION

1. A series is geometric when the ratio of every term to the one before it is the same constant.
2. P: $1, 6, 11, 16, \ldots$ has constant differences $6 - 1 = 11 - 6 = 5$, but the ratios $\frac{6}{1} = 6$ and $\frac{11}{6}$ are unequal. So P is arithmetic, not geometric.
3. Q: $9, 6, 3, 0, -3, \ldots$ has constant differences -3, but the ratios $\frac{6}{9} = \frac{2}{3}$ and $\frac{3}{6} = \frac{1}{2}$ are unequal. The term 0 would also make the next ratio $\frac{-3}{0}$ undefined. So Q is arithmetic, not geometric.
4. R: $\frac{3}{1} = \frac{9}{3} = \frac{27}{9} = \frac{81}{27} = 3$. The ratio is constant, so R is geometric.
5. S: $\frac{-8}{4} = \frac{16}{-8} = \frac{-32}{16} = \frac{64}{-32} = -2$. The ratio is constant, so S is geometric.
6. Only R and S are geometric, which is option (B).

KEY IDEA
A geometric series has a constant ratio between consecutive terms; an arithmetic series has a constant difference. Test the ratio of each pair of neighbours.

WATCH OUT FOR
Calling P and Q geometric because their terms change by a regular pattern. A constant difference makes a series arithmetic, not geometric.

Q.14 MCQ · 1 MARK

General Biology › Enzymes

Which one of the following statements is CORRECT for enzyme catalyzed reactions? (ΔG is Gibbs free energy change, K_{eq} is equilibrium constant)

(A) Enzymes affect ΔG, but not K_{eq}

(B) Enzymes affect K_{eq}, but not ΔG

(C) Enzymes affect both ΔG and K_{eq}

(D) Enzymes do not affect ΔG or K_{eq}

Official answer: **D**

SOLUTION

1. An enzyme is a catalyst. It lowers the activation energy $\Delta G^{\ddagger}$ of the reaction by stabilising the transition state, so the reaction reaches equilibrium faster.
2. The overall free energy change depends only on the free energies of the initial and final states: $\Delta G = G_{\text{products}} - G_{\text{reactants}}$. An enzyme changes neither state, so ΔG is unchanged.
3. The equilibrium constant is fixed by the standard free energy change: $\Delta G^{\circ} = -RT \ln K_{eq}$. Since ΔG° is unchanged, K_{eq} is unchanged.
4. The enzyme speeds the forward and reverse reactions by the same factor, so the ratio $k_f/k_r = K_{eq}$ stays the same.
5. (A) is wrong because ΔG is not changed. (B) is wrong because K_{eq} is not changed, and a change in K_{eq} would need a change in ΔG°. (C) is wrong because both stay the same.
6. (D) is correct. The enzyme alters only the rate (the activation barrier), not ΔG or K_{eq}.

KEY IDEA

A catalyst lowers the activation barrier and speeds the forward and reverse reactions equally. It does not change the free energy of the reactants or products, so it leaves ΔG and K_{eq} unchanged.

WATCH OUT FOR

Thinking that a faster reaction means a more favourable one. An enzyme changes how fast equilibrium is reached, not where equilibrium lies.

Q.15 MCQ · 1 MARK

Fundamentals of Biological Engineering › Growth kinetics

Which one of the following can NOT be a limiting substrate if Monod's growth kinetics is applicable?

(A) Extracellular carbon source

(B) Extracellular nitrogen source

(C) Dissolved oxygen

(D) Intracellular carbon source

Official answer: **D**

SOLUTION

1. The Monod model: $\mu = \dfrac{\mu_{max} S}{K_s + S}$. Here μ is the specific growth rate (h^{-1}), μ_{max} is its maximum value, S is the concentration of the limiting substrate and K_s is the saturation constant (the value of S at which $\mu = \mu_{max}/2$).
2. In the Monod model, S is the concentration of the substrate **in the medium around the cells**. The model is empirical and unstructured: it treats the cell as a black box with no internal state. Growth rate therefore depends only on the concentration of a nutrient the cell takes up from outside.
3. (A) An extracellular carbon source such as glucose is the classic Monod limiting substrate. It **can** be limiting.

4. (B) An extracellular nitrogen source such as NH_4^+ can limit growth in the same way, with its own K_s. It **can** be limiting.
5. (C) Dissolved oxygen is a substrate taken up from the liquid phase. When aerobic growth is limited by oxygen, the same form applies: $\mu = \frac{\mu_{max} C_{O_2}}{K_{O_2} + C_{O_2}}$, where C_{O_2} is the dissolved-oxygen concentration and K_{O_2} is its saturation constant. It **can** be limiting.
6. (D) An intracellular carbon source, such as a stored reserve, is inside the cell. It is not a concentration in the medium, so it cannot stand in for S, and the unstructured Monod model has no variable for anything inside the cell. It **cannot** be the limiting substrate.
7. Answer: (D).

KEY IDEA

Monod kinetics is an unstructured, black-box model. Its limiting substrate S is always a concentration in the medium, meaning a nutrient taken up from outside the cell. That can be a carbon source, a nitrogen source or dissolved oxygen, but never a pool inside the cell.

WATCH OUT FOR

Picking (C) because oxygen is thought of as an electron acceptor rather than a 'substrate'. Dissolved oxygen is routinely modelled as a Monod limiting substrate with its own saturation constant K_{O_2}. The option that fails is the intracellular one, because the model only sees what is in the medium.

Q.16 MCQ · 1 MARK

Q.16 Which one of the following is the unit of heat transfer coefficient?

(A) $W\ m^2\ K^{-1}$ (B) $W\ m^{-2}\ K$ (C) $W\ m^{-2}\ K^{-1}$ (D) $W\ m^2\ K$

Official answer: **C**

Q.17 MCQ · 1 MARK

Fundamentals of Biological Engineering › Growth kinetics

Which one of the following is catabolized during endogenous metabolism in a batch bacterial cultivation?

(A) internal reserves

(B) extracellular substrates

(C) extracellular products

(D) toxic substrates

Official answer: **A**

SOLUTION

1. **Definition of endogenous metabolism:** the cell catabolises its own material, meaning stored polymers first and then other cell constituents, to get the energy it needs to stay alive (maintenance). Exogenous metabolism is the opposite case, where the cell catabolises substrate taken up from the medium.
2. **When it matters in a batch culture:** endogenous metabolism goes on all the time. It becomes the cell's main energy source in the stationary and death phases, once the limiting extracellular substrate has run out. The cells still need maintenance energy, for example to hold the membrane potential and ion gradients and to repair proteins and DNA. With nothing left in the medium, they draw on reserves they built up earlier.
3. **What the internal reserves are:** intracellular storage polymers such as glycogen, poly-β-hydroxybutyrate (PHB) and polyphosphate. When these run low, the cell starts to break down its own RNA and proteins as well.
4. **Kinetic view (Herbert's endogenous-metabolism model):**

$$\frac{dX}{dt} = (\mu_g - k_e)X$$

Here X ($\mathrm{g\,L^{-1}}$) is the biomass concentration, μ_g ($\mathrm{h^{-1}}$) is the gross specific growth rate and k_e ($\mathrm{h^{-1}}$) is the rate constant of endogenous metabolism. The $-k_eX$ term is biomass being used up by the cell itself. That is why the net specific growth rate $\mu_g - k_e$ is lower than μ_g, and why X falls once $\mu_g \to 0$ after the substrate is gone.

5. **Eliminate the other options:** (B) Catabolising extracellular substrates is exogenous metabolism, which is the normal growth mode. (C) Extracellular products are metabolites the cell has secreted. If a cell does take one back up and use it (acetate, for example), it takes it from the medium, so that is exogenous metabolism too. (D) Degrading a toxic substrate also means using a compound from outside the cell, so it is exogenous and has nothing to do with the definition.
6. So the material catabolised during endogenous metabolism is the cell's **internal reserves**, option (A).

KEY IDEA

Endogenous means the energy source is inside the cell. Exogenous means the source comes from the medium. Endogenous metabolism burns the cell's own internal reserves (storage polymers, then cell constituents) to meet maintenance demand. It becomes dominant in the stationary and death phases of a batch culture, once the external substrate has run out.

WATCH OUT FOR

Choosing (C) because cells in the stationary phase sometimes re-consume products they secreted earlier, such as acetate. That product is taken up from the medium, so its use is exogenous metabolism. Another mistake is to connect 'endogenous' with stress and pick (D). Whether a metabolism is endogenous depends only on where the material being catabolised comes from.

Q.18 MCQ · 1 MARK

Q.18 Which one of the following need NOT be conserved in a biochemical reaction?

(A) Total mass
(B) Total moles
(C) Number of atoms of each element
(D) Total energy

Official answer: **B**

Q.19 NAT · 1 MARK

Recombinant DNA Technology and Tools › Bioinformatics

The number of possible rooted trees in a phylogeny of three species is ___.

Official answer: **3**

SOLUTION

1. For 3 species (X, Y, Z), a rooted bifurcating (binary) phylogenetic tree groups exactly two of them as a sister pair, with the root node joining this pair's most recent common ancestor to the third species (the outgroup).
2. The number of ways to choose which two species form the sister pair is $\binom{3}{2} = 3$: (X,Y) with Z as outgroup, (X,Z) with Y as outgroup, or (Y,Z) with X as outgroup.
3. Each choice of sister pair produces a structurally distinct rooted tree. Since a phylogenetic tree has no left/right ordering, swapping the two members within a sister pair, or swapping the pair with the outgroup label, does not create a new topology; it only relabels the same tree.
4. This matches the general combinatorial formula for the number of distinct rooted bifurcating trees on n labeled taxa: $(2n-3)!! = 1 \times 3 \times 5 \times \cdots \times (2n-3)$.
5. Substituting $n = 3$: $(2 \times 3 - 3)!! = 3!! = 3 \times 1 = 3$.
6. Hence the number of possible rooted trees for a phylogeny of three species is 3.

KEY IDEA

For n labeled taxa, the number of distinct rooted bifurcating (binary) phylogenetic trees is $(2n-3)!! = 1 \times 3 \times 5 \times \cdots \times (2n-3)$. For $n = 3$, this gives $3!! = 3$: choose which 2 of the 3 species form a sister clade (root joins their common ancestor to the third species), and there are $\binom{3}{2} = 3$ such choices.

WATCH OUT FOR

Confusing the ROOTED tree count with the UNROOTED tree count for 3 taxa: an unrooted tree topology for 3 species is unique (all three star-like arrangements are the same tree once the root is removed), so students sometimes answer 1. The question asks specifically for rooted trees, where placing the root creates 3 distinguishable topologies.

Q.20 NAT · 1 MARK

Engineering Mathematics › Linear algebra

Matrix A = [[0, 6],[p, 0]] will be skew-symmetric when p = _____.

Official answer: **-6**

SOLUTION

1. A matrix is skew-symmetric when $A^T = -A$, that is $a_{ij} = -a_{ji}$ for all i, j.
2. Here $A = \begin{bmatrix} 0 & 6 \\ p & 0 \end{bmatrix}$, so $A^T = \begin{bmatrix} 0 & p \\ 6 & 0 \end{bmatrix}$ and $-A = \begin{bmatrix} 0 & -6 \\ -p & 0 \end{bmatrix}$.
3. Equating $A^T = -A$ entry by entry, the $(1,2)$ entries give $p = -6$ and the $(2,1)$ entries give $6 = -p$. Both conditions agree.
4. The diagonal entries are 0, and $a_{ii} = -a_{ii}$ forces exactly that, so they impose no further condition.
5. Hence $p = -6$.

KEY IDEA

Skew-symmetric means $A^T = -A$: the diagonal is zero and each off-diagonal entry is the negative of its mirror entry, so $a_{21} = -a_{12}$.

WATCH OUT FOR

Taking $p = 6$, which makes the matrix symmetric rather than skew-symmetric. The mirror entry must have the opposite sign.

Q.21 NAT · 1 MARK

Engineering Mathematics › Calculus

The solution of $\lim_{x \to 8} \left(\frac{x^2 - 64}{x - 8} \right)$ is _____.

Official answer: **16**

SOLUTION

1. At $x = 8$ the expression is $\dfrac{8^2 - 64}{8 - 8} = \dfrac{0}{0}$, which is indeterminate, so simplify before taking the limit.
2. Factorise the numerator as a difference of squares: $x^2 - 64 = (x - 8)(x + 8)$.
3. In a limit $x \neq 8$, so the common factor cancels: $\dfrac{(x-8)(x+8)}{x-8} = x + 8$.
4. Take the limit: $\lim_{x \to 8}(x + 8) = 16$.
5. Check with L'Hopital's rule, which applies because the form is $\frac{0}{0}$: $\lim_{x \to 8} \dfrac{2x}{1} = 16$.

KEY IDEA

A $\frac{0}{0}$ form means a common factor can be cancelled. Factorise $x^2 - 64$ as $(x - 8)(x + 8)$, cancel $(x - 8)$, then substitute $x = 8$.

WATCH OUT FOR

Substituting $x = 8$ straight away and writing the limit as $\frac{0}{0}$ or "undefined". Another slip is to read the limit as the derivative of $x^2 - 64$ at 8 and get $2x$ wrong, or to forget the factor 2 in $2x$ when using L'Hopital's rule.

Q.22 NAT · 1 MARK

Engineering Mathematics › Probability & statistics

The median value for the dataset (12, 10, 16, 8, 90, 50, 30, 24) is _____.

Official answer: **20**

SOLUTION

1. Sort the eight values in ascending order: $8,\ 10,\ 12,\ 16,\ 24,\ 30,\ 50,\ 90$.
2. The number of observations is $n = 8$, which is even, so the median is the mean of the $\frac{n}{2}$-th and $\left(\frac{n}{2}+1\right)$-th ordered values.
3. These are the 4th and 5th values: 16 and 24.
4. $$\text{Median} = \frac{16 + 24}{2} = 20$$
5. The outlier 90 does not affect the median, because the median depends only on the middle ordered values.

KEY IDEA

Sort the data first. With an even number of observations, the median is the average of the two middle ordered values.

WATCH OUT FOR

Taking the middle of the data in its given order, or picking only the 4th or 5th sorted value instead of averaging both. The mean, 30, is also pulled up by the outlier 90 and is not the median.

Q.23 NAT · 1 MARK

Fundamentals of Biological Engineering › Growth kinetics

The degree of reduction for acetic acid ($C_2H_4O_2$) is _____.

Official answer: **4**

SOLUTION

1. The degree of reduction γ is the number of available electrons per **carbon atom** (per C-mole). It is counted against the reference compounds CO_2, H_2O and NH_3, which have $\gamma = 0$. The valences used are C = +4, H = +1, O = −2 and N = −3.
2. For a compound $C_wH_xO_yN_z$:
$$\gamma = \frac{4w + x - 2y - 3z}{w}$$
3. Acetic acid $C_2H_4O_2$ has $w = 2$, $x = 4$, $y = 2$ and $z = 0$.
4. Available electrons per molecule: $4(2) + 4 - 2(2) - 3(0) = 8 + 4 - 4 = 8$.
5. Divide by the number of carbon atoms:
$$\gamma = \frac{8}{2} = 4$$
6. Check with the C-mole formula: $C_2H_4O_2$ divided by 2 gives CH_2O, so $\gamma = 4 + 2 - 2(1) = 4$. This is the same as glucose, whose C-mole formula is also CH_2O.

KEY IDEA

Degree of reduction is counted per carbon atom (per C-mole): $\gamma = (4w + x - 2y - 3z)/w$ for $C_wH_xO_yN_z$, using C = +4, H = +1, O = −2, N = −3. Acetic acid has the same C-mole formula as glucose (CH_2O), so it has the same $\gamma = 4$.

WATCH OUT FOR

Answering 8, the available electrons for the whole molecule, and forgetting to divide by the 2 carbon atoms. Another mistake is taking O as +2 or leaving out the oxygen term.

Q.24 NAT · 1 MARK

Q.24 The mass of 1 kmol of oxygen molecules is _____ g (rounded off to the nearest integer).

BT 3/10

Official answer: **31800 to 32000**

Q.25 NAT · 1 MARK

Recombinant DNA Technology and Tools › Assays & electrophoresis

Protein concentration of a crude enzyme preparation was 10 mg mL^{-1}. 10 µL of this sample gave an activity of 5 µmol min^{-1} under standard assay conditions. The specific activity of this crude enzyme preparation is _____ units mg^{-1}.

Official answer: **50**

SOLUTION

1. Definition: one unit (U) of enzyme activity is the amount of enzyme that converts 1 µmol of substrate per minute under standard assay conditions. The assay on the 10 µL aliquot gave 5 µmol min^{-1}, so that aliquot contains 5 units of activity.
2. Definition: specific activity = enzyme activity (in units) per mg of total protein present in that same aliquot.
3. Protein mass in the 10 µL aliquot: $10\ \text{mg mL}^{-1} \times 10\ \mu\text{L} = 10\ \text{mg mL}^{-1} \times 0.01\ \text{mL} = 0.1\ \text{mg}$.
4. Specific activity $= \dfrac{5\ \text{units}}{0.1\ \text{mg}} = 50\ \text{units mg}^{-1}$.

KEY IDEA

One enzyme unit (U) is defined as the amount of enzyme that converts 1 µmol of substrate (or produces 1 µmol of product) per minute under the stated assay conditions; specific activity is that activity expressed per mg of total protein in the same sample.

WATCH OUT FOR

Using the protein concentration (10 mg mL^{-1}) directly as "mg protein" instead of first converting it to the mass of protein actually present in the 10 µL aliquot that was assayed (0.1 mg), which would wrongly give 5/10 = 0.5 units mg^{-1}.

Q.26 MCQ · 2 MARKS

General Biology › Biomolecules

In general, which one of the following statements is NOT CORRECT?

(A) Hydrogen bonds result from electrostatic interactions

(B) Hydrogen bonds contribute to the folding energy of proteins

(C) Hydrogen bonds are weaker than van der Waals interactions

(D) Hydrogen bonds are directional

Official answer: **C**

SOLUTION

1. We need the statement that is false, so test each option against what is known about non-covalent forces.
2. (A) A hydrogen bond is mainly an electrostatic (dipole-dipole) attraction between a donor X-H (with X = N, O, F) and an acceptor lone pair. The statement is correct.
3. (B) Backbone and side-chain hydrogen bonds stabilise α-helices, β-sheets and tertiary structure, so they contribute to the folding energy of proteins. The statement is correct.
4. (C) A hydrogen bond has an energy of about 12 to $30\ \text{kJ/mol}$. A van der Waals contact is only about 0.4 to $4\ \text{kJ/mol}$. So hydrogen bonds are stronger than van der Waals interactions, and the statement

that they are weaker is false.

5. (D) Hydrogen bonds are strongest when the donor, hydrogen and acceptor are nearly collinear, so they are directional. The statement is correct.
6. The statement that is NOT correct is (C).

KEY IDEA

Typical strength order of non-covalent forces: ionic and hydrogen bonds (roughly 12 to 30 kJ/mol) are stronger than van der Waals contacts (roughly 0.4 to 4 kJ/mol). Hydrogen bonds are electrostatic in origin and directional.

WATCH OUT FOR

Treating hydrogen bonds as 'weak' and assuming they are weaker than every other non-covalent force. They are weak compared with covalent bonds, but stronger than van der Waals forces, and much of their value comes from being directional.

Q.27 MCQ · 2 MARKS

Recombinant DNA Technology and Tools › Editing & interactions

For site-directed mutagenesis, which one of the following restriction enzymes is used to digest methylated DNA?

(A) KpnI

(B) DpnI

(C) XhoI

(D) MluI

Official answer: **B**

SOLUTION

1. In PCR-based site-directed mutagenesis, the template plasmid is isolated from a dam$^+$ strain of E. coli, so the adenine in each of its GATC sites is methylated by Dam methylase.
2. The mutant strands are made in vitro by PCR, so they carry no Dam methylation.
3. DpnI cuts GATC only when the adenine is methylated (methylated or hemimethylated DNA). Treating the reaction with DpnI therefore digests the parental template and leaves the unmethylated, mutated DNA intact, which enriches the mutant plasmid.
4. KpnI, XhoI and MluI are ordinary sequence-specific restriction enzymes; none of them cuts only methylated DNA. The answer is (B) DpnI.

KEY IDEA

In PCR-based site-directed mutagenesis (e.g. QuikChange), the parental plasmid template (isolated from a dam+ E. coli strain) is Dam-methylated at GATC sites, while the newly synthesized mutant strand made in vitro is unmethylated. DpnI is methylation-dependent and cleaves only methylated/hemimethylated GATC, so treating the PCR product with DpnI selectively destroys the parental template and enriches for the mutant plasmid.

WATCH OUT FOR

Confusing DpnI (cuts only methylated DNA) with the many restriction enzymes that are blocked by methylation (cut only unmethylated DNA), or picking a sequence-specific enzyme (KpnI, XhoI, MluI) that has no relationship to methylation status at all.

Q.28 MCQ · 2 MARKS

Genetics, Cell and Molecular Biology › Cell biology

Match the organelles in Group I with their functions in Group II.

Group I:

P. Lysosome

Q. Smooth ER

R. Golgi apparatus
S. Nucleolus

Group II:
1. Digestion of foreign substances
2. Protein targeting
3. Lipid synthesis
4. Protein synthesis
5. rRNA synthesis

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

(B) P-1, Q-4, R-5, S-3

(C) P-2, Q-5, R-3, S-4

(D) P-1, Q-3, R-4, S-5

Official answer: **A**

SOLUTION

1. Lysosome (P) contains hydrolytic enzymes that digest foreign/phagocytosed material and worn-out cell components → matches function 1 (Digestion of foreign substances).
2. Smooth ER (Q) lacks bound ribosomes and is the principal site of lipid and steroid synthesis; protein synthesis (via bound ribosomes) is a rough ER function, not smooth ER → matches function 3 (Lipid synthesis), ruling out function 4.
3. Golgi apparatus (R) receives proteins made on the rough ER, chemically modifies them (e.g., glycosylation), and sorts/packages them into vesicles for delivery to their correct destinations; this is protein targeting, not protein synthesis → matches function 2 (Protein targeting), which rules out option (D)'s R-4 pairing.
4. Nucleolus (S) is the site of rRNA synthesis/processing and ribosomal subunit assembly → matches function 5 (rRNA synthesis).
5. Combining all four matches: P-1, Q-3, R-2, S-5, which is option (A).
6. Checking the distractors confirms (A) is uniquely correct: (B) swaps Golgi and Smooth ER's roles with rRNA/lipid synthesis (both wrong); (C) mismatches every pair; (D) is correct for P, Q, and S but incorrectly assigns protein synthesis (4) instead of protein targeting (2) to the Golgi apparatus.

KEY IDEA

Each organelle has a defining, distinguishing biochemical role: lysosomes digest material via hydrolytic enzymes, smooth ER synthesizes lipids (rough ER, not smooth, is associated with protein synthesis via bound ribosomes), the Golgi apparatus modifies, sorts, and targets proteins to their destinations (it does not synthesize proteins itself), and the nucleolus is the site of rRNA synthesis and ribosome subunit assembly.

WATCH OUT FOR

Confusing Golgi apparatus's role (protein targeting/sorting/packaging) with protein synthesis (which occurs on ribosomes, often on rough ER); this trap is embedded in option (D), which correctly matches P, Q, and S but wrongly assigns R-4 (protein synthesis) to the Golgi instead of R-2 (protein targeting).

Q.29 MCQ · 2 MARKS

Recombinant DNA Technology and Tools › Bioinformatics

Which of the following statements are CORRECT when a protein sequence database is searched using the BLAST algorithm?

P. A larger E-value indicates higher sequence similarity
Q. E-value < 10^-10 indicates sequence homology

R. A higher BLAST score indicates higher sequence similarity
S. E-value > 10^10 indicates sequence homology

(A) P, Q and R only

(B) Q and R only

(C) P, R and S only

(D) P and S only

Official answer: **B**

SOLUTION

1. BLAST's E-value is the expected number of chance alignments with a score at least as good as the one observed in a database of that size; the BLAST score is a direct measure of alignment quality built from substitution-matrix rewards and gap penalties. Smaller E-value = less likely to be chance = higher significance/homology; higher score = better alignment = higher similarity; the two measures move in opposite directions relative to 'better'.
2. P claims a LARGER E-value indicates higher similarity. This is backwards: a larger E-value means the match is more likely to be a chance occurrence, i.e. lower significance/similarity, not higher. P is FALSE.
3. Q states E-value < 10^{-10} indicates sequence homology. Such a vanishingly small E-value means the alignment would essentially never be expected by chance, so it strongly indicates true sequence homology. Q is TRUE.
4. R states a higher BLAST score indicates higher sequence similarity. Since the score accumulates positive contributions for matches/conservative substitutions and is penalized for mismatches and gaps, a higher score directly corresponds to a better, more similar alignment. R is TRUE.
5. S states E-value > 10^{10} indicates sequence homology. An E-value this large means on the order of 10^{10} equally good chance matches would be expected in the search. This is the signature of NO homology, not evidence for it. S is FALSE.
6. Only Q and R are correct statements, which is option (B).

KEY IDEA

In BLAST, the E-value is the expected number of alignments of that score or better occurring purely by chance in a database search, so a SMALLER E-value means the match is less likely to be chance, i.e. more significant/homologous. The BLAST score, by contrast, is a direct measure of alignment quality (built from substitution-matrix rewards/penalties for matches, mismatches and gaps): a HIGHER score means a better, more similar alignment. The two measures move in opposite directions relative to "better," which is exactly why this question mixes them.

WATCH OUT FOR

Treating "larger/higher" as uniformly "better" for both quantities: assuming a larger E-value or a higher E-value threshold also signals stronger homology, when only a very small E-value (like P < 10^{-10}) indicates true homology, while a very large E-value (like > 10^{10}) indicates the match is essentially indistinguishable from random chance, i.e. no evidence of homology.

Q.30 MCQ · 2 MARKS

Genetics, Cell and Molecular Biology › Mendelian genetics

Which one of the following is coded by the ABO blood group locus in the human genome?

(A) Acyl transferase

(B) Galactosyltransferase

(C) Transposase

(D) β-Galactosidase

Official answer: **B**

SOLUTION

1. The ABO locus encodes an enzyme that transfers a sugar residue onto the H antigen precursor displayed on red blood cell surfaces, converting it into the A or B antigen.
2. The *A* allele's product adds N-acetylgalactosamine to the H antigen; the *B* allele's product adds galactose. Both are sugar-transferring enzymes of the glycosyltransferase family, which the question's options label as "galactosyltransferase."
3. Option (A) Acyl transferase: wrong; these enzymes transfer acyl groups (e.g., in lipid or acetylation chemistry) and have no role in ABO antigen formation.
4. Option (B) Galactosyltransferase: correct; the ABO locus encodes a glycosyltransferase-type enzyme that adds a sugar residue to the H antigen, which is exactly the product of this locus.
5. Option (C) Transposase: wrong; transposases move transposable elements within the genome and are unrelated to antigen biosynthesis.
6. Option (D) β-Galactosidase: wrong; this is a hydrolase that cleaves a terminal galactose (e.g., in lactose breakdown), the reverse reaction of a sugar-adding transferase.
7. By elimination and by the known biochemistry of the ABO locus product, the correct choice is (B) Galactosyltransferase.

KEY IDEA

The ABO locus encodes a glycosyltransferase enzyme that attaches a terminal sugar residue onto the H antigen precursor on the red blood cell surface, generating the A or B antigen; this class of enzyme is grouped under "galactosyltransferase."

WATCH OUT FOR

Confusing this transferase (which ADDS a sugar to build the antigen) with β-galactosidase, a hydrolase that REMOVES/cleaves a sugar (as in the *lacZ* system); the two enzyme classes catalyze opposite reactions and are easy to swap under time pressure.

Q.31 MCQ · 2 MARKS

Recombinant DNA Technology and Tools › PCR & sequencing

Which of the following factors affect the fidelity of DNA polymerase in polymerase chain reaction?
P. Mg2+ concentration
Q. pH
R. Annealing temperature

(A) P and Q only

(B) P and R only

(C) Q and R only

(D) P, Q and R

Official answer: **A**

SOLUTION

1. Define the term first. The **fidelity** of a DNA polymerase is how accurately it copies the template: how often it inserts the correct complementary dNTP opposite each template base. It is measured as an error rate, for example misincorporations per base per duplication. **Specificity** is a different property of a PCR. It describes whether the primers anneal only at the intended target sites, so that only the intended product is amplified. The question asks about fidelity only.
2. **P. Mg^{2+} concentration affects fidelity.** Mg^{2+} is the catalytic cofactor in the polymerase active site, and it also forms the Mg^{2+}–dNTP complex that the enzyme actually uses as its substrate. Free Mg^{2+} in excess of the total dNTP concentration stabilises mispaired primer termini and lets the enzyme extend

mismatches more easily, so the error rate rises. When Mg^{2+} is kept close to the total dNTP concentration, fidelity is higher. P is correct.

3. **Q. pH affects fidelity.** pH sets the ionisation state of the catalytic and base-selecting residues in the active site, and it also changes how readily the enzyme extends a mismatched terminus. The measured error rate of Taq polymerase changes with the pH of the reaction buffer; it is lower at mildly acidic pH (around 5–6) than at the usual pH of about 8–9. Q is correct.
4. **R. Annealing temperature does not affect fidelity.** Annealing temperature controls how stringently the primers hybridise to the template. If it is too low, primers bind at partially matched, off-target sites, which gives non-specific bands and primer-dimers. If it is too high, the primers bind poorly and the yield falls. These are problems of **specificity and yield**. Annealing temperature does not change how accurately the polymerase chooses each nucleotide during extension. Even a mis-primed product is copied at the enzyme's normal per-base error rate, because the polymerase still reads the template base by base. R is therefore not a fidelity factor.
5. Eliminate the options. (B), (C) and (D) all include R, so each of them is wrong. Only (A) contains both fidelity factors, P and Q, and excludes R.
6. Answer: **(A) P and Q only**.

KEY IDEA
Fidelity is the polymerase's per-base copying accuracy, and specificity is where the primers bind. Reaction chemistry at the active site changes fidelity: free Mg^{2+} in excess of dNTPs, pH, and an unbalanced dNTP pool. Annealing temperature changes primer–template stringency, which affects specificity and yield, not fidelity.

WATCH OUT FOR
Treating 'fidelity' as meaning 'anything that gives a wrong PCR product', and so choosing (D). A low annealing temperature causes mispriming and non-specific bands. That is a failure of specificity, not a change in how accurately the polymerase inserts nucleotides.

Q.32 MCQ · 2 MARKS

Recombinant DNA Technology and Tools › Microscopy & spectroscopy

Group I lists spectroscopic methods and Group II lists biomolecular applications of these methods. Match the methods in Group I with the applications in Group II.

Group I
P. Infrared
Q. Circular Dichroism
R. Nuclear Magnetic Resonance

Group II
1. Identification of functional groups
2. Determination of secondary structure
3. Estimation of molecular weight
4. Determination of 3-D structure

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

Official answer: **C**

SOLUTION

1. Infrared (IR) spectroscopy measures vibrational absorption frequencies characteristic of specific chemical bonds and functional groups (C=O, N-H, O-H, etc.), making it the classical tool for

identification of functional groups, so P matches 1.

2. Circular Dichroism (CD) measures the differential absorption of left- and right-circularly polarized light by chiral chromophores in a molecule. The far-UV CD spectrum of a protein gives distinct, well-characterized band shapes for alpha-helix, beta-sheet and random-coil content, making CD the standard rapid tool for determination of secondary structure, so Q matches 2.
3. Nuclear Magnetic Resonance (NMR), particularly multidimensional techniques such as COSY and NOESY, yields inter-proton distance restraints (from NOE cross-peaks) and torsion-angle information (from coupling constants) sufficient to compute a complete three-dimensional solution structure of a biomolecule, so R matches 4.
4. Estimation of molecular weight (Group II, option 3) is not a function performed by IR, CD, or NMR in this context: that role belongs to techniques such as mass spectrometry, gel filtration, or SDS-PAGE, so option 3 is correctly left unused among P, Q, R.
5. Combining the matches P-1, Q-2, R-4 gives exactly option (C).

KEY IDEA

Each spectroscopic method has one signature application: IR probes bond vibrations (functional groups), CD probes chiral secondary-structure content, and multidimensional NMR provides distance/angle restraints for full 3-D structure determination; molecular weight is estimated by other techniques (e.g., mass spectrometry), not by these three.

WATCH OUT FOR

Confusing CD with 3-D structure determination (since it is a "structural" technique) instead of secondary structure, or assuming NMR is used for molecular weight estimation because NMR-active nuclei are also used in mass-related contexts (e.g., MS), leading to a mismatch with option 3.

Q.33 MCQ · 2 MARKS

Recombinant DNA Technology and Tools › Assays & electrophoresis

The hexapeptide P has an isoelectric point (pI) of 6.9. Hexapeptide Q is a variant of P that contains valine instead of glutamate at position 3. The two peptides are analyzed by polyacrylamide gel electrophoresis at pH 8.0. Which one of the following statements is CORRECT?

(A) P will migrate faster than Q towards the anode

(B) P will migrate faster than Q towards the cathode

(C) Both P and Q will migrate together

(D) Q will migrate faster than P towards the anode

Official answer: **A**

SOLUTION

1. Rule: at running pH > pI, a peptide is net negatively charged; at pH < pI it is net positively charged. Here P has pI = 6.9 and the gel runs at pH 8.0 > 6.9, so P carries a net negative charge during the run.
2. Q differs from P only at position 3, where the acidic residue glutamate (negatively charged side chain at pH 8.0) is replaced by valine (a neutral, nonpolar side chain). This removes one negative charge from the molecule.
3. Losing an acidic (negative-contributing) residue makes the peptide less acidic overall, so its isoelectric point rises: pI(Q) > pI(P) = 6.9.
4. Losing just one acidic residue out of six is not enough to push the pI past 8.0, so Q is still net negatively charged at pH 8.0, but its net negative charge is smaller in magnitude than P's, because 8.0 is closer to Q's (higher) pI than it is to P's pI.
5. Rule: negatively charged species migrate towards the anode in electrophoresis (positively charged species migrate towards the cathode); a larger net charge magnitude gives faster migration when

size/shape are essentially unchanged, as is the case for these near-identical hexapeptides.

6. Therefore both P and Q migrate towards the anode, but P, carrying the larger net negative charge, migrates faster than Q.
7. Checking the options: (A) matches this conclusion exactly: correct. (B) wrongly directs migration to the cathode, which applies to net positive charge: incorrect. (C) would require equal net charge, which is false here: incorrect. (D) reverses which peptide is faster; Q, with the smaller charge, is the slower one: incorrect.

KEY IDEA

A protein/peptide run in a gel above its pI carries a net negative charge and migrates towards the anode; the size of that net negative charge (and hence migration speed) depends on how far the running pH is above the pI. Removing an acidic (negatively charged) residue raises the pI, which, at a fixed running pH above both pI values, reduces the net negative charge and therefore the migration speed towards the anode.

WATCH OUT FOR

Confusing which peptide is "more negative": students often assume that because Q has one fewer negative side chain it must be the more mobile one, or they send the negatively charged species towards the cathode instead of the anode (cathode attracts cations, anode attracts anions).

Q.34 MCQ · 2 MARKS

Plant, Animal and Microbial Biotechnology › Hybridomas & transgenics

Antibody-producing hybridoma cells are generated by the fusion of a

(A) T cell with a myeloma cell

(B) B cell with a myeloma cell

(C) macrophage with a myeloma cell

(D) T cell and a B cell

Official answer: **B**

SOLUTION

1. A hybridoma is a hybrid cell line made to give a continuous supply of one monoclonal antibody (the Kohler and Milstein technique).
2. Antibody production is the property of B lymphocytes (plasma cells), so the antibody-producing partner must be a B cell, usually taken from the spleen of an immunised animal.
3. A normal B cell cannot divide indefinitely in culture, so it is fused with an immortal myeloma (B-cell tumour) cell, which supplies unlimited growth.
4. The myeloma partner is chosen to be deficient in HGPRT and to secrete no antibodies of its own. In HAT medium the unfused myeloma cells die because they cannot use the salvage pathway, and the unfused B cells die because they have a limited life span in culture. Only the fused hybridoma cells survive.
5. Option (A) is wrong: T cells do not make antibodies. They carry T cell receptors and regulate immunity.
6. Option (C) is wrong: macrophages present antigen and phagocytose, but they do not secrete antibodies.
7. Option (D) is wrong: both partners are normal, mortal lymphocytes. A fusion of a T cell and a B cell has no immortal partner, so it would not form a stable, indefinitely growing antibody-secreting line.
8. Therefore the antibody-producing hybridoma arises from fusing a B cell with a myeloma cell, option (B).

KEY IDEA
A hybridoma combines the antibody-making ability of a B cell with the unlimited growth of a myeloma cell. HAT selection then keeps only the fused cells.

WATCH OUT FOR
Choosing a T cell because it is an immune cell, or a macrophage because it is an antigen-presenting cell. Only B cells (plasma cells) make antibodies. Also, fusing two normal lymphocytes gives no immortal partner.

Q.35 MCQ · 2 MARKS

Plant, Animal and Microbial Biotechnology › Animal cell culture

Which of the following statements are CORRECT about the function of fetal bovine serum in animal cell culture?
P. It stimulates cell growth
Q. It enhances cell attachment
R. It provides hormones and minerals
S. It maintains pH at 7.4

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

Official answer: **C**

SOLUTION

1. Fetal bovine serum (FBS) is the usual supplement added to animal cell culture media, typically at 5 to 10 percent. It supplies what a basal medium of salts, sugars, amino acids and vitamins lacks. Judge each statement by asking whether it is a function serum is added for.
2. P is correct. Serum carries growth factors such as PDGF, EGF and FGF, and insulin-like growth factors. These stimulate cells to divide, which is the main reason serum is added.
3. Q is correct. Serum contains attachment and spreading factors, mainly fibronectin and vitronectin. They adsorb to the culture surface and let anchorage-dependent cells attach and spread.
4. R is correct. Serum supplies hormones (for example insulin and hydrocortisone) and minerals and trace elements (for example iron carried by transferrin, zinc and selenium), along with lipids.
5. S is not correct. Holding the medium at pH 7.4 is the job of the medium's buffer system: sodium bicarbonate in equilibrium with the CO_2 atmosphere of the incubator (usually 5 percent CO_2), sometimes with HEPES added. Serum proteins have only a minor buffering effect, and serum is not what sets or maintains the pH; serum-free media hold pH 7.4 perfectly well with the same buffer system. So pH maintenance is not a function of FBS.
6. Only P, Q and R are true, so the answer is option (C). Option (A) leaves out R, and options (B) and (D) include the false statement S.

KEY IDEA
Serum supplies growth factors (P), attachment factors such as fibronectin (Q), and hormones, minerals and trace elements (R). The pH of the culture is controlled by the medium's buffer (bicarbonate with incubator CO_2, or HEPES), not by serum.

WATCH OUT FOR
Choosing (D) because serum proteins buffer a little. That small buffering effect is not what serum is added for. The bicarbonate and CO_2 system (or HEPES) maintains pH 7.4, and serum-free media hold that pH without any serum.

Q.36 MCQ · 2 MARKS

Genetics, Cell and Molecular Biology › Gene expression

Which one of the following covalent linkages exists between 7-Methyl guanosine (m^7G) and mRNAs?

(A) 2'–3' triphosphate

(B) 3'–5' triphosphate

(C) 5'–5' triphosphate

(D) 2'–5' triphosphate

Official answer: **C**

SOLUTION

1. The question asks for the covalent linkage joining the 7-methylguanosine (m^7G) cap to the 5' end of the mRNA transcript.
2. During co-transcriptional capping, RNA triphosphatase removes the terminal (γ) phosphate from the 5' end of the nascent transcript, leaving a 5' diphosphate.
3. Guanylyltransferase then transfers GMP from GTP onto this 5' diphosphate end. This joins the 5'-carbon of the incoming guanosine to the 5'-carbon of the transcript through a bridge of three phosphates: an unusual 5'–5' triphosphate linkage, not the standard 3'–5' phosphodiester bond used elsewhere along the RNA chain.
4. Guanine-N7 methyltransferase subsequently methylates this terminal guanosine at N7 to produce m^7G; this methylation step modifies the base, not the linkage already formed.
5. Option (A) 2'–3' triphosphate: incorrect: no such bond exists in cap chemistry.
6. Option (B) 3'–5' triphosphate: incorrect: this describes ordinary internucleotide phosphodiester geometry (normally one phosphate), not the cap junction.
7. Option (C) 5'–5' triphosphate: correct; the hallmark 'head-to-head' bond created by guanylyltransferase linking the cap GMP's 5' carbon to the transcript's 5' carbon via three phosphates.
8. Option (D) 2'–5' triphosphate: incorrect; 2'–5' linkages occur elsewhere in biology (e.g., the 2-5A system, lariat branch points) but not in the cap structure.
9. Therefore the covalent linkage between m^7G and the mRNA is the 5'–5' triphosphate bridge.

KEY IDEA

mRNA 5' capping installs m^7G via a unique 5'–5' triphosphate linkage (not the standard 3'–5' phosphodiester bond of the rest of the chain), formed when guanylyltransferase adds GMP to the diphosphate 5' end left after RNA triphosphatase removes the γ-phosphate; N7-methylation of the added guanosine follows and does not alter the linkage.

WATCH OUT FOR

Assuming the cap is attached by the usual 3'–5' phosphodiester bond used for all other internucleotide linkages in RNA, rather than recognizing the atypical 5'-to-5' triphosphate bridge unique to capping.

Q.37 MCQ · 2 MARKS

General Biology › Biomolecules

Which one of the following amino acid residues will destabilize an α-helix when inserted in the middle of the helix?

(A) Pro

(B) Val

(C) Ile

(D) Leu

Official answer: **A**

Q.38 MCQ · 2 MARKS

Engineering Mathematics › Differential equations

What is the solution of the differential equation $\frac{dy}{dx} = \frac{x}{y}$, with the initial condition, at $x = 0$, $y = 1$?

(A) $x^2 = y^2 + 1$
(B) $y^2 = x^2 + 1$
(C) $y^2 = 2x^2 + 1$
(D) $x^2 - y^2 = 0$

Official answer: **B**

SOLUTION

1. The equation is separable: $y\,dy = x\,dx$.
2. Integrate both sides: $\frac{y^2}{2} = \frac{x^2}{2} + C$, so $y^2 = x^2 + 2C$.
3. Apply the initial condition $x = 0,\ y = 1$: $1 = 0 + 2C$, so $2C = 1$.
4. Therefore $y^2 = x^2 + 1$.
5. Check: differentiating gives $2y\,y' = 2x$, so $y' = x/y$, as required, and at $x = 0$ we get $y^2 = 1$. This is option (B).

KEY IDEA

Separate the variables, integrate both sides, then use the initial condition to fix the constant.

WATCH OUT FOR

Forgetting the factor of 2 when integrating $y\,dy$ and $x\,dx$ gives $y = x + C$ or a wrong constant. Option (A) swaps the roles of x and y, and option (D) fails the condition $y(0) = 1$.

Q.39 MCQ · 2 MARKS

Engineering Mathematics › Differential equations

The Laplace transform of the function $f(t) = t^2 + 2t + 1$ is

(A) $\frac{1}{s^3} + \frac{3}{s^2} + \frac{1}{s}$
(B) $\frac{4}{s^3} + \frac{4}{s^2} + \frac{1}{s}$
(C) $\frac{1}{s^3} + \frac{2}{s^2} + \frac{1}{s}$
(D) $\frac{2}{s^3} + \frac{2}{s^2} + \frac{1}{s}$

Official answer: **D**

SOLUTION

1. The Laplace transform is linear, so transform each term separately: $\mathcal{L}\{t^2 + 2t + 1\} = \mathcal{L}\{t^2\} + 2\,\mathcal{L}\{t\} + \mathcal{L}\{1\}$.
2. Use the standard result $\mathcal{L}\{t^n\} = \frac{n!}{s^{n+1}}$ for $n = 0, 1, 2, \ldots$.
3. For $n = 2$: $\mathcal{L}\{t^2\} = \frac{2!}{s^3} = \frac{2}{s^3}$.
4. For $n = 1$: $\mathcal{L}\{t\} = \frac{1!}{s^2} = \frac{1}{s^2}$, so $2\,\mathcal{L}\{t\} = \frac{2}{s^2}$.
5. For $n = 0$: $\mathcal{L}\{1\} = \frac{0!}{s} = \frac{1}{s}$.
6. Add the three terms:

$$F(s) = \frac{2}{s^3} + \frac{2}{s^2} + \frac{1}{s}$$

7. This matches option (D).

KEY IDEA
Laplace transform is linear, and $\mathcal{L}\{t^n\} = n!/s^{n+1}$. The factorial gives the 2 in the t^2 term, and the coefficient 2 of t multiplies $1/s^2$.

WATCH OUT FOR
Forgetting the 2! in the numerator and writing $1/s^3$ for $\mathcal{L}\{t^2\}$, which leads to options (A) or (C). Another slip is dropping or mishandling the coefficient 2 on t.

Q.40 MCQ · 2 MARKS

Fundamentals of Biological Engineering › Growth kinetics

Which of the following factors can influence the lag phase of a microbial culture in a batch fermentor?

P. Inoculum size
Q. Inoculum age
R. Medium composition

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

Official answer: **D**

SOLUTION

1. **What the lag phase is.** It is the period right after inoculation when the cell number barely rises, because the cells are adjusting to the new environment. They are making the enzymes, ribosomes and cofactors the new medium needs. Anything that changes how much adjusting the cells must do changes how long the lag lasts.
2. **P, inoculum size.** A small inoculum gives a long lag. Essential metabolites and cofactors that leak out of the cells (and dissolved CO_2, which some cultures need) are diluted into a large volume, so the cells have to rebuild them before they can grow. A large inoculum (typically 5–10% by volume) keeps these at a useful level and shortens the lag. So P matters.
3. **Q, inoculum age.** Cells taken from the mid-exponential phase of the seed culture are already metabolically active and start growing almost at once. Cells taken from the stationary or death phase must repair damage and rebuild their machinery first, so their lag is longer. So Q matters.
4. **R, medium composition.** If the fermentor medium differs from the seed medium (a different carbon source, missing growth factors, a different pH or osmolarity), the cells must switch on new enzymes, so the lag is longer. A seed grown in the same medium shows almost no lag. A medium holding two carbon sources can even give a second lag when the preferred one runs out and the cells switch to the other (diauxic growth). So R matters.
5. **All three matter, so the answer is P, Q and R, option (D).**

KEY IDEA
The lag phase is the time cells spend adapting before they divide. Anything that changes how much adapting they must do changes its length. A small inoculum dilutes the metabolites cells leak out, an old inoculum needs repair first, and an unfamiliar medium forces the cells to make new enzymes. So all three factors lengthen or shorten the lag.

WATCH OUT FOR
Treating the lag phase as a property of the organism alone and dropping inoculum size (P), on the idea that more cells only shift the curve up. A small inoculum really does lengthen the lag, because leaked metabolites and cofactors are diluted. Some students also drop medium composition (R), forgetting that a change of medium between seed and fermentor is the main reason cells have to adapt at all.

Q.41 MCQ · 2 MARKS

Fundamentals of Biological Engineering › Process control

Which one of the following statements is CORRECT about proportional controllers?

(A) The initial change in control output signal is relatively slow

(B) The initial corrective action is greater for larger error

(C) They have no offset

(D) There is no corrective action if the error is a constant

Official answer: **B**

SOLUTION

1. Proportional (P) control law: $c(t) = \bar{c} + K_c\, e(t)$, where $e(t) = y_{sp}(t) - y_m(t)$ is the error (set point y_{sp} minus measured value y_m), K_c is the controller gain and $\bar{c}$ is the bias, the controller output when $e = 0$. In deviation form $c'(t) = c(t) - \bar{c} = K_c\, e(t)$, so the transfer function is $G_c(s) = K_c$: a pure gain with no dynamics.
2. (A) Because $G_c(s) = K_c$ has no lag, the output changes the moment the error appears. A step error $e = M$ gives a step change in output of $K_c M$ at $t = 0^+$. The initial change is immediate, not slow, so (A) is false.
3. (B) The corrective action is $\Delta c = K_c\, e$, directly proportional to the error. A larger initial error gives a proportionally larger initial correction, so (B) is true.
4. (C) Offset check: take a first-order process $G_p(s) = \dfrac{K_p}{\tau s + 1}$ (process gain K_p, time constant τ) in a unity-feedback loop with P control and a unit step in set point. The closed-loop response is $Y(s) = \dfrac{K_c K_p}{\tau s + 1 + K_c K_p} \cdot \dfrac{1}{s}$. By the final-value theorem, $y(\infty) = \lim_{s \to 0} s\, Y(s) = \dfrac{K_c K_p}{1 + K_c K_p}$, so the offset is $1 - y(\infty) = \dfrac{1}{1 + K_c K_p} \neq 0$ for any finite K_c. P control leaves a steady-state offset, so (C) is false.
5. Physical reason for the offset: to hold the process at a new steady state, the controller output must stay away from $\bar{c}$. Since $c - \bar{c} = K_c\, e$, that requires a nonzero error. Removing the offset needs integral action.
6. (D) With a constant error $e = M$, the P output stays at $\bar{c} + K_c M$, which is a steady, nonzero corrective action. Giving zero action for a constant error is how derivative control behaves ($\tau_D \dfrac{de}{dt} = 0$ when e is constant, where τ_D is the derivative time), not proportional control. So (D) is false.
7. The only correct statement is (B).

KEY IDEA

A P controller is a pure gain, $c - \bar{c} = K_c\, e$. It acts at once and in proportion to the error, so a bigger error gets a bigger correction. It still acts on a constant error, and it cannot remove offset, because holding a new steady state needs a nonzero error.

WATCH OUT FOR

Mixing up the three control modes. Zero action for a constant error describes derivative control (D), and eliminating offset describes integral control (C). A slow initial response belongs to lag-type or integral action (A). None of these describes proportional control.

Q.42 MCQ · 2 MARKS

Fundamentals of Biological Engineering › Process control

Match the instruments in Group I with their corresponding measurements in Group II.

GROUP I	GROUP II
P. Manometer	1. Agitator speed
Q. Rotameter	2. Pressure difference
R. Tachometer	3. Cell number
S. Haemocytometer	4. Air flow rate

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

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

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

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

Official answer: **C**

SOLUTION

1. **P, Manometer:** a U-tube partly filled with a liquid of density ρ_m. The two limbs are connected to two points in the line, and the difference h between the liquid levels gives the pressure difference between them, $\Delta P = (\rho_m - \rho)\, g\, h$, where ρ is the density of the fluid above the manometer liquid. For a gas, $\rho \ll \rho_m$, so $\Delta P \approx \rho_m g h$. So P-2.
2. **Q, Rotameter:** a variable-area flow meter. A float rises in a tapered, vertical glass tube until drag and buoyancy balance its weight, and the height of the float gives the volumetric flow rate. On a fermenter it is the standard meter for the air (gas) flow into the sparger. So Q-4.
3. **R, Tachometer:** measures rotational speed, in rpm. On a bioreactor that is the speed of the agitator (impeller) shaft. So R-1.
4. **S, Haemocytometer:** a counting chamber of known depth with an etched grid. The cells in a known volume are counted under the microscope, which gives the cell number (cell concentration). So S-3.
5. Matching: P-2, Q-4, R-1, S-3. Only option (C) has this. Each of the other options breaks at least one pair: (A) puts the manometer on air flow rate, (B) puts the manometer on cell number and the haemocytometer on pressure difference, and (D) swaps the rotameter and the tachometer.

KEY IDEA

Match each instrument to the physical quantity it senses. A manometer reads a liquid-column height, so it gives a pressure difference. A rotameter reads the height of a float in a tapered tube, so it gives a flow rate (on a fermenter, the air flow to the sparger). A tachometer reads the speed of a rotating shaft (the agitator). A haemocytometer is a counting chamber of known volume, so it gives the cell number.

WATCH OUT FOR

Mixing up the rotameter and the tachometer because both names suggest rotation, which leads to option (D). The rotameter's float spins, but what it measures is flow rate. The tachometer is the instrument that measures rotational speed (rpm).

Q.43 MCQ · 2 MARKS

Fundamentals of Biological Engineering › Bioreactor operation

Which of the following statements is ALWAYS CORRECT about an ideal chemostat?

P. Substrate concentration inside the chemostat is equal to that in the exit stream

Q. Optimal dilution rate is lower than critical dilution rate

R. Biomass concentration increases with increase in dilution rate

S. Cell recirculation facilitates operation beyond critical dilution rate

(A) P and Q only

(B) P, R and S only

(C) P and S only

(D) P, Q and S only

Official answer: **D**

SOLUTION

1. **P (true).** An ideal chemostat is a perfectly mixed continuous stirred-tank reactor, so the composition is the same at every point in the vessel and the outlet stream is a sample of the vessel contents.

Therefore $S_{\text{inside}} = S_{\text{exit}}$.

2. **Setting up Q and R.** Take Monod kinetics, $\mu = \dfrac{\mu_{max} S}{K_s + S}$. Here μ is the specific growth rate, μ_{max} is its maximum value and K_s is the saturation constant. At chemostat steady state $\mu = D$, where $D = F/V$ is the dilution rate. Solving for the substrate concentration gives $S = \dfrac{K_s D}{\mu_{max} - D}$, and the substrate balance gives $X = Y_{X/S}(S_0 - S)$. In these, S_0 is the feed substrate concentration, X is the biomass concentration and $Y_{X/S}$ is the biomass yield on substrate.
3. **Critical (washout) dilution rate.** Washout happens when no substrate is used up, i.e. $S \to S_0$. Putting $S = S_0$ into $S = \dfrac{K_s D}{\mu_{max} - D}$ gives
$$D_{crit} = \frac{\mu_{max} S_0}{K_s + S_0} = \mu_{max}(1 - a), \qquad a = \frac{K_s}{K_s + S_0},\ 0 < a < 1$$
4. **Optimal dilution rate.** This is the D at which biomass productivity $DX = Y_{X/S}\, D \left(S_0 - \dfrac{K_s D}{\mu_{max} - D} \right)$ is highest. Setting $\dfrac{d(DX)}{dD} = 0$ gives $S_0 = \dfrac{K_s D(2\mu_{max} - D)}{(\mu_{max} - D)^2}$. Now put $u = \mu_{max} - D$, so that $D(2\mu_{max} - D) = \mu_{max}^2 - u^2$. The condition becomes $u^2(S_0 + K_s) = K_s \mu_{max}^2$, so $u = \mu_{max}\sqrt{a}$ and
$$D_{opt} = \mu_{max}\left(1 - \sqrt{a}\right)$$
5. **Q (true).** When $0 < a < 1$, $\sqrt{a} > a$, so $D_{opt} < D_{crit}$ for every choice of K_s, S_0 and μ_{max}. There is also a direct argument: productivity DX is zero at $D = 0$ and zero again at washout ($X = 0$), and positive in between. Its maximum must therefore come before D_{crit}.
6. **R (false).** $S = \dfrac{K_s D}{\mu_{max} - D}$ goes up as D goes up. So $X = Y_{X/S}(S_0 - S)$ goes **down** as D increases and reaches $X = 0$ at D_{crit}. The statement is not always correct.
7. **S (true).** Suppose a fraction α of the feed flow is recycled, carrying cells at βX with concentration factor $\beta > 1$. The steady-state biomass balance on the vessel is $\alpha F \beta X - (1 + \alpha) F X + \mu X V = 0$, which gives $\mu = D(1 + \alpha - \alpha\beta) < D$. The cells therefore only need to grow more slowly than the dilution rate. Washout now occurs only when $D > \dfrac{D_{crit}}{1 + \alpha - \alpha\beta}$, so a steady state can be kept above the simple chemostat's D_{crit}.
8. P, Q and S are always correct and R is not, so the answer is option (D).

KEY IDEA

In a steady-state chemostat $\mu = D$. So $S = K_s D/(\mu_{max} - D)$ rises with D, and $X = Y_{X/S}(S_0 - S)$ falls with D. Productivity DX is zero at $D = 0$ and at washout, so it peaks strictly below D_{crit}. Cell recycle keeps μ below D, which is what lets the reactor run above the simple chemostat's washout rate.

WATCH OUT FOR

Picking R because a higher dilution rate brings in more substrate. In fact, raising D forces cells to grow faster, which needs a higher residual S, and that leaves less substrate to turn into biomass. The other common mistake is to confuse the optimal dilution rate (maximum productivity DX) with the critical one (washout) and so reject Q.

Q.44 MCQ · 2 MARKS

Plant, Animal and Microbial Biotechnology › Plant tissue culture

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

Assertion [a]: It is possible to regenerate a whole plant from a single plant cell.
Reason [r]: It is easier to introduce transgenes in to plants than animals.

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

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

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

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

Official answer: **B**

SOLUTION

1. Test the assertion first. Plant cells are totipotent: a single cell, or a protoplast, grown on a medium with a suitable auxin to cytokinin balance forms callus and then shoots and roots, giving a whole plant. So [a] is true.
2. Test the reason. Plant cells take up foreign DNA readily, for example through Agrobacterium tumefaciens (Ti plasmid) or the gene gun, and a transformed cell can be grown into a complete transgenic plant. Animal transgenesis needs embryo microinjection or embryonic stem cells, and the change must reach the germline. So [r] is a fair general statement and is true.
3. Now ask whether [r] explains [a]. The assertion is about totipotency, a developmental property of plant cells. It holds whether or not any transgene is introduced, and the ease of gene transfer says nothing about why a single cell can regenerate.
4. The link actually runs the other way. Totipotency is one reason transgenes are easier to use in plants, because a transformed single cell can be regenerated into a whole plant. So [r] does not account for [a].
5. Option (A) fails because [r] is not the explanation for [a]. Option (C) fails because both statements are true. Option (D) fails because [r] is true. Option (B) is correct.

KEY IDEA
In an assertion-reason question, check each statement on its own, then ask whether the reason explains the assertion. Totipotency is a property of plant cells. The ease of transgene transfer is a consequence of it, not the cause.

WATCH OUT FOR
Choosing (A) because both statements are true and both concern plant biotechnology. The reason does not explain the assertion, and if anything the explanation runs from [a] to [r].

Q.45 NAT · 2 MARKS

Recombinant DNA Technology and Tools › Microscopy & spectroscopy

A UV-visible spectrophotometer has a minimum detectable absorbance of 0.02. The minimum concentration of a protein sample that can be measured reliably in this instrument with a cuvette of 1 cm path length is _____ µM. The molar extinction coefficient of the protein is 10,000 L mol^{-1} cm^{-1}.

Official answer: **2**

SOLUTION

1. Beer-Lambert law: $A = \varepsilon c l$, where A is absorbance, ε is the molar extinction coefficient, c is concentration, and l is the path length.
2. Given: minimum detectable absorbance $A = 0.02$, $\varepsilon = 10{,}000\ \text{L mol}^{-1}\text{cm}^{-1}$, $l = 1\ \text{cm}$.
3. Rearranging for concentration:
$$c = \frac{A}{\varepsilon l}$$
4. Substituting the values:
$$c = \frac{0.02}{10000 \times 1} = 2 \times 10^{-6}\ \text{mol L}^{-1}$$
5. Converting to μM (since $1\ \text{mol L}^{-1} = 10^{6}\ \mu M$):
$$2 \times 10^{-6}\ \text{mol L}^{-1} = 2\ \mu M$$
6. So the minimum concentration that can be measured reliably is $2\ \mu M$.

KEY IDEA
The Beer-Lambert law (A = εcl) directly relates absorbance to concentration through the molar extinction coefficient and path length; a spectrophotometer's detection limit in absorbance units translates into a minimum measurable concentration via this same relation.

WATCH OUT FOR
Forgetting to convert the resulting mol/L answer into µM (a factor of 10^6), or mixing up which quantity is being solved for (rearranging incorrectly to isolate ε or l instead of c).

Q.46 NAT · 2 MARKS

General Biology › Biomolecules

The difference in concentrations of an uncharged solute between two compartments is 1.6-fold. The energy required for active transport of the solute across the membrane separating the two compartments is ___ cal mol^-1 (rounded off to the nearest integer). (R = 1.987 cal mol^-1 K^-1, T = 37 °C)

Official answer: **280 to 295**

SOLUTION

1. For an uncharged solute there is no membrane-potential term, so the free energy needed to move it against a concentration gradient is $\Delta G = RT \ln \dfrac{C_2}{C_1}$.
2. The concentration ratio is $C_2/C_1 = 1.6$, so $\ln 1.6 = 0.4700$.
3. Convert the temperature to kelvin: $T = 37 + 273 = 310\ \mathrm{K}$ (using $310.15\ \mathrm{K}$ gives the same integer).
4. $RT = 1.987\ \mathrm{cal\ mol^{-1}K^{-1}} \times 310\ \mathrm{K} \approx 616\ \mathrm{cal\ mol^{-1}}$.
5. $\Delta G = 616 \times 0.4700 \approx 289.5 \approx 290\ \mathrm{cal\ mol^{-1}}$, so active transport must supply about 290 cal per mole.

KEY IDEA
Active transport of an uncharged solute against a concentration gradient costs $\Delta G = RT \ln(C_2/C_1)$, with no electrical term, and T must be in kelvin.

WATCH OUT FOR
Using T = 37 in degrees Celsius instead of kelvin, using log base 10 in place of the natural log, or adding a membrane-potential term $zF\Delta\psi$ that does not apply to an uncharged solute.

Q.47 NAT · 2 MARKS

Genetics, Cell and Molecular Biology › Mendelian genetics

In pea plants, purple color of flowers is determined by the dominant allele while white color is determined by the recessive allele. A genetic cross between two purple flower-bearing plants results in an offspring with white flowers. The probability that the third offspring from these parents will have purple flowers is _____ (rounded off to 2 decimal places).

Official answer: **0.75**

SOLUTION

1. Purple is the dominant phenotype (allele P) and white is recessive (allele p); an offspring with white flowers must be homozygous recessive, genotype pp.
2. Both parents show the purple (dominant) phenotype, yet one of their offspring is pp. Since a pp offspring must receive a recessive allele from each parent, neither parent can be homozygous dominant PP (a PP parent could never contribute a p allele). Hence both purple-flowered parents must be heterozygous: $Pp \times Pp$.
3. A monohybrid cross $Pp \times Pp$ gives the genotypic ratio $1\,PP : 2\,Pp : 1\,pp$, i.e. a phenotypic ratio of 3 purple : 1 white. So for any single offspring of this cross, $P(\text{purple}) = \dfrac{3}{4}$ and $P(\text{white}) = \dfrac{1}{4}$.
4. Each offspring arises from an independent fertilization event, so the phenotype of one offspring (here, the first offspring being white) gives no information about, and does not change, the probability

distribution for any other offspring, including the third.

5. Therefore the probability that the third offspring has purple flowers is

$$P(\text{purple}) = \frac{3}{4} = 0.75$$

KEY IDEA
Each offspring's genotype is determined independently at fertilization (each is an independent Mendelian trial), so the phenotype of one sibling gives no information about another; the probability for the third offspring is simply the parental cross's phenotypic ratio.

WATCH OUT FOR
Treating the white first offspring as changing the probability for later offspring (e.g., trying to condition on "since one was already white, the remaining must balance to a 3:1 ratio" or halving/adjusting 3/4), when in fact fertilizations are independent Bernoulli trials and each offspring's probability of being purple is always 3/4 regardless of siblings' phenotypes.

Q.48 NAT · 2 MARKS

Genetics, Cell and Molecular Biology › Gene expression

The molecular mass of a protein is 22 kDa. The size of the cDNA (excluding the untranslated regions) that codes for this protein is _____ kb (rounded off to 1 decimal place).

Official answer: **0.6**

SOLUTION

1. Given: molecular mass of the protein = 22 kDa = 22,000 Da.
2. Standard approximation used in molecular biology: the average molecular mass of one amino acid residue in a protein ≈ 110 Da.
3. Number of amino acid residues in the protein $= \frac{22000\ \text{Da}}{110\ \text{Da}} = 200$ amino acids.
4. The genetic code is triplet: each amino acid in the protein is specified by one codon of 3 nucleotides in the coding (mRNA/cDNA) sequence.
5. Length of the coding sequence (cDNA, excluding untranslated regions) $= 200 \times 3 = 600\ \text{nucleotides} = 600\ \text{bp}$.
6. Convert to kilobases: $600\ \text{bp} = 0.6\ \text{kb}$ (since $1\ \text{kb} = 1000\ \text{bp}$).
7. Rounded to 1 decimal place, the size of the cDNA coding region $= 0.6\ \text{kb}$.

KEY IDEA
The average molecular mass of an amino acid residue in a protein is taken as ~110 Da; each amino acid is encoded by one codon (3 nucleotides) in the coding (cDNA) sequence.

WATCH OUT FOR
Forgetting to convert the answer from base pairs (600 bp) to kilobases (0.6 kb), or using an incorrect average amino acid residue mass instead of the standard ~110 Da approximation, or forgetting that each amino acid needs 3 nucleotides (one codon).

Q.49 NAT · 2 MARKS

Engineering Mathematics › Probability & statistics

A new game is being introduced in a casino. A player can lose Rs. 100, break even, win Rs. 100, or win Rs. 500. The probabilities (P(X)) of each of these outcomes (X) are given in the following table: X (in Rs.): -100, 0, 100, 500 with P(X): 0.25, 0.5, 0.2, 0.05. The standard deviation (σ) for the casino payout is Rs. _____ (rounded off to the nearest integer).

Official answer: **128 to 130**

SOLUTION

1. The probabilities sum to $0.25 + 0.5 + 0.2 + 0.05 = 1$, so this is a valid discrete distribution.
2. Mean: $E[X] = \sum x\,P(X) = (-100)(0.25) + 0(0.5) + 100(0.2) + 500(0.05) = -25 + 0 + 20 + 25 = 20$.

3. Second moment: $E[X^2] = \sum x^2 P(X) = 10000(0.25) + 0(0.5) + 10000(0.2) + 250000(0.05) = 2500 + 0 + 2000 + 12500 = 17000$.
4. Variance: $\sigma^2 = E[X^2] - (E[X])^2 = 17000 - 20^2 = 16600$.
5. Standard deviation: $\sigma = \sqrt{16600} \approx 128.84$, which rounds to 129.

KEY IDEA

For a discrete distribution, compute the mean $E[X]$ and the second moment $E[X^2]$ from the table. Then $\sigma = \sqrt{E[X^2] - (E[X])^2}$.

WATCH OUT FOR

Forgetting to subtract the square of the mean (giving $\sqrt{17000} \approx 130.4$, which falls outside the accepted range). Another slip is taking the standard deviation of the four listed values and ignoring their probabilities.

Q.50 NAT · 2 MARKS

Engineering Mathematics › Numerical methods

Q.50 $\int_{-1}^{1} f(x)dx$ calculated using trapezoidal rule for the values given in the table is _____ (rounded off to 2 decimal places).

x	-1	$-2/3$	$-1/3$	0	$1/3$	$2/3$	1
$f(x)$	0.37	0.51	0.71	1.0	1.40	1.95	2.71

Official answer: **2.20 to 2.50**

SOLUTION

1. The seven tabulated points $x = -1, -\frac{2}{3}, -\frac{1}{3}, 0, \frac{1}{3}, \frac{2}{3}, 1$ are equally spaced, so the step size is $h = \frac{1}{3}$ and there are 6 sub-intervals between -1 and 1.
2. Composite trapezoidal rule with step $h = \frac{1}{3}$:
$$\int_{-1}^{1} f(x)\,dx \approx \frac{h}{2}\left[f_0 + f_6 + 2\left(f_1 + f_2 + f_3 + f_4 + f_5\right)\right].$$
3. End values: $f_0 + f_6 = 0.37 + 2.71 = 3.08$.
4. Interior values: $f_1 + f_2 + f_3 + f_4 + f_5 = 0.51 + 0.71 + 1.0 + 1.40 + 1.95 = 5.57$, so $2 \times 5.57 = 11.14$.
5. Bracket: $3.08 + 11.14 = 14.22$.
6. Integral: $\frac{h}{2} \times 14.22 = \frac{1}{6} \times 14.22 = 2.37$.

KEY IDEA

With equally spaced data, the composite trapezoidal rule is $\frac{h}{2}[\text{first} + \text{last} + 2(\text{all interior values})]$. Here $h = \frac{1}{3}$ and there are 6 sub-intervals.

WATCH OUT FOR

Using $h = \frac{2}{3}$ (the width of the whole interval over 3), or giving the interior values weight 1 instead of 2. Another slip is counting 7 sub-intervals instead of 6 and so using the wrong h.

Q.51 NAT · 2 MARKS

Fundamentals of Biological Engineering › Growth kinetics

Yeast biomass ($C_6H_{10}O_3N$) grown on glucose is described by the stoichiometric equation given below:

$$C_6H_{12}O_6 + 0.48\,NH_3 + 3\,O_2 \rightarrow 0.48\,C_6H_{10}O_3N + 3.12\,CO_2 + 4.32\,H_2O$$

The amount of glucose needed for the production of $50\ \text{g L}^{-1}$ of yeast biomass in a batch reactor with a working volume of 1,00,000 L is _____ kg (rounded off to the nearest integer).

Official answer: **12500 to 14500**

SOLUTION

1. Total biomass to be produced: $m_X = 50\ \text{g L}^{-1} \times 1{,}00{,}000\ \text{L} = 5 \times 10^6\ \text{g} = 5000\ \text{kg}$.

2. Molar masses (C = 12, H = 1, O = 16, N = 14): biomass $C_6H_{10}O_3N$: $72 + 10 + 48 + 14 = 144\ \text{g mol}^{-1}$; glucose $C_6H_{12}O_6$: $72 + 12 + 96 = 180\ \text{g mol}^{-1}$.
3. From the stoichiometric equation, 1 mol of glucose gives 0.48 mol of biomass. The biomass yield on substrate, $Y_{X/S}$ (grams of biomass formed per gram of glucose consumed), is therefore
$$Y_{X/S} = \frac{0.48 \times 144}{1 \times 180} = \frac{69.12}{180} = 0.384\ \text{g biomass (g glucose)}^{-1}$$
4. Glucose required:
$$m_S = \frac{m_X}{Y_{X/S}} = \frac{5000\ \text{kg}}{0.384} = 13020.8\ \text{kg} \approx 13021\ \text{kg}$$
5. Check by moles: $n_X = \frac{5 \times 10^6\ \text{g}}{144\ \text{g mol}^{-1}} = 34722.2\ \text{mol}$; $n_S = \frac{34722.2}{0.48} = 72338.0\ \text{mol}$; $m_S = 72338.0 \times 180\ \text{g} = 1.30208 \times 10^7\ \text{g} \approx 13021\ \text{kg}$.

KEY IDEA

The coefficients in a balanced growth equation are in moles. Multiply each one by its molar mass to get a mass yield: $Y_{X/S} = (0.48 \times 144)/180 = 0.384\ \text{g g}^{-1}$. The glucose needed is then the total biomass divided by $Y_{X/S}$. The equation balances for C, H, O and N, so its coefficients can be used as printed. Only the biomass and glucose coefficients matter here; NH3, O2, CO2 and H2O play no part in the answer.

WATCH OUT FOR

Treating 0.48 as a mass ratio, which gives $5000/0.48 \approx 10417$ kg (outside the key), or forgetting to convert the molar ratio to a mass ratio with the two molar masses (144 and 180). Another slip is misreading the volume: 1,00,000 L in Indian digit grouping is 10^5 L. Reading it as 10^6 L makes every figure ten times too large.

Q.52 NAT · 2 MARKS

Fundamentals of Biological Engineering › Bioreactor operation

Phenolic wastewater discharged from an industry was treated with *Pseudomonas* sp. in an aerobic bioreactor. The influent and effluent concentrations of phenol were 10,000 and 10 ppm, respectively. The inlet feed rate of wastewater was $80\ \text{L h}^{-1}$. The kinetic properties of the organism are as follows:

Maximum specific growth rate $(\mu_m) = 1\ \text{h}^{-1}$

Saturation constant $(K_S) = 100\ \text{mg L}^{-1}$

Cell death rate $(k_d) = 0.01\ \text{h}^{-1}$

Assuming that the bioreactor operates under 'chemostat' mode, the working volume required for this process is _____ L (rounded off to the nearest integer).

Official answer: **970 to 1010**

SOLUTION

1. Symbols: μ = specific growth rate, μ_m = maximum specific growth rate, K_S = Monod saturation constant, k_d = specific cell death rate, F = feed rate, V = working volume, $D = F/V$ = dilution rate, S = phenol concentration in the reactor, X = biomass concentration. A chemostat is well mixed, so the effluent concentration equals the concentration inside the reactor: $S = 10\ \text{ppm} = 10\ \text{mg L}^{-1}$ (for a dilute aqueous solution, $1\ \text{ppm} \approx 1\ \text{mg L}^{-1}$).
2. Monod growth rate at the reactor concentration:
$$\mu = \frac{\mu_m S}{K_S + S} = \frac{1 \times 10}{100 + 10} = \frac{1}{11} = 0.0909\ \text{h}^{-1}$$
3. Biomass balance at steady state with a sterile feed and cell death:
$$\frac{dX}{dt} = \mu X - k_d X - DX = 0 \ \Rightarrow\ D = \mu - k_d$$
4. Dilution rate:
$$D = \frac{1}{11} - 0.01 = \frac{100 - 11}{1100} = \frac{89}{1100} = 0.08091\ \text{h}^{-1}$$

5. Working volume:

$$V = \frac{F}{D} = \frac{80}{89/1100} = \frac{88000}{89} = 988.76\ \text{L}$$

6. The influent phenol concentration ($10{,}000\ \text{ppm}$) fixes how much biomass is formed ($X = Y_{X/S}(S_0 - S)$), not the residence time, so it does not enter the volume. Rounded to the nearest integer, $V \approx 989\ \text{L}$.

KEY IDEA

At steady state in a chemostat with cell death, the biomass balance gives $D = \mu - k_d$, where μ is the Monod rate at the effluent (reactor) concentration. Once you have D, the volume is $V = F/D$. The inlet concentration S_0 only sets how much biomass is formed. It does not change the dilution rate.

WATCH OUT FOR

Ignoring death and taking $D = \mu$ gives $V = 880\ \text{L}$, which is outside the key. Adding death with the wrong sign ($D = \mu + k_d$) gives about $793\ \text{L}$. Putting the influent $10{,}000\ \text{ppm}$ into the Monod equation instead of the effluent $10\ \text{ppm}$ is also wrong, because in a well-mixed chemostat the cells only ever see the outlet concentration.

Q.53 NAT · 2 MARKS

Fundamentals of Biological Engineering › Downstream

In a cross-flow filtration process, the pressure drop (ΔP) driving the fluid flow is 2 atm, inlet feed pressure (P_i) is 3 atm and filtrate pressure (P_f) is equal to atmospheric pressure. The average transmembrane pressure drop (ΔP_m) is _____ atm.

Official answer: **1**

SOLUTION

1. In cross-flow (tangential-flow) filtration the feed flows along the membrane surface. The pressure drop ΔP that drives this flow along the channel is the fall from the inlet feed pressure P_i to the outlet (retentate) pressure P_o: $\Delta P = P_i - P_o$.
2. Retentate outlet pressure: $P_o = P_i - \Delta P = 3 - 2 = 1\ \text{atm}$.
3. The feed-side pressure falls along the membrane from P_i to P_o, so the average feed-side pressure is taken as the arithmetic mean of the inlet and outlet values: $\bar{P}_{feed} = \frac{P_i + P_o}{2} = \frac{3+1}{2} = 2\ \text{atm}$.
4. The filtrate (permeate) side is at atmospheric pressure. Since the feed pressures are given as absolute values, $P_f = 1\ \text{atm}$.
5. The average transmembrane pressure drop is the average feed-side pressure minus the filtrate pressure:

$$\Delta P_m = \frac{P_i + P_o}{2} - P_f = 2 - 1 = 1\ \text{atm}$$

Equivalently, $\Delta P_m = P_i - \frac{\Delta P}{2} - P_f = 3 - 1 - 1 = 1\ \text{atm}$.

KEY IDEA

In cross-flow filtration, $\Delta P = P_i - P_o$ is the pressure drop along the channel and $\Delta P_m = \frac{P_i + P_o}{2} - P_f$ is the average pressure difference across the membrane. Put together, $\Delta P_m = P_i - \frac{\Delta P}{2} - P_f$.

WATCH OUT FOR

Taking atmospheric pressure as $P_f = 0$ (a gauge value) while $P_i = 3\ \text{atm}$ is an absolute value. That gives $2\ \text{atm}$. The other common slip is subtracting P_f from the inlet pressure alone ($3 - 1 = 2\ \text{atm}$) instead of from the average feed-side pressure, which ignores the pressure drop along the membrane.

Q.54 NAT · 2 MARKS

Fundamentals of Biological Engineering › Upstream

An industrial fermentor containing 10,000 L of medium needs to be sterilized. The initial spore concentration in the medium is 10^6 spores mL^{-1}. The desired probability of contamination after sterilization is 10^{-3}. The

death rate of spores at 121 °C is $4\ \text{min}^{-1}$. Assume that there is no cell death during heating and cooling phases. The holding time of the sterilization process is _____ min (rounded off to the nearest integer).

Official answer: **9 to 10**

SOLUTION

1. Total spores at the start, N_0 = concentration × volume. Here $10{,}000\ \text{L} = 10^4\ \text{L} \times 10^3\ \text{mL L}^{-1} = 10^7\ \text{mL}$, so $N_0 = 10^6\ \text{spores mL}^{-1} \times 10^7\ \text{mL} = 10^{13}$ spores.
2. A contamination probability of 10^{-3} means the expected number of surviving spores in the whole batch after sterilization is $N = 10^{-3}$. In other words, one batch in 1000 still carries a viable spore.
3. Thermal death of spores follows first-order kinetics: $\frac{dN}{dt} = -k_d N$, which integrates at constant temperature to $\ln \frac{N_0}{N} = k_d\, t$. Here $k_d = 4\ \text{min}^{-1}$ is the specific death rate constant of the spores at 121 °C.
4. No spores die during heating or cooling, so the whole required reduction, the design (Del) factor $\nabla = \ln \frac{N_0}{N}$, must be delivered by the holding stage:
$$\nabla = \ln \frac{10^{13}}{10^{-3}} = \ln 10^{16} = 16 \times 2.3026 = 36.84$$
5. Holding time at 121 °C:
$$t_{hold} = \frac{\ln(N_0/N)}{k_d} = \frac{36.84}{4\ \text{min}^{-1}} = 9.21\ \text{min}$$
6. Rounded to the nearest integer, $t_{hold} \approx 9$ min.

KEY IDEA

In batch sterilization, N_0 is the TOTAL spore count in the whole vessel (concentration × volume), and the target N is the contamination probability, read as the expected number of survivors per batch. With first-order death at constant temperature, $\ln(N_0/N) = k_d\, t$. Since heating and cooling kill nothing here, the holding stage has to deliver the whole Del factor.

WATCH OUT FOR

Using the spore concentration (10^6 per mL) as N_0 instead of the total count in 10,000 L (10^{13}), which gives $\ln 10^9/4 = 5.2$ min. Two other slips: forgetting that 1 L = 1000 mL, and using $\log_{10}$ instead of $\ln$ (this gives $16/4 = 4$ min).

Q.55 NAT · 2 MARKS

Fundamentals of Biological Engineering › Bioreactor operation

The dimensions and operating condition of a lab-scale fermentor are as follows:
Volume = 1 L
Diameter = 20 cm
Agitator speed = 600 rpm
Ratio of impeller diameter to fermentor diameter = 0.3
This fermentor needs to be scaled up to 8,000 L for a large scale industrial application. If the scale-up is based on constant impeller tip speed, the speed of the agitator in the larger reactor is _____ rpm. Assume that the scale-up factor is the cube root of the ratio of fermentor volumes.

Official answer: **30**

SOLUTION

1. Geometric similarity means every length, including the impeller diameter D_i, grows by the same scale factor. The question sets that factor as the cube root of the volume ratio, where V_1 and V_2 are the lab and large working volumes:
$$\frac{D_{i,2}}{D_{i,1}} = \left(\frac{V_2}{V_1}\right)^{1/3} = \left(\frac{8000\ \text{L}}{1\ \text{L}}\right)^{1/3} = 20$$

2. The impeller-to-vessel diameter ratio stays at 0.3 in both vessels, so the impeller diameter also scales by 20. The lab impeller is $0.3 \times 20\ \text{cm} = 6\ \text{cm}$, so the large one is $6 \times 20 = 120\ \text{cm}$. Only the ratio of the two affects the answer.
3. Impeller tip speed: $u_{tip} = \pi N D_i$, where N is the agitator speed (revolutions per unit time) and D_i is the impeller diameter.
4. Constant tip speed: $\pi N_1 D_{i,1} = \pi N_2 D_{i,2}$, so $N_2 = N_1 \dfrac{D_{i,1}}{D_{i,2}}$.
5. $$N_2 = 600\ \text{rpm} \times \frac{1}{20} = 30\ \text{rpm}$$
6. Check: $u_{tip} = \pi \times 600\ \text{min}^{-1} \times 0.06\ \text{m} \approx 113\ \text{m min}^{-1}$ in the lab vessel and $\pi \times 30\ \text{min}^{-1} \times 1.2\ \text{m} \approx 113\ \text{m min}^{-1}$ in the large one, so the tip speed is the same in both.

KEY IDEA

Tip speed is $\pi N D_i$. Keeping it constant makes N inversely proportional to D_i. In a geometrically similar vessel, D_i grows as $(V_2/V_1)^{1/3}$, so $N_2 = N_1 (V_1/V_2)^{1/3}$.

WATCH OUT FOR

The usual slips are scaling the speed by the volume ratio (600/8000) instead of the length ratio (600/20), or using the constant power-per-volume rule ($N \propto D_i^{-2/3}$, which gives about 81 rpm) when the question asks for constant tip speed. The 20 cm vessel diameter and the 0.3 impeller ratio are not needed, because both vessels keep the same impeller ratio.

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