GATE Biotechnology

Sample Paper – 5

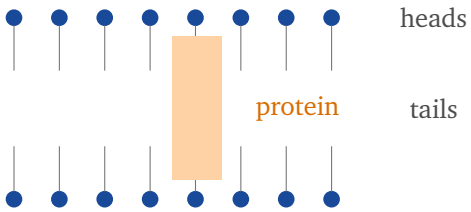
Duration: 128 Minutes **Maximum Marks: 72**

Instructions

- This paper contains **46 questions** covering the core **Biotechnology** subject of the GATE paper conducted by the IITs and IISc (General Aptitude and Engineering Mathematics are provided as separate papers).
- **Q1–Q20 carry 1 mark each** and **Q21–Q46 carry 2 marks each**, for a total of **72 marks**.
- Each question carries **negative marking of one-third of its allotted marks**: a wrong 1-mark question costs **0.33** and a wrong 2-mark question costs **0.67**. Unattempted questions carry no penalty.
- Every question here is a single-correct **MCQ**. The real GATE paper also has Multiple Select (MSQ) and Numerical Answer Type (NAT) questions, and **those carry no negative marking**.
- Attempt this paper in one timed sitting of about **128 minutes**, the share this core subject earns at GATE's overall pace of 180 minutes for 65 questions. Use $R = 8.314$ J mol^{-1}K^{-1} and take $\ln 2 = 0.693$ where required, unless stated otherwise.

Biochemistry

Q1. The biological membrane sketched below is built from a phospholipid bilayer with globular proteins embedded in it. The model that pictures this membrane as a two-dimensional fluid in which the lipids and proteins can diffuse laterally is the: [1 mark]



(A) the static unit-membrane (rigid tri-layer) model

(B) the fluid mosaic model of Singer and Nicolson

(C) a pure lipid-monolayer model

(D) a protein-sheet sandwich model

Q2. Oleic acid (an 18:1 fatty acid) and stearic acid (an 18:0 fatty acid) both have eighteen carbon atoms, yet oleic acid melts at a much lower temperature. Structurally, oleic acid differs from stearic acid by the presence of: **[1 mark]**

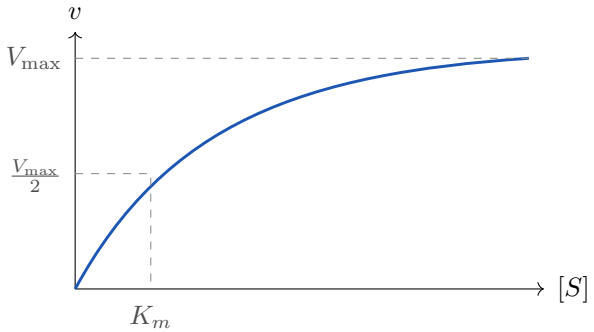
(A) one extra hydroxyl group on the chain

(B) one cis carbon–carbon double bond

(C) a branched methyl side group

(D) two additional carbon atoms

Q3. An enzyme obeys Michaelis–Menten kinetics with a maximum velocity $V_{\max} = 90\ \mu$mol min^{-1} and a Michaelis constant $K_m = 2$ mM, as sketched below. The initial reaction velocity when the substrate concentration $[S] = 6$ mM is: **[1 mark]**



(A) $90\ \mu$mol min^{-1}

(B) $45\ \mu$mol min^{-1}

(C) $22.5\ \mu\text{mol min}^{-1}$

(D) $67.5\ \mu\text{mol min}^{-1}$

Q4. A membrane transport process moves a solute across the plasma membrane *against* its concentration gradient, using the free energy released by the direct hydrolysis of ATP at the carrier protein. This process is classified as: **[1 mark]**

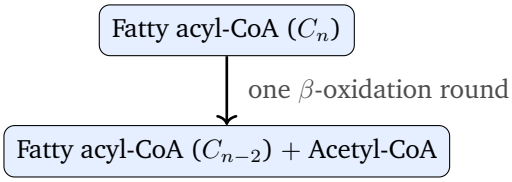
(A) primary active transport

(B) simple diffusion

(C) facilitated diffusion

(D) osmosis

Q5. The diagram summarises one round of the β-oxidation of a saturated fatty-acyl-CoA. Each such round shortens the fatty-acyl chain by two carbon atoms and, besides the shortened acyl-CoA, releases one molecule each of: **[1 mark]**



(A) two NADH and one CO_2

(B) one ATP and one acetyl-CoA only

(C) one $FADH_2$, one NADH and one acetyl-CoA

(D) two acetyl-CoA and one GTP

Q6. Palmitic acid, a fully saturated fatty acid with a 16-carbon straight chain, is completely degraded to acetyl-CoA by β-oxidation. The number of rounds (cycles) of β-oxidation needed to break it down completely is: **[1 mark]**

(A) 8

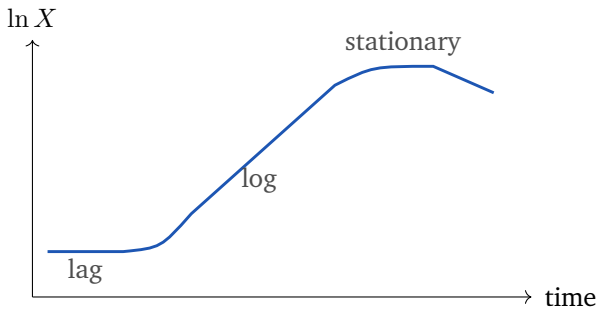
(B) 7

(C) 16

(D) 6

Microbiology

Q7. The batch growth curve of a bacterial culture, plotted as $\ln X$ against time, is shown below. The phase in which nutrients are running low, the rate of new cell formation is balanced by the rate of cell death, and the viable count stays almost constant is the: **[1 mark]**



(A) lag phase

(B) exponential (log) phase

(C) stationary phase

(D) death (decline) phase

Q8. A suspension of bacterial spores has a decimal reduction time (D-value) of 1.5 min at 121 °C. To reduce the viable spore count from 10^6 down to 10^0 (a six-log reduction) by moist-heat sterilisation, the holding time required at 121 °C is: **[1 mark]**

(A) 9 min

(B) 1.5 min

(C) 6 min

(D) 4.5 min

Q9. Certain medium components – such as heat-labile vitamins, some sugars and most antibiotics – are destroyed by the high temperature of an au-

toclave. The recommended way to sterilise such heat-sensitive solutions is: [1 mark]

(A) autoclaving at $121\ ^\circ$C for 15 min

(B) dry heat in a hot-air oven at $160\ ^\circ$C

(C) boiling at $100\ ^\circ$C for 10 min

(D) filtration through a $0.22\ \mu$m membrane filter

Q10. A culture medium in which every ingredient and its exact amount are known and specified, prepared entirely from pure chemical compounds, is described as a: [1 mark]

(A) complex medium containing peptone and yeast extract

(B) enriched blood medium

(C) selective medium with a single inhibitor

(D) chemically defined (synthetic) medium

Q11. An organism that uses organic compounds as its source of carbon and also obtains its energy by oxidising organic chemical compounds is nutritionally classified as a: [1 mark]

(A) chemoheterotroph

(B) photoautotroph

(C) chemoautotroph

(D) photoheterotroph

Cell Biology and Molecular Biology

Q12. A point mutation replaces one purine by the other purine (A $\leftrightarrow$ G), or one pyrimidine by the other pyrimidine (C $\leftrightarrow$ T), so that the chemical class of the base is preserved. Such a base substitution is called a: [1 mark]

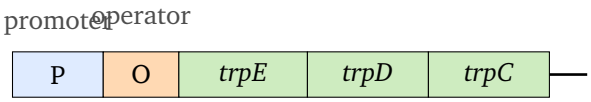
(A) transversion

(B) frameshift mutation

(C) nonsense mutation

(D) transition

Q13. The organisation of the *trp* (tryptophan) operon of *Escherichia coli* is shown below. When intracellular tryptophan is abundant, it binds the *trp* repressor and only then can the repressor switch off transcription. In this system tryptophan therefore acts as a: [1 mark]



(A) an inducer

(B) a corepressor

(C) a transcriptional activator

(D) a sigma factor

Q14. Exposure of DNA to ultraviolet light causes covalent bonds to form between two adjacent pyrimidine bases on the same strand, distorting the double helix and blocking replication. These UV-induced lesions are: [1 mark]

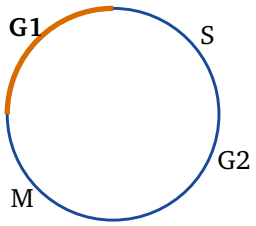
(A) pyrimidine (thymine) dimers

(B) apurinic (AP) sites

(C) deaminated cytosines

(D) single-strand nicks

Q15. The eukaryotic cell cycle is drawn below as a circle, with one quadrant highlighted. The major checkpoint known as the restriction point, at which the cell commits (or not) to entering S phase and replicating its DNA, is located at the end of the phase marked: [1 mark]



(A) G1 phase

(B) S phase

(C) G2 phase

(D) M phase

Q16. Human cells repair UV-induced pyrimidine dimers by cutting out a short single-stranded stretch of DNA that contains the damaged bases and then resynthesising it. This repair pathway, defective in the disease xeroderma pigmentosum, is: **[1 mark]**

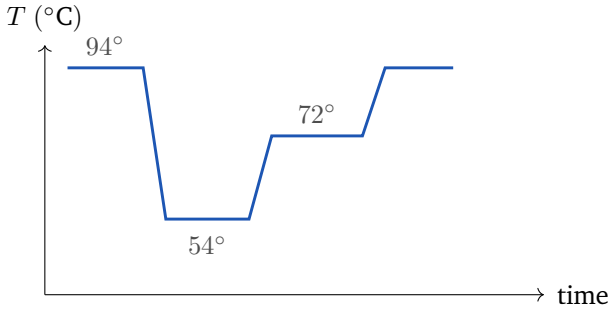
(A) mismatch repair

(B) base excision repair

(C) direct photoreactivation

(D) nucleotide excision repair

Q17. The temperature programme of one cycle of the polymerase chain reaction (PCR) is shown below. The high-temperature step at about 94–95 °C, at which the two strands of the double-stranded template are separated into single strands, is called: **[1 mark]**



(A) annealing

(B) denaturation

(C) extension (elongation)

(D) ligation

Q18. The addition or loss of a single nucleotide within the protein-coding region of a gene changes the way every codon downstream of that point is read. This type of mutation is called a: **[1 mark]**

(A) silent (synonymous) mutation

(B) transition

(C) frameshift mutation

(D) conservative substitution

Genetics, Immunology and Evolution

Q19. A large randomly mating population is at Hardy–Weinberg equilibrium for a single gene with two alleles. The frequency of the dominant allele is $p = 0.6$. The expected frequency of homozygous dominant individuals in this population is: [1 mark]

(A) 0.60

(B) 0.36

(C) 0.16

(D) 0.48

Q20. Among the five classes of human immunoglobulins, the class that is secreted across mucosal surfaces (appearing in saliva, tears, colostrum and intestinal secretions), typically as a dimer joined by a J chain and secretory component, is: [1 mark]

(A) IgG

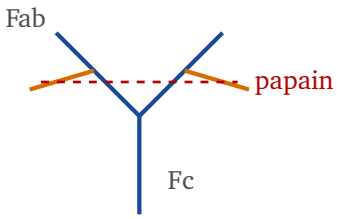
(B) IgM

(C) IgA

(D) IgD

Genetics, Immunology and Evolution (continued)

Q21. The schematic below shows an IgG monomer being cleaved by the protease papain. Papain cuts the antibody on the amino-terminal side of the hinge disulphide bonds. Digestion of one IgG molecule by papain therefore yields: [2 marks]



(A) one F(ab')$_2$ fragment plus several small peptides

(B) two identical Fab fragments and one Fc fragment

(C) two Fc fragments and one Fab fragment

(D) two free light chains only

Q22. Different antibodies recognise a huge variety of antigens even though their overall structure is similar. The part of the antibody molecule that differs greatly from one antibody to another and actually forms the antigen-binding site is the: **[2 marks]**

(A) constant region of the heavy chain

(B) Fc region

(C) variable regions of the heavy and light chains

(D) hinge region

Q23. A clinical laboratory quantifies a specific protein antigen in a patient's serum by capturing it with an immobilised antibody and detecting it with a second, enzyme-linked antibody that generates a measurable colour change. This antigen–antibody assay is called: **[2 marks]**

(A) ELISA (enzyme-linked immunosorbent assay)

(B) the polymerase chain reaction

(C) Southern blotting

(D) Gram staining

Q24. In a test cross involving two linked genes, 1000 progeny are scored and 80 of them are found to be recombinant (parental-type broken) individuals. The genetic map distance between the two loci is: **[2 marks]**

(A) 80 centimorgan

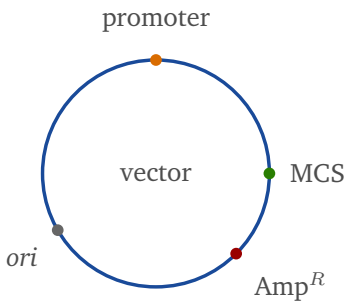
(B) 20 centimorgan

(C) 12 centimorgan

(D) 8 centimorgan

Recombinant DNA Technology and Bioinformatics

Q25. The map of an *expression* plasmid used to make a recombinant protein in *E. coli* is shown below. The element that determines where transcription of the cloned gene begins and how strongly the gene is transcribed into mRNA is the: **[2 marks]**



(A) the origin of replication

(B) the promoter

(C) the antibiotic-resistance gene

(D) the multiple cloning site

Q26. In the widely used pET expression system for *E. coli*, transcription of the cloned gene is driven by a very strong promoter that is recognised only by a bacteriophage RNA polymerase and is switched on by adding IPTG. This promoter is the: **[2 marks]**

(A) native *lac* promoter

(B) *trp* promoter

(C) SV40 early promoter

(D) T7 promoter

Q27. A DNA molecule created in the laboratory by joining together DNA sequences that come from two different biological sources – for example a human gene inserted into a bacterial plasmid – is called: [2 marks]

(A) recombinant DNA

(B) complementary DNA only

(C) satellite DNA

(D) highly repetitive DNA

Q28. To obtain a recombinant protein only *after* the host culture has grown to a high cell density, the cloned gene is placed under a promoter that stays silent during growth and is then deliberately switched on by adding a chemical such as IPTG. A promoter that can be turned on in this way is described as: [2 marks]

(A) constitutive

(B) permanently repressed

(C) inducible

(D) silenced by methylation

Q29. In the output of a BLAST similarity search, each hit is ranked by a statistical score that estimates how many alignments of at least that quality would be expected purely by chance in a database of the given size, so that a smaller value means a more significant match. This quantity is the: [2 marks]

(A) E-value (expect value)

(B) melting temperature T_m

(C) codon adaptation index

(D) isoelectric point

Q30. A recombinant therapeutic protein must be produced in a correctly folded form with authentic human-type glycosylation (added sugar chains). To meet this requirement, the preferred expression host is usually a: [2 marks]

(A) strain of *Escherichia coli*

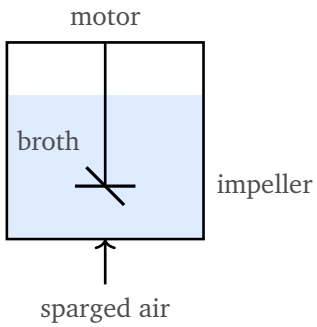
(B) mammalian (for example CHO) cell line

(C) bacteriophage particle

(D) cell-free plasmid solution

Bioprocess Engineering and Process Biotechnology

Q31. In the stirred-tank bioreactor shown, mixing is provided by a rotating impeller. The dimensionless group that expresses the ratio of inertial to viscous forces around the impeller, and hence decides whether the flow in the vessel is laminar or turbulent, is the: **[2 marks]**



(A) the Sherwood number

(B) the Damköhler number

(C) the Peclet number

(D) the Reynolds number

Q32. A Rushton turbine impeller of diameter $D = 0.1$ m rotates at $N = 5$ s^{-1} in a fermentation broth of density $\rho = 1000$ kg m^{-3} and viscosity $\mu = 0.001$ Pa s. Using the impeller Reynolds number $Re = \dfrac{\rho N D^2}{\mu}$, its value is: **[2 marks]**

(A) 5×10^4

(B) 5×10^3

(C) 5×10^5

(D) 5×10^2

Q33. When an aerobic fermentation is scaled up from a pilot vessel to a large production vessel of the same geometry, the single criterion most commonly held constant so that the oxygen-transfer coefficient $k_L a$ is preserved is constant: [2 marks]

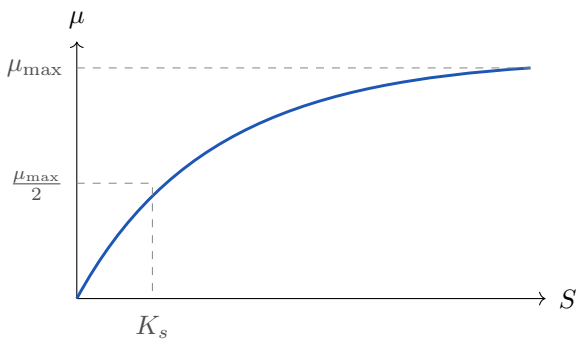
(A) agitation speed, N

(B) total power input, P

(C) power input per unit volume, P/V

(D) vessel diameter

Q34. The specific growth rate μ of a microbe depends on the limiting-substrate concentration S through the Monod model $\mu = \dfrac{\mu_{\max} S}{K_s + S}$, shown below. When the substrate is present in large excess, so that $S \gg K_s$, the specific growth rate approaches: [2 marks]



(A) $\mu_{\max}$

(B) $\dfrac{\mu_{\max}}{2}$

(C) zero

(D) $2\,\mu_{\max}$

Q35. In an aerobic submerged culture the oxygen transfer rate is OTR $= k_L a\,(C^* - C_L)$. If a dense, oxygen-hungry culture is becoming oxygen-limited, the most effective measure to raise the oxygen supply is to: [2 marks]

(A) increase the impeller speed to raise $k_L a$

(B) reduce the air-flow (aeration) rate

(C) raise the broth temperature above $45\ ^\circ$C

(D) allow C_L to rise above C^*

Q36. An aerobic fermenter has a volumetric oxygen-transfer coefficient $k_La = 200\ \text{h}^{-1}$. The saturation dissolved-oxygen concentration is $C^* = 8$ mg L^{-1} and the culture is held at a dissolved-oxygen level of $C_L = 2$ mg L^{-1}. The oxygen transfer rate OTR $= k_La\,(C^* - C_L)$ is: **[2 marks]**

(A) 400 mg $\text{L}^{-1}\text{h}^{-1}$

(B) 1600 mg $\text{L}^{-1}\text{h}^{-1}$

(C) 1200 mg $\text{L}^{-1}\text{h}^{-1}$

(D) 40 mg $\text{L}^{-1}\text{h}^{-1}$

Q37. A fed-batch fermentation reaches a final product concentration of 90 g L^{-1} at the end of 30 hours of operation. The overall volumetric productivity of the product for this run is: **[2 marks]**

(A) 30 g $\text{L}^{-1}\text{h}^{-1}$

(B) 0.33 g $\text{L}^{-1}\text{h}^{-1}$

(C) 2700 g $\text{L}^{-1}\text{h}^{-1}$

(D) 3 g $\text{L}^{-1}\text{h}^{-1}$

Q38. A bioreactor is run in a mode in which fresh nutrient medium is added gradually during the course of the run while nothing is withdrawn until the end, so that the working volume steadily increases with time. This mode of operation is called: **[2 marks]**

(A) continuous (chemostat) operation

(B) fed-batch operation

(C) simple batch operation

(D) turbidostat operation

Plant and Animal Biotechnology

Q39. Bt cotton and Bt maize are transgenic crops that resist attack by insect pests because they carry a gene coding for an insecticidal crystal (Cry) protein. This insecticidal gene is derived from the soil bacterium: [2 marks]

(A) *Agrobacterium tumefaciens*

(B) *Escherichia coli*

(C) *Bacillus thuringiensis*

(D) *Pseudomonas fluorescens*

Q40. The Cry (Bt) protein is harmless to the plant and to mammals but toxic to susceptible caterpillars. After a larva eats the transgenic tissue, the crystal protein is solubilised, proteolytically activated, and then kills the insect by binding gut receptors and creating pores. This activation and pore formation take place in the: [2 marks]

(A) acidic stomach of a mammal

(B) hard outer cuticle of the insect

(C) chloroplast of the plant cell

(D) alkaline midgut of the larva, where it forms pores in the gut epithelial cells

Q41. *Agrobacterium* transfers genes poorly into most cereals. To insert the Bt gene directly into the cells of such crops, a common physical method fires DNA-coated gold or tungsten microparticles into the plant tissue. This technique is the: [2 marks]

(A) electroporation of naked protoplasts

(B) *Agrobacterium* co-cultivation

(C) gene gun (biolistic particle bombardment)

(D) direct microinjection into the nucleus

Q42. Transgenic livestock can be engineered so that a valuable human therapeutic protein is secreted into their milk, from which it is then purified.

This use of transgenic animals as living factories for pharmaceutical proteins is called: [2 marks]

(A) molecular pharming (gene pharming)

(B) somatic hybridisation

(C) micropropagation

(D) apomixis

Q43. When a plant is transformed, only a small fraction of the treated cells actually take up and integrate the transgene. To let only these transformed cells grow on the selection medium, a selectable marker is co-introduced. A commonly used plant selectable marker, carried by the *nptII* gene, confers resistance to the antibiotic: [2 marks]

(A) ampicillin

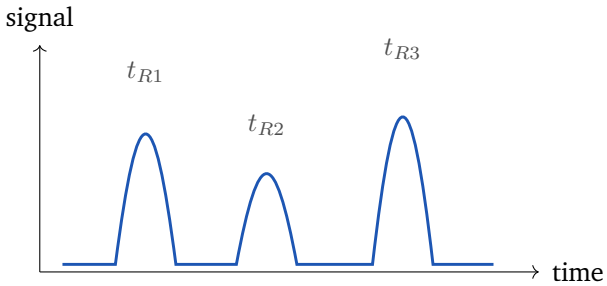
(B) tetracycline

(C) chloramphenicol

(D) kanamycin

Analytical Techniques

Q44. The chromatogram below is obtained from a high-performance liquid chromatography (HPLC) separation, in which several compounds appear as peaks emerging at different times. For a given compound, the elapsed time between sample injection and the appearance of its peak at the detector is called its: [2 marks]



(A) the void time only

(B) the dead volume

(C) the retention time

(D) the theoretical plate height

Q45. In reversed-phase HPLC the stationary phase is non-polar (for example a C_{18}-bonded silica) while the mobile phase is comparatively polar. Under these conditions, the compounds that leave the column *first* (with the shortest retention time) are the: **[2 marks]**

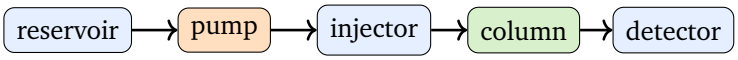
(A) most non-polar (most hydrophobic) compounds

(B) most polar (least hydrophobic) compounds

(C) highest molecular-weight compounds

(D) most positively charged compounds

Q46. The block diagram below shows the main components of an HPLC system, connected in the order in which the mobile phase flows. The component that generates the high, steady pressure needed to push the mobile phase through the tightly packed column at a constant flow rate is the: **[2 marks]**



(A) the detector

(B) the high-pressure pump

(C) the injector loop

(D) the data recorder

Detailed Solutions

Q1.

Solution

Concept – how modern cell biology describes the membrane: The plasma membrane is not a rigid sheet but a mobile assembly of lipids and proteins.

Step 1 – read the diagram: It shows a continuous phospholipid bilayer, with the polar heads facing the water on both sides and the non-polar tails buried inside.

Step 2 – note the embedded proteins: A globular protein spans the bilayer, floating within it rather than sitting on a fixed lattice.

Step 3 – name the model: This picture, of a fluid lipid bilayer in which proteins are dispersed like tiles in a mosaic and can diffuse sideways, is the fluid mosaic model proposed by Singer and Nicolson in 1972.

Why the other options are wrong:

- A: the older unit-membrane model treated the membrane as a static, rigid tri-layer.
- C and D: a single lipid monolayer or a protein-sheet sandwich do not describe the observed bilayer-with-embedded-proteins.

Final Answer: the fluid mosaic model $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q1

Q2.

Solution

Concept – saturated versus unsaturated fatty acids: The notation $18{:}1$ means 18 carbons and 1 carbon–carbon double bond, whereas $18{:}0$ means 18 carbons and no double bond.

Step 1 – compare the two chains: Stearic acid $(18{:}0)$ is fully saturated; oleic acid $(18{:}1)$ has one double bond.

Step 2 – locate the difference: That single double bond in oleic acid is in the cis configuration.

Step 3 – link structure to the melting point: The cis double bond puts a rigid kink in the chain, so the molecules pack together less tightly and the melting temperature falls – exactly the behaviour described.

Why the other options are wrong:

- A, C and D: neither an extra hydroxyl, nor a methyl branch, nor two more carbons is implied by the 18:1 versus 18:0 description.

Final Answer: one *cis* carbon–carbon double bond $\Rightarrow$ B

Answer: (B) Go Back to Q2

Q3.

Solution

Concept – the Michaelis–Menten rate equation: $v = \dfrac{V_{\max}[S]}{K_m + [S]}$ links the initial velocity to the substrate concentration.

Step 1 – list the data: $V_{\max} = 90\ \mu\text{mol min}^{-1}$, $K_m = 2$ mM and $[S] = 6$ mM.

Step 2 – substitute the values: $v = \dfrac{90 \times 6}{2 + 6}$

Step 3 – evaluate the numerator: $90 \times 6 = 540$

Step 4 – evaluate the denominator: $2 + 6 = 8$

Step 5 – divide: $v = \dfrac{540}{8}$

$v = 67.5\ \mu\text{mol min}^{-1}$

Final Answer: $v = 67.5\ \mu\text{mol min}^{-1} \Rightarrow$ D

Answer: (D) Go Back to Q3

Q4.

Solution

Concept – classes of membrane transport: Movement against a concentration gradient is uphill and needs an input of free energy.

Step 1 – note the direction: The solute is moved against its gradient, so the process cannot be spontaneous on its own.

Step 2 – note the energy source: The energy comes from the direct hydrolysis of ATP at the carrier protein.

Step 3 – name the process: Transport that is powered by the immediate hydrolysis of ATP is primary active transport (as in the Na^+/K^+-ATPase).

Why the other options are wrong:

- B and C: simple and facilitated diffusion move solutes *down* the gradient and use no ATP.

- D: osmosis is the passive movement of water, not active solute pumping.

Final Answer: primary active transport $\Rightarrow$ A

Answer: (A) Go Back to Q4

Q5.

Solution

Concept – one round of β-oxidation: Fatty acids are broken down two carbons at a time in the mitochondrial matrix through a repeating four-step sequence.

Step 1 – list the four reactions of a round: oxidation (by FAD), hydration, a second oxidation (by NAD^+), and thiolytic cleavage.

Step 2 – account for the reduced coenzymes: The first oxidation reduces FAD to $FADH_2$; the second oxidation reduces NAD^+ to NADH.

Step 3 – account for the carbon product: The final thiolysis snips off a two-carbon unit as one acetyl-CoA and leaves an acyl chain shortened by two carbons.

Step 4 – collect the products of one round: So each round yields one $FADH_2$, one NADH and one acetyl-CoA.

Final Answer: one $FADH_2$, one NADH and one acetyl-CoA $\Rightarrow$ C

Answer: (C) Go Back to Q5

Q6.

Solution

Concept – counting the rounds of β-oxidation: A saturated fatty acid with an even number of carbons C is cut into $C/2$ acetyl-CoA units, and the number of rounds is one fewer than the number of units.

Step 1 – find the number of acetyl-CoA units: Palmitic acid has 16 carbons, so it gives $\frac{16}{2} = 8$ acetyl-CoA units.

Step 2 – relate rounds to units: Number of rounds $=$ (number of acetyl-CoA units) -1.

Step 3 – substitute: $= 8 - 1$

$= 7$

Step 4 – reason it out: The last round cleaves a four-carbon unit into two acetyl-CoA at once, so one fewer round than the total number of units is needed.

Final Answer: 7 rounds of β-oxidation $\Rightarrow$ B

Answer: (B) Go Back to Q6

Q7.

Solution

Concept – the phases of a batch growth curve: A batch culture moves through lag, exponential, stationary and death phases.

Step 1 – describe the phase in question: Nutrients are depleting and toxic products are building up, so cell birth and cell death come into balance.

Step 2 – effect on the viable count: With birth balancing death, the number of live cells stays almost constant, giving a flat plateau on the $\ln X$ plot.

Step 3 – name that plateau: This flat, top portion of the curve is the stationary phase.

Why the other options are wrong:

- A, lag phase: cells are adapting and are not yet dividing.
- B, exponential phase: cells divide at the maximum rate, so the curve rises steeply.
- D, death phase: the viable count *falls*, so the curve slopes downward.

Final Answer: the stationary phase $\Rightarrow$ C

Answer: (C) Go Back to Q7

Q8.

Solution

Concept – the decimal reduction time (D-value): The D-value is the time needed at a given temperature to kill 90% of the population, that is to cut the viable count by one factor of ten (one log).

Step 1 – find how many logs must be removed: Going from 10^6 to 10^0 is a reduction of 6 orders of magnitude, i.e. 6 log cycles.

Step 2 – relate holding time to D-value: Holding time $=$ (number of log reductions) $\times$ D-value.

Step 3 – substitute the numbers: $= 6 \times 1.5$ min

Step 4 – evaluate: $= 9$ min

Final Answer: 9 min at 121 °C $\Rightarrow$ A

Answer: (A) Go Back to Q8

Q9.

Solution

Concept – sterilising heat-sensitive solutions: Some medium components lose activity when heated, so they cannot be autoclaved.

Step 1 – identify the problem: Vitamins, certain sugars and antibiotics are heat-labile and would be destroyed at $121\ ^\circ$C.

Step 2 – choose a non-thermal method: Passing the solution through a membrane filter with a pore size of $0.22\ \mu$m physically removes bacteria and spores without any heating.

Step 3 – confirm it works: Because $0.22\ \mu$m is smaller than bacterial cells, the filtrate is sterile while the delicate molecules remain intact.

Why the other options are wrong:

- A and B: autoclaving and dry heat both apply high temperature and would destroy the components.
- C, boiling: does not reliably kill spores and still heats the solution.

Final Answer: filtration through a $0.22\ \mu$m membrane $\Rightarrow$ D

Answer: (D) Go Back to Q9

Q10.

Solution

Concept – defined versus complex media: Media are classified by how precisely their chemical composition is known.

Step 1 – read the key phrase: Every ingredient and its exact amount are specified, and everything is a pure chemical compound.

Step 2 – match to the definition: A medium whose exact chemical make-up is fully known is a chemically defined (synthetic) medium.

Why the other options are wrong:

- A, complex medium: contains peptone or yeast extract, whose precise composition is unknown.
- B, enriched medium: adds rich, chemically undefined supplements such as blood.

- C, selective medium: is defined by an added inhibitor, not by having a fully known composition.

Final Answer: a chemically defined (synthetic) medium $\Rightarrow$ D

Answer: (D) Go Back to Q10

Q11.

Solution

Concept – nutritional classification of microbes: Organisms are grouped by their carbon source (auto- versus hetero-) and their energy source (photo- versus chemo-).

Step 1 – classify the carbon source: The organism uses organic compounds for carbon, so it is a heterotroph.

Step 2 – classify the energy source: It gets energy by oxidising organic chemical compounds, so it is a chemotroph.

Step 3 – combine the two: Chemo (energy from chemicals) + heterotroph (organic carbon) = chemoheterotroph.

Why the other options are wrong:

- B and D, photo-: obtain energy from light, not chemicals.
- C, chemoautotroph: uses CO_2, an inorganic carbon source, not organic carbon.

Final Answer: a chemoheterotroph $\Rightarrow$ A

Answer: (A) Go Back to Q11

Q12.

Solution

Concept – transitions versus transversions: Base substitutions are classified by whether the base class (purine or pyrimidine) is preserved.

Step 1 – read the change: A purine is replaced by the other purine, or a pyrimidine by the other pyrimidine.

Step 2 – note the class is conserved: Purine stays purine and pyrimidine stays pyrimidine, so the chemical class of the base does not change.

Step 3 – name the substitution: A substitution that keeps the base class is a

transition.

Why the other options are wrong:

- A, transversion: swaps a purine for a pyrimidine (or vice versa), changing the class.
- B, frameshift: is an insertion or deletion, not a substitution.
- C, nonsense: creates a stop codon; that is an *effect*, not this class of change.

Final Answer: a transition $\Rightarrow$ D

Answer: (D) Go Back to Q12

Q13.

Solution

Concept – repressible control of the *trp* operon: The *trp* operon makes the enzymes for tryptophan biosynthesis and is switched off when the end product is plentiful.

Step 1 – state of the repressor alone: By itself, the *trp* repressor cannot bind the operator; it is inactive.

Step 2 – role of tryptophan: When tryptophan is abundant it binds the repressor and converts it into its active, DNA-binding form.

Step 3 – name that role: A small molecule that must combine with a repressor to let it shut off transcription is a corepressor.

Why the other options are wrong:

- A, inducer: turns a system *on* by inactivating a repressor (the *lac* logic), the opposite of what happens here.
- C, activator: increases transcription by binding DNA directly.
- D, sigma factor: helps RNA polymerase recognise promoters and is unrelated to this control.

Final Answer: a corepressor $\Rightarrow$ B

Answer: (B) Go Back to Q13

Q14.

Solution

Concept – UV damage to DNA: Ultraviolet light drives a photochemical reaction between neighbouring bases.

Step 1 – identify which bases react: Two adjacent pyrimidines (most often two thymines) on the same strand become covalently linked.

Step 2 – name the lesion: The linked pair is a pyrimidine (thymine) dimer, typically a cyclobutane pyrimidine dimer.

Step 3 – note the consequence: The dimer kinks the helix and stalls DNA and RNA polymerases, so it must be repaired.

Why the other options are wrong:

- B, apurinic site: is a base lost by hydrolysis, not a UV cross-link.
- C, deaminated cytosine: arises from deamination (giving uracil), a different chemistry.
- D, single-strand nick: is a break in the backbone, not a base–base bond.

Final Answer: pyrimidine (thymine) dimers $\Rightarrow \boxed{\text{A}}$

Answer: (A) Go Back to Q14

Q15.

Solution

Concept – the cell-cycle phases and the restriction point: The eukaryotic cycle runs G1 $\rightarrow$ S $\rightarrow$ G2 $\rightarrow$ M, and each transition is guarded by a checkpoint.

Step 1 – locate the checkpoint described: The restriction point decides whether the cell will commit to replicating its DNA.

Step 2 – identify the phase that precedes S: DNA replication happens in S phase, and the phase just before S is G1.

Step 3 – place the checkpoint: So the restriction point sits at the end of G1, at the G1/S boundary, exactly the highlighted quadrant.

Why the other options are wrong:

- B, S phase: is where replication actually occurs, after the commitment is made.
- C, G2 phase: ends at the G2/M checkpoint, which guards entry into mitosis.
- D, M phase: is mitosis itself, controlled by the spindle-assembly checkpoint.

Final Answer: the G1 phase $\Rightarrow$ A

Answer: (A) Go Back to Q15

Q16.

Solution

Concept – repair of bulky DNA lesions: Damage that distorts the helix, such as a pyrimidine dimer, is removed by cutting out a patch of the damaged strand.

Step 1 – describe the mechanism given: An oligonucleotide containing the lesion is excised, and the gap is filled by DNA polymerase and sealed by ligase.

Step 2 – name that pathway: Excising a short single-stranded stretch that carries a bulky lesion is nucleotide excision repair (NER).

Step 3 – confirm with the disease clue: NER is defective in xeroderma pigmentosum, whose patients are extremely sensitive to sunlight – the clue given in the question.

Why the other options are wrong:

- A, mismatch repair: corrects base-pairing errors left after replication.
- B, base excision repair: removes a single damaged base through a glycosylase, not a bulky helix-distorting dimer.
- C, photoreactivation: directly reverses dimers using photolyase and is absent in placental mammals.

Final Answer: nucleotide excision repair $\Rightarrow$ D

Answer: (D) Go Back to Q16

Q17.

Solution

Concept – the three temperature steps of a PCR cycle: Each cycle uses denaturation, annealing and extension at different temperatures.

Step 1 – read the highest-temperature step: The plateau at about 94–95 °C is the hottest part of the cycle.

Step 2 – state what happens there: At this temperature the hydrogen bonds holding the two strands together break, separating the double-stranded template into single strands.

Step 3 – name the step: Melting the template into single strands is the denatura-

tion step.

Why the other options are wrong:

- A, annealing: happens at the lower ~ 54 °C step, where primers bind.
- C, extension: happens at ~ 72 °C, where Taq polymerase synthesises new DNA.
- D, ligation: is not a step of standard PCR at all.

Final Answer: denaturation $\Rightarrow$ B

Answer: (B) Go Back to Q17

Q18.

Solution

Concept – the reading frame of a gene: The ribosome reads the coding sequence in consecutive, non-overlapping triplets starting from a fixed point.

Step 1 – describe the change: A single nucleotide is inserted or deleted within the coding region.

Step 2 – trace the effect downstream: Because the triplets are counted from the start, adding or removing one base shifts every codon after that point.

Step 3 – name the mutation: A mutation that shifts the reading frame in this way is a frameshift mutation, and it usually scrambles the protein and often creates a premature stop.

Why the other options are wrong:

- A, silent mutation: changes a base but not the encoded amino acid, and does not shift the frame.
- B, transition: is a base substitution, which keeps the frame intact.
- D, conservative substitution: swaps one amino acid for a similar one, again with no frame shift.

Final Answer: a frameshift mutation $\Rightarrow$ C

Answer: (C) Go Back to Q18

Q19.

Solution

Concept – Hardy–Weinberg genotype frequencies: With allele frequencies p (dominant) and q (recessive), the genotypes occur as $p^2 : 2pq : q^2$.

Step 1 – identify the genotype asked for: Homozygous dominant individuals have frequency p^2.

Step 2 – insert the value of p: $p^2 = (0.6)^2$

Step 3 – evaluate: $= 0.36$

Step 4 – sanity check: Then $q = 1 - 0.6 = 0.4$, giving $q^2 = 0.16$ and $2pq = 0.48$, and $0.36 + 0.48 + 0.16 = 1.00$, so the frequencies add up correctly.

Final Answer: homozygous dominant frequency $= 0.36 \Rightarrow$ B

Answer: (B) Go Back to Q19

Q20.

Solution

Concept – immunoglobulin classes and their locations: The five human antibody classes differ in structure and in where they act.

Step 1 – read the defining features: The class described is secreted at mucosal surfaces, appears in saliva, tears and colostrum, and is a dimer carrying a J chain and secretory component.

Step 2 – match to a class: Secretory (mucosal) antibody that is a J-chain-linked dimer is IgA.

Why the other options are wrong:

- A, IgG: is the main *serum* antibody and a monomer, not a mucosal dimer.
- B, IgM: is a pentamer and is the first antibody made in a primary response, mainly in blood.
- D, IgD: sits on naive B-cell surfaces and is scarce in secretions.

Final Answer: IgA $\Rightarrow$ C

Answer: (C) Go Back to Q20

Q21.

Solution

Concept – proteolytic fragments of IgG: Cutting an antibody with a protease at a defined site produces characteristic fragments.

Step 1 – locate the papain cut: Papain cleaves each heavy chain on the amino-terminal side of the hinge disulphide bonds, above the point where the two heavy chains are joined.

Step 2 – work out the pieces released: Cutting above the inter-heavy-chain disulphides separates the two arms from the stem.

Step 3 – name the pieces: This gives two identical antigen-binding fragments (Fab), each with one binding site, plus one crystallisable stem fragment (Fc).

Why the other options are wrong:

- A, $F(ab')_2$: results from *pepsin*, which cuts *below* the hinge and keeps the two arms joined.
- C: papain does not produce two Fc pieces.
- D: the light chains are not released as free chains by papain.

Final Answer: two Fab fragments and one Fc fragment $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q21

Q22.

Solution

Concept – variable and constant regions of an antibody: Each heavy and light chain has a variable (V) domain at the amino-terminus and one or more constant (C) domains.

Step 1 – identify what changes between antibodies: The amino-acid sequence of the variable domains differs enormously from one antibody clone to another.

Step 2 – link that variation to function: The variable domains of the paired heavy and light chains fold together to form the antigen-binding site, whose shape gives each antibody its specificity.

Step 3 – state the answer: So the antigen-binding site is formed by the variable regions of the heavy and light chains.

Why the other options are wrong:

- A and B: the constant region and the Fc are relatively invariant and mediate

effector functions, not antigen recognition.
- D, hinge: gives the molecule flexibility but does not bind antigen.

Final Answer: the variable regions of the heavy and light chains $\Rightarrow$ C

Answer: (C) Go Back to Q22

Q23.

Solution

Concept – enzyme-based immunoassays: Antigens can be measured by exploiting the tight, specific binding of antibodies together with an enzyme reporter.

Step 1 – read the method: The antigen is captured by an immobilised antibody and revealed by a second, enzyme-linked antibody that produces a colour.

Step 2 – match to the assay name: An immunosorbent assay that uses an enzyme-linked antibody to give a measurable colour is an ELISA.

Step 3 – note the readout: The intensity of the colour is proportional to the amount of antigen, allowing quantification.

Why the other options are wrong:

- B, PCR: amplifies DNA, not a protein antigen.
- C, Southern blot: detects specific DNA sequences.
- D, Gram staining: classifies bacteria and is not an antigen assay.

Final Answer: ELISA $\Rightarrow$ A

Answer: (A) Go Back to Q23

Q24.

Solution

Concept – map distance from recombination frequency: For linked genes, the genetic map distance in centimorgan equals the recombination frequency expressed as a percentage.

Step 1 – compute the recombination frequency: $\text{RF} = \dfrac{\text{recombinant progeny}}{\text{total progeny}} = \dfrac{80}{1000}$

Step 2 – convert to a percentage: $= 0.08 = 8\%$

Step 3 – convert to map units: 1% recombination $= 1$ centimorgan, so $8\% = 8$

centimorgan.

Final Answer: 8 centimorgan $\Rightarrow$ D

Answer: (D) Go Back to Q24

Q25.

Solution

Concept – the parts of an expression vector: An expression plasmid carries an origin, a selectable marker, a cloning site and, crucially, a promoter to drive the insert.

Step 1 – identify what controls transcription: Transcription starts at, and its strength is set by, the promoter that lies just upstream of the cloned gene.

Step 2 – read that element off the map: The element marked "promoter" is the one that determines where and how strongly the gene is transcribed into mRNA.

Why the other options are wrong:

- A, origin of replication: controls plasmid copy number, not transcription.
- C, antibiotic-resistance gene: lets transformed cells be selected but does not drive the insert.
- D, multiple cloning site: is only the array of restriction sites where the insert is placed.

Final Answer: the promoter $\Rightarrow$ B

Answer: (B) Go Back to Q25

Q26.

Solution

Concept – the pET / T7 expression system: The pET vectors give very high-level protein production in *E. coli* by using a phage promoter and polymerase.

Step 1 – recall the promoter used: In pET vectors the cloned gene sits behind a T7 promoter.

Step 2 – note which polymerase reads it: Only T7 RNA polymerase (supplied by the host on induction) recognises this promoter, so the host's own polymerase ignores it.

Step 3 – note the induction: Adding IPTG switches on the T7 RNA polymerase, which then transcribes the gene strongly.

Why the other options are wrong:

- A, *lac* promoter: is weaker and is read by the host polymerase.
- B, *trp* promoter: is a bacterial biosynthetic promoter, not the pET driver.
- C, SV40 promoter: works in mammalian cells, not in *E. coli*.

Final Answer: the T7 promoter $\Rightarrow$ D

Answer: (D) Go Back to Q26

Q27.

Solution

Concept – what "recombinant DNA" means: Recombinant DNA technology joins DNA from different sources into one molecule.

Step 1 – read the definition given: Sequences from two different biological sources are joined together, e.g. a human gene placed into a bacterial plasmid.

Step 2 – name the product: A DNA molecule assembled from two different sources is, by definition, recombinant DNA.

Why the other options are wrong:

- B, cDNA: is DNA copied from mRNA; it is not defined by joining two sources.
- C, satellite DNA: is highly repetitive genomic DNA.
- D, repetitive DNA: is naturally repeated genomic sequence, not an engineered join.

Final Answer: recombinant DNA $\Rightarrow$ A

Answer: (A) Go Back to Q27

Q28.

Solution

Concept – inducible expression of a cloned gene: Separating growth from production is achieved by controlling when the gene is switched on.

Step 1 – read the behaviour wanted: The promoter stays silent while the cells grow and is turned on only later by adding a chemical (IPTG).

Step 2 – name that behaviour: A promoter that can be switched on by an external signal is an inducible promoter.

Step 3 – note the benefit: This lets the culture first reach high density and only

then divert resources to making the product, which is often useful when the product is toxic or a metabolic burden.

Why the other options are wrong:

- A, constitutive: is always on, so it cannot be delayed.
- B, permanently repressed: would never make the product.
- D, silenced by methylation: describes epigenetic shut-off, not a controllable IPTG switch.

Final Answer: inducible $\Rightarrow$ C

Answer: (C) Go Back to Q28

Q29.

Solution

Concept – scoring hits in a BLAST search: BLAST ranks alignments by a statistic that reflects how likely a match of that quality is by chance.

Step 1 – read the definition given: The quantity estimates the number of hits of at least that score expected purely by chance in a database of the given size.

Step 2 – name it: That is the E-value (expect value).

Step 3 – interpret its size: A very small E-value (for example 10^{-50}) means the match is very unlikely to be chance, so it is highly significant.

Why the other options are wrong:

- B, T_m: is the DNA melting temperature, unrelated to alignment scoring.
- C, codon adaptation index: gauges how well codons match a host's preference.
- D, isoelectric point: is a protein property, not a search statistic.

Final Answer: the E-value $\Rightarrow$ A

Answer: (A) Go Back to Q29

Q30.

Solution

Concept – choosing an expression host by post-translational needs: The right host depends on whether the protein needs folding help and glycosylation.

Step 1 – read the requirement: The protein must be correctly folded and must carry authentic human-type sugar chains (glycosylation).

Step 2 – eliminate bacteria: *E. coli* cannot perform mammalian glycosylation and often misfolds large secreted proteins.

Step 3 – choose the host: A mammalian cell line such as CHO carries out human-like glycosylation and folding, so it is preferred for such therapeutics.

Why the other options are wrong:

- A, *E. coli*: lacks the glycosylation machinery.
- C, bacteriophage: is a virus and cannot itself make the folded glycoprotein.
- D, cell-free plasmid: performs no glycosylation.

Final Answer: a mammalian (CHO) cell line $\Rightarrow$ B

Answer: (B) Go Back to Q30

Q31.

Solution

Concept – the impeller Reynolds number: Mixing regimes in a stirred tank are set by the ratio of inertial to viscous forces.

Step 1 – recall the relevant group: For an impeller of diameter D turning at speed N in a fluid of density ρ and viscosity μ, this ratio is $Re = \dfrac{\rho N D^2}{\mu}$.

Step 2 – interpret it: Re compares inertial forces to viscous forces; a high value means inertial forces dominate and the flow is turbulent.

Step 3 – name the group: This dimensionless number is the Reynolds number.

Why the other options are wrong:

- A, Sherwood number: relates to mass-transfer coefficients.
- B, Damköhler number: compares reaction rate with transport rate.
- C, Peclet number: compares convective with diffusive transport.

Final Answer: the Reynolds number $\Rightarrow$ D

Answer: (D) Go Back to Q31

Q32.

Solution

Concept – computing the impeller Reynolds number: $Re = \dfrac{\rho N D^2}{\mu}$, with all quantities in SI units.

Step 1 – list the data: $\rho = 1000$ kg m^{-3}, $N = 5$ s^{-1}, $D = 0.1$ m and $\mu = 0.001$ Pa s.

Step 2 – evaluate D^2: $D^2 = (0.1)^2 = 0.01$ m^2

Step 3 – form the numerator: $\rho N D^2 = 1000 \times 5 \times 0.01 = 50$

Step 4 – divide by the viscosity: $Re = \dfrac{50}{0.001}$

Step 5 – evaluate: $Re = 50000 = 5 \times 10^4$

Step 6 – interpret: $Re > 10^4$ confirms fully turbulent mixing, as intended in an aerated fermenter.

Final Answer: $Re = 5 \times 10^4 \Rightarrow \boxed{\text{A}}$

Answer: (A) Go Back to Q32

Q33.

Solution

Concept – scale-up criteria for aerobic fermenters: On scale-up, one operating variable is held constant to preserve oxygen transfer.

Step 1 – identify the target to preserve: Adequate oxygen supply means keeping the volumetric mass-transfer coefficient k_La roughly the same at large scale.

Step 2 – pick the matching criterion: k_La correlates strongly with the power dissipated per unit volume, so keeping P/V constant is the most widely used single criterion.

Step 3 – state the answer: Therefore scale-up is done at constant power input per unit volume, P/V.

Why the other options are wrong:

- A, constant N: cannot be held because tip speed and power would rise sharply with size.
- B, constant total power P: ignores the much larger volume and would starve the big vessel of mixing energy per litre.

- D, constant diameter: geometric similarity is assumed, not a transfer criterion.

Final Answer: constant power input per unit volume, $P/V \Rightarrow$ C

Answer: (C) Go Back to Q33

Q34.

Solution

Concept – the Monod model at high substrate: $\mu = \dfrac{\mu_{\max} S}{K_s + S}$ describes how growth rate saturates as substrate rises.

Step 1 – apply the limit $S \gg K_s$: When S is much larger than K_s, the denominator $K_s + S \approx S$.

Step 2 – simplify the expression: $\mu \approx \dfrac{\mu_{\max} S}{S}$

Step 3 – cancel S: $\mu \approx \mu_{\max}$

Step 4 – read it from the curve: The plot flattens toward the horizontal asymptote $\mu_{\max}$ at large S, confirming the result.

Final Answer: $\mu \to \mu_{\max} \Rightarrow$ A

Answer: (A) Go Back to Q34

Q35.

Solution

Concept – boosting the oxygen transfer rate: OTR $= k_L a\,(C^* - C_L)$, so OTR rises if either $k_L a$ or the driving force $(C^* - C_L)$ is increased.

Step 1 – pick the practical lever: $k_L a$ can be raised by more vigorous agitation, which breaks bubbles into smaller ones and increases interfacial area.

Step 2 – state the action: Increasing the impeller speed raises $k_L a$ and hence the OTR.

Why the other options are wrong:

- B, lowering aeration: reduces the gas supply and interfacial area, lowering OTR.
- C, raising temperature above 45 °C: harms the culture and *lowers* oxygen solubility C^*.
- D, $C_L > C^*$: is physically impossible at steady operation and would reverse the driving force.

Final Answer: increase the impeller speed to raise $k_La \Rightarrow$ A

Answer: (A) Go Back to Q35

Q36.

Solution

Concept – computing the oxygen transfer rate: OTR $= k_La\,(C^* - C_L)$.

Step 1 – list the data: $k_La = 200$ h^{-1}, $C^* = 8$ mg L^{-1} and $C_L = 2$ mg L^{-1}.

Step 2 – find the driving force: $C^* - C_L = 8 - 2 = 6$ mg L^{-1}

Step 3 – multiply by k_La: OTR $= 200 \times 6$

Step 4 – evaluate: OTR $= 1200$ mg L^{-1}h^{-1}

Final Answer: OTR $= 1200$ mg L^{-1}h$^{-1} \Rightarrow$ C

Answer: (C) Go Back to Q36

Q37.

Solution

Concept – overall volumetric productivity: Productivity is the amount of product formed per unit volume per unit time, i.e. final concentration divided by total time.

Step 1 – list the data: Final product concentration $= 90$ g L^{-1}, total time $= 30$ h.

Step 2 – write the formula: Productivity $= \dfrac{\text{final product concentration}}{\text{total time}}$

Step 3 – substitute: $= \dfrac{90}{30}$

Step 4 – evaluate: $= 3$ g L^{-1}h^{-1}

Final Answer: 3 g L^{-1}h$^{-1} \Rightarrow$ D

Answer: (D) Go Back to Q37

Q38.

Solution

Concept – modes of bioreactor operation: Batch, fed-batch and continuous modes differ in how medium is added and broth removed.

Step 1 – read the operating description: Fresh medium is added gradually during the run, but nothing is withdrawn until the end.

Step 2 – note the consequence: Because material enters but does not leave, the working volume increases with time.

Step 3 – name the mode: Adding feed without withdrawal, so the volume grows, is fed-batch operation.

Why the other options are wrong:

- A, continuous: adds and removes at the same rate, holding the volume constant.
- C, batch: adds nothing after the start.
- D, turbidostat: is a continuous system that controls cell density, again at constant volume.

Final Answer: fed-batch operation $\Rightarrow$ B

Answer: (B) Go Back to Q38

Q39.

Solution

Concept – the source of the Bt insecticidal gene: Bt crops are named after the bacterium that provides their pest-resistance gene.

Step 1 – recall what "Bt" stands for: "Bt" is short for *Bacillus thuringiensis*, a soil bacterium.

Step 2 – link to the Cry protein: This bacterium naturally makes insecticidal crystal (Cry) proteins during sporulation, and its *cry* genes are engineered into the crops.

Step 3 – conclude: So the insecticidal gene of Bt cotton and Bt maize comes from *Bacillus thuringiensis*.

Why the other options are wrong:

- A, *Agrobacterium*: is used as a gene-delivery vector, not as the source of the toxin gene.
- B and D, *E. coli* and *Pseudomonas*: do not make the Cry insecticidal crystal proteins.

Final Answer: *Bacillus thuringiensis* $\Rightarrow$ C

Answer: (C) Go Back to Q39

Q40.

Solution

Concept – the mode of action of the Cry (Bt) toxin: The crystal protein is a protoxin that only becomes lethal under specific gut conditions.

Step 1 – ingestion and solubilisation: A susceptible larva eats the transgenic tissue, and the alkaline environment of its midgut dissolves the crystal protein.

Step 2 – activation: Gut proteases then cleave the solubilised protoxin into the active toxin.

Step 3 – pore formation: The active toxin binds specific receptors on the midgut epithelial cells and inserts to form pores, so the gut cells swell and burst and the larva stops feeding and dies.

Step 4 – identify the site: All of this happens in the alkaline midgut of the larva.

Why the other options are wrong:

- A: the mammalian stomach is acidic and lacks the specific receptors, which is why Bt crops are safe to eat.
- B, cuticle: the toxin must be ingested; it does not act on the outer cuticle.
- C, chloroplast: is a plant organelle and is not where the insect toxicity occurs.

Final Answer: the alkaline midgut, forming pores in the gut cells $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q40

Q41.

Solution

Concept – direct gene transfer into cereals: Cereals are recalcitrant to *Agrobacterium*, so physical DNA-delivery methods are used.

Step 1 – read the method described: DNA-coated gold or tungsten microparticles are fired into the plant tissue.

Step 2 – name the technique: Shooting DNA-coated metal microprojectiles into cells is the gene gun, or biolistic particle bombardment.

Step 3 – note why it is used here: Because it is purely physical, it works even in species that *Agrobacterium* infects poorly, such as maize and wheat.

Why the other options are wrong:

- A, electroporation: introduces DNA by electric pulses into protoplasts, not by firing particles.

- B, *Agrobacterium*: is exactly the method said to work poorly for cereals.
- D, microinjection: delivers DNA into single cells with a fine needle and is not particle bombardment.

Final Answer: the gene gun (biolistic particle bombardment) $\Rightarrow$ C

Answer: (C) Go Back to Q41

Q42.

Solution

Concept – transgenic animals as protein factories: Foreign genes can be engineered so that their product is secreted into an easily harvested fluid.

Step 1 – read the application: A human therapeutic protein is secreted into the milk of transgenic livestock and then purified.

Step 2 – name the strategy: Using transgenic animals (or plants) as living factories for pharmaceutical proteins is called molecular pharming, or gene pharming.

Why the other options are wrong:

- B, somatic hybridisation: is a plant protoplast-fusion technique.
- C, micropropagation: is clonal plant multiplication in culture.
- D, apomixis: is seed formation without fertilisation and is unrelated.

Final Answer: molecular pharming (gene pharming) $\Rightarrow$ A

Answer: (A) Go Back to Q42

Q43.

Solution

Concept – selectable markers in plant transformation: Only a few treated cells integrate the transgene, so a marker is used to let just those cells grow.

Step 1 – recall the classic plant marker: The *nptII* gene encodes neomycin phosphotransferase II.

Step 2 – state what it confers: This enzyme inactivates aminoglycoside antibiotics, giving resistance to kanamycin (and neomycin).

Step 3 – apply the selection: On kanamycin-containing medium, only transformed cells carrying *nptII* survive and regenerate.

Why the other options are wrong:

- A, ampicillin: its resistance (bla) is a common *bacterial* marker, not the plant-cell selection here.
- B and C, tetracycline and chloramphenicol: are not the resistance conferred by *nptII*.

Final Answer: kanamycin $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q43

Q44.

Solution

Concept – reading an HPLC chromatogram: In HPLC the detector records a signal versus time, and each analyte appears as a peak.

Step 1 – define the quantity asked for: It is the time from sample injection to the moment the compound's peak reaches the detector.

Step 2 – name it: This characteristic time is the retention time, t_R, of that compound.

Step 3 – note its use: Under fixed conditions each compound has a reproducible t_R, so retention time helps identify it.

Why the other options are wrong:

- A, void time: is the time for an unretained species, not for a given retained compound.
- B, dead volume: is a volume of the system, not the elapsed time of a peak.
- D, plate height: measures column efficiency, not elution time.

Final Answer: the retention time $\Rightarrow$ $\boxed{\text{C}}$

Answer: (C) Go Back to Q44

Q45.

Solution

Concept – elution order in reversed-phase HPLC: Separation depends on how strongly each compound interacts with the non-polar stationary phase.

Step 1 – describe the phases: The stationary phase is non-polar (C_{18}) and the mobile phase is relatively polar.

Step 2 – reason about retention: Non-polar (hydrophobic) compounds stick

strongly to the C_{18} surface and are held back, so they elute late.

Step 3 – identify what elutes first: Polar (hydrophilic) compounds interact weakly with the non-polar surface, spend more time in the mobile phase and therefore elute first.

Why the other options are wrong:

- A: the most non-polar compounds are the most strongly retained and elute *last*.
- C and D: in reversed-phase HPLC separation is governed by polarity/hydrophobicity, not primarily by molecular weight or charge.

Final Answer: the most polar (least hydrophobic) compounds $\Rightarrow$ B

Answer: (B) Go Back to Q45

Q46.

Solution

Concept – the components of an HPLC system: The mobile phase flows reservoir $\rightarrow$ pump $\rightarrow$ injector $\rightarrow$ column $\rightarrow$ detector.

Step 1 – identify the demanding requirement: HPLC columns are packed with very small particles, so a high, steady pressure is needed to keep the mobile phase moving at a constant flow rate.

Step 2 – match the component: The high-pressure pump is what generates and maintains this pressure and flow.

Step 3 – confirm by elimination of the rest: The injector introduces the sample, the column separates it, and the detector senses the eluting bands – none of these produces the pressure.

Why the other options are wrong:

- A, detector: only measures the separated compounds.
- C, injector loop: only loads the sample onto the flow.
- D, data recorder: only stores and displays the signal.

Final Answer: the high-pressure pump $\Rightarrow$ B

Answer: (B) Go Back to Q46

Answer Key

Q	Ans	Q	Ans	Q	Ans	Q	Ans	Q	Ans
1	B	2	B	3	D	4	A	5	C
6	B	7	C	8	A	9	D	10	D
11	A	12	D	13	B	14	A	15	A
16	D	17	B	18	C	19	B	20	C
21	B	22	C	23	A	24	D	25	B
26	D	27	A	28	C	29	A	30	B
31	D	32	A	33	C	34	A	35	A
36	C	37	D	38	B	39	C	40	D
41	C	42	A	43	D	44	C	45	B
46	B								