GATE Biotechnology

Sample Paper – 8

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 flavin coenzyme FAD (flavin adenine dinucleotide), which acts as an electron carrier in the citric-acid-cycle enzyme succinate dehydrogenase, is biosynthetically derived from which water-soluble vitamin? **[1 mark]**

(A) niacin (vitamin B_3)

(B) thiamine (vitamin B_1)

(C) riboflavin (vitamin B_2)

(D) pyridoxine (vitamin B_6)

Q2. Coenzyme A (CoA), the universal carrier of acyl groups in reactions such as fatty-acid oxidation and the pyruvate-dehydrogenase step, contains at its core a molecule of which vitamin? **[1 mark]**

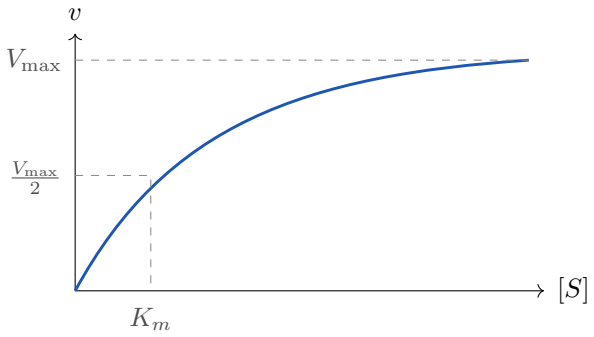
(A) biotin (vitamin B_7)

(B) folic acid (vitamin B_9)

(C) cobalamin (vitamin B_{12})

(D) pantothenic acid (vitamin B_5)

Q3. An enzyme obeys Michaelis–Menten kinetics with $V_{\max} = 80$ μmol min^{-1} and $K_m = 4$ mM, as sketched below. The initial reaction velocity at a substrate concentration $[S] = 12$ mM is: **[1 mark]**



(A) 60 μmol min^{-1}

(B) 40 μmol min^{-1}

(C) 20 μmol min^{-1}

(D) 80 μmol min^{-1}

Q4. Thiamine pyrophosphate (TPP), the coenzyme that assists the decarboxylation of α-keto acids in the pyruvate-dehydrogenase complex, is a derivative of which vitamin? **[1 mark]**

(A) riboflavin (vitamin B_2)

(B) niacin (vitamin B_3)

(C) thiamine (vitamin B_1)

(D) pyridoxine (vitamin B_6)

Q5. Pyridoxal phosphate (PLP), the coenzyme that shuttles amino groups during transamination reactions catalysed by aminotransferases, is derived from which vitamin? [1 mark]

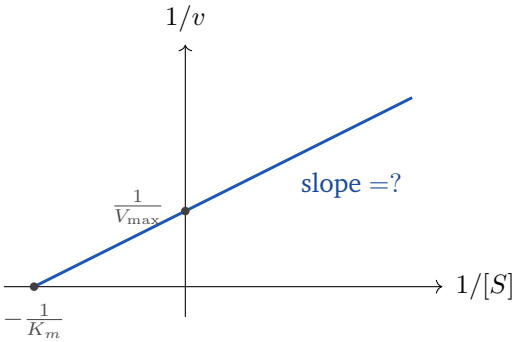
(A) thiamine (vitamin B_1)

(B) riboflavin (vitamin B_2)

(C) niacin (vitamin B_3)

(D) pyridoxine (vitamin B_6)

Q6. The Lineweaver–Burk (double-reciprocal) plot of an enzyme-catalysed reaction is shown below. The *slope* of the straight line drawn on these axes is equal to: [1 mark]



(A) $\dfrac{1}{V_{\max}}$

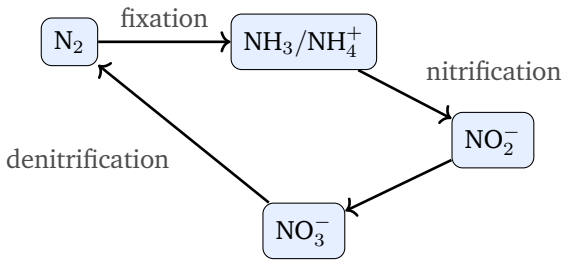
(B) $-\dfrac{1}{K_m}$

(C) $\dfrac{1}{K_m}$

(D) $\dfrac{K_m}{V_{\max}}$

Microbiology

Q7. The nitrogen cycle in soil is summarised below. The two-step microbial oxidation of ammonia first to nitrite and then to nitrate, carried out by chemoautotrophs such as *Nitrosomonas* and *Nitrobacter*, is called: [1 mark]



(A) nitrification

(B) denitrification

(C) nitrogen fixation

(D) ammonification

Q8. Biological nitrogen fixation reduces atmospheric dinitrogen (N_2) to ammonia. The oxygen-sensitive enzyme complex that catalyses this energy-demanding reduction in diazotrophic bacteria is: **[1 mark]**

(A) nitrate reductase

(B) nitrogenase

(C) urease

(D) catalase

Q9. In a legume field, a soil bacterium invades root hairs, triggers the formation of root nodules and there fixes atmospheric nitrogen in a mutualistic partnership with the host plant. This symbiotic nitrogen-fixing genus is: **[1 mark]**

(A) *Nitrosomonas*

(B) *Azotobacter*

(C) *Rhizobium*

(D) *Clostridium*

Q10. During exponential growth a bacterial population increases from 10^2 cells to 10^8 cells in exactly 3 hours. The number of generations (doublings) completed during this period is nearest to: **[1 mark]**

(A) 20

(B) 10

(C) 6

(D) 100

Q11. In waterlogged, oxygen-poor soils, certain facultative anaerobes use nitrate as a terminal electron acceptor and reduce it stepwise to gaseous N_2, which escapes to the atmosphere. This nitrogen-cycle step is: [1 mark]

(A) nitrification

(B) ammonification

(C) denitrification

(D) nitrogen assimilation

Cell Biology and Molecular Biology

Q12. A controlled, energy-dependent form of cell death proceeds through caspase activation, chromatin condensation, membrane blebbing and packaging of the cell into apoptotic bodies, all without leakage of contents or inflammation. This process is: [1 mark]

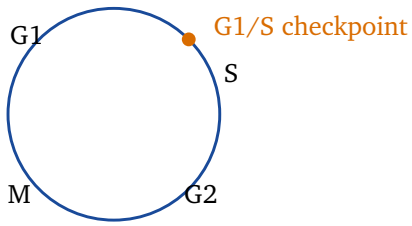
(A) apoptosis

(B) necrosis

(C) autophagy

(D) mitosis

Q13. The eukaryotic cell cycle is shown below, with the G1/S restriction point highlighted. Passage through this checkpoint, which commits the cell to DNA replication, is driven mainly by the activity of: [1 mark]



(A) p53 acting alone

(B) DNA ligase

(C) cyclin–CDK (cyclin-dependent kinase) complexes

(D) telomerase

Q14. In the intrinsic (mitochondrial) pathway of apoptosis, an internal stress signal permeabilises the outer mitochondrial membrane and releases a small haem protein into the cytosol, where it helps assemble the apoptosome and activate caspase-9. This released molecule is: **[1 mark]**

(A) free calcium ions

(B) ATP

(C) cytochrome c

(D) glucose

Q15. A tumour-suppressor protein senses DNA damage and responds by arresting the cell cycle for repair or, if the damage is severe, by triggering apoptosis; because of this gate-keeping role it is often called the "guardian of the genome". This protein is: **[1 mark]**

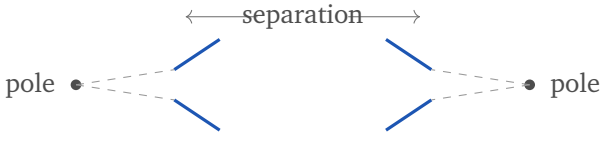
(A) p53

(B) Ras

(C) Myc

(D) cyclin B

Q16. The stage of mitosis sketched below is the point at which the cohesion between sister chromatids is lost and the two chromatids of each chromosome are pulled by spindle fibres toward opposite poles of the cell. This stage is: **[1 mark]**



(A) metaphase

(B) anaphase

(C) prophase

(D) telophase

Q17. A sample of double-stranded DNA is found to contain 30% adenine among its total bases. Using Chargaff's base-pairing rules, the percentage of guanine in the same DNA is: **[1 mark]**

(A) 30%

(B) 20%

(C) 40%

(D) 70%

Q18. In the maturation of a eukaryotic pre-mRNA, the non-coding intron sequences are precisely removed and the coding exon sequences are joined together by the spliceosome. This processing step is called: **[1 mark]**

(A) $5'$ capping

(B) polyadenylation

(C) transcription

(D) splicing

Genetics, Immunology and Evolution

Q19. Vaccines such as the BCG vaccine and the oral polio vaccine use pathogens whose virulence has been reduced by repeated culture so that they replicate weakly and stimulate strong, long-lasting immunity without causing disease. This kind of vaccine is a/an: **[1 mark]**

(A) live attenuated vaccine

(B) toxoid vaccine

(C) subunit vaccine

(D) DNA vaccine

Q20. A patient with a deep wound is given an injection of ready-made anti-tetanus antibodies (antiserum) for immediate protection. The type of immunity conferred by such pre-formed antibodies is: [1 mark]

(A) active immunity

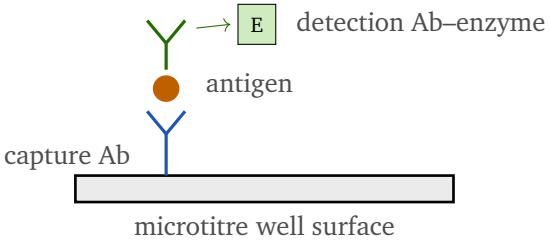
(B) passive immunity

(C) innate immunity

(D) autoimmunity

Genetics, Immunology and Evolution (continued)

Q21. The sandwich ELISA sketched below is used to measure the concentration of an antigen. The antigen is trapped between a plate-bound capture antibody and a detection antibody, and the detection antibody is conjugated to an enzyme that converts a colourless substrate into a coloured product. The enzyme most commonly used for this colour reaction is: [2 marks]



(A) horseradish peroxidase (HRP)

(B) DNA polymerase

(C) nitrogenase

(D) lysozyme

Q22. A large randomly mating population is at Hardy–Weinberg equilibrium for a single gene with two alleles. The frequency of the recessive homozygous genotype (aa) is observed to be 0.09. The frequency of the recessive allele, q, in this population is: [2 marks]

(A) 0.3

(B) 0.09

(C) 0.7

(D) 0.03

Q23. During a primary immune response, one immunoglobulin class appears earliest in the serum and, because it is a large pentamer that is not retained for long, its presence is used as a serological marker of a recent or acute infection. This class is: [2 marks]

(A) IgG

(B) IgM

(C) IgA

(D) IgE

Q24. In a small, isolated population the frequencies of alleles change from one generation to the next purely because of random sampling of gametes, with no role for natural selection. Over time this may fix or eliminate alleles by chance. This evolutionary mechanism is called: [2 marks]

(A) natural selection

(B) gene flow

(C) mutation pressure

(D) genetic drift

Recombinant DNA Technology and Bioinformatics

Q25. For the low-cost, high-level production of a simple non-glycosylated recombinant protein, the host of first choice is a bacterium that grows rapidly on inexpensive media and whose genetics is very well understood, even though it cannot add sugar chains to proteins. This host is: [2 marks]

(A) *Escherichia coli*

(B) cultured human liver cells

(C) tobacco leaf tissue

(D) silkworm larvae

Q26. In a widely used bacterial expression vector the cloned gene sits downstream of a strong, tightly regulated promoter that is switched on by adding the lactose analogue IPTG to the culture. This inducible promoter arrangement is the: [2 marks]

(A) SV40 early promoter

(B) T7/*lac* promoter system

(C) CaMV 35S promoter

(D) nopaline synthase (nos) promoter

Q27. A *linear* DNA molecule of total length 10 kb carries two *Eco*RI recognition sites, located at the 2 kb and 7 kb positions from the left end, as shown. Complete digestion of this DNA with *Eco*RI produces fragments of: [2 marks]

(A) 2 kb and 8 kb

(B) 5 kb and 5 kb

(C) 2 kb, 5 kb and 3 kb

(D) 10 kb only (single uncut piece)

Q28. A recombinant protein is engineered to carry a tail of six consecutive histidine residues. This tag lets the protein be captured from a crude lysate in a single step by its tight binding to immobilised Ni^{2+} ions on a column. This purification method is: [2 marks]

(A) size-exclusion (gel-filtration) chromatography

(B) ion-exchange chromatography

(C) SDS–PAGE

(D) nickel-affinity (immobilised-metal, IMAC) chromatography

Q29. A BLAST search returns a database hit whose alignment with the query sequence has an extremely small expectation value, $E \approx 1 \times 10^{-50}$. The correct interpretation of this very low E-value is that the match is: [2 marks]

(A) most likely a random, chance alignment

(B) almost certainly a sequencing artefact

(C) a region of no real similarity

(D) highly significant and very unlikely to have arisen by chance

Q30. To express a typical eukaryotic gene in *Escherichia coli*, the reverse-transcribed cDNA of the gene is cloned rather than its genomic DNA. The essential reason is that the bacterial host cannot: [2 marks]

(A) remove introns from the primary transcript (it cannot splice)

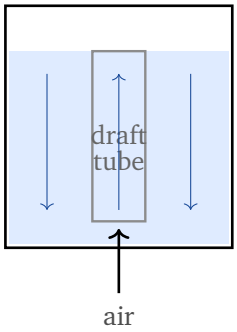
(B) translate messenger RNA into protein

(C) replicate a plasmid vector

(D) form peptide bonds

Bioprocess Engineering and Process Biotechnology

Q31. The bioreactor sketched below has no mechanical impeller; instead, sterile air sparged at the base of a draft tube makes the broth rise on the gassed side and sink on the ungassed side, giving gentle circulation well suited to shear-sensitive cells. This reactor type is a/an: [2 marks]



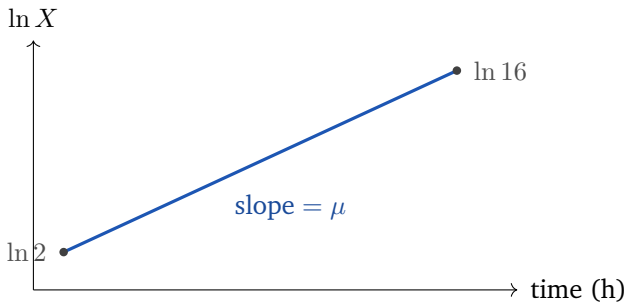
(A) mechanically stirred-tank reactor

(B) packed-bed reactor

(C) airlift bioreactor

(D) membrane bioreactor

Q32. In a batch stirred-tank bioreactor, an organism grows exponentially and its biomass concentration rises from 2 g L^{-1} to 16 g L^{-1} over a period of 9 hours, as plotted below. The specific growth rate μ during this exponential phase is nearest to: **[2 marks]**



(A) 0.10 h^{-1}

(B) 0.69 h^{-1}

(C) 0.46 h^{-1}

(D) 0.23 h^{-1}

Q33. A chemostat has a constant working volume of 5 L and is fed with sterile medium at a volumetric flow rate of 1.5 L h^{-1}. The dilution rate at which the vessel operates is: **[2 marks]**

(A) 3.33 h^{-1}

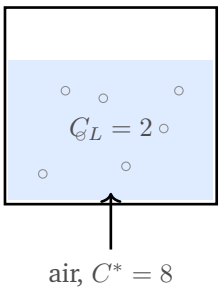
(B) 0.60 h^{-1}

(C) 0.30 h^{-1}

(D) 1.50 h^{-1}

Q34. In the aerobic fermenter shown, oxygen passes from the sparged gas bubbles into the broth. The volumetric mass-transfer coefficient is $k_La = 100$ h^{-1}, the saturation dissolved-oxygen concentration is $C^* = 8$ mg L^{-1}

and the actual dissolved-oxygen level is $C_L = 2$ mg L^{-1}. The oxygen transfer rate (OTR) is: [2 marks]



(A) 600 mg $L^{-1}h^{-1}$

(B) 800 mg $L^{-1}h^{-1}$

(C) 200 mg $L^{-1}h^{-1}$

(D) 100 mg $L^{-1}h^{-1}$

Q35. When an aerobic stirred-tank fermentation is scaled up from the laboratory to production size, one criterion is very commonly held constant so that the oxygen-transfer capability of the large vessel matches that of the small one. This criterion is constant: [2 marks]

(A) impeller rotational speed

(B) power input per unit liquid volume (P/V)

(C) medium temperature only

(D) total power drawn by the motor

Q36. Continuous (high-temperature, short-time) sterilisation of fermentation medium is often preferred over batch sterilisation of the same medium. The principal advantage of the continuous route is that it causes: [2 marks]

(A) a much higher energy consumption in every case

(B) greater destruction of heat-sensitive nutrients

(C) less thermal damage to nutrients, because the hold time at high temperature is short

(D) no requirement for any heating at all

Q37. A fed-batch mode, in which fresh substrate is metered into the bioreactor gradually during the run, is chosen in preference to a simple batch when the aim is to: [2 marks]

(A) keep the substrate concentration low so as to avoid substrate inhibition or overflow metabolism

(B) withdraw all of the product continuously

(C) hold the culture permanently at zero growth

(D) sterilise the medium more rapidly

Q38. A bioreactor is filled with a solid support (such as beads or a matrix) that carries immobilised enzyme or cells, and the substrate solution is pumped through this fixed bed. This reactor configuration is a/an: [2 marks]

(A) chemostat

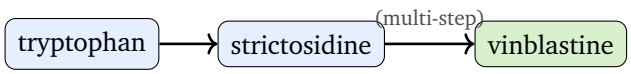
(B) packed-bed reactor

(C) airlift reactor

(D) conventional stirred-tank reactor

Plant and Animal Biotechnology

Q39. Cell-suspension cultures are grown commercially to obtain the anticancer alkaloids vincristine and vinblastine, whose simplified biosynthetic route from a common precursor is sketched below. These valuable terpenoid indole alkaloids are secondary metabolites of the plant: [2 marks]



(A) *Escherichia coli*

(B) *Catharanthus roseus* (Madagascar periwinkle)

(C) *Rhizobium leguminosarum*

(D) baker's yeast (*Saccharomyces cerevisiae*)

Q40. Plant secondary metabolites such as alkaloids, terpenoids and phenolic compounds are not required for the basic growth and metabolism of the plant. Their principal biological role is to: [2 marks]

(A) carry out photosynthesis

(B) serve as the plant's primary energy-storage molecules

(C) replicate the nuclear DNA

(D) defend the plant and mediate ecological interactions (against herbivores, pathogens and competitors)

Q41. Fast-growing, highly branched cultures that produce secondary metabolites and grow on hormone-free medium can be induced by infecting plant tissue with *Agrobacterium rhizogenes*, whose Ri plasmid transforms the cells. The transformed cultures obtained in this way are called: [2 marks]

(A) callus cultures only

(B) isolated protoplasts

(C) somatic embryos

(D) hairy-root cultures

Q42. Transgenic farm animals can be engineered so that a valuable therapeutic protein (for example a human blood-clotting factor) is secreted in their milk, from which it is then purified. Using such animals as living factories for recombinant proteins is known as molecular pharming, and the animals are described as living: [2 marks]

(A) xenografts

(B) bioreactors (gene pharming / molecular pharming)

(C) clones, and nothing more

(D) hybridomas

Q43. To raise the yield of a desired secondary metabolite, a plant cell culture is deliberately treated with a signalling agent such as a fungal cell-wall

extract or methyl jasmonate, which switches on the relevant biosynthetic pathway. This strategy of stimulating secondary-metabolite production is called: [2 marks]

(A) somaclonal variation

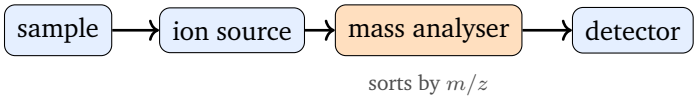
(B) elicitation

(C) micropropagation

(D) hardening

Analytical Techniques

Q44. The block diagram below shows the main stages of a mass spectrometer: the sample is ionised, the ions are sorted in the analyser, and they strike a detector. In the analyser, the gas-phase ions are separated according to their: [2 marks]



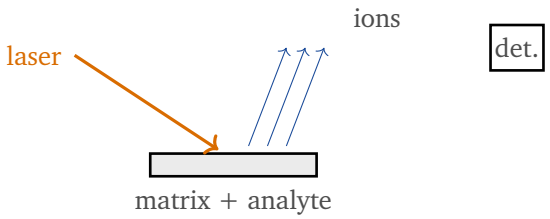
(A) physical size alone

(B) net charge alone

(C) mass-to-charge ratio (m/z)

(D) isoelectric point (pI)

Q45. The soft-ionisation technique sketched below embeds the analyte in a solid, light-absorbing matrix and fires a pulsed laser at the spot; the desorbed ions are then accelerated down a flight tube and timed. This technique, widely used for protein and peptide mass fingerprinting, is: [2 marks]



(A) gas chromatography (GC)

(B) MALDI (matrix-assisted laser desorption/ionisation)

(C) nuclear magnetic resonance (NMR)

(D) ultraviolet–visible (UV–Vis) spectroscopy

Q46. A purified protein solution is read in a spectrophotometer at 280 nm using a cuvette of path length 1 cm, giving an absorbance of 0.90. If the molar absorptivity of the protein at this wavelength is $45000\ \text{M}^{-1}\text{cm}^{-1}$, then by the Beer–Lambert law $A = \varepsilon\, c\, l$ the molar concentration of the protein is: **[2 marks]**

(A) 2×10^{-4} M

(B) 4.5×10^{-4} M

(C) 2×10^{-6} M

(D) 2×10^{-5} M

Detailed Solutions

Q1.

Solution

Concept – vitamins as coenzyme precursors: Several B-group vitamins are the chemical starting materials from which cells build essential coenzymes.

Step 1 – identify the coenzyme: FAD (flavin adenine dinucleotide) is a flavin coenzyme; its reactive part is the flavin (isoalloxazine) ring.

Step 2 – trace the vitamin source: The flavin ring is supplied by **riboflavin (vitamin B_2)**, which is first converted to FMN and then to FAD.

Step 3 – confirm the role: FAD/FMN accept a pair of electrons (and protons) in oxidation–reduction reactions such as the succinate-to-fumarate step of the citric acid cycle.

Why the other options are wrong:

- A, niacin: is the precursor of $NAD^+/NADP^+$, not FAD.
- B, thiamine: gives rise to thiamine pyrophosphate.
- D, pyridoxine: gives rise to pyridoxal phosphate.

Final Answer: riboflavin (vitamin B_2) $\Rightarrow$ C

Answer: (C) Go Back to Q1

Q2.

Solution

Concept – coenzyme A and its vitamin core: Coenzyme A carries acyl groups through a reactive thiol ($-SH$) end, and its backbone is built around a specific vitamin.

Step 1 – recall the structure of CoA: Coenzyme A is assembled from adenosine-3',5'-bisphosphate, pantothenic acid and β-mercaptoethylamine.

Step 2 – pick out the vitamin: The central unit of that chain is **pantothenic acid (vitamin B_5)**.

Step 3 – link to function: Acyl groups attach to the terminal $-SH$ of CoA (for example forming acetyl-CoA), so a shortage of vitamin B_5 impairs acyl-transfer metabolism.

Why the other options are wrong:

- A, biotin: is the carboxyl-carrying coenzyme of carboxylases.
- B, folic acid: gives tetrahydrofolate for one-carbon transfers.
- C, cobalamin: is the coenzyme for certain isomerase/methyl-transfer reactions.

Final Answer: pantothenic acid (vitamin B_5) $\Rightarrow$ D

Answer: (D) Go Back to Q2

Q3.

Solution

Concept – the Michaelis–Menten rate law: $v = \dfrac{V_{\max}\,[S]}{K_m + [S]}$ gives the initial velocity for a given substrate concentration.

Step 1 – list the data: $V_{\max} = 80\ \mu$mol min^{-1}, $K_m = 4$ mM, $[S] = 12$ mM.

Step 2 – substitute into the equation: $v = \dfrac{80 \times 12}{4 + 12}$

Step 3 – evaluate the denominator: $4 + 12 = 16$

Step 4 – evaluate the numerator: $80 \times 12 = 960$

Step 5 – complete the arithmetic: $v = \dfrac{960}{16} = 60\ \mu$mol min^{-1}

Step 6 – sanity check: Since $[S] = 3K_m$, the fraction $[S]/(K_m + [S]) = 12/16 = 0.75$, so $v = 0.75\,V_{\max} = 60$, which agrees.

Final Answer: $v = 60\ \mu$mol min^{-1} $\Rightarrow$ A

Answer: (A) Go Back to Q3

Q4.

Solution

Concept – thiamine and its coenzyme: Thiamine pyrophosphate (TPP) is the active coenzyme form of a specific vitamin and is needed for decarboxylation of α-keto acids.

Step 1 – name the parent vitamin: TPP is made from **thiamine (vitamin B_1)** by transfer of a pyrophosphate group.

Step 2 – state where it acts: TPP is the coenzyme of the pyruvate-dehydrogenase and α-ketoglutarate-dehydrogenase complexes and of transketolase.

Step 3 – link to deficiency: A lack of vitamin B_1 impairs these reactions and causes beriberi, underlining that thiamine is the source of TPP.

Why the other options are wrong:

- A, riboflavin: gives FAD/FMN.
- B, niacin: gives NAD^+/$NADP^+$.
- D, pyridoxine: gives pyridoxal phosphate.

Final Answer: thiamine (vitamin B_1) $\Rightarrow$ C

Answer: (C) Go Back to Q4

Q5.

Solution

Concept – pyridoxal phosphate in amino-acid metabolism: PLP is the coenzyme that carries the amino group during transamination, and it comes from one particular vitamin.

Step 1 – name the parent vitamin: Pyridoxal phosphate is derived from **pyridoxine (vitamin B_6)**.

Step 2 – describe the reaction it serves: In transamination, PLP forms a Schiff base with the substrate and shuttles the $-NH_2$ group between an amino acid and an α-keto acid.

Step 3 – broaden the role: PLP is also the coenzyme for decarboxylations and racemisations of amino acids, so vitamin B_6 is central to amino-acid metabolism.

Why the other options are wrong:

- A, thiamine: gives TPP for keto-acid decarboxylation.
- B, riboflavin: gives FAD.
- C, niacin: gives the nicotinamide nucleotides.

Final Answer: pyridoxine (vitamin B_6) $\Rightarrow$ D

Answer: (D) Go Back to Q5

Q6.

Solution

Concept – the Lineweaver–Burk straight line: Inverting the Michaelis–Menten equation gives $\frac{1}{v} = \frac{K_m}{V_{\max}} \cdot \frac{1}{[S]} + \frac{1}{V_{\max}}$, which has the form $y = mx + c$.

Step 1 – identify the variables: Here $y = 1/v$ and $x = 1/[S]$.

Step 2 – read off the slope: The coefficient of x is the slope, $m = \dfrac{K_m}{V_{\max}}$.

Step 3 – read off the intercepts (for contrast): The y-intercept is $\dfrac{1}{V_{\max}}$ and the x-intercept is $-\dfrac{1}{K_m}$.

Step 4 – match to the options: The requested slope is $\dfrac{K_m}{V_{\max}}$.

Why the other options are wrong:

- A, $1/V_{\max}$: is the y-intercept, not the slope.
- B, $-1/K_m$: is the x-intercept.
- C, $1/K_m$: is neither intercept nor slope of this line.

Final Answer: slope $= \dfrac{K_m}{V_{\max}} \Rightarrow$ D

Answer: (D) Go Back to Q6

Q7.

Solution

Concept – the microbial nitrogen cycle: Nitrogen passes between N_2, ammonia, nitrite and nitrate through distinct microbial transformations.

Step 1 – read the step described: Ammonia is oxidised first to nitrite ($NH_3 \rightarrow NO_2^-$) and then to nitrate ($NO_2^- \rightarrow NO_3^-$).

Step 2 – name the process: This aerobic oxidation of ammonia to nitrate by chemoautotrophs is **nitrification**.

Step 3 – name the organisms: *Nitrosomonas* performs the first step and *Nitrobacter* the second, using the energy released to fix CO_2.

Why the other options are wrong:

- B, denitrification: reduces nitrate back to N_2, the reverse direction.
- C, nitrogen fixation: converts N_2 to ammonia.
- D, ammonification: releases ammonia from organic nitrogen.

Final Answer: nitrification $\Rightarrow$ A

Answer: (A) Go Back to Q7

Q8.

Solution

Concept – biological nitrogen fixation: Reducing the very stable N $\equiv$ N triple bond to ammonia requires a specialised enzyme and a large input of ATP.

Step 1 – write the reaction: $N_2 + 8H^+ + 8e^- + 16\,ATP \rightarrow 2NH_3 + H_2 + 16\,ADP + 16\,P_i$.

Step 2 – name the catalyst: This reduction is catalysed by **nitrogenase**, a two-component metalloenzyme (Fe protein plus MoFe protein).

Step 3 – note its oxygen sensitivity: Nitrogenase is irreversibly inactivated by oxygen, which is why diazotrophs protect it (for example inside heterocysts or root nodules).

Why the other options are wrong:

- A, nitrate reductase: reduces nitrate, not N_2.
- C, urease: hydrolyses urea to ammonia and CO_2.
- D, catalase: breaks down hydrogen peroxide.

Final Answer: nitrogenase $\Rightarrow$ B

Answer: (B) Go Back to Q8

Q9.

Solution

Concept – symbiotic nitrogen fixation in legumes: Some bacteria fix nitrogen only in partnership with a host plant, inside specially formed root structures.

Step 1 – read the clues: The bacterium invades root hairs, induces *root nodules* and fixes nitrogen in a mutualism with a legume.

Step 2 – identify the genus: This is ***Rhizobium***, the classic legume-nodulating diazotroph.

Step 3 – note the exchange: The plant supplies carbon and a low-oxygen, leghaemoglobin-buffered environment; the bacteroids supply fixed ammonia.

Why the other options are wrong:

- A, *Nitrosomonas*: is a nitrifier, not a nitrogen fixer.
- B, *Azotobacter*: fixes nitrogen but is free-living, not nodule-forming.
- D, *Clostridium*: is a free-living anaerobic fixer, not symbiotic.

Final Answer: *Rhizobium* $\Rightarrow$ C

Answer: (C) Go Back to Q9

Q10.

Solution

Concept – counting generations in exponential growth: The number of doublings is $n = \log_2\left(\frac{X}{X_0}\right) = \frac{\ln(X/X_0)}{\ln 2}$.

Step 1 – list the data: $X_0 = 10^2$, $X = 10^8$, time $= 3$ h.

Step 2 – find the fold increase: $\frac{X}{X_0} = \frac{10^8}{10^2} = 10^6$

Step 3 – take the log base 2: $n = \log_2(10^6) = 6 \times \log_2(10) = 6 \times 3.322$

Step 4 – evaluate: $n \approx 19.93$

Step 5 – round to the nearest option: $n \approx 20$ generations.

Final Answer: ≈ 20 generations $\Rightarrow$ A

Answer: (A) Go Back to Q10

Q11.

Solution

Concept – returning nitrogen to the atmosphere: Under low-oxygen conditions some microbes respire using nitrate instead of oxygen, reducing it to gaseous nitrogen.

Step 1 – follow the reduction sequence: $NO_3^- \rightarrow NO_2^- \rightarrow NO \rightarrow N_2O \rightarrow N_2$.

Step 2 – name the process: This anaerobic reduction of nitrate to N_2 gas is **denitrification**.

Step 3 – note its ecological effect: It removes fixed nitrogen from the soil and releases it to the air, closing the nitrogen cycle (but also lowering soil fertility).

Why the other options are wrong:

- A, nitrification: oxidises ammonia to nitrate (opposite direction).
- B, ammonification: converts organic N to ammonia.
- D, assimilation: incorporates inorganic N into biomass.

Final Answer: denitrification $\Rightarrow$ C

Answer: (C) Go Back to Q11

Q12.

Solution

Concept – apoptosis versus other forms of cell death: Apoptosis is a neat, regulated "cell suicide" distinct from the messy, accidental death of necrosis.

Step 1 – match the described features: Caspase activation, chromatin condensation, membrane blebbing and formation of apoptotic bodies are the hallmarks of **apoptosis**.

Step 2 – note the absence of inflammation: Because the cell is packaged into membrane-bound bodies and cleared by phagocytes, no contents leak out and there is no inflammation.

Why the other options are wrong:

- B, necrosis: cells swell and burst, spilling contents and causing inflammation.
- C, autophagy: is self-digestion of components for recycling, not primarily a death programme.
- D, mitosis: is cell division, not cell death.

Final Answer: apoptosis $\Rightarrow$ A

Answer: (A) Go Back to Q12

Q13.

Solution

Concept – driving the cell cycle past its checkpoints: Progression through the cycle is controlled by enzymes whose activity rises and falls in a set order.

Step 1 – identify the control enzymes: The engines of the cycle are the **cyclin-dependent kinases (CDKs)**, which are active only when bound to their partner cyclins.

Step 2 – apply to the G1/S restriction point: Rising cyclin D– and cyclin E–CDK activity phosphorylates the retinoblastoma protein (Rb), releasing E2F and committing the cell to S phase.

Step 3 – state the answer: So passage through the highlighted G1/S checkpoint is driven by cyclin–CDK complexes.

Why the other options are wrong:

- A, p53 alone: is a brake that can *halt* the cycle at damage, not the positive driver of the transition.

- B, DNA ligase: seals DNA nicks and does not regulate the checkpoint.
- D, telomerase: extends chromosome ends and is unrelated to this switch.

Final Answer: cyclin–CDK complexes $\Rightarrow$ C

Answer: (C) Go Back to Q13

Q14.

Solution

Concept – the intrinsic apoptotic pathway: Internal stresses converge on the mitochondrion, which releases a signal that switches on the caspase cascade.

Step 1 – follow the pathway: Pro-apoptotic Bcl-2-family proteins permeabilise the outer mitochondrial membrane.

Step 2 – name the released molecule: This releases **cytochrome** c from the intermembrane space into the cytosol.

Step 3 – state the downstream effect: Cytosolic cytochrome c binds Apaf-1 to build the apoptosome, which activates caspase-9 and then the executioner caspases.

Why the other options are wrong:

- A, calcium ions: modulate many pathways but are not the apoptosome trigger released here.
- B, ATP: is a cofactor of apoptosome assembly, not the signal released from the mitochondrion.
- D, glucose: is a metabolite with no role in triggering apoptosis.

Final Answer: cytochrome c $\Rightarrow$ C

Answer: (C) Go Back to Q14

Q15.

Solution

Concept – the "guardian of the genome": One tumour-suppressor protein integrates DNA-damage signals and decides between repair and death.

Step 1 – match the description: Sensing DNA damage, arresting the cycle for repair, or ordering apoptosis, and the nickname "guardian of the genome", all point to **p53**.

Step 2 – state its mechanism: Activated p53 is a transcription factor that switches on genes such as *p21* (cell-cycle arrest) and pro-apoptotic genes.

Step 3 – note its clinical importance: The *TP53* gene is mutated in a large fraction of human cancers, removing this safeguard.

Why the other options are wrong:

- B, Ras: is a proto-oncogene that promotes proliferation.
- C, Myc: is a proliferation-driving transcription factor.
- D, cyclin B: drives entry into mitosis and is not a DNA-damage guardian.

Final Answer: p53 $\Rightarrow$ A

Answer: (A) Go Back to Q15

Q16.

Solution

Concept – the stages of mitosis: Mitosis proceeds as prophase, metaphase, anaphase and telophase, each marked by a characteristic chromosome movement.

Step 1 – read the key event: Sister chromatids lose their cohesion and are pulled toward opposite poles.

Step 2 – name the stage: This separation and poleward movement of chromatids defines **anaphase**.

Step 3 – fit the neighbours: It follows metaphase (chromosomes aligned at the equator) and precedes telophase (nuclei re-forming at each pole).

Why the other options are wrong:

- A, metaphase: chromosomes are lined up but not yet separated.
- C, prophase: chromosomes condense and the spindle forms.
- D, telophase: chromatids have already reached the poles and nuclei reassemble.

Final Answer: anaphase $\Rightarrow$ B

Answer: (B) Go Back to Q16

Q17.

Solution

Concept – Chargaff's base-pairing rules: In double-stranded DNA, $\%A = \%T$ and $\%G = \%C$, and all four must sum to 100%.

Step 1 – use the given value: $\%A = 30$, so $\%T = 30$ as well.

Step 2 – find the combined G+C: $\%A + \%T + \%G + \%C = 100$

$30 + 30 + \%G + \%C = 100$

$\%G + \%C = 40$

Step 3 – split G and C equally: Since $\%G = \%C$, each is half of 40: $\%G = \frac{40}{2} = 20$

Step 4 – state the result: $\%G = 20\%$.

Final Answer: $\%G = 20\% \Rightarrow \boxed{\text{B}}$

Answer: (B) Go Back to Q17

Q18.

Solution

Concept – processing of eukaryotic pre-mRNA: A primary transcript must be modified before it can be translated: capping, splicing and polyadenylation.

Step 1 – read the event described: Introns are excised and exons are joined together.

Step 2 – name the step: This cutting-and-joining is **splicing**, carried out by the spliceosome (snRNPs).

Step 3 – note the outcome: The mature mRNA now contains only the continuous coding information of the joined exons.

Why the other options are wrong:

- A, $5'$ capping: adds a 7-methylguanosine cap to the $5'$ end.
- B, polyadenylation: adds a poly(A) tail at the $3'$ end.
- C, transcription: is the synthesis of the RNA itself, before this processing.

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

Answer: (D) Go Back to Q18

Q19.

Solution

Concept – classes of vaccine: Vaccines differ by what form of the pathogen or antigen they present to the immune system.

Step 1 – read the description: The pathogen is whole and still able to replicate weakly, but its virulence has been reduced.

Step 2 – name the type: A weakened but living pathogen defines a **live attenuated vaccine** (for example BCG and oral polio).

Step 3 – note the advantage: Because the organism replicates a little, it usually gives strong, long-lasting humoral and cell-mediated immunity from a single dose.

Why the other options are wrong:

- B, toxoid vaccine: uses an inactivated bacterial toxin, not a live organism.
- C, subunit vaccine: uses only a purified antigen fragment.
- D, DNA vaccine: delivers a gene encoding the antigen, not the live pathogen.

Final Answer: live attenuated vaccine $\Rightarrow$ A

Answer: (A) Go Back to Q19

Q20.

Solution

Concept – active versus passive immunity: Immunity is "active" when the body makes its own antibodies and "passive" when ready-made antibodies are supplied from outside.

Step 1 – read the scenario: The patient receives pre-formed anti-tetanus antibodies (antiserum) directly.

Step 2 – classify the immunity: Because protection comes from externally supplied antibodies, this is **passive immunity**.

Step 3 – note its properties: Passive immunity acts immediately but is short-lived, since no memory cells are generated in the recipient.

Why the other options are wrong:

- A, active immunity: would require the patient's own response, as after vaccination or infection.
- C, innate immunity: is the non-specific first line of defence, not antibody transfer.

- D, autoimmunity: is a harmful response against self, not protection.

Final Answer: passive immunity $\Rightarrow$ B

Answer: (B) Go Back to Q20

Q21.

Solution

Concept – the enzyme label in a sandwich ELISA: In ELISA the detection antibody carries an enzyme that turns a colourless substrate into a coloured product, giving a signal proportional to antigen amount.

Step 1 – recall the common reporter enzymes: The two enzymes routinely conjugated to detection antibodies are horseradish peroxidase and alkaline phosphatase.

Step 2 – pick the option offered: Among the choices, **horseradish peroxidase (HRP)** is the standard ELISA reporter; with a substrate such as TMB it produces a blue colour.

Step 3 – link colour to concentration: More antigen means more bound detection antibody, more enzyme, and a deeper colour read as higher absorbance.

Why the other options are wrong:

- B, DNA polymerase: synthesises DNA and gives no colorimetric antigen signal.
- C, nitrogenase: fixes nitrogen and is unrelated to ELISA.
- D, lysozyme: cleaves bacterial cell walls and is not a reporter enzyme.

Final Answer: horseradish peroxidase (HRP) $\Rightarrow$ A

Answer: (A) Go Back to Q21

Q22.

Solution

Concept – Hardy–Weinberg genotype frequencies: For two alleles with frequencies p and q, the genotype frequencies are p^2 (dominant homozygote), $2pq$ (heterozygote) and q^2 (recessive homozygote).

Step 1 – link the recessive homozygote to q: Frequency of $aa = q^2$.

Step 2 – substitute the data: $q^2 = 0.09$

Step 3 – solve for q: $q = \sqrt{0.09}$

Step 4 – evaluate: $q = 0.3$

Step 5 – sanity check: Then $p = 1 - 0.3 = 0.7$, and $p^2 + 2pq + q^2 = 0.49 + 0.42 + 0.09 = 1.00$, so the values are consistent.

Final Answer: $q = 0.3 \Rightarrow$ A

Answer: (A) Go Back to Q22

Q23.

Solution

Concept – the immunoglobulin of the primary response: Different antibody classes appear at different times; one is the earliest marker of a new infection.

Step 1 – recall the timing: In a primary response, **IgM** is synthesised and secreted first, before class switching to IgG.

Step 2 – use its structure: Secreted IgM is a pentamer with high avidity, effective early even at low affinity.

Step 3 – apply as a marker: Because it appears early and does not persist long, detecting antigen-specific IgM signals a recent or acute infection.

Why the other options are wrong:

- A, IgG: dominates the later, secondary response and long-term memory.
- C, IgA: guards mucosal surfaces and secretions.
- D, IgE: is involved in allergy and anti-parasite responses.

Final Answer: IgM $\Rightarrow$ B

Answer: (B) Go Back to Q23

Q24.

Solution

Concept – random change in allele frequencies: Evolution can occur without selection when chance alone alters which alleles are passed on, especially in small populations.

Step 1 – read the description: Allele frequencies change from generation to generation purely by random sampling of gametes, with no fitness differences involved.

Step 2 – name the mechanism: This is **genetic drift**.

Step 3 – note its effects: Drift is strongest in small populations and can fix or lose alleles by chance, reducing genetic variation (as in bottleneck and founder effects).

Why the other options are wrong:

- A, natural selection: acts on fitness differences, which are explicitly excluded here.
- B, gene flow: is the movement of alleles between populations by migration.
- C, mutation pressure: is the introduction of new alleles, not random sampling of existing ones.

Final Answer: genetic drift $\Rightarrow$ D

Answer: (D) Go Back to Q24

Q25.

Solution

Concept – choosing a host for recombinant protein production: The ideal expression host balances growth rate, cost, ease of genetic manipulation and the ability to fold and modify the protein.

Step 1 – match the stated requirements: Rapid growth on cheap media, very well-known genetics, but no glycosylation, all describe a bacterium.

Step 2 – name the host: This is ***Escherichia coli***, the workhorse for simple, non-glycosylated recombinant proteins (for example recombinant insulin).

Step 3 – note the limitation: Because *E. coli* cannot add glycan chains or perform many eukaryotic modifications, glycoproteins are instead made in yeast or mammalian cells.

Why the other options are wrong:

- B, human liver cells: grow slowly and are costly, though they glycosylate well.
- C, tobacco leaf: is used in plant molecular farming but is not the low-cost first choice described.
- D, silkworm larvae: are a baculovirus-based system, more complex than bacterial culture.

Final Answer: *Escherichia coli* $\Rightarrow$ A

Answer: (A) Go Back to Q25

Q26.

Solution

Concept – inducible bacterial expression: Strong recombinant expression is usually kept off until the culture is dense, then switched on by an inducer.

Step 1 – identify the inducer: IPTG is a non-metabolisable lactose analogue that relieves *lac* repression.

Step 2 – name the promoter system: IPTG-controlled expression uses the **T7/*lac* promoter system**, in which IPTG switches on T7 RNA polymerase, which then drives the cloned gene.

Step 3 – explain the strategy: Cells are grown to high density with the gene silent (avoiding toxicity), then IPTG is added to trigger a burst of protein synthesis.

Why the other options are wrong:

- A, SV40 promoter: drives expression in mammalian cells.
- C, CaMV 35S promoter: is a constitutive plant promoter.
- D, nos promoter: is used in plant transformation, not IPTG-induced bacterial expression.

Final Answer: T7/*lac* promoter system $\Rightarrow$ B

Answer: (B) Go Back to Q26

Q27.

Solution

Concept – cutting a linear DNA at internal sites: On a *linear* molecule, k cuts give $k+1$ fragments; the fragment sizes are the distances between successive cut points and the two ends.

Step 1 – list the data: Length $= 10$ kb; sites at 2 kb and 7 kb from the left end.

Step 2 – fragment from the left end to the first site: $2 - 0 = 2$ kb.

Step 3 – fragment between the two sites: $7 - 2 = 5$ kb.

Step 4 – fragment from the second site to the right end: $10 - 7 = 3$ kb.

Step 5 – state the three fragments: 2 kb, 5 kb and 3 kb (two cuts on a linear molecule give three pieces).

Step 6 – check the sum: $2 + 5 + 3 = 10$ kb, the full length, so the accounting is

complete.

Final Answer: 2 kb, 5 kb and 3 kb $\Rightarrow$ C

Answer: (C) Go Back to Q27

Q28.

Solution

Concept – affinity purification with a His-tag: A short peptide tag lets a recombinant protein be pulled out of a crude mixture by specific binding to an immobilised ligand.

Step 1 – read the tag and ligand: Six histidines bind tightly to immobilised Ni^{2+} ions.

Step 2 – name the method: This is **nickel-affinity chromatography**, a form of immobilised-metal affinity chromatography (IMAC).

Step 3 – describe the elution: Contaminants wash through, and the His-tagged protein is then released by imidazole, which competes for the nickel.

Why the other options are wrong:

- A, gel filtration: separates by size, not by a specific tag.
- B, ion exchange: separates by net charge.
- C, SDS–PAGE: is an analytical size separation, not a preparative capture step.

Final Answer: nickel-affinity (IMAC) chromatography $\Rightarrow$ D

Answer: (D) Go Back to Q28

Q29.

Solution

Concept – the meaning of the BLAST E-value: The E-value is the number of alignments as good as (or better than) the observed one that would be expected purely by chance in a database of that size.

Step 1 – interpret a small E-value: A very small E-value means almost no such match is expected by chance.

Step 2 – apply the number: $E \approx 1 \times 10^{-50}$ is extremely small, so the alignment is **highly significant and very unlikely to be random**.

Step 3 – draw the biological conclusion: Such a hit strongly suggests genuine homology (shared ancestry or conserved function) between query and subject.

Why the other options are wrong:

- A, random: describes a *large* E-value, the opposite case.
- B, sequencing artefact: is not what the E-value measures.
- C, no similarity: contradicts a strong, low-E alignment.

Final Answer: highly significant, unlikely by chance $\Rightarrow$ D

Answer: (D) Go Back to Q29

Q30.

Solution

Concept – why cDNA is used for eukaryotic genes in bacteria: Eukaryotic genes contain introns that must be removed, but bacteria lack the machinery to do so.

Step 1 – recall the difference: Genomic eukaryotic DNA has exons interrupted by introns; the mature mRNA has the introns already spliced out.

Step 2 – identify the bacterial limitation: *E. coli* has no spliceosome, so it **cannot remove introns** from a transcript.

Step 3 – state the solution: Reverse-transcribing the mature mRNA gives intron-free cDNA, which the bacterium can transcribe and translate into the correct protein.

Why the other options are wrong:

- B, translate mRNA: bacteria translate mRNA readily.
- C, replicate plasmids: bacteria replicate plasmid vectors well.
- D, form peptide bonds: bacterial ribosomes form peptide bonds normally.

Final Answer: it cannot splice out introns $\Rightarrow$ A

Answer: (A) Go Back to Q30

Q31.

Solution

Concept – gas-driven (pneumatic) bioreactors: Some bioreactors mix and aerate the broth using the sparged gas itself rather than a stirrer, which lowers shear.

Step 1 – read the design cues: No impeller; air sparged at the base of a draft tube; broth rises on the gassed side and falls on the ungassed side; gentle circulation for shear-sensitive cells.

Step 2 – name the reactor: These features define an **airlift bioreactor**, in which the density difference between gassed and ungassed liquid drives a loop flow.

Step 3 – note the benefit: Because there is no high-shear impeller, airlift designs suit fragile plant, animal and mycelial cultures.

Why the other options are wrong:

- A, stirred-tank: uses a mechanical impeller for mixing.
- B, packed-bed: holds a fixed bed of solid support with liquid pumped through it.
- D, membrane bioreactor: separates biomass with a membrane and is defined by that filtration step.

Final Answer: airlift bioreactor $\Rightarrow$ C

Answer: (C) Go Back to Q31

Q32.

Solution

Concept – specific growth rate in exponential batch culture: For $X = X_0 e^{\mu t}$, the specific growth rate is $\mu = \dfrac{1}{t}\ln\dfrac{X}{X_0}$.

Step 1 – list the data: $X_0 = 2$ g L^{-1}, $X = 16$ g L^{-1}, $t = 9$ h.

Step 2 – form the ratio: $\dfrac{X}{X_0} = \dfrac{16}{2} = 8$

Step 3 – take the natural log: $\ln 8 = \ln 2^3 = 3\ln 2 = 3 \times 0.693 = 2.079$

Step 4 – divide by the time: $\mu = \dfrac{2.079}{9}$

Step 5 – evaluate: $\mu \approx 0.231$ h^{-1} ≈ 0.23 h^{-1}

Final Answer: $\mu \approx 0.23$ h^{-1} $\Rightarrow$ D

Answer: (D) Go Back to Q32

Q33.

Solution

Concept – dilution rate of a chemostat: The dilution rate is the feed flow rate divided by the working volume, $D = \dfrac{F}{V}$.

Step 1 – list the data: $F = 1.5$ L h^{-1}, $V = 5$ L.

Step 2 – substitute: $D = \dfrac{1.5}{5}$

Step 3 – evaluate: $D = 0.30\ \text{h}^{-1}$

Step 4 – check the units: $\dfrac{\text{L h}^{-1}}{\text{L}} = \text{h}^{-1}$, a reciprocal time, as a dilution rate should be.

Final Answer: $D = 0.30\ \text{h}^{-1} \Rightarrow \boxed{\text{C}}$

Answer: (C) Go Back to Q33

Q34.

Solution

Concept – oxygen transfer rate in an aerobic bioreactor: OTR $= k_L a\,(C^* - C_L)$, the product of the volumetric mass-transfer coefficient and the concentration driving force.

Step 1 – list the data: $k_L a = 100\ \text{h}^{-1}$, $C^* = 8\ \text{mg L}^{-1}$, $C_L = 2\ \text{mg L}^{-1}$.

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

Step 3 – multiply: OTR $= 100 \times 6$

Step 4 – evaluate: OTR $= 600\ \text{mg L}^{-1}\text{h}^{-1}$

Step 5 – check the units: $\text{h}^{-1} \times \text{mg L}^{-1} = \text{mg L}^{-1}\text{h}^{-1}$, the correct rate unit.

Final Answer: OTR $= 600\ \text{mg L}^{-1}\text{h}^{-1} \Rightarrow \boxed{\text{A}}$

Answer: (A) Go Back to Q34

Q35.

Solution

Concept – scale-up criteria for aerobic fermenters: When enlarging a fermenter, engineers keep one parameter constant so that oxygen supply on the large scale matches the small scale.

Step 1 – link oxygen transfer to power: The mass-transfer coefficient $k_L a$ correlates strongly with the power delivered to the broth per unit volume and the gas flow.

Step 2 – state the usual criterion: The most common scale-up rule is **constant power input per unit volume (P/V)**, which tends to preserve $k_L a$.

Step 3 – explain why others fail: Holding impeller speed or total power constant does not keep P/V (and hence oxygen transfer) the same across very different volumes.

Why the other options are wrong:

- A, constant impeller speed: gives very different power densities at different scales.
- C, temperature only: does not address oxygen transfer.
- D, total power: a fixed total power is spread thin in a large vessel, lowering P/V.

Final Answer: constant $P/V \Rightarrow$ B

Answer: (B) Go Back to Q35

Q36.

Solution

Concept – continuous versus batch sterilisation of media: Killing microbes and degrading nutrients both speed up with temperature, but killing is far more temperature-sensitive, favouring brief high-temperature treatment.

Step 1 – compare the thermal histories: Batch sterilisation heats the whole tank slowly and holds it hot for a long time; continuous sterilisation exposes the medium to high temperature only briefly.

Step 2 – state the consequence: The short hold time of continuous sterilisation means **less thermal damage to heat-sensitive nutrients** while still achieving the required kill.

Step 3 – give the reason: Because sterilisation has a higher activation energy than nutrient destruction, high-temperature short-time processing kills spores efficiently with minimal nutrient loss.

Why the other options are wrong:

- A, higher energy always: continuous sterilisation usually recovers heat and is not necessarily more energy-intensive.
- B, greater nutrient destruction: is the drawback of *batch*, not continuous, sterilisation.
- D, no heating at all: sterilisation still requires heat.

Final Answer: less thermal damage to nutrients $\Rightarrow$ C

Answer: (C) Go Back to Q36

Q37.

Solution

Concept – why fed-batch is chosen: In fed-batch operation the substrate is supplied gradually rather than all at once, letting the operator hold its concentration in a favourable range.

Step 1 – identify the problem being solved: A high initial substrate concentration can inhibit growth or trigger wasteful overflow metabolism (for example acetate or ethanol formation).

Step 2 – state the fed-batch benefit: By metering substrate in slowly, fed-batch **keeps the substrate concentration low**, avoiding inhibition and overflow while sustaining high cell densities.

Step 3 – give an example: This is why baker's yeast and many recombinant-protein fermentations are run fed-batch on a controlled glucose feed.

Why the other options are wrong:

- B, withdraw all product: describes continuous operation, not fed-batch.
- C, zero growth: is not the aim; fed-batch supports active growth.
- D, faster sterilisation: is unrelated to the feeding strategy.

Final Answer: to keep substrate low and avoid inhibition/overflow $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q37

Q38.

Solution

Concept – reactors with immobilised biocatalyst: Enzymes or cells fixed on a solid support can be packed into a column through which substrate flows, allowing reuse of the biocatalyst.

Step 1 – read the configuration: A fixed bed of solid support carrying immobilised enzyme/cells, with substrate pumped through it.

Step 2 – name the reactor: This is a **packed-bed reactor** (also called a fixed-bed reactor).

Step 3 – note its use: Packed-bed reactors are common for continuous biotransformations (for example immobilised glucose isomerase producing high-fructose syrup).

Why the other options are wrong:

- A, chemostat: is a well-mixed continuous *suspension* culture, not a fixed bed.
- C, airlift: circulates a suspension using sparged gas.
- D, stirred-tank: mixes a suspension with an impeller.

Final Answer: packed-bed reactor $\Rightarrow$ B

Answer: (B) Go Back to Q38

Q39.

Solution

Concept – plant sources of pharmaceutical alkaloids: Several life-saving drugs are secondary metabolites obtained from specific plants, sometimes through cell culture.

Step 1 – identify the drugs: Vincristine and vinblastine are terpenoid indole alkaloids used in cancer chemotherapy.

Step 2 – trace the source plant: They are produced by ***Catharanthus roseus*** (the Madagascar periwinkle), from a pathway that begins with tryptophan and strictosidine as shown.

Step 3 – link to biotechnology: Because yields in the whole plant are low, cell-suspension and elicited cultures of *C. roseus* are studied for alkaloid production.

Why the other options are wrong:

- A, *E. coli*: is a bacterium and does not make these plant alkaloids naturally.
- C, *Rhizobium*: is a nitrogen-fixing bacterium.
- D, baker's yeast: is a fungus and not the natural source of vinca alkaloids.

Final Answer: *Catharanthus roseus* $\Rightarrow$ B

Answer: (B) Go Back to Q39

Q40.

Solution

Concept – the role of plant secondary metabolites: Unlike primary metabolites, secondary metabolites are not needed for basic growth; they serve adaptive, ecological functions.

Step 1 – classify the compounds: Alkaloids, terpenoids and phenolics are the major classes of plant secondary metabolites.

Step 2 – state their principal role: Their main job is **defence and ecological interaction**: deterring herbivores, inhibiting pathogens, attracting pollinators or seed dispersers, and competing with other plants.

Step 3 – connect to human use: Many of these defensive chemicals are exploited by humans as drugs, flavours, dyes and pesticides.

Why the other options are wrong:

- A, photosynthesis: is carried out by chlorophyll and primary machinery.
- B, energy storage: is the role of starch and lipids (primary metabolites).
- C, DNA replication: is unrelated to secondary metabolites.

Final Answer: defence and ecological interactions $\Rightarrow$ D

Answer: (D) Go Back to Q40

Q41.

Solution

Concept – *Agrobacterium rhizogenes* and hairy roots: Just as *A. tumefaciens* causes crown gall, *A. rhizogenes* transforms plant cells to produce a distinctive root culture.

Step 1 – read the clues: Fast-growing, highly branched cultures that grow without added hormones and make secondary metabolites, induced by *A. rhizogenes* carrying the Ri plasmid.

Step 2 – name the culture: These are **hairy-root cultures**, formed after transfer of the root-inducing (Ri) T-DNA into the plant genome.

Step 3 – note the advantage: Hairy roots are genetically stable and productive, making them useful for continuous production of root-derived secondary metabolites.

Why the other options are wrong:

- A, callus: is an unorganised mass that usually needs added hormones.
- B, protoplasts: are wall-less cells, not a rooted culture.
- C, somatic embryos: are embryo-like structures for propagation, not *A. rhizogenes* products.

Final Answer: hairy-root cultures $\Rightarrow$ D

Answer: (D) Go Back to Q41

Q42.

Solution

Concept – transgenic animals as protein factories: A recombinant gene can be engineered so that its protein is secreted in an animal's milk, making the animal a living production system.

Step 1 – read the scenario: A therapeutic protein is secreted into milk and later purified from it.

Step 2 – name the concept: Using transgenic animals in this way is molecular pharming (gene pharming), and the animals act as living **bioreactors**.

Step 3 – note a real example: Recombinant human antithrombin has been produced in the milk of transgenic goats by exactly this approach.

Why the other options are wrong:

- A, xenografts: are tissue/organ transplants between species, a different idea.
- C, clones: identical copies do not, by themselves, secrete a recombinant drug.
- D, hybridomas: are fused cells that make monoclonal antibodies in culture, not milk-secreting animals.

Final Answer: living bioreactors (molecular pharming) $\Rightarrow$ B

Answer: (B) Go Back to Q42

Q43.

Solution

Concept – boosting secondary-metabolite yield: Plant cultures can be prompted to make more of a target compound by exposing them to a stress or signalling molecule.

Step 1 – read the treatment: A fungal cell-wall extract or methyl jasmonate is added to switch on the biosynthetic pathway.

Step 2 – name the strategy: Deliberately adding such a signal (an elicitor) to raise metabolite production is called **elicitation**.

Step 3 – explain the mechanism: The elicitor mimics a stress/defence cue, activating the genes and enzymes of the secondary-metabolite pathway, so accumulation increases.

Why the other options are wrong:

- A, somaclonal variation: is genetic/epigenetic variation arising during culture, not a deliberate yield boost by a signal.
- C, micropropagation: is rapid clonal multiplication of plants.
- D, hardening: is acclimatising plantlets to external conditions before transfer.

Final Answer: elicitation $\Rightarrow$ B

Answer: (B) Go Back to Q43

Q44.

Solution

Concept – the basis of separation in mass spectrometry: A mass spectrometer ionises molecules and then sorts the ions in an analyser according to a single physical quantity.

Step 1 – follow the instrument: Sample $\rightarrow$ ion source (ionisation) $\rightarrow$ mass analyser (separation) $\rightarrow$ detector.

Step 2 – state the separation basis: In the analyser, ions are separated by their **mass-to-charge ratio (m/z)**, since their motion in electric/magnetic fields depends on both mass and charge.

Step 3 – read the output: The detector records ion abundance against m/z, giving the mass spectrum from which molecular masses are deduced.

Why the other options are wrong:

- A, size alone: physical size is not what the analyser measures.
- B, charge alone: charge matters only through the m/z ratio, not by itself.
- D, isoelectric point: governs isoelectric focusing, not mass spectrometry.

Final Answer: mass-to-charge ratio (m/z) $\Rightarrow$ C

Answer: (C) Go Back to Q44

Q45.

Solution

Concept – soft ionisation of large biomolecules: Proteins and peptides are fragile, so they are ionised gently by embedding them in a matrix and using a laser pulse.

Step 1 – read the description: Analyte mixed into a light-absorbing solid matrix,

a pulsed laser fired at the spot, and ions accelerated down a flight tube.

Step 2 – name the technique: This is **MALDI** (matrix-assisted laser desorption/ionisation), usually paired with a time-of-flight (TOF) analyser.

Step 3 – state its use: MALDI-TOF is a mainstay of protein/peptide mass fingerprinting and of rapid microbial identification.

Why the other options are wrong:

- A, GC: is a chromatographic separation, not an ionisation method for large biomolecules.
- C, NMR: probes nuclear spin environments, not ion masses.
- D, UV–Vis: measures light absorption, not molecular mass.

Final Answer: MALDI $\Rightarrow$ B

Answer: (B) Go Back to Q45

Q46.

Solution

Concept – the Beer–Lambert law: $A = \varepsilon\, c\, l$, where A is absorbance, ε the molar absorptivity, c the concentration and l the path length.

Step 1 – list the data: $A = 0.90$, $\varepsilon = 45000\ \text{M}^{-1}\text{cm}^{-1}$, $l = 1$ cm.

Step 2 – rearrange for concentration: $c = \dfrac{A}{\varepsilon\, l}$

Step 3 – substitute: $c = \dfrac{0.90}{45000 \times 1}$

Step 4 – evaluate: $c = \dfrac{0.90}{45000} = 2.0 \times 10^{-5}\ \text{M}$

Step 5 – check the units: $\dfrac{1}{\text{M}^{-1}\text{cm}^{-1} \times \text{cm}} = \text{M}$, confirming a molar concentration.

Final Answer: $c = 2 \times 10^{-5}\ \text{M} \Rightarrow$ D

Answer: (D) Go Back to Q46

Answer Key

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