GATE Biotechnology

Sample Paper – 1

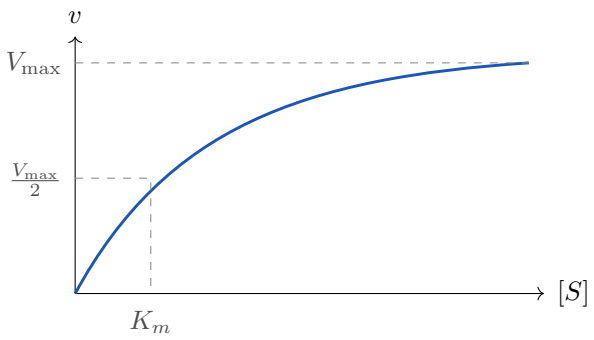
Duration: 128 Minutes **Maximum Marks: 72**

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. An enzyme obeys Michaelis–Menten kinetics with a maximum velocity $V_{\max} = 60\ \mu$mol min^{-1} and a Michaelis constant $K_m = 5$ mM, as sketched below. The initial reaction velocity when the substrate concentration $[S] = 5$ mM is: **[1 mark]**



(A) $60\ \mu\text{mol min}^{-1}$

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

(C) $30\ \mu\text{mol min}^{-1}$

(D) $15\ \mu\text{mol min}^{-1}$

Q2. A single linear polypeptide chain is made up of 100 amino-acid residues joined end to end. The number of peptide bonds present in this chain is: **[1 mark]**

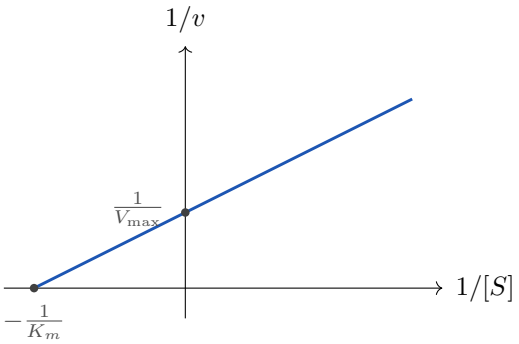
(A) 100

(B) 101

(C) 200

(D) 99

Q3. The Lineweaver–Burk (double-reciprocal) plot of an enzyme-catalysed reaction is shown below. The intercept made by the straight line on the horizontal $(1/[S])$ axis is equal to: **[1 mark]**



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

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

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

(D) $-\dfrac{1}{V_{\max}}$

Q4. At standard biochemical conditions the hydrolysis of adenosine triphosphate (ATP) to adenosine diphosphate (ADP) and inorganic phosphate (P_i) is exergonic. Its standard free-energy change $\Delta G^{\circ\prime}$ is closest to: **[1 mark]**

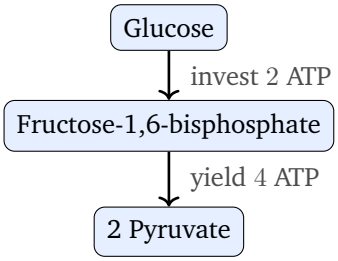
(A) -30.5 kJ mol^{-1}

(B) -14.2 kJ mol^{-1}

(C) $+30.5$ kJ mol^{-1}

(D) -61.0 kJ mol^{-1}

Q5. The glycolytic (Embden–Meyerhof) pathway converts one molecule of glucose into two molecules of pyruvate, as summarised below. Accounting for both the investment and the payoff phases, the *net* yield of ATP per molecule of glucose is: **[1 mark]**



(A) 4

(B) 2

(C) 6

(D) 8

Q6. A reversible inhibitor competes with the substrate for the active site of an enzyme. Compared with the uninhibited reaction, the presence of such a *competitive* inhibitor causes: **[1 mark]**

(A) $V_{\max}$ to decrease while K_m stays unchanged

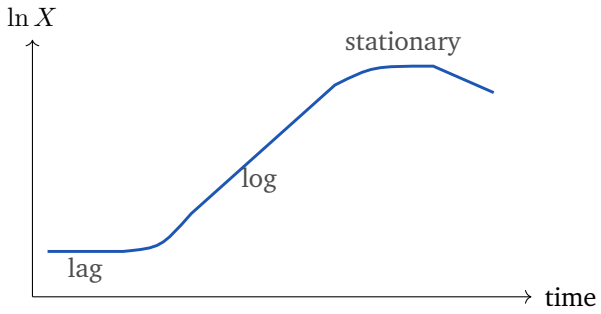
(B) the apparent K_m to increase while $V_{\max}$ stays unchanged

(C) both K_m and $V_{\max}$ to decrease

(D) the apparent K_m to decrease while $V_{\max}$ stays unchanged

Microbiology

Q7. The batch growth curve of a bacterial culture, plotted as $\ln X$ against time, is shown below. The phase in which the cells divide at a constant maximum rate and the specific growth rate is at its highest is the: **[1 mark]**



(A) exponential (log) phase

(B) lag phase

(C) stationary phase

(D) death (decline) phase

Q8. During exponential growth a bacterial population increases from 10^3 cells to 10^6 cells in exactly 6 hours. The generation (doubling) time of this culture is nearest to: **[1 mark]**

(A) 18 min

(B) 36 min

(C) 60 min

(D) 72 min

Q9. In the Gram-staining procedure, the dye that is retained by Gram-positive cells (giving them a purple appearance) even after the alcohol decolourisation step is: [1 mark]

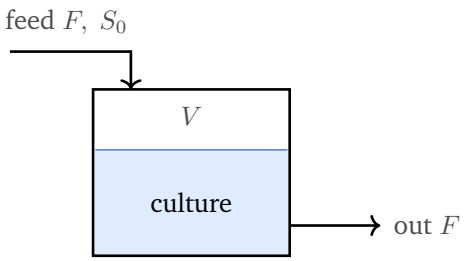
(A) crystal violet

(B) safranin

(C) methylene blue

(D) malachite green

Q10. An ideal chemostat is operated as shown, with sterile feed entering and culture leaving at the same volumetric flow rate. At steady state, the specific growth rate μ of the organism becomes equal to: [1 mark]



(A) $\mu_{\max}$

(B) zero

(C) the dilution rate D

(D) the saturation constant K_s

Q11. The most widely used standard condition for moist-heat (steam) sterilisation of microbiological media in an autoclave is: [1 mark]

(A) $100\ ^\circ$C at atmospheric pressure for 30 min

(B) $160\ ^\circ$C dry heat for 2 hours

(C) $134\ ^\circ$C at 30 psi for 60 min

(D) $121\ ^\circ$C at 15 psi for 15 min

Cell Biology and Molecular Biology

Q12. During DNA replication one of the two new strands is synthesised discontinuously, as a series of short Okazaki fragments that are later joined together. This strand is the: **[1 mark]**

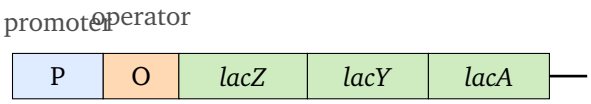
(A) lagging strand

(B) leading strand

(C) parental template strand

(D) both new strands equally

Q13. The organisation of the *lac* operon of *Escherichia coli* is shown below. In the absence of lactose, the active *lac* repressor protein switches off transcription by binding to the: **[1 mark]**



(A) promoter

(B) CAP (activator) site

(C) structural genes

(D) operator

Q14. The standard genetic code has 64 codons in all. Of these, the number of *sense* codons (that is, codons that specify an amino acid) is: **[1 mark]**

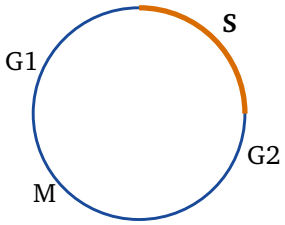
(A) 64

(B) 20

(C) 3

(D) 61

Q15. The eukaryotic cell cycle is represented by the circular diagram below, with one quadrant highlighted. The replication (synthesis) of nuclear DNA takes place during the phase marked: **[1 mark]**



(A) G1 phase

(B) M phase

(C) S phase

(D) G2 phase

Q16. The enzyme that catalyses the synthesis of a messenger RNA molecule using a DNA strand as the template, during transcription, is: **[1 mark]**

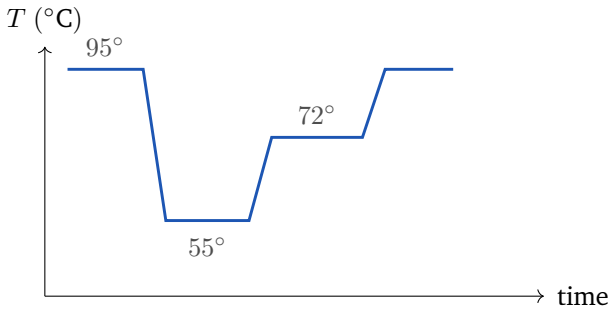
(A) DNA polymerase

(B) DNA ligase

(C) RNA polymerase

(D) reverse transcriptase

Q17. The temperature programme of one cycle of the polymerase chain reaction (PCR) is shown below. The step carried out at about 50–60 °C, at which the primers hybridise to their complementary sequences on the template, is called: **[1 mark]**



(A) denaturation

(B) annealing

(C) extension (elongation)

(D) ligation

Q18. Starting from a single double-stranded DNA template molecule and assuming ideal doubling in every cycle, the theoretical number of copies of the target sequence after 30 cycles of PCR is: **[1 mark]**

(A) 2^{15}

(B) 2^{30}

(C) 30

(D) 2×30

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 recessive allele is $q = 0.2$. The expected frequency of heterozygous individuals in the population is: **[1 mark]**

(A) 0.04

(B) 0.64

(C) 0.16

(D) 0.32

Q20. Among the five classes of human immunoglobulins, the class that is present at the highest concentration in normal adult serum is: **[1 mark]**

(A) IgM

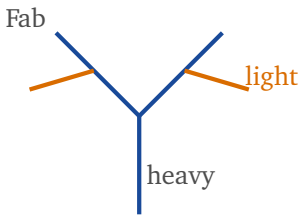
(B) IgA

(C) IgG

(D) IgE

Genetics, Immunology and Evolution (continued)

Q21. The schematic below shows the basic structure of an IgG antibody monomer. In terms of its polypeptide chains and antigen-binding sites, an IgG monomer consists of: **[2 marks]**



(A) two identical heavy chains and one light chain, giving one antigen-binding site

(B) four heavy chains and four light chains, giving four antigen-binding sites

(C) two identical heavy chains and two identical light chains, giving two antigen-binding sites

(D) one heavy chain and one light chain, giving one antigen-binding site

Q22. Two genes on different chromosomes assort independently. In a cross between two double heterozygotes, $AaBb \times AaBb$, both dominant alleles being completely dominant, the phenotypic ratio expected in the F_2 generation is: **[2 marks]**

(A) $9:3:3:1$

(B) $3:1$

(C) $1:2:1$

(D) $1:1:1:1$

Q23. Inside an infected cell, viral proteins synthesised in the cytosol are processed and their peptide fragments are displayed at the cell surface for recognition by cytotoxic ($CD8^+$) T cells. These endogenous antigenic peptides are presented on: **[2 marks]**

(A) MHC class II molecules

(B) secreted antibodies

(C) MHC class I molecules

(D) the B-cell receptor

Q24. In a two-point test cross, two linked genes are found to recombine with a frequency of 10%. The corresponding genetic map distance between the two loci is: **[2 marks]**

(A) 10 centimorgan

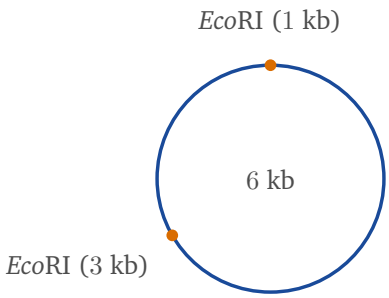
(B) 1 centimorgan

(C) 90 centimorgan

(D) 100 centimorgan

Recombinant DNA Technology and Bioinformatics

Q25. A circular plasmid of total length 6 kb carries two recognition sites for the restriction enzyme *Eco*RI, located at the 1 kb and 3 kb positions measured around the circle, as shown. Complete digestion of the plasmid with *Eco*RI produces DNA fragments of: **[2 marks]**



(A) 2 kb and 4 kb

(B) 1 kb and 3 kb

(C) 3 kb and 3 kb

(D) 6 kb only (single linearised piece)

Q26. In a gene-cloning experiment, a DNA insert and a linearised vector, both cut with the same restriction enzyme, are to be joined together. The enzyme that seals the insert into the vector by forming the phosphodiester bonds between them is: **[2 marks]**

(A) a restriction endonuclease

(B) DNA ligase

(C) DNA polymerase I

(D) alkaline phosphatase

Q27. A researcher wishes to detect one specific protein in a mixture. The proteins are separated by gel electrophoresis, transferred (blotted) onto a membrane and then probed with a labelled antibody specific to the target protein. This technique is called: [2 marks]

(A) Southern blotting

(B) Northern blotting

(C) dot blotting for DNA

(D) Western blotting

Q28. In sequence-based bioinformatics analysis, the program most commonly used to search a large database for regions of local similarity to a given query sequence, and to rank hits by an E-value, is: [2 marks]

(A) PCR

(B) BLAST

(C) SDS-PAGE

(D) ELISA

Q29. In the Sanger (chain-termination) method of DNA sequencing, synthesis of the growing DNA strand stops each time the DNA polymerase incorporates a special nucleotide that lacks a $3'$-hydroxyl group. These chain-terminating nucleotides are the: [2 marks]

(A) deoxynucleotides (dNTPs)

(B) RNA primers

(C) dideoxynucleotides (ddNTPs)

(D) methylated bases

Q30. In blue–white screening on X-gal plates, an insert is cloned into the multiple cloning site within the *lacZ*α gene of the vector. A bacterial colony that carries a plasmid *with* an insert (a recombinant) appears: [2 marks]

(A) blue

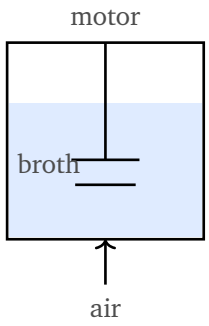
(B) white

(C) red

(D) green

Bioprocess Engineering and Process Biotechnology

Q31. In the batch stirred-tank bioreactor shown, an organism grows exponentially and the biomass concentration rises from 1 g L^{-1} to 8 g L^{-1} in 6 hours. The specific growth rate μ during this period is nearest to: **[2 marks]**



(A) 0.12 h^{-1}

(B) 0.23 h^{-1}

(C) 0.69 h^{-1}

(D) 0.35 h^{-1}

Q32. In a fermentation, 20 g of dry cell biomass is produced while 50 g of glucose is consumed as the carbon and energy source. The biomass yield coefficient on substrate, $Y_{X/S}$, is: **[2 marks]**

(A) 2.5 g g^{-1}

(B) 0.4 g g^{-1}

(C) 0.8 g g^{-1}

(D) 0.2 g g^{-1}

Q33. A chemostat has a constant working volume of 2 L and is fed with sterile medium at a volumetric flow rate of 0.5 L h^{-1}. The dilution rate at which it operates is: **[2 marks]**

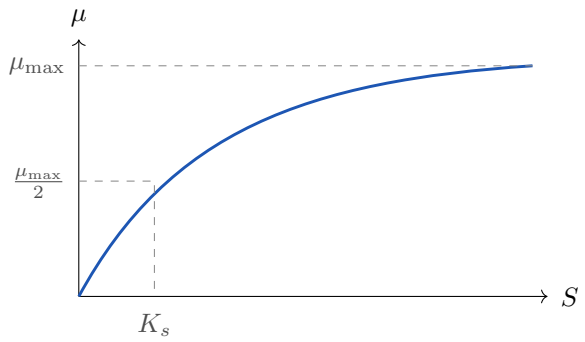
(A) $1.0\ \text{h}^{-1}$

(B) $0.5\ \text{h}^{-1}$

(C) $0.25\ \text{h}^{-1}$

(D) $4.0\ \text{h}^{-1}$

Q34. The dependence of specific growth rate μ on the limiting-substrate concentration S follows the Monod model $\mu = \dfrac{\mu_{\max} S}{K_s + S}$, shown below. When the substrate concentration equals the saturation constant, $S = K_s$, the specific growth rate is: **[2 marks]**



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

(B) $\mu_{\max}$

(C) zero

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

Q35. In an aerobic submerged fermentation, oxygen is supplied to the broth across the gas–liquid interface. The volumetric rate of oxygen transfer (OTR) from the gas to the liquid is correctly expressed as: **[2 marks]**

(A) $\dfrac{k_L a}{C^* - C_L}$

(B) $k_L a\, C^*$ only

(C) $\dfrac{C^* - C_L}{k_L a}$

(D) $k_L a\,(C^* - C_L)$

Q36. In the design of batch thermal sterilisation of a fermentation medium, the extent of sterilisation is measured by the Del factor ∇, defined in

terms of the initial and final numbers of viable organisms, N_0 and N. The Del factor is: [2 marks]

(A) $\frac{N}{N_0}$

(B) $\frac{N_0}{N}$

(C) $\ln\frac{N}{N_0}$

(D) $\ln\frac{N_0}{N}$

Q37. In a batch fermentation, the product concentration reaches its maximum value of 40 g L^{-1} at the end of 20 hours of operation. The overall volumetric productivity of the product for this batch is: [2 marks]

(A) 0.5 g $L^{-1}h^{-1}$

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

(C) 2 g $L^{-1}h^{-1}$

(D) 20 g $L^{-1}h^{-1}$

Q38. A bioreactor is run in a mode in which sterile fresh medium is added continuously while culture broth is withdrawn at the same rate, so that the working volume is held constant and a steady state can be maintained. This mode of operation is called: [2 marks]

(A) batch operation

(B) fed-batch operation

(C) continuous operation

(D) solid-state fermentation

Plant and Animal Biotechnology

Q39. The capacity of a single differentiated plant cell to divide, dedifferentiate and regenerate into a complete, fertile plant when placed on a suitable culture medium is known as: [2 marks]

(A) totipotency

(B) pluripotency

(C) senescence

(D) apoptosis

Q40. In *Agrobacterium tumefaciens*-mediated genetic transformation of plants, the specific segment of the Ti plasmid that is excised, transferred into the plant cell and integrated into the plant nuclear genome is the: **[2 marks]**

(A) *vir* region

(B) origin of replication

(C) opine-catabolism region

(D) T-DNA

Q41. Most animal cell cultures are grown in bicarbonate-buffered media inside incubators kept at about 5% CO_2. The main purpose of maintaining this elevated CO_2 level is to: **[2 marks]**

(A) supply carbon as a nutrient for the cells

(B) stabilise the pH of the medium through the bicarbonate buffer system

(C) sterilise the culture medium

(D) provide oxygen for cellular respiration

Q42. Monoclonal antibodies of a single specificity are produced in the laboratory from hybridoma cells. A hybridoma is created by fusing an antibody-secreting B lymphocyte with a: **[2 marks]**

(A) myeloma (immortal tumour) cell

(B) mature red blood cell

(C) plant protoplast

(D) bacterial cell

Q43. Somatic hybridisation is a method of producing hybrid plants without going through sexual crossing. The technique is based on the fusion of: [2 marks]

(A) male and female gametes

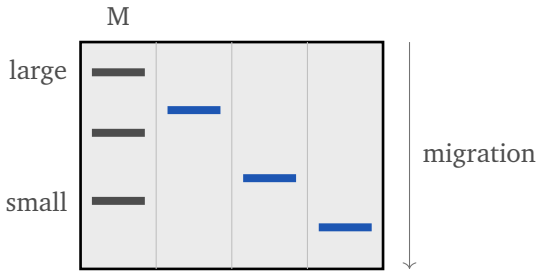
(B) protoplasts from two somatic cells

(C) pollen grains with each other

(D) two zygotes

Analytical Techniques

Q44. The SDS–PAGE gel shown below separates a protein mixture, with a molecular-weight marker (lane M) alongside. Because the bound SDS gives every polypeptide an essentially uniform charge-to-mass ratio, the proteins are separated mainly according to their: [2 marks]



(A) net charge in the native state

(B) isoelectric point (pI)

(C) molecular shape alone

(D) molecular weight (size)

Q45. A coloured solution is analysed by spectrophotometry. Its absorbing species has a molar absorptivity of $6000\ \text{M}^{-1}\text{cm}^{-1}$. Measured in a cuvette of path length 1 cm, the solution shows an absorbance of 0.60. Using the Beer–Lambert law $A = \varepsilon\, c\, l$, the molar concentration of the solution is: [2 marks]

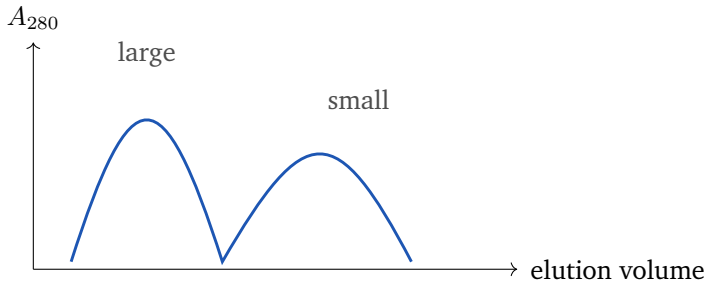
(A) 1×10^{-4} M

(B) 1×10^{-3} M

(C) 6×10^{-4} M

(D) 1×10^{-5} M

Q46. A mixture of proteins is separated on a size-exclusion (gel-filtration) column, giving the elution profile shown. Because large molecules are excluded from the pores of the beads and pass through in the void volume, the molecules that emerge *first* from the column are the: **[2 marks]**



(A) largest molecules

(B) smallest molecules

(C) most highly charged molecules

(D) most hydrophobic molecules

Detailed Solutions

Q1.

Solution

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

Step 1 – list the data: $V_{\max} = 60\ \mu\text{mol min}^{-1}$, $K_m = 5$ mM and $[S] = 5$ mM.

Step 2 – note the special case $[S] = K_m$: When the substrate concentration equals K_m, the velocity is exactly half of $V_{\max}$.

Step 3 – substitute the values: $v = \dfrac{60 \times 5}{5 + 5}$

Step 4 – evaluate the denominator: $5 + 5 = 10$

Step 5 – complete the arithmetic: $v = \dfrac{300}{10}$

$v = 30\ \mu\text{mol min}^{-1}$

Final Answer: $v = 30\ \mu\text{mol min}^{-1} \Rightarrow \boxed{\text{C}}$

Answer: (C) Go Back to Q1

Q2.

Solution

Concept – peptide bonds link successive residues: Each peptide bond joins two neighbouring amino acids, so a chain of n residues is held together by $n - 1$ such bonds.

Step 1 – read the residue count: $n = 100$ amino-acid residues.

Step 2 – apply the relation: Number of peptide bonds $= n - 1$

Step 3 – substitute: $= 100 - 1$

$= 99$

Step 4 – reason it out: The first residue keeps its free amino end and the last keeps its free carboxyl end, so one fewer bond than residues is formed.

Final Answer: 99 peptide bonds $\Rightarrow \boxed{\text{D}}$

Answer: (D) Go Back to Q2

Q3.

Solution

Concept – the Lineweaver–Burk (double-reciprocal) equation: Taking reciprocals of the Michaelis–Menten equation gives $\frac{1}{v} = \frac{K_m}{V_{\max}} \cdot \frac{1}{[S]} + \frac{1}{V_{\max}}$, which is a straight line in $1/v$ versus $1/[S]$.

Step 1 – identify the intercepts of this line: The y-intercept (at $1/[S] = 0$) is $\frac{1}{V_{\max}}$.

Step 2 – find the x-intercept: Set $1/v = 0$ and solve for $1/[S]$: $0 = \frac{K_m}{V_{\max}} \cdot \frac{1}{[S]} + \frac{1}{V_{\max}}$

Step 3 – rearrange: $\frac{K_m}{V_{\max}} \cdot \frac{1}{[S]} = -\frac{1}{V_{\max}}$

Step 4 – cancel $V_{\max}$ and solve: $\frac{1}{[S]} = -\frac{1}{K_m}$

Step 5 – interpret: The line therefore crosses the horizontal axis at $-\frac{1}{K_m}$, exactly as marked on the plot.

Final Answer: x-intercept $= -\frac{1}{K_m} \Rightarrow$ B

Answer: (B) Go Back to Q3

Q4.

Solution

Concept – ATP is the cell's energy currency: The hydrolysis of the terminal phosphoanhydride bond of ATP releases a substantial, well-defined amount of free energy under standard biochemical conditions.

Step 1 – recall the standard value: ATP + $H_2O \rightarrow$ ADP + P_i, with $\Delta G^{\circ\prime} = -30.5$ kJ mol^{-1}.

Step 2 – check the sign: The reaction is exergonic (energy releasing), so $\Delta G^{\circ\prime}$ must be *negative*; this rules out the positive option.

Step 3 – check the magnitude: -30.5 kJ mol^{-1} corresponds to about -7.3 kcal mol^{-1}, the standard textbook figure.

Why the other options are wrong:

- B, -14.2 kJ mol^{-1}: too small; this is closer to a low-energy phosphate ester such as glucose-6-phosphate.
- C, $+30.5$ kJ mol^{-1}: has the wrong sign and would make hydrolysis endergonic.

- D, -61.0 kJ mol^{-1}: about double the true value.

Final Answer: $\Delta G^{\circ\prime} \approx -30.5$ kJ mol^{-1} $\Rightarrow$ A

Answer: (A) Go Back to Q4

Q5.

Solution

Concept – glycolysis has an investment phase and a payoff phase: Some ATP is spent early to activate the sugar, and more ATP is generated later; the net yield is the difference.

Step 1 – count the ATP invested: Two ATP are consumed (at the hexokinase and phosphofructokinase steps).

Step 2 – count the ATP produced: Four ATP are generated in the payoff phase (two each at the phosphoglycerate-kinase and pyruvate-kinase steps, for the two triose molecules).

Step 3 – take the net: Net ATP $= 4 - 2$

$= 2$

Step 4 – note the reducing power (aside): Glycolysis also yields 2 NADH per glucose, but the question asks only about the *net ATP*, which is 2.

Final Answer: net ATP $= 2$ per glucose $\Rightarrow$ B

Answer: (B) Go Back to Q5

Q6.

Solution

Concept – competitive inhibitors compete for the active site: A competitive inhibitor resembles the substrate and binds the free enzyme's active site, but it can be out-competed by raising the substrate concentration.

Step 1 – effect on $V_{\max}$: Because excess substrate can displace the inhibitor, the same maximum velocity is still reachable, so $V_{\max}$ is **unchanged**.

Step 2 – effect on K_m: More substrate is now needed to reach half-maximal velocity, so the *apparent* K_m **increases** (the enzyme appears to have lower affinity).

Step 3 – match to the options: Apparent K_m up, $V_{\max}$ constant $\Rightarrow$ option B.

Why the other options are wrong:

- A: lowering $V_{\max}$ at constant K_m describes a **non-competitive** inhibitor.

- C and D: neither a fall in both, nor a fall in K_m, fits competitive inhibition.

Final Answer: apparent K_m increases, $V_{\max}$ unchanged $\Rightarrow$ B

Answer: (B) Go Back to Q6

Q7.

Solution

Concept – the four phases of a batch growth curve: A batch culture passes through lag, exponential (log), stationary and death phases; the slope of $\ln X$ against time is the specific growth rate μ.

Step 1 – link slope to growth rate: On the $\ln X$ plot the steepest, straight-line portion has the largest slope, and slope $= \mu$.

Step 2 – identify that portion: The steepest straight segment is the middle rising part, which is the exponential (log) phase.

Step 3 – confirm the biology: During this phase nutrients are ample and cells divide at their maximum constant rate, so $\mu = \mu_{\max}$.

Why the other options are wrong:

- B, lag phase: cells are adapting and hardly dividing, so $\mu \approx 0$.
- C, stationary phase: growth balances death, so the net $\mu \approx 0$.
- D, death phase: viable count falls, so μ is negative.

Final Answer: the exponential (log) phase $\Rightarrow$ A

Answer: (A) Go Back to Q7

Q8.

Solution

Concept – generations during exponential growth: The number of doublings is $n = \dfrac{\ln(X/X_0)}{\ln 2}$, and the generation time is $t_d = \dfrac{t}{n}$.

Step 1 – list the data: $X_0 = 10^3$, $X = 10^6$, total time $t = 6$ h $= 360$ min.

Step 2 – find the fold increase: $\dfrac{X}{X_0} = \dfrac{10^6}{10^3} = 10^3 = 1000$

Step 3 – compute the number of generations: $n = \log_2(1000) = \dfrac{\ln 1000}{\ln 2} = \dfrac{6.908}{0.693}$

$n \approx 9.97$

Step 4 – compute the generation time: $t_d = \dfrac{360}{9.97}$

$t_d \approx 36.1$ min

Step 5 – round to the nearest option: $t_d \approx 36$ min.

Final Answer: $t_d \approx 36$ min $\Rightarrow$ B

Answer: (B) Go Back to Q8

Q9.

Solution

Concept – the sequence of Gram-stain reagents: The stain uses crystal violet (primary), Gram's iodine (mordant), alcohol/acetone (decolouriser) and safranin (counterstain).

Step 1 – what happens in Gram-positive cells: Their thick peptidoglycan wall traps the crystal violet–iodine complex during decolourisation.

Step 2 – identify the retained dye: The retained (primary) dye is therefore **crystal violet**, giving a purple colour.

Step 3 – contrast with Gram-negative cells: Their thin wall loses the complex on decolourisation and instead takes up the pink safranin counterstain.

Why the other options are wrong:

- B, safranin: is the counterstain retained by Gram-*negative* cells.
- C and D: methylene blue and malachite green are not part of the standard Gram procedure.

Final Answer: crystal violet $\Rightarrow$ A

Answer: (A) Go Back to Q9

Q10.

Solution

Concept – steady state in a chemostat: A chemostat is a continuous stirred-tank reactor in which the dilution rate is $D = F/V$; at steady state the cell concentration does not change with time.

Step 1 – write the biomass balance: Rate of change = growth − washout: $\dfrac{dX}{dt} = \mu X - DX$.

Step 2 – impose steady state: At steady state $\frac{dX}{dt} = 0$, so $\mu X - DX = 0$.

Step 3 – solve for μ: Dividing by X (with $X \neq 0$): $\mu - D = 0$, hence $\mu = D$.

Step 4 – interpret: The operator sets the growth rate simply by choosing the feed flow rate; the culture self-adjusts so that μ equals D.

Final Answer: $\mu = D$ (the dilution rate) $\Rightarrow$ C

Answer: (C) Go Back to Q10

Q11.

Solution

Concept – moist-heat sterilisation conditions: Saturated steam under pressure is far more lethal to microbes than dry heat at the same temperature.

Step 1 – recall the standard autoclave cycle: 121 °C, at a gauge pressure of about 15 psi (≈ 103 kPa), held for 15 minutes.

Step 2 – why these values: 15 psi of steam raises the boiling point of water to 121 °C, and 15 minutes at that temperature reliably kills bacterial endospores.

Why the other options are wrong:

- A, 100 °C at atmospheric pressure: does not kill resistant spores.
- B, 160 °C for 2 h: is a *dry-heat* (hot-air oven) cycle, not autoclaving.
- C, 134 °C at 30 psi for 60 min: is not the standard laboratory cycle.

Final Answer: 121 °C at 15 psi for 15 min $\Rightarrow$ D

Answer: (D) Go Back to Q11

Q12.

Solution

Concept – leading versus lagging strand: DNA polymerase synthesises DNA only in the $5' \rightarrow 3'$ direction, so the two antiparallel template strands are copied differently.

Step 1 – the strand copied continuously: The template read $3' \rightarrow 5'$ toward the fork allows continuous synthesis; this new strand is the leading strand.

Step 2 – the strand copied discontinuously: The other template forces synthesis away from the fork, so it is made in short pieces called Okazaki fragments.

Step 3 – name that strand: That discontinuously made strand is the **lagging**

strand.

Step 4 – finishing step: The Okazaki fragments are later sealed by DNA ligase to give one continuous strand.

Final Answer: the lagging strand $\Rightarrow$ A

Answer: (A) Go Back to Q12

Q13.

Solution

Concept – negative control of the *lac* operon: The *lac* repressor controls transcription by binding a specific DNA site that overlaps the start of the operon.

Step 1 – state of the operon without lactose: With no lactose (hence no inducer allolactose), the repressor is in its active DNA-binding form.

Step 2 – identify the binding site: The active repressor binds the **operator**, the site located between the promoter and the structural genes.

Step 3 – consequence: Repressor bound at the operator physically blocks RNA polymerase from transcribing *lacZ*, *lacY* and *lacA*, so the operon is switched off.

Why the other options are wrong:

- A, promoter: is where RNA polymerase binds, not the repressor.
- B, CAP site: binds the activator CAP–cAMP, which is positive control.
- C, structural genes: are transcribed, not bound by the repressor.

Final Answer: the operator $\Rightarrow$ D

Answer: (D) Go Back to Q13

Q14.

Solution

Concept – composition of the genetic code: There are $4^3 = 64$ possible triplet codons, but not all of them specify amino acids.

Step 1 – write the total: Total codons $= 64$.

Step 2 – remove the stop codons: Three codons (UAA, UAG, UGA) are stop (nonsense) codons and code for no amino acid.

Step 3 – count the sense codons: Sense codons $= 64 - 3 = 61$.

Step 4 – note the degeneracy: These 61 sense codons specify only 20 amino

acids, so the code is degenerate (several codons per amino acid), but the *number of sense codons* is still 61.

Final Answer: 61 sense codons $\Rightarrow$ D

Answer: (D) Go Back to Q14

Q15.

Solution

Concept – phases of the eukaryotic cell cycle: Interphase is divided into G1 (growth), S (DNA synthesis) and G2 (growth), followed by M (mitosis).

Step 1 – locate DNA replication: Chromosomal DNA is copied only during the synthesis phase.

Step 2 – name that phase: That phase is the **S phase**, highlighted in the diagram.

Step 3 – track the DNA content: A cell's DNA content doubles from $2C$ to $4C$ across S phase, then halves again at the end of mitosis.

Why the other options are wrong:

- A, G1: the cell grows and prepares for replication but no DNA is made yet.
- B, M: chromosomes are separated, not replicated.
- D, G2: the cell checks the copied DNA and prepares for mitosis.

Final Answer: the S phase $\Rightarrow$ C

Answer: (C) Go Back to Q15

Q16.

Solution

Concept – transcription and its enzyme: Transcription copies a gene's DNA sequence into RNA, following base-pairing rules with uracil in place of thymine.

Step 1 – identify the reaction: DNA template $\rightarrow$ complementary mRNA.

Step 2 – name the catalyst: This synthesis is carried out by **RNA polymerase**, which needs no primer.

Why the other options are wrong:

- A, DNA polymerase: makes DNA, not RNA, and needs a primer.
- B, DNA ligase: seals nicks in DNA; it does not polymerise nucleotides on a template.

- D, reverse transcriptase: makes DNA from an RNA template, the opposite of transcription.

Final Answer: RNA polymerase $\Rightarrow$ C

Answer: (C) Go Back to Q16

Q17.

Solution

Concept – the three temperature steps of a PCR cycle: Each cycle has denaturation (high T), annealing (intermediate T) and extension (about 72 °C).

Step 1 – match the step to the temperature: The step at about 50–60 °C is the middle-temperature step in the profile.

Step 2 – what happens there: At this temperature the short primers base-pair with their complementary sequences flanking the target; this is **annealing**.

Step 3 – fit the neighbours: It is preceded by denaturation at about 95 °C (strand separation) and followed by extension at about 72 °C (Taq polymerase synthesis).

Why the other options are wrong:

- A, denaturation: occurs at about 95 °C.
- C, extension: occurs at about 72 °C.
- D, ligation: is not a PCR step at all.

Final Answer: annealing $\Rightarrow$ B

Answer: (B) Go Back to Q17

Q18.

Solution

Concept – exponential amplification in PCR: Ideally the number of target copies doubles every cycle, so after n cycles it is multiplied by 2^n.

Step 1 – write the amplification law: Copies $=$ (starting number) $\times\, 2^n$.

Step 2 – substitute the data: Starting number $= 1$ molecule and $n = 30$ cycles.

Step 3 – evaluate: Copies $= 1 \times 2^{30} = 2^{30}$.

Step 4 – put a value to it: $2^{30} \approx 1.07 \times 10^9$, roughly a billion copies, which is why a trace of DNA becomes visible.

Final Answer: 2^{30} copies $\Rightarrow$ B

Answer: (B) Go Back to Q18

Q19.

Solution

Concept – Hardy–Weinberg genotype frequencies: For two alleles with frequencies p and q ($p+q=1$), the genotype frequencies are p^2, $2pq$ and q^2; heterozygotes are $2pq$.

Step 1 – list the data: $q = 0.2$ (recessive allele).

Step 2 – find the dominant-allele frequency: $p = 1 - q = 1 - 0.2 = 0.8$

Step 3 – compute the heterozygote frequency: $2pq = 2 \times 0.8 \times 0.2$

Step 4 – multiply: $= 2 \times 0.16$

$= 0.32$

Step 5 – sanity check the total: $p^2 + 2pq + q^2 = 0.64 + 0.32 + 0.04 = 1.00$, so the split is consistent.

Final Answer: heterozygote frequency $= 0.32 \Rightarrow$ D

Answer: (D) Go Back to Q19

Q20.

Solution

Concept – serum levels of immunoglobulin classes: The five classes (IgG, IgA, IgM, IgD, IgE) occur at very different concentrations in serum.

Step 1 – rank the classes: IgG is by far the most abundant, making up about 75–80% of total serum antibody.

Step 2 – note its roles: IgG is the main antibody of the secondary immune response and the only class that crosses the placenta.

Why the other options are wrong:

- A, IgM: is the first antibody made in a response but is present at lower serum levels than IgG.
- B, IgA: dominates mucosal secretions, not serum.
- D, IgE: is present only in trace amounts and mediates allergy.

Final Answer: IgG $\Rightarrow$ C

Answer: (C) Go Back to Q20

Q21.

Solution

Concept – the four-chain structure of IgG: The basic antibody unit is a Y-shaped molecule built from heavy and light chains linked by disulphide bonds.

Step 1 – count the chains: An IgG monomer has two identical *heavy* chains and two identical *light* chains.

Step 2 – locate the antigen-binding sites: Each arm (Fab) is formed by one heavy and one light chain and carries one antigen-binding site.

Step 3 – total the binding sites: Two Fab arms give **two** identical antigen-binding sites, so IgG is bivalent.

Step 4 – match to the options: Two heavy + two light chains, two binding sites $\Rightarrow$ option C.

Why the other options are wrong:

- A and D: give too few chains and only one binding site.
- B: four heavy and four light chains describes an IgM-like pentamer subunit count, not an IgG monomer.

Final Answer: two heavy + two light chains, two binding sites $\Rightarrow$ $\boxed{\text{C}}$

Answer: (C) Go Back to Q21

Q22.

Solution

Concept – the dihybrid F_2 ratio: For two genes assorting independently, each with complete dominance, the F_2 of a double-heterozygote cross follows Mendel's classic ratio.

Step 1 – treat each gene separately: $Aa \times Aa$ gives 3 dominant : 1 recessive, and likewise $Bb \times Bb$ gives $3:1$.

Step 2 – combine by the product rule: $(3:1) \times (3:1)$ over both traits gives the joint phenotype ratio.

Step 3 – expand the product: 9 (both dominant) : 3 (dominant A, recessive b) : 3 (recessive a, dominant B) : 1 (both recessive).

Step 4 – state the ratio: $9:3:3:1$.

Step 5 – check the total: $9+3+3+1=16$, matching the 4×4 Punnett square.

Final Answer: $9:3:3:1 \Rightarrow \boxed{\text{A}}$

Answer: (A) Go Back to Q22

Q23.

Solution

Concept – the two antigen-presentation pathways: Endogenous (cytosolic) antigens and exogenous (engulfed) antigens are presented on different MHC molecules to different T cells.

Step 1 – classify the antigen: Viral proteins made in the cytosol are *endogenous* antigens.

Step 2 – match to the MHC class: Endogenous peptides are loaded onto **MHC class I** molecules.

Step 3 – match to the T cell: MHC class I–peptide complexes are recognised by $CD8^+$ cytotoxic T cells, exactly the cells named in the question.

Why the other options are wrong:

- A, MHC class II: presents exogenous antigens to $CD4^+$ helper T cells.
- B, antibodies: recognise free antigen, not MHC-presented peptides.
- D, B-cell receptor: binds native antigen and is unrelated to this pathway.

Final Answer: MHC class I $\Rightarrow$ C

Answer: (C) Go Back to Q23

Q24.

Solution

Concept – recombination frequency and map distance: One map unit (centimorgan, cM) is defined as a recombination frequency of 1% between two loci.

Step 1 – read the recombination frequency: Recombination frequency $= 10\%$.

Step 2 – convert to map units: Map distance $= 10\% \times \dfrac{1 \text{ cM}}{1\%}$

Step 3 – evaluate: $= 10$ cM.

Step 4 – note the validity range: This direct proportionality holds well for small frequencies (up to about $\leq 20\%$), where double crossovers are rare.

Final Answer: 10 cM $\Rightarrow$ A

Answer: (A) Go Back to Q24

Q25.

Solution

Concept – fragments from cutting a circular DNA: Each restriction cut on a *circular* molecule with k sites yields k linear fragments; the fragment sizes are the arc lengths between neighbouring sites.

Step 1 – list the data: Total size $= 6$ kb; *Eco*RI sites at the 1 kb and 3 kb positions.

Step 2 – fragment between the two sites: Going from 1 kb to 3 kb around the circle: $3 - 1 = 2$ kb.

Step 3 – the remaining fragment: The rest of the circle: $6 - 2 = 4$ kb.

Step 4 – state the two fragments: 2 kb and 4 kb (two cuts $\Rightarrow$ two pieces).

Step 5 – check the sum: $2 + 4 = 6$ kb, the full plasmid length, so the accounting is complete.

Final Answer: 2 kb and 4 kb $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q25

Q26.

Solution

Concept – joining insert to vector: After a restriction enzyme creates compatible ends, a separate enzyme is needed to make the backbone continuous.

Step 1 – what bond must form: The gap between insert and vector is closed by forming phosphodiester bonds in the sugar–phosphate backbone.

Step 2 – name the enzyme: This is done by **DNA ligase** (typically T4 DNA ligase), using ATP.

Why the other options are wrong:

- A, restriction endonuclease: *cuts* DNA; it does the opposite job.
- C, DNA polymerase I: fills gaps by adding nucleotides but does not seal the final nick between two duplexes here.
- D, alkaline phosphatase: removes $5'$-phosphates to prevent self-ligation of the vector; it cannot join fragments.

Final Answer: DNA ligase $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q26

Q27.

Solution

Concept – the blotting family of techniques: Southern (DNA), Northern (RNA) and Western (protein) blots differ by the target molecule and the probe used.

Step 1 – identify the target: Here the separated molecules are *proteins*, probed with a specific antibody.

Step 2 – name the technique: Protein transfer followed by antibody detection is the **Western blot**.

Why the other options are wrong:

- A, Southern blot: detects a specific *DNA* sequence with a nucleic-acid probe.
- B, Northern blot: detects a specific *RNA* with a nucleic-acid probe.
- C, dot blot for DNA: spots nucleic acid without electrophoretic separation and does not use an antibody against protein.

Final Answer: Western blotting $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q27

Q28.

Solution

Concept – sequence-similarity searching: Finding regions of local similarity between a query and a database is a core bioinformatics task with a dedicated algorithm.

Step 1 – recall the standard tool: The Basic Local Alignment Search Tool (**BLAST**) performs exactly this local-similarity search.

Step 2 – note its output: BLAST ranks hits by an E-value, the number of matches of that quality expected by chance, so smaller E-values are more significant.

Why the other options are wrong:

- A, PCR: is a laboratory amplification method, not a search program.
- C, SDS-PAGE: is a protein-separation technique.
- D, ELISA: is an antibody-based detection assay.

Final Answer: BLAST $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q28

Q29.

Solution

Concept – the Sanger chain-termination method: Sequencing uses a mixture of normal dNTPs and a small fraction of chain-terminating analogues.

Step 1 – identify the terminator: The terminators are **dideoxynucleotides (ddNTPs)**, which lack the $3'$-OH group.

Step 2 – explain the termination: Without a $3'$-OH, no further phosphodiester bond can form, so the growing chain stops wherever a ddNTP is incorporated.

Step 3 – link to read-out: The nested set of terminated fragments, sorted by length, reveals the sequence.

Why the other options are wrong:

- A, dNTPs: are the normal substrates that *extend* the chain.
- B, RNA primers: only start synthesis; they do not terminate it.
- D, methylated bases: are not the basis of Sanger termination.

Final Answer: dideoxynucleotides (ddNTPs) $\Rightarrow$ C

Answer: (C) Go Back to Q29

Q30.

Solution

Concept – blue–white screening: The vector carries *lacZ*α; a functional product plus X-gal gives blue colonies, and disruption of the gene gives white colonies.

Step 1 – what an insert does: Cloning a DNA fragment into the multiple cloning site interrupts *lacZ*α, so no active β-galactosidase is made.

Step 2 – effect on colour: With no functional enzyme, X-gal is not cleaved, so the recombinant colony stays **white**.

Step 3 – the contrast: A non-recombinant colony (empty vector, intact *lacZ*α) cleaves X-gal and turns blue.

Final Answer: recombinant colonies are white $\Rightarrow$ B

Answer: (B) Go Back to Q30

Q31.

Solution

Concept – specific growth rate from exponential growth: In batch exponential growth $X = X_0 e^{\mu t}$, so $\mu = \dfrac{1}{t}\ln\dfrac{X}{X_0}$.

Step 1 – list the data: $X_0 = 1$ g L^{-1}, $X = 8$ g L^{-1}, $t = 6$ h.

Step 2 – form the ratio: $\dfrac{X}{X_0} = \dfrac{8}{1} = 8$

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: $\mu = \dfrac{2.079}{6}$

Step 5 – evaluate: $\mu \approx 0.347$ h^{-1} ≈ 0.35 h^{-1}

Final Answer: $\mu \approx 0.35$ h^{-1} $\Rightarrow$ D

Answer: (D) Go Back to Q31

Q32.

Solution

Concept – biomass yield coefficient: $Y_{X/S} = \dfrac{\text{mass of biomass formed}}{\text{mass of substrate consumed}}$.

Step 1 – list the data: Biomass formed $= 20$ g; glucose consumed $= 50$ g.

Step 2 – substitute: $Y_{X/S} = \dfrac{20}{50}$

Step 3 – simplify: $Y_{X/S} = 0.4$ g g^{-1}

Step 4 – interpret: Each gram of glucose consumed yields 0.4 g of cells; the rest of the carbon goes into products, CO_2 and maintenance.

Final Answer: $Y_{X/S} = 0.4$ g g^{-1} $\Rightarrow$ B

Answer: (B) Go Back to Q32

Q33.

Solution

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

Step 1 – list the data: $F = 0.5$ L h^{-1}, $V = 2$ L.

Step 2 – substitute: $D = \dfrac{0.5}{2}$

Step 3 – evaluate: $D = 0.25$ h^{-1}

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

Final Answer: $D = 0.25\ \text{h}^{-1} \Rightarrow \boxed{\text{C}}$

Answer: (C) Go Back to Q33

Q34.

Solution

Concept – meaning of the Monod saturation constant: K_s is the substrate concentration at which the specific growth rate is half its maximum, analogous to K_m in enzyme kinetics.

Step 1 – write the Monod equation: $\mu = \frac{\mu_{\max} S}{K_s + S}$

Step 2 – set $S = K_s$: $\mu = \frac{\mu_{\max} K_s}{K_s + K_s}$

Step 3 – simplify the denominator: $K_s + K_s = 2K_s$

Step 4 – cancel K_s: $\mu = \frac{\mu_{\max} K_s}{2K_s} = \frac{\mu_{\max}}{2}$

Final Answer: $\mu = \frac{\mu_{\max}}{2} \Rightarrow \boxed{\text{A}}$

Answer: (A) Go Back to Q34

Q35.

Solution

Concept – oxygen transfer in aerobic bioreactors: Oxygen moves from gas bubbles into the liquid at a rate set by the mass-transfer coefficient and the concentration driving force.

Step 1 – write the OTR expression: $\text{OTR} = k_L a\,(C^* - C_L)$.

Step 2 – identify the terms: $k_L a$ is the volumetric mass-transfer coefficient, C^* the saturation (equilibrium) dissolved-oxygen concentration, and C_L the actual dissolved-oxygen concentration in the broth.

Step 3 – interpret the driving force: The transfer rate is proportional to the concentration gap $(C^* - C_L)$; when the broth is oxygen-starved this gap, and hence the transfer, is large.

Why the other options are wrong:

- A and C: place the driving force in the wrong position (division instead of

multiplication), giving wrong units.
- B: drops the C_L term, so it ignores the oxygen already dissolved.

Final Answer: OTR $= k_L a\,(C^* - C_L) \Rightarrow$ D

Answer: (D) Go Back to Q35

Q36.

Solution

Concept – the Del factor in sterilisation design: The Del factor ∇ measures the reduction in the number of viable organisms achieved by a heat treatment.

Step 1 – write the definition: $\nabla = \ln\dfrac{N_0}{N}$, where N_0 is the initial and N the final number of viable organisms.

Step 2 – check the sign: Since sterilisation lowers the count, $N_0 > N$, so $N_0/N > 1$ and $\ln(N_0/N) > 0$; the Del factor is a positive number, as it must be.

Step 3 – typical magnitude: A design Del factor of about $\nabla \approx 30$ or more is used to reduce even a large initial spore load to a negligible survival probability.

Why the other options are wrong:

- A and B: bare ratios are not the defined (logarithmic) Del factor.
- C, $\ln(N/N_0)$: is negative and has the ratio inverted.

Final Answer: $\nabla = \ln\dfrac{N_0}{N} \Rightarrow$ D

Answer: (D) Go Back to Q36

Q37.

Solution

Concept – volumetric productivity: Overall volumetric productivity $= \dfrac{\text{final product concentration}}{\text{total batch time}}$.

Step 1 – list the data: Product concentration $= 40$ g L^{-1}; batch time $= 20$ h.

Step 2 – substitute: Productivity $= \dfrac{40}{20}$

Step 3 – evaluate: $= 2$ g L^{-1}h^{-1}

Step 4 – interpret: On average the process makes 2 g of product per litre of broth per hour over the whole run.

Final Answer: $2\ \text{g L}^{-1}\text{h}^{-1} \Rightarrow \boxed{\text{C}}$

Answer: (C) Go Back to Q37

Q38.

Solution

Concept – modes of bioreactor operation: Bioreactors are run in batch, fed-batch or continuous mode, distinguished by how feed and product streams are handled.

Step 1 – read the description: Sterile medium is added continuously *and* broth is removed at the same rate, keeping the volume constant.

Step 2 – match the mode: Continuous inflow and outflow at equal rates with constant volume defines **continuous** operation (for example a chemostat).

Step 3 – note the key feature: Only continuous operation can hold a genuine time-invariant steady state.

Why the other options are wrong:

- A, batch: has no inflow or outflow during the run.
- B, fed-batch: adds feed but does not withdraw, so the volume rises.
- D, solid-state fermentation: is carried out on a moist solid substrate with little free water, a different concept.

Final Answer: continuous operation $\Rightarrow \boxed{\text{C}}$

Answer: (C) Go Back to Q38

Q39.

Solution

Concept – totipotency of plant cells: A key property exploited in plant tissue culture is that many plant cells retain the full genetic capacity to regenerate an entire organism.

Step 1 – read the definition given: A single differentiated cell dedifferentiates and regenerates a whole, fertile plant.

Step 2 – name the property: This capacity is **totipotency**.

Step 3 – link to practice: Totipotency underlies micropropagation, where explants form callus and then whole plantlets on suitable hormone media.

Why the other options are wrong:

- B, pluripotency: the ability to form many (but not all) cell types, a term used mainly for animal stem cells.
- C, senescence: programmed ageing and decline, the opposite idea.
- D, apoptosis: programmed cell death.

Final Answer: totipotency $\Rightarrow$ A

Answer: (A) Go Back to Q39

Q40.

Solution

Concept – *Agrobacterium*-mediated gene transfer: The Ti (tumour-inducing) plasmid of *Agrobacterium* naturally moves a defined DNA segment into plant cells.

Step 1 – identify the transferred segment: The segment excised and integrated into the plant nuclear genome is the **T-DNA**, bordered by the left and right border repeats.

Step 2 – role of the *vir* genes: The *vir* (virulence) genes process and transfer the T-DNA but are themselves *not* transferred.

Step 3 – link to engineering: In a disarmed vector the tumour genes within the T-DNA are replaced by the gene of interest, which then integrates into the plant.

Why the other options are wrong:

- A, *vir* region: acts in *trans* and stays in the bacterium.
- B, origin of replication: maintains the plasmid in the bacterium; it is not transferred.
- C, opine-catabolism region: lets the bacterium use opines and is not part of the transferred DNA.

Final Answer: the T-DNA $\Rightarrow$ D

Answer: (D) Go Back to Q40

Q41.

Solution

Concept – the bicarbonate buffer in cell culture: Most media use a CO_2/HCO_3^- buffer whose pH depends on the partial pressure of CO_2 above the medium.

Step 1 – write the equilibrium: $CO_2 + H_2O \rightleftharpoons H_2CO_3 \rightleftharpoons H^+ + HCO_3^-$.

Step 2 – see the role of the 5% CO_2: Holding the gas phase at about 5% CO_2 fixes this equilibrium so the medium stays near physiological pH (≈ 7.4).

Step 3 – conclude the purpose: The main purpose is therefore to **stabilise the medium pH** through the bicarbonate buffer, not to feed or oxygenate the cells.

Why the other options are wrong:

- A: cells get carbon mainly from glucose and glutamine, not from atmospheric CO_2.
- C: CO_2 does not sterilise the medium.
- D: oxygen, not CO_2, supports respiration.

Final Answer: to buffer the medium pH via the bicarbonate system $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q41

Q42.

Solution

Concept – hybridoma technology: Monoclonal antibodies are made by immortalising a single antibody-producing cell through cell fusion.

Step 1 – the two fusion partners: An antibody-secreting B lymphocyte (specific but short-lived) is fused with a **myeloma** (immortal tumour) cell.

Step 2 – the resulting cell: The fused hybridoma inherits antibody production from the B cell and immortal growth from the myeloma.

Step 3 – the outcome: A single hybridoma clone secretes one antibody of a single specificity: a monoclonal antibody.

Why the other options are wrong:

- B, red blood cell: has no nucleus and cannot confer immortal growth.
- C, plant protoplast: is used in plant somatic hybridisation, not antibody production.
- D, bacterial cell: cannot fuse with a mammalian B cell to form a hybridoma.

Final Answer: a myeloma (immortal tumour) cell $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q42

Q43.

Solution

Concept – somatic hybridisation in plants: This technique combines the genomes of two plants without sexual crossing, by fusing cells stripped of their walls.

Step 1 – prepare the cells: Enzymatic removal of the cell wall yields wall-less *protoplasts* from two somatic cells.

Step 2 – carry out the fusion: The protoplasts are fused (chemically with PEG or by electrofusion) to give a hybrid cell.

Step 3 – regenerate: The fused cell is cultured to regenerate a somatic hybrid plant carrying both parental genomes.

Why the other options are wrong:

- A, gametes: their fusion is normal sexual fertilisation, not somatic hybridisation.
- C, pollen grains: are male gametophytes and are not fused in this technique.
- D, zygotes: are already products of fertilisation.

Final Answer: protoplasts from two somatic cells $\Rightarrow$ B

Answer: (B) Go Back to Q43

Q44.

Solution

Concept – basis of separation in SDS–PAGE: SDS coats every polypeptide with negative charge in proportion to its length, masking the protein's own charge and shape.

Step 1 – effect of SDS: Because the charge-to-mass ratio becomes essentially the same for all proteins, charge no longer distinguishes them.

Step 2 – what remains to separate them: Movement through the gel's sieving matrix then depends only on size: smaller proteins migrate faster and farther.

Step 3 – conclude the basis: So SDS–PAGE separates proteins primarily by **molecular weight (size)**, with the smallest bands nearest the bottom of the gel.

Why the other options are wrong:

- A, native charge: is deliberately masked by SDS.
- B, isoelectric point: is the basis of isoelectric focusing, not SDS–PAGE.
- C, shape alone: is removed because SDS denatures and linearises the proteins.

Final Answer: molecular weight (size) $\Rightarrow$ D

Answer: (D) Go Back to Q44

Q45.

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: $A = 0.60$, $\varepsilon = 6000\ \text{M}^{-1}\text{cm}^{-1}$, $l = 1$ cm.

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

Step 3 – substitute: $c = \dfrac{0.60}{6000 \times 1}$

Step 4 – evaluate: $c = \dfrac{0.60}{6000} = 1.0 \times 10^{-4}\ \text{M}$

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

Final Answer: $c = 1 \times 10^{-4}\ \text{M} \Rightarrow$ A

Answer: (A) Go Back to Q45

Q46.

Solution

Concept – separation in size-exclusion chromatography: Gel-filtration beads have pores; molecules are sorted by how much of the internal pore volume they can access.

Step 1 – fate of large molecules: Large molecules are too big to enter the pores, so they are excluded and travel only through the space between beads (the void volume).

Step 2 – consequence for elution order: Taking the shortest path, the largest molecules elute *first*, in the void volume, exactly as the first peak shows.

Step 3 – fate of small molecules: Small molecules diffuse into the pores, take a longer effective path, and therefore elute later.

Why the other options are wrong:

- B, smallest molecules: elute last, not first.
- C and D: charge and hydrophobicity govern ion-exchange and hydrophobic-interaction chromatography, not size exclusion.

Final Answer: the largest molecules $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q46

Answer Key

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