GATE Biotechnology

Sample Paper – 4

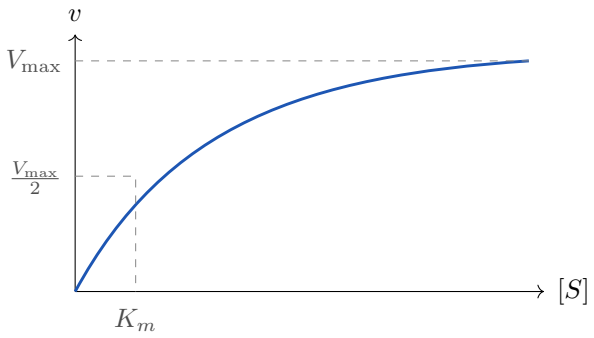
Duration: 128 Minutes **Maximum Marks: 72**

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 following Michaelis–Menten kinetics has a maximum velocity $V_{\max} = 120$ μmol min^{-1} and a Michaelis constant $K_m = 4$ mM, as sketched below. The initial reaction velocity when the substrate concentration $[S] = 12$ mM is: [1 mark]



(A) $120\ \mu\text{mol min}^{-1}$

(B) $108\ \mu\text{mol min}^{-1}$

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

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

Q2. A reversible inhibitor binds to a site on the enzyme other than the active site and lowers the turnover of the enzyme without affecting how tightly the substrate binds. Compared with the uninhibited reaction, such a classical *non-competitive* inhibitor causes: **[1 mark]**

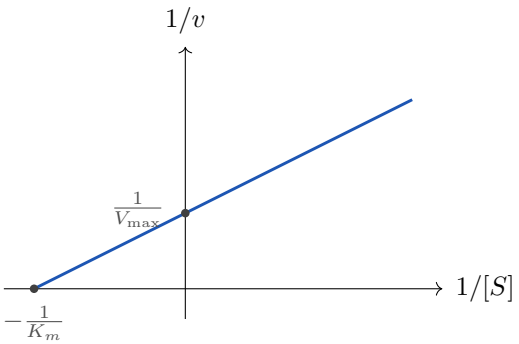
(A) the apparent K_m to increase while $V_{\max}$ stays unchanged

(B) both K_m and $V_{\max}$ to increase

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

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

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



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

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

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

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

Q4. An enzyme has a catalytic rate constant (turnover number) $k_{\text{cat}} = 1000\ \text{s}^{-1}$ and a Michaelis constant $K_m = 2 \times 10^{-4}$ M. Its catalytic efficiency, defined as k_{cat}/K_m, is: **[1 mark]**

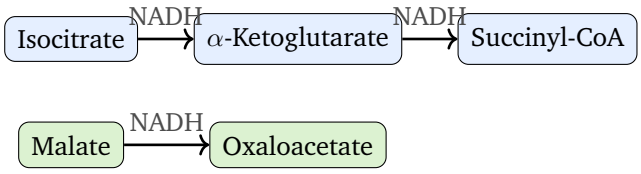
(A) $2 \times 10^{-7}\ \text{M}^{-1}\text{s}^{-1}$

(B) $5 \times 10^{-6}\ \text{M}^{-1}\text{s}^{-1}$

(C) $5 \times 10^{6}\ \text{M}^{-1}\text{s}^{-1}$

(D) $2 \times 10^{7}\ \text{M}^{-1}\text{s}^{-1}$

Q5. The citric acid (Krebs) cycle oxidises one molecule of acetyl-CoA to two molecules of CO_2. Three of its steps are shown below, each transferring electrons to NAD^+. The number of NADH molecules generated in one complete turn of the cycle is: **[1 mark]**



(A) 1

(B) 2

(C) 4

(D) 3

Q6. A reversible inhibitor binds only to the enzyme–substrate (ES) complex and not to the free enzyme. Compared with the uninhibited reaction, the presence of such an *uncompetitive* inhibitor causes: **[1 mark]**

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

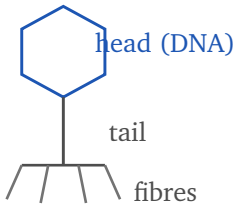
(B) the apparent K_m to increase while $V_{\max}$ stays unchanged

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

(D) both the apparent K_m and $V_{\max}$ to decrease

Microbiology

Q7. A bacteriophage of the structure shown below infects *Escherichia coli*, immediately hijacks the host machinery, replicates, assembles new virions and bursts the cell to release progeny within about 30 minutes. This reproductive pathway of the phage is the: **[1 mark]**



(A) lytic cycle

(B) lysogenic cycle

(C) binary fission

(D) budding

Q8. Tobacco mosaic virus (TMV) is a classic rod-shaped plant virus whose helical capsid encloses its genome. The genetic material carried inside a TMV particle is: **[1 mark]**

(A) double-stranded DNA

(B) single-stranded DNA

(C) single-stranded RNA

(D) double-stranded RNA

Q9. At the very end of the lytic cycle, a bacteriophage must break open the host cell wall so that the newly assembled virions can escape. The phage-encoded enzyme that degrades the bacterial peptidoglycan to burst the cell is: **[1 mark]**

(A) lysozyme (endolysin)

(B) integrase

(C) reverse transcriptase

(D) DNA gyrase

Q10. In a plaque assay, a dilute suspension of bacteriophage is mixed with excess host bacteria and poured over an agar plate, producing a confluent lawn dotted with clear zones. Each individual clear plaque in the lawn arises from: **[1 mark]**

(A) a single bacterial colony

(B) a spontaneously resistant mutant

(C) a single infectious virus particle

(D) a bacterial endospore

Q11. A temperate bacteriophage such as λ can enter a dormant state in which its DNA is inserted into and replicated along with the host chromosome, without immediately killing the cell. In this integrated state the phage genome is called a: **[1 mark]**

(A) prophage

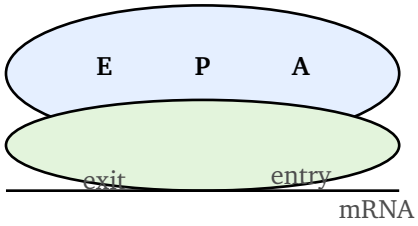
(B) mature virion

(C) capsomere

(D) plaque

Cell Biology and Molecular Biology

Q12. The elongation phase of translation on a ribosome uses three tRNA-binding sites, shown below. The site into which each incoming aminoacyl-tRNA (charged with the next amino acid) first enters is the: **[1 mark]**



(A) P site

(B) A site

(C) E site

(D) the $5'$ cap

Q13. Translation always begins at a specific initiator codon on the messenger RNA, which is read by a special initiator tRNA. In the standard genetic code this start codon, AUG, specifies the amino acid: **[1 mark]**

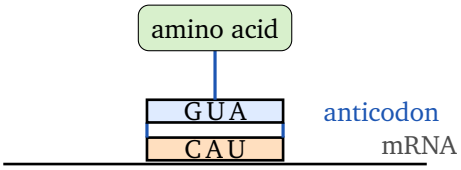
(A) valine

(B) leucine

(C) tryptophan

(D) methionine

Q14. During translation the codon on the mRNA is decoded by an adaptor molecule whose complementary anticodon base-pairs with it, and which carries the matching amino acid to the ribosome, as shown. This adaptor molecule is: **[1 mark]**



(A) messenger RNA (mRNA)

(B) transfer RNA (tRNA)

(C) ribosomal RNA (rRNA)

(D) small nuclear RNA (snRNA)

Q15. During the elongation cycle of translation, the ribosome must move exactly one codon along the mRNA after each peptide bond is formed, a step catalysed by elongation factor EF-G. The energy that drives this translocation comes from the hydrolysis of: **[1 mark]**

(A) ATP

(B) a transmembrane proton gradient

(C) NADH

(D) GTP

Q16. Elongation of the polypeptide continues until the ribosome reaches a codon that specifies no amino acid and is instead read by a release factor, ending translation. In the standard genetic code the number of such stop (termination) codons is: **[1 mark]**

(A) 1

(B) 2

(C) 4

(D) 3

Q17. On the ribosome the actual peptide bond between the growing chain and the next amino acid is formed by peptidyl transferase, a catalytic activity that resides in the large-subunit ribosomal RNA (a ribozyme). The chemical bond formed between the two amino acids is a: **[1 mark]**

(A) peptide bond

(B) phosphodiester bond

(C) glycosidic bond

(D) hydrogen bond

Q18. Consider the flow of genetic information during protein synthesis. The correct description of the polarity of reading and building is that: **[1 mark]**

(A) the mRNA is read $3' \rightarrow 5'$ while the polypeptide grows from its carboxyl to its amino terminus

(B) the mRNA is read $5' \rightarrow 3'$ while the polypeptide grows from its amino to its carboxyl terminus

(C) the mRNA is read $5' \rightarrow 3'$ while the polypeptide grows from its carboxyl to its amino terminus

(D) the mRNA is read $3' \rightarrow 5'$ while the polypeptide grows from its amino to its carboxyl terminus

Genetics, Immunology and Evolution

Q19. Two genes lie very close together on the same chromosome, so that they usually pass together into the same gamete and produce only a small proportion of recombinant offspring. Such genes are said to show: [1 mark]

(A) strong linkage, giving mostly parental-type gametes and few recombinants

(B) independent assortment giving a $1:1:1:1$ gamete ratio

(C) a recombination frequency of exactly 50%

(D) epistasis between the two loci

Q20. When a two-point test cross between two genes yields a recombination frequency of 50%, the two genes behave, for practical purposes of inheritance, as though they are: [1 mark]

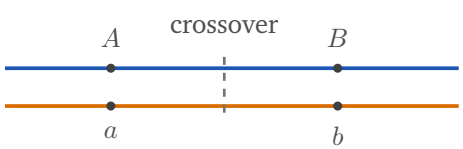
(A) completely linked

(B) exactly 5 map units apart

(C) genetically unlinked and assorting independently

(D) two alleles of the same gene

Q21. In a two-point test cross between linked genes, 1000 progeny are scored and 80 of them are found to be recombinant, as indicated by the crossover in the schematic below. The map distance between the two loci is: [2 marks]



(A) 8 centimorgan

(B) 80 centimorgan

(C) 0.8 centimorgan

(D) 92 centimorgan

Q22. In hybridoma technology, fused cells are selected in HAT (hypoxanthine–aminopterin–thymidine) medium. Aminopterin blocks the de novo synthesis of nucleotides, so only cells with a working salvage pathway survive. The unfused myeloma cells die in HAT medium because they lack the enzyme: **[2 marks]**

(A) hypoxanthine-guanine phosphoribosyltransferase (HGPRT)

(B) DNA polymerase

(C) reverse transcriptase

(D) RNA polymerase

Q23. In a three-point test cross, the frequency of observed double-crossover progeny is 0.006, whereas the frequency expected from the two single-crossover distances is 0.010. The coefficient of coincidence is 0.6; the corresponding interference is: **[2 marks]**

(A) 0.006

(B) 0.6

(C) 0.4

(D) 1.6

Q24. A single hybridoma clone is expanded in culture and its secreted antibody is collected. A defining property of the monoclonal antibodies obtained from one such clone is that they are: **[2 marks]**

(A) a mixture recognising many different epitopes on the antigen

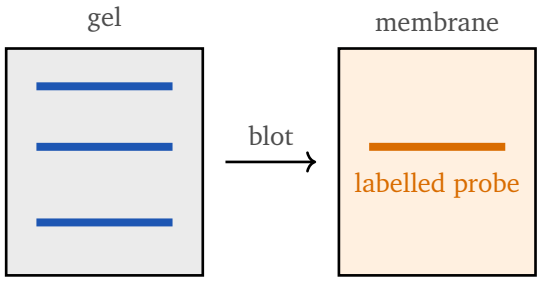
(B) of continually changing specificity from cell to cell

(C) unable to bind the original antigen

(D) all identical and directed against a single epitope

Recombinant DNA Technology and Bioinformatics

Q25. To detect one specific DNA sequence in a genome, total DNA is cut with restriction enzymes, separated by agarose gel electrophoresis, transferred (blotted) onto a membrane and then hybridised with a labelled complementary nucleic-acid probe, as sketched below. This technique is: [2 marks]



(A) Western blotting

(B) Northern blotting

(C) Southern blotting

(D) Eastern blotting

Q26. In modern automated Sanger (chain-termination) sequencing, the four chain-terminating dideoxynucleotides are run together in a single reaction and then separated by capillary electrophoresis. The feature that lets the instrument tell the four terminating bases apart as they pass the detector is: [2 marks]

(A) their different molecular weights only

(B) four distinct fluorescent dyes, one per ddNTP

(C) the radioactivity of the dNTPs

(D) antibody probes specific to each base

Q27. A researcher wants to measure how strongly a particular gene is expressed by detecting its messenger RNA transcript. The RNA is separated by gel electrophoresis, transferred to a membrane and probed with a labelled complementary sequence. This technique is: [2 marks]

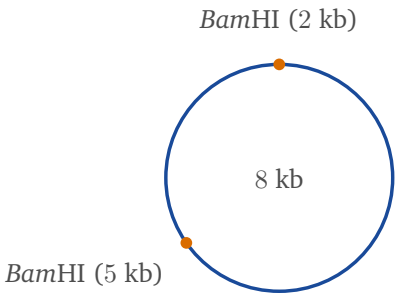
(A) Southern blotting

(B) Western blotting

(C) Northern blotting

(D) Southwestern blotting

Q28. A circular plasmid of total length 8 kb carries two recognition sites for *Bam*HI, located at the 2 kb and 5 kb positions measured around the circle, as shown. Complete digestion of the plasmid with *Bam*HI produces DNA fragments of: **[2 marks]**



(A) 3 kb and 5 kb

(B) 2 kb and 5 kb

(C) 4 kb and 4 kb

(D) 8 kb only (single linearised piece)

Q29. When a query protein sequence is compared against a database using BLAST, each reported hit is assigned an E-value. A very low (close to zero) E-value for an alignment indicates that: **[2 marks]**

(A) the alignment is likely to have arisen by chance

(B) the match is highly significant and unlikely to be random

(C) the query sequence is unusually long

(D) the two sequences have a high GC content

Q30. Before the dideoxy method became dominant, DNA could be sequenced by the Maxam–Gilbert method. Unlike the Sanger approach, the Maxam–Gilbert method reads a sequence on the basis of: **[2 marks]**

(A) base-specific chemical modification and cleavage of end-labelled DNA

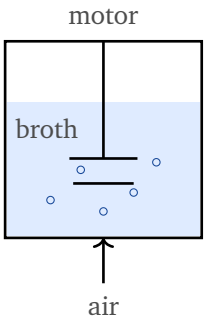
(B) chain termination by dideoxynucleotides

(C) hybridisation of the DNA to a microarray

(D) measuring the mass of each nucleotide by mass spectrometry

Bioprocess Engineering and Process Biotechnology

Q31. In the aerated stirred-tank fermenter shown, air is sparged into the broth and oxygen transfers across the gas–liquid interface. The volumetric mass-transfer coefficient is $k_La = 100\ \text{h}^{-1}$, the saturation dissolved-oxygen concentration is $C^* = 8$ mg L^{-1} and the actual dissolved-oxygen concentration in the broth is $C_L = 2$ mg L^{-1}. The oxygen transfer rate (OTR) is: **[2 marks]**



(A) 800 mg $\text{L}^{-1}\text{h}^{-1}$

(B) 600 mg $\text{L}^{-1}\text{h}^{-1}$

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

(D) 1000 mg $\text{L}^{-1}\text{h}^{-1}$

Q32. In an aerobic fermentation held at a steady dissolved-oxygen level, the growing cells take up oxygen at a specific rate $q_{O_2} = 8$ mmol O_2 $\text{g}^{-1}\text{h}^{-1}$, and the biomass concentration is $X = 5$ g L^{-1}. The oxygen uptake rate (OUR) of the culture, which the transfer must match, is: **[2 marks]**

(A) 8 mmol $\text{L}^{-1}\text{h}^{-1}$

(B) 1.6 mmol $\text{L}^{-1}\text{h}^{-1}$

(C) 13 mmol $\text{L}^{-1}\text{h}^{-1}$

(D) 40 mmol $L^{-1}h^{-1}$

Q33. Oxygen transfer in an aerobic bioreactor is written as OTR $= k_L a\,(C^* - C_L)$, where the driving force $(C^* - C_L)$ has units of concentration and OTR has units of concentration per time. The volumetric oxygen-transfer coefficient $k_L a$ therefore has units of: **[2 marks]**

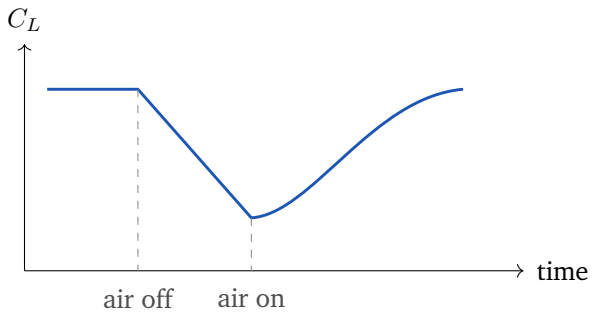
(A) reciprocal time (for example h^{-1})

(B) mg L^{-1}

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

(D) dimensionless

Q34. The dynamic (gassing-out) method used to characterise an aerobic fermenter is illustrated below: the air is first switched off so the respiring cells drive the dissolved oxygen down, and then the air is switched back on and the recovery of dissolved oxygen with time is recorded and analysed. The parameter obtained from this experiment is: **[2 marks]**



(A) the biomass yield coefficient $Y_{X/S}$

(B) the Monod saturation constant K_s

(C) the volumetric oxygen-transfer coefficient $k_L a$

(D) the maintenance coefficient m

Q35. In a stirred-tank aerobic fermenter, the engineer needs to raise the oxygen-transfer capacity to keep a dense culture from becoming oxygen limited. Increasing the impeller (agitation) speed, while other conditions are held fixed, generally: **[2 marks]**

(A) increases k_La by producing smaller bubbles and a larger interfacial area

(B) decreases k_La by coalescing the bubbles

(C) has no effect on k_La

(D) lowers the saturation concentration C^*

Q36. In a chemostat operating on Monod kinetics, the operator slowly raises the feed flow rate, and hence the dilution rate D. Washout, in which the cells are removed faster than they can grow and the culture is lost, sets in once D exceeds: **[2 marks]**

(A) the saturation constant K_s

(B) the maximum specific growth rate $\mu_{\max}$

(C) zero

(D) the yield coefficient $Y_{X/S}$

Q37. In a batch fermentation, 60 g L^{-1} of glucose is completely consumed and 15 g L^{-1} of dry cell biomass is formed. The observed biomass yield coefficient on substrate, $Y_{X/S}$, is: **[2 marks]**

(A) 4.0 g g^{-1}

(B) 0.25 g g^{-1}

(C) 0.5 g g^{-1}

(D) 0.15 g g^{-1}

Q38. Oxygen is only sparingly soluble in fermentation broth, which is the fundamental reason why oxygen transfer, rather than oxygen availability in the gas, so often limits aerobic cultures. At about 25 °C and in equilibrium with air, the saturation concentration of dissolved oxygen in water, C^*, is closest to: **[2 marks]**

(A) about 7–8 mg L^{-1}

(B) about 210 mg L^{-1}

(C) about 1000 mg L^{-1}

(D) about 50 mg L^{-1}

Plant and Animal Biotechnology

Q39. Many therapeutic monoclonal antibodies first raised in mice are re-engineered so that most of the antibody sequence is of human origin before they are given to patients. The main reason this "humanisation" is carried out is to: **[2 marks]**

(A) increase the overall size of the antibody

(B) reduce the antibody's immunogenicity so the patient's immune system does not reject it

(C) allow the antibody to bind many unrelated antigens at once

(D) enable the antibody to be produced in bacteria

Q40. Hybridomas for monoclonal-antibody production are made by fusing an antibody-secreting B lymphocyte with an immortal myeloma cell. The chemical agent most commonly used to promote the fusion of the two cell membranes is: **[2 marks]**

(A) trypsin

(B) collagenase

(C) calcium chloride alone

(D) polyethylene glycol (PEG)

Q41. A crop plant is genetically engineered to express the *cry* gene encoding the Cry (Bt) protein from the soil bacterium *Bacillus thuringiensis*. The trait that this transgene confers on the plant is: **[2 marks]**

(A) tolerance to a broad-spectrum herbicide

(B) tolerance to drought and salinity

(C) delayed ripening of the fruit

(D) resistance to insect pests

Q42. A common physical method for introducing foreign DNA into cultured animal cells applies a brief, high-voltage electric pulse that transiently opens pores in the plasma membrane, allowing DNA to enter. This transfection method is called: [2 marks]

(A) lipofection

(B) electroporation

(C) microinjection

(D) the gene gun (biolistics)

Q43. In a home pregnancy test kit and in a sandwich ELISA, the reagent immobilised on the strip or plate that specifically captures the target antigen (for example the hormone hCG) is: [2 marks]

(A) a restriction endonuclease

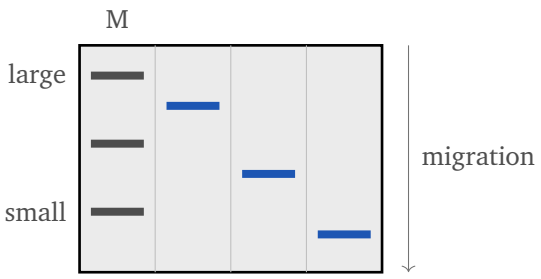
(B) a monoclonal antibody

(C) a single-stranded DNA probe

(D) a ribozyme

Analytical Techniques

Q44. In preparing a sample for reducing SDS–PAGE, the loading buffer contains, besides SDS, a reagent such as β-mercaptoethanol or dithiothreitol. The specific purpose of adding this reducing agent before running the gel shown below is to: [2 marks]



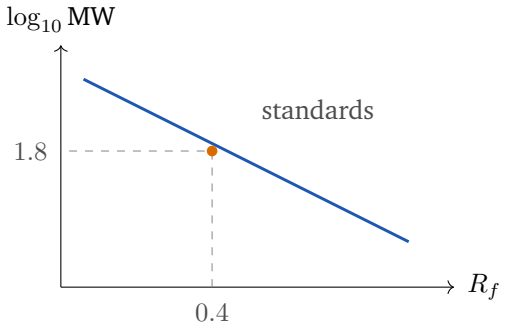
(A) add extra negative charge to the polypeptides

(B) stain the separated protein bands

(C) break the disulphide bonds so that the polypeptide subunits separate and migrate individually

(D) cross-link the polyacrylamide gel matrix

Q45. On an SDS–PAGE gel, a set of standards gives a calibration line $\log_{10}(\text{MW in kDa}) = -1.5\,R_f + 2.4$, where R_f is the relative migration distance. An unknown protein band migrates with $R_f = 0.4$. Its estimated molecular weight is closest to: **[2 marks]**



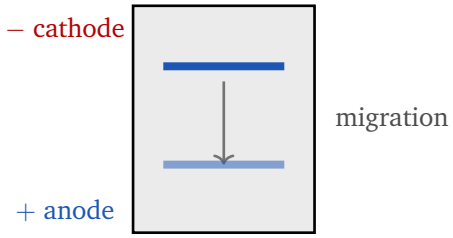
(A) 25 kDa

(B) 63 kDa

(C) 100 kDa

(D) 15 kDa

Q46. When an SDS-treated protein sample is loaded near the cathode of a vertical slab gel and the current is switched on, the polypeptides move down through the gel toward the opposite electrode, as shown. They migrate in this direction because the bound SDS gives every polypeptide: **[2 marks]**



(A) a net positive charge, so they run toward the cathode

(B) essentially no net charge

(C) a charge that depends on the protein's own isoelectric point

(D) a uniform net negative charge, so they run toward the anode

Detailed Solutions

Q1.

Solution

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

Step 1 – list the data: $V_{\max} = 120\ \mu$mol min^{-1}, $K_m = 4$ mM and $[S] = 12$ mM.

Step 2 – substitute into the equation: $v = \dfrac{120 \times 12}{4 + 12}$

Step 3 – evaluate the numerator: $120 \times 12 = 1440$

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

Step 5 – complete the division: $v = \dfrac{1440}{16}$

$v = 90\ \mu$mol min^{-1}

Step 6 – sanity check: Since $[S] = 12$ mM is three times $K_m = 4$ mM, the velocity should be $\dfrac{3}{4}V_{\max} = 90$, which matches.

Final Answer: $v = 90\ \mu$mol min^{-1} $\Rightarrow$ C

Answer: (C) Go Back to Q1

Q2.

Solution

Concept – non-competitive inhibition: A classical non-competitive inhibitor binds equally to the free enzyme and to the ES complex at a site away from the active site, so it removes a fraction of enzyme from productive catalysis but does not change substrate binding.

Step 1 – effect on $V_{\max}$: Because some enzyme is effectively taken out of action no matter how much substrate is added, the maximum attainable velocity falls, so $V_{\max}$ **decreases**.

Step 2 – effect on K_m: The inhibitor does not compete with substrate for the active site, so the substrate's apparent affinity is unchanged and K_m **stays the same**.

Step 3 – match to the options: $V_{\max}$ down, K_m unchanged $\Rightarrow$ option C.

Why the other options are wrong:

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

- B and D: neither a rise in K_m nor a fall in K_m fits pure non-competitive inhibition.

Final Answer: $V_{\max}$ decreases, K_m unchanged $\Rightarrow$ C

Answer: (C) Go Back to Q2

Q3.

Solution

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

Step 1 – identify the vertical intercept: The y-intercept occurs where $1/[S] = 0$.

Step 2 – substitute $1/[S] = 0$: $\frac{1}{v} = \frac{K_m}{V_{\max}} \times 0 + \frac{1}{V_{\max}}$

Step 3 – simplify: $\frac{1}{v} = \frac{1}{V_{\max}}$

Step 4 – interpret: The line therefore crosses the vertical $(1/v)$ axis at $\frac{1}{V_{\max}}$, exactly as marked on the plot.

Why the other options are wrong:

- A, $-\frac{1}{K_m}$: is the *horizontal*-axis intercept, not the vertical one.
- B, $\frac{K_m}{V_{\max}}$: is the slope of the line.
- C, $-\frac{1}{V_{\max}}$: has the wrong sign.

Final Answer: y-intercept $= \frac{1}{V_{\max}} \Rightarrow$ D

Answer: (D) Go Back to Q3

Q4.

Solution

Concept – catalytic efficiency: The ratio k_{cat}/K_m (the specificity constant) measures how efficiently an enzyme converts substrate to product at low substrate concentration.

Step 1 – list the data: $k_{\text{cat}} = 1000\ \text{s}^{-1}$ and $K_m = 2 \times 10^{-4}$ M.

Step 2 – write the ratio: $\frac{k_{\text{cat}}}{K_m} = \frac{1000}{2 \times 10^{-4}}$

Step 3 – separate the numbers and the powers of ten: $= \frac{1000}{2} \times \frac{1}{10^{-4}}$

Step 4 – evaluate each part: $\frac{1000}{2} = 500$ and $\frac{1}{10^{-4}} = 10^4$

Step 5 – combine: $= 500 \times 10^4 = 5 \times 10^6\ \text{M}^{-1}\text{s}^{-1}$

Step 6 – interpret: A value near 10^6–$10^8\ \text{M}^{-1}\text{s}^{-1}$ marks a very efficient enzyme, approaching the diffusion limit.

Final Answer: $k_{\text{cat}}/K_m = 5 \times 10^6\ \text{M}^{-1}\text{s}^{-1} \Rightarrow \boxed{\text{C}}$

Answer: (C) Go Back to Q4

Q5.

Solution

Concept – the redox steps of the citric acid cycle: One turn of the Krebs cycle oxidises acetyl-CoA and transfers electrons to NAD^+ and FAD; the three NAD^+-linked dehydrogenase steps each make one NADH.

Step 1 – list the NADH-producing steps: (i) isocitrate $\rightarrow$ α-ketoglutarate (isocitrate dehydrogenase).

Step 2 – continue: (ii) α-ketoglutarate $\rightarrow$ succinyl-CoA (α-ketoglutarate dehydrogenase).

Step 3 – continue: (iii) malate $\rightarrow$ oxaloacetate (malate dehydrogenase).

Step 4 – count them: Number of NADH per turn $= 3$.

Step 5 – note the other carriers (aside): The cycle also makes 1 FADH_2 (at succinate dehydrogenase) and 1 GTP, but the question asks only for NADH.

Final Answer: 3 NADH per turn $\Rightarrow \boxed{\text{D}}$

Answer: (D) Go Back to Q5

Q6.

Solution

Concept – uncompetitive inhibition: An uncompetitive inhibitor binds *only* to the enzyme–substrate complex, ES, and not to the free enzyme.

Step 1 – effect on $V_{\max}$: By tying up ES, the inhibitor lowers the amount of complex that can turn over, so the maximum velocity falls; $V_{\max}$ **decreases**.

Step 2 – effect on K_m: Removing ES from the equilibrium pulls more free enzyme

and substrate into complex (Le Chatelier), so the substrate appears to bind more tightly and the apparent K_m also **decreases**.

Step 3 – key signature: Both $V_{\max}$ and K_m fall by the same factor, so their ratio $V_{\max}/K_m$ stays constant; on a Lineweaver–Burk plot the lines are *parallel*.

Step 4 – match to the options: Both apparent K_m and $V_{\max}$ decrease $\Rightarrow$ option D.

Why the other options are wrong:

- A: $V_{\max}$ down with K_m unchanged is *non-competitive* inhibition.
- B: K_m up with $V_{\max}$ unchanged is *competitive* inhibition.
- C: no change at all describes no inhibition.

Final Answer: both apparent K_m and $V_{\max}$ decrease $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q6

Q7.

Solution

Concept – the two lifestyles of a bacteriophage: A phage can follow a lytic cycle (immediate replication and cell lysis) or a lysogenic cycle (integration and dormancy).

Step 1 – read the described behaviour: The phage takes over the host at once, replicates, assembles progeny and *bursts* the cell to release them.

Step 2 – match to a cycle: Rapid multiplication ending in host lysis is the definition of the **lytic cycle**.

Step 3 – confirm the timescale: A burst within roughly 30 minutes releasing many virions is typical of virulent lytic phages such as T4.

Why the other options are wrong:

- B, lysogenic cycle: the phage DNA integrates and stays dormant as a prophage; the cell is not immediately lysed.
- C, binary fission: is how bacteria divide, not how viruses reproduce.
- D, budding: is a release mechanism of some enveloped animal viruses, not of a lytic tailed phage.

Final Answer: the lytic cycle $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q7

Q8.

Solution

Concept – the genome of tobacco mosaic virus: Different virus families store their genetic information as DNA or RNA, single- or double-stranded.

Step 1 – recall TMV's classification: TMV is the archetypal positive-sense, single-stranded RNA plant virus with a helical capsid.

Step 2 – state the genome: Its genetic material is **single-stranded RNA**.

Step 3 – historical note: The reconstitution experiments of Fraenkel-Conrat and Singer showed that the RNA of TMV, not its coat protein, carries the infectivity and genetic information.

Why the other options are wrong:

- A, dsDNA: is the genome of phages like T4 or of herpesviruses, not TMV.
- B, ssDNA: is found in viruses such as ϕX174, not TMV.
- D, dsRNA: is characteristic of reoviruses, not TMV.

Final Answer: single-stranded RNA $\Rightarrow$ C

Answer: (C) Go Back to Q8

Q9.

Solution

Concept – how a phage escapes at the end of the lytic cycle: To release its progeny, a phage must destroy the bacterial cell wall, which is made of peptidoglycan.

Step 1 – identify the target: The barrier is the peptidoglycan (murein) layer of the cell wall.

Step 2 – name the enzyme: The phage-encoded **lysozyme (endolysin)** hydrolyses the glycosidic bonds of peptidoglycan, weakening the wall so the cell bursts.

Step 3 – fit the mechanism: Together with a holin that permeabilises the membrane, endolysin causes the timed lysis that releases the new virions.

Why the other options are wrong:

- B, integrase: inserts phage DNA into the host chromosome during lysogeny; it does not lyse the wall.
- C, reverse transcriptase: copies RNA into DNA in retroviruses and is unrelated here.

- D, DNA gyrase: is a host topoisomerase, not a wall-degrading enzyme.

Final Answer: lysozyme (endolysin) $\Rightarrow$ A

Answer: (A) Go Back to Q9

Q10.

Solution

Concept – the plaque assay: A plaque is a clear zone in a bacterial lawn where cells have been lysed by successive rounds of phage infection.

Step 1 – how a plaque forms: One infectious phage infects a single cell, lyses it, and the released progeny infect neighbouring cells, spreading a visible cleared circle.

Step 2 – identify the origin of each plaque: Each separate plaque therefore traces back to **a single infectious virus particle** (one plaque-forming unit).

Step 3 – use in quantification: Counting plaques and multiplying by the dilution factor gives the phage titre in plaque-forming units per millilitre (PFU/mL).

Why the other options are wrong:

- A, a bacterial colony: colonies are opaque growth, not clear lysis zones.
- B, a resistant mutant: would grow *within* the lawn, not clear it.
- D, an endospore: is a survival structure, unrelated to plaque formation.

Final Answer: a single infectious virus particle $\Rightarrow$ C

Answer: (C) Go Back to Q10

Q11.

Solution

Concept – lysogeny and the prophage: A temperate phage such as λ can integrate its DNA into the host chromosome and be passively replicated with it.

Step 1 – describe the integrated state: The phage DNA is inserted into the bacterial chromosome and copied each time the cell divides, without producing new virions.

Step 2 – name it: In this integrated, dormant form the phage genome is called a **prophage**.

Step 3 – note induction: Stress (for example UV damage) can trigger the

prophage to excise and switch to the lytic cycle.

Why the other options are wrong:

- B, mature virion: is the complete infectious particle outside the cell, not integrated DNA.
- C, capsomere: is a protein subunit of the capsid.
- D, plaque: is the clear zone seen in a plaque assay, not the integrated genome.

Final Answer: a prophage $\Rightarrow$ A

Answer: (A) Go Back to Q11

Q12.

Solution

Concept – the three tRNA sites of the ribosome: During elongation the ribosome has an A (aminoacyl), a P (peptidyl) and an E (exit) site, through which tRNAs pass in that order.

Step 1 – trace the path of a tRNA: A charged aminoacyl-tRNA first enters at one site, is then shifted as the peptide grows, and finally leaves.

Step 2 – name the entry site: The incoming aminoacyl-tRNA delivering the *next* amino acid enters the **A site**.

Step 3 – follow the sequence: After peptide-bond formation and translocation it moves to the P site, and then out through the E site.

Why the other options are wrong:

- A, P site: holds the tRNA carrying the growing peptide, not the newly arriving one.
- C, E site: is where the deacylated tRNA exits.
- D, the $5'$ cap: is a feature of eukaryotic mRNA, not a tRNA-binding site.

Final Answer: the A site $\Rightarrow$ B

Answer: (B) Go Back to Q12

Q13.

Solution

Concept – the start codon: Translation begins at a defined initiator codon recognised by a special initiator tRNA.

Step 1 – recall the start codon: The universal start codon is AUG.

Step 2 – read out the amino acid: AUG specifies **methionine** (formyl-methionine in bacteria), so almost every nascent polypeptide starts with methionine.

Step 3 – note downstream trimming: The initiator methionine is often removed later by methionine aminopeptidase, but it is still the amino acid placed first.

Why the other options are wrong:

- A, valine (GUN codons), B, leucine (CUN and others) and C, tryptophan (UGG) are all coded by different codons, none of which is the start codon AUG.

Final Answer: methionine $\Rightarrow$ D

Answer: (D) Go Back to Q13

Q14.

Solution

Concept – the adaptor of translation: Crick's adaptor hypothesis predicted a molecule that reads the codon and carries the matching amino acid.

Step 1 – what the molecule does: It base-pairs with the mRNA codon through a complementary *anticodon* and delivers a specific amino acid to the ribosome.

Step 2 – name it: This adaptor is the **transfer RNA (tRNA)**.

Step 3 – confirm with the figure: The mRNA codon CAU pairs with the tRNA anticodon GUA, and the tRNA carries its amino acid at the other end, exactly as drawn.

Why the other options are wrong:

- A, mRNA: carries the coding message; it does not itself carry amino acids.
- C, rRNA: forms the ribosome's structural and catalytic core, not the adaptor.
- D, snRNA: functions in splicing of pre-mRNA, not in decoding codons.

Final Answer: transfer RNA (tRNA) $\Rightarrow$ B

Answer: (B) Go Back to Q14

Q15.

Solution

Concept – energy source for translocation: Both the delivery of aminoacyl-tRNA (by EF-Tu) and translocation of the ribosome (by EF-G) are powered by GTP-dependent elongation factors.

Step 1 – identify the step: Translocation moves the ribosome one codon along the mRNA after each peptide bond, driven by EF-G.

Step 2 – identify the fuel: EF-G binds GTP and hydrolyses it; the energy from **GTP hydrolysis** drives the conformational change that shifts the tRNAs and mRNA.

Step 3 – generalise: Each elongation cycle consumes GTP twice (once at aminoacyl-tRNA delivery, once at translocation).

Why the other options are wrong:

- A, ATP: is used to *charge* tRNAs with amino acids, not for translocation.
- B, a proton gradient: drives ATP synthesis in mitochondria, not ribosome movement.
- C, NADH: is an electron carrier, not the direct energy source here.

Final Answer: GTP hydrolysis $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q15

Q16.

Solution

Concept – termination of translation: Elongation ends when the ribosome reaches a stop codon, which is read not by a tRNA but by a release factor.

Step 1 – list the stop codons: The three stop codons are UAA, UAG and UGA.

Step 2 – count them: Number of stop codons $= 3$.

Step 3 – explain their action: None of them pairs with a tRNA; instead a release factor binds and triggers hydrolysis of the finished polypeptide from the tRNA.

Why the other options are wrong:

- A, 1, and B, 2: undercount the termination codons.
- C, 4: overcounts them; there are exactly three.

Final Answer: 3 stop codons $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q16

Q17.

Solution

Concept – the bond made by peptidyl transferase: The ribosome's large-subunit rRNA catalyses joining of successive amino acids during translation.

Step 1 – name the reaction: Peptidyl transferase links the carboxyl group of the growing chain to the amino group of the incoming amino acid.

Step 2 – name the bond: This covalent link between two amino acids is a **peptide bond** (an amide bond).

Step 3 – note the catalyst: Because the catalytic activity resides in rRNA, the ribosome is a ribozyme.

Why the other options are wrong:

- B, phosphodiester bond: joins nucleotides in nucleic acids, not amino acids.
- C, glycosidic bond: links sugars in carbohydrates.
- D, hydrogen bond: is a weak, non-covalent interaction, not the backbone link between residues.

Final Answer: a peptide bond $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q17

Q18.

Solution

Concept – polarity of reading and synthesis: Translation has a fixed directionality both for reading the message and for building the protein.

Step 1 – direction of reading the mRNA: The ribosome reads the mRNA from its $5'$ end toward its $3'$ end.

Step 2 – direction of building the protein: Amino acids are added starting at the amino (N) terminus and finishing at the carboxyl (C) terminus.

Step 3 – combine the two: So the mRNA is read $5' \rightarrow 3'$ while the polypeptide grows N $\rightarrow$ C.

Step 4 – match to the options: This is exactly option B.

Why the other options are wrong:

- A and D: state the mRNA is read $3' \rightarrow 5'$, which is incorrect.
- C: keeps the correct mRNA direction but reverses the protein direction.

Final Answer: mRNA read $5' \to 3'$, protein N $\to$ C $\Rightarrow$ B

Answer: (B) Go Back to Q18

Q19.

Solution

Concept – linkage: Genes physically close on the same chromosome are inherited together more often than chance, because a crossover rarely falls between them.

Step 1 – describe the outcome: Most gametes keep the parental combination of alleles, and only a few recombinant gametes are produced.

Step 2 – name the phenomenon: This tendency to be inherited together is **linkage**, and the closer the genes, the stronger it is.

Step 3 – link to map distance: The rarity of recombinants translates into a small recombination frequency and a short map distance.

Why the other options are wrong:

- B, independent assortment: is what *unlinked* genes on different chromosomes show.
- C, 50% recombination: is the value for genes so far apart that they behave as unlinked.
- D, epistasis: is an interaction affecting the phenotype, not the co-inheritance of loci.

Final Answer: strong linkage with few recombinants $\Rightarrow$ A

Answer: (A) Go Back to Q19

Q20.

Solution

Concept – the upper limit of recombination frequency: Recombination frequency between two loci can range from 0% (completely linked) up to a maximum of 50%.

Step 1 – interpret a 50% value: A recombination frequency of 50% means recombinant and parental gametes appear in equal numbers.

Step 2 – compare with independent assortment: Genes on *different* chromosomes also give 50% recombinants by independent assortment.

Step 3 – conclude: So loci at 50% recombination are indistinguishable from **un-**

linked genes that assort independently, even if they happen to sit far apart on the same chromosome.

Why the other options are wrong:

- A, completely linked: corresponds to 0% recombination, the opposite extreme.
- B, 5 map units: would mean only 5% recombination.
- D, the same gene: alleles of one gene do not recombine at all.

Final Answer: genetically unlinked, assorting independently $\Rightarrow$ $\boxed{\text{C}}$

Answer: (C) Go Back to Q20

Q21.

Solution

Concept – recombination frequency and map distance: Map distance in centimorgan (cM) equals the percentage of recombinant progeny, since 1 cM $= 1\%$ recombination.

Step 1 – list the data: Total progeny $= 1000$; recombinant progeny $= 80$.

Step 2 – compute the recombination frequency: $\text{RF} = \dfrac{\text{recombinants}}{\text{total}} = \dfrac{80}{1000}$

Step 3 – convert to a percentage: $= 0.08 = 8\%$

Step 4 – convert to map units: $8\% \times \dfrac{1 \text{ cM}}{1\%} = 8$ cM.

Step 5 – note validity: At only 8% recombination double crossovers are negligible, so the direct conversion is accurate.

Final Answer: 8 cM $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q21

Q22.

Solution

Concept – HAT selection in hybridoma technology: HAT medium forces cells to make nucleotides by the salvage pathway, because aminopterin blocks the de novo pathway.

Step 1 – what aminopterin does: Aminopterin inhibits dihydrofolate reductase, shutting down de novo synthesis of purines and pyrimidines.

Step 2 – the only escape: Cells can still survive if they use hypoxanthine and

thymidine through the *salvage* pathway.

Step 3 – the missing enzyme: The myeloma line used in fusions is chosen to be deficient in **HGPRT**, so it cannot run the salvage pathway and dies in HAT if it stays unfused.

Step 4 – why only hybridomas survive: A fused hybridoma gets HGPRT from the B-cell partner (salvage restored) and immortality from the myeloma partner, so only true hybridomas grow.

Final Answer: hypoxanthine-guanine phosphoribosyltransferase (HGPRT) $\Rightarrow$ A

Answer: (A) Go Back to Q22

Q23.

Solution

Concept – coefficient of coincidence and interference: The coefficient of coincidence (CoC) compares observed double crossovers with those expected, and interference is $I = 1 - \text{CoC}$.

Step 1 – write the CoC: $\text{CoC} = \dfrac{\text{observed double crossovers}}{\text{expected double crossovers}}$

Step 2 – substitute the data: $\text{CoC} = \dfrac{0.006}{0.010}$

Step 3 – evaluate: $\text{CoC} = 0.6$

Step 4 – compute interference: $I = 1 - \text{CoC} = 1 - 0.6$

$I = 0.4$

Step 5 – interpret: A positive interference of 0.4 means one crossover reduces the chance of a second nearby crossover, so fewer doubles appear than predicted.

Final Answer: interference $= 0.4 \Rightarrow$ C

Answer: (C) Go Back to Q23

Q24.

Solution

Concept – what "monoclonal" means: Because a hybridoma is derived from a single fused B cell, every cell in the clone makes the identical antibody.

Step 1 – trace the origin: All the cells descend from one parent hybridoma, so they carry the same rearranged antibody genes.

Step 2 – describe the product: Every secreted antibody molecule is therefore **identical** and binds the same single epitope (antigenic determinant).

Step 3 – contrast with polyclonal serum: A conventional antiserum contains a mixture of antibodies from many B-cell clones, recognising many epitopes; monoclonals avoid that heterogeneity.

Why the other options are wrong:

- A: recognising many epitopes describes a *polyclonal* antibody preparation.
- B: a single clone does not change its specificity from cell to cell.
- C: monoclonal antibodies do bind the original antigen; that is the point of selecting the clone.

Final Answer: all identical, directed against a single epitope $\Rightarrow$ D

Answer: (D) Go Back to Q24

Q25.

Solution

Concept – the blotting family: Southern (DNA), Northern (RNA) and Western (protein) blots are distinguished by the target molecule and the probe.

Step 1 – identify the target: Here the molecules separated and blotted are *DNA* fragments.

Step 2 – identify the probe: They are detected with a labelled complementary *nucleic-acid* probe that hybridises to the target sequence.

Step 3 – name the technique: Detecting a specific DNA sequence this way is **Southern blotting**, named after Edwin Southern.

Why the other options are wrong:

- A, Western blot: detects *protein* with an antibody.
- B, Northern blot: detects *RNA* with a nucleic-acid probe.
- D, Eastern blot: is a less standard term for detecting post-translational modifications, not this DNA method.

Final Answer: Southern blotting $\Rightarrow$ C

Answer: (C) Go Back to Q25

Q26.

Solution

Concept – dye-terminator sequencing: Modern automated Sanger sequencing runs all four ddNTPs in one tube and reads them optically.

Step 1 – the key labelling trick: Each of the four dideoxynucleotides (ddA, ddC, ddG, ddT) carries a *different* fluorescent dye.

Step 2 – how the read-out works: As the size-sorted fragments pass a laser detector during capillary electrophoresis, the colour of the fluorescence at each position reveals the terminating base.

Step 3 – the advantage: Because the four bases are colour-coded, a single lane (capillary) reads the whole sequence, instead of four separate lanes.

Why the other options are wrong:

- A: molecular weight sets the migration order but does not by itself identify the base.
- C: radiolabelling of dNTPs was the older, manual approach and does not colour-code bases.
- D: antibodies are not used to read sequencing ladders.

Final Answer: four distinct fluorescent dyes, one per ddNTP $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q26

Q27.

Solution

Concept – the blotting family, RNA version: Detecting a specific RNA transcript uses the same logic as Southern blotting but with RNA as the target.

Step 1 – identify the target: Here the molecule to be detected is the *messenger RNA* of a gene.

Step 2 – name the method: Separating RNA by electrophoresis, blotting it and probing with a labelled complementary sequence is **Northern blotting**.

Step 3 – what it reveals: The intensity of the band reports the abundance of that transcript, and its position reports the transcript size.

Why the other options are wrong:

- A, Southern blot: targets DNA, not RNA.
- B, Western blot: targets protein with an antibody.

- D, Southwestern blot: detects DNA-binding *proteins*, not mRNA levels.

Final Answer: Northern blotting $\Rightarrow$ C

Answer: (C) Go Back to Q27

Q28.

Solution

Concept – fragments from cutting a circular DNA: A circular molecule with k restriction sites gives k linear fragments, whose sizes are the arc lengths between neighbouring sites.

Step 1 – list the data: Total size $= 8$ kb; *Bam*HI sites at the 2 kb and 5 kb positions.

Step 2 – fragment between the two sites: From 2 kb to 5 kb around the circle: $5 - 2 = 3$ kb.

Step 3 – the remaining fragment: The rest of the circle: $8 - 3 = 5$ kb.

Step 4 – state the two fragments: 3 kb and 5 kb (two cuts on a circle give two pieces).

Step 5 – check the sum: $3 + 5 = 8$ kb, the full plasmid length, so the accounting is complete.

Final Answer: 3 kb and 5 kb $\Rightarrow$ A

Answer: (A) Go Back to Q28

Q29.

Solution

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

Step 1 – interpret a low E-value: A very small E-value means such a good match would almost never occur at random.

Step 2 – conclude significance: So a low E-value marks a **highly significant** hit, likely reflecting real homology.

Step 3 – the direction of the scale: Larger E-values (approaching 1 or more) indicate matches that could easily arise by chance and are therefore weak.

Why the other options are wrong:

- A: a chance match corresponds to a *high* E-value, not a low one.

- C: query length affects the raw score but is not what the E-value directly reports.
- D: GC content is unrelated to the statistical significance encoded by the E-value.

Final Answer: a highly significant, non-random match $\Rightarrow$ B

Answer: (B) Go Back to Q29

Q30.

Solution

Concept – the Maxam–Gilbert method: The Maxam–Gilbert (chemical) method sequences DNA by cleaving it at specific bases rather than by synthesising new strands.

Step 1 – label the DNA: An end of the DNA is radioactively labelled.

Step 2 – chemically modify and cleave: Separate reactions use chemicals that modify and then break the DNA preferentially at particular bases (for example G, or A+G, or C, or C+T).

Step 3 – read the ladder: The nested set of end-labelled fragments is separated by gel electrophoresis, and the sequence is read from the pattern of cleavage.

Step 4 – contrast with Sanger: Sanger sequencing instead *synthesises* new strands and stops them with ddNTPs, so the two methods differ fundamentally.

Why the other options are wrong:

- B: chain termination by ddNTPs is the *Sanger* method.
- C: microarray hybridisation is a different technology (sequencing by hybridisation).
- D: mass spectrometry of single nucleotides is not the basis of Maxam–Gilbert.

Final Answer: base-specific chemical cleavage of end-labelled DNA $\Rightarrow$ A

Answer: (A) Go Back to Q30

Q31.

Solution

Concept – the oxygen transfer rate (OTR): 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 – compute the driving force: $C^* - C_L = 8 - 2 = 6\ \text{mg L}^{-1}$

Step 3 – substitute into the OTR equation: OTR $= 100 \times 6$

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

Step 5 – check the units: $\text{h}^{-1} \times \text{mg L}^{-1} = \text{mg L}^{-1}\text{h}^{-1}$, a rate of concentration change, as required.

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

Answer: (B) Go Back to Q31

Q32.

Solution

Concept – the oxygen uptake rate (OUR): OUR $= q_{O_2} X$, the specific oxygen uptake rate times the biomass concentration.

Step 1 – list the data: $q_{O_2} = 8\ \text{mmol O}_2\ \text{g}^{-1}\text{h}^{-1}$ and $X = 5\ \text{g L}^{-1}$.

Step 2 – substitute: OUR $= 8 \times 5$

Step 3 – evaluate: OUR $= 40\ \text{mmol L}^{-1}\text{h}^{-1}$

Step 4 – check the units: $\text{mmol g}^{-1}\text{h}^{-1} \times \text{g L}^{-1} = \text{mmol L}^{-1}\text{h}^{-1}$, a volumetric consumption rate.

Step 5 – interpret: At steady dissolved oxygen the transfer must supply this same $40\ \text{mmol L}^{-1}\text{h}^{-1}$, so OTR = OUR.

Final Answer: OUR $= 40\ \text{mmol L}^{-1}\text{h}^{-1} \Rightarrow \boxed{\text{D}}$

Answer: (D) Go Back to Q32

Q33.

Solution

Concept – dimensional analysis of $k_L a$: The units of $k_L a$ follow from rearranging the OTR equation.

Step 1 – rearrange for $k_L a$: $k_L a = \dfrac{\text{OTR}}{C^* - C_L}$

Step 2 – insert the units: $k_L a = \dfrac{\text{mg L}^{-1}\text{h}^{-1}}{\text{mg L}^{-1}}$

Step 3 – cancel the concentration units: The mg L^{-1} cancels top and bottom, leaving h^{-1}.

Step 4 – state the result: $k_L a$ has units of **reciprocal time**, such as h^{-1} or s^{-1}.

Why the other options are wrong:

- B, mg L^{-1}: are the units of a concentration such as C^*, not $k_L a$.
- C, mg $\text{L}^{-1}\text{h}^{-1}$: are the units of the whole OTR, not of $k_L a$ alone.
- D, dimensionless: is incorrect, since $k_L a$ carries a time dimension.

Final Answer: reciprocal time (for example h^{-1}) $\Rightarrow$ A

Answer: (A) Go Back to Q33

Q34.

Solution

Concept – the dynamic (gassing-out) method: This is a standard way to measure the oxygen-transfer capacity of a working fermenter from the response of the dissolved-oxygen probe.

Step 1 – switch off the air: With aeration stopped, the respiring cells consume dissolved oxygen and C_L falls (the descending part of the curve).

Step 2 – switch the air back on: Aeration resumes and C_L rises back toward C^* (the recovery part of the curve).

Step 3 – analyse the recovery: The rate of recovery, $\dfrac{dC_L}{dt} = k_L a\,(C^* - C_L) - \text{OUR}$, is fitted to extract the transfer coefficient.

Step 4 – name the parameter obtained: The experiment yields the **volumetric oxygen-transfer coefficient** $k_L a$.

Why the other options are wrong:

- A, $Y_{X/S}$: comes from biomass and substrate measurements, not from a DO transient.
- B, K_s: is found from growth-rate versus substrate data.
- D, maintenance coefficient: is obtained from chemostat substrate balances, not this method.

Final Answer: the volumetric oxygen-transfer coefficient $k_L a$ $\Rightarrow$ C

Answer: (C) Go Back to Q34

Q35.

Solution

Concept – how agitation affects oxygen transfer: k_La depends on the interfacial area a per unit volume and on the liquid-side coefficient k_L.

Step 1 – effect of faster stirring on bubble size: Higher impeller speed shears the sparged gas into *smaller* bubbles.

Step 2 – effect on interfacial area: Smaller bubbles at the same gas hold-up present a much *larger* total gas–liquid interfacial area a.

Step 3 – effect on turbulence: Greater turbulence also thins the liquid film, raising k_L; both effects push k_La up.

Step 4 – conclude: Therefore increasing agitation speed generally **increases** k_La, which is the usual way to relieve oxygen limitation.

Why the other options are wrong:

- B: faster stirring breaks up bubbles rather than coalescing them, so k_La does not fall.
- C: agitation clearly does affect k_La.
- D: C^* is set by temperature, pressure and gas composition, not by stirrer speed.

Final Answer: increases k_La (smaller bubbles, larger area) $\Rightarrow$ A

Answer: (A) Go Back to Q35

Q36.

Solution

Concept – washout in a chemostat: At steady state $\mu = D$; if the demanded growth rate exceeds what the organism can achieve, cells are removed faster than they grow.

Step 1 – write the steady-state relation: For a chemostat the cells grow at $\mu = D$ as long as a steady state exists.

Step 2 – recognise the ceiling: The specific growth rate cannot exceed the maximum value $\mu_{\max}$ set by the organism.

Step 3 – find the washout condition: If D is raised above $\mu_{\max}$, the required

$\mu = D$ is unattainable, so $\dfrac{dX}{dt} < 0$ and the biomass is progressively diluted out.

Step 4 – state the critical value: Washout therefore begins once $D > \mu_{\max}$ (strictly, at $D = D_{\text{crit}} \approx \mu_{\max}$ for a saturating feed).

Why the other options are wrong:

- A, K_s: is a substrate concentration, not a rate that sets washout.
- C, zero: a dilution rate above zero is normal operation, not washout.
- D, $Y_{X/S}$: is a yield, not a growth rate.

Final Answer: D exceeding $\mu_{\max} \Rightarrow$ B

Answer: (B) Go Back to Q36

Q37.

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 $= 15$ g L^{-1}; glucose consumed $= 60$ g L^{-1}.

Step 2 – substitute: $Y_{X/S} = \dfrac{15}{60}$

Step 3 – simplify: $Y_{X/S} = 0.25$ g g^{-1}

Step 4 – interpret: Each gram of glucose consumed produces 0.25 g of cells; the remaining carbon goes to products, CO_2 and maintenance.

Final Answer: $Y_{X/S} = 0.25$ g g$^{-1} \Rightarrow$ B

Answer: (B) Go Back to Q37

Q38.

Solution

Concept – the low solubility of oxygen: Oxygen is poorly soluble in aqueous media, which is why aerobic fermentations are so often transfer-limited.

Step 1 – recall the saturation value: In water at about 25 °C in equilibrium with air, the dissolved-oxygen saturation C^* is only about 7–8 mg L^{-1}.

Step 2 – put it in perspective: This tiny reservoir would be exhausted by a dense culture in seconds if it were not continuously replenished by transfer from the sparged air.

Step 3 – link to design: Because C^* is so small, the driving force $(C^* - C_L)$

is small, so a high k_La (vigorous aeration and agitation) is needed to meet the oxygen demand.

Why the other options are wrong:

- B, 210 mg L^{-1}: confuses the $\approx 21\%$ oxygen in air with its dissolved concentration.
- C, 1000 mg L^{-1}: is far too high for dissolved O_2.
- D, 50 mg L^{-1}: still greatly overstates the real solubility.

Final Answer: about 7–8 mg $L^{-1} \Rightarrow$ A

Answer: (A) Go Back to Q38

Q39.

Solution

Concept – humanising a monoclonal antibody: Mouse antibodies given to patients are seen as foreign and provoke an immune response, so they are re-engineered to look human.

Step 1 – the problem with a mouse antibody: Repeated dosing of a fully murine antibody triggers a human anti-mouse antibody (HAMA) response that neutralises the drug and can cause reactions.

Step 2 – the fix: Humanisation replaces most of the mouse sequence with human framework and constant regions, keeping only the antigen-binding loops from the mouse.

Step 3 – the outcome: This **reduces immunogenicity**, so the patient's immune system tolerates the antibody and the therapeutic works for longer.

Why the other options are wrong:

- A: humanisation is not about changing overall size.
- C: it preserves the original single specificity; it does not broaden binding.
- D: humanised antibodies are still made in mammalian cells, not bacteria.

Final Answer: to reduce immunogenicity and avoid rejection $\Rightarrow$ B

Answer: (B) Go Back to Q39

Q40.

Solution

Concept – fusing cells to make a hybridoma: Producing monoclonal antibodies requires physically merging a B cell with a myeloma cell.

Step 1 – the requirement: The two plasma membranes must be induced to fuse so the two nuclei end up in one cell.

Step 2 – the standard agent: Polyethylene glycol (PEG) is the chemical most commonly used; it dehydrates and brings the membranes into close contact so they fuse.

Step 3 – alternatives: Electrofusion (an electric pulse) is the other common physical method, but among the chemical choices listed PEG is the answer.

Why the other options are wrong:

- A, trypsin: is a protease used to detach cells, not to fuse them.
- B, collagenase: digests extracellular matrix; it does not promote fusion.
- C, calcium chloride alone: is used to make bacteria competent for DNA uptake, not to fuse mammalian cells.

Final Answer: polyethylene glycol (PEG) $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q40

Q41.

Solution

Concept – Bt crops: The *cry* gene of *Bacillus thuringiensis* encodes an insecticidal crystal (Cry) protein.

Step 1 – what the Cry protein does: When a susceptible insect larva eats the plant, the Cry protein is activated in its alkaline gut and punches pores in the gut epithelium, killing the larva.

Step 2 – the resulting trait: A plant expressing this transgene is protected against those insect pests, so the trait is **insect-pest resistance**.

Step 3 – real examples: Bt cotton and Bt maize are commercial crops that use exactly this strategy.

Why the other options are wrong:

- A, herbicide tolerance: comes from genes like *EPSPS* (for example Roundup Ready crops), not *cry*.

- B, drought and salinity tolerance: involves stress-response genes, not Bt.
- C, delayed ripening: is the Flavr Savr type trait using antisense polygalacturonase, unrelated to *cry*.

Final Answer: resistance to insect pests $\Rightarrow$ D

Answer: (D) Go Back to Q41

Q42.

Solution

Concept – electroporation: Foreign DNA can be driven into cells by transiently permeabilising the membrane with electricity.

Step 1 – describe the method: A brief, high-voltage electric pulse creates temporary pores in the plasma membrane.

Step 2 – how DNA enters: DNA in the surrounding buffer passes through these pores into the cytoplasm before the membrane reseals.

Step 3 – name it: This physical transfection method is **electroporation**.

Why the other options are wrong:

- A, lipofection: uses cationic lipid–DNA complexes, not an electric pulse.
- C, microinjection: physically injects DNA through a fine needle into individual cells.
- D, the gene gun (biolistics): fires DNA-coated metal particles into cells and is used mainly for plants.

Final Answer: electroporation $\Rightarrow$ B

Answer: (B) Go Back to Q42

Q43.

Solution

Concept – antibody-based detection assays: Immunoassays such as ELISA and lateral-flow pregnancy tests rely on antibodies that specifically capture the target antigen.

Step 1 – what is immobilised: The capture reagent fixed to the plate or strip must bind the antigen (for example hCG) with high specificity.

Step 2 – identify the reagent: That reagent is a **monoclonal antibody** directed

against the antigen.

Step 3 – how the read-out works: A second, labelled antibody then binds a different epitope of the captured antigen (a sandwich), producing the colour or line that signals a positive result.

Why the other options are wrong:

- A, restriction endonuclease: cuts DNA and has no role in capturing a protein antigen.
- C, single-stranded DNA probe: detects nucleic acids by hybridisation, not proteins.
- D, ribozyme: is a catalytic RNA, not an antigen-capture reagent.

Final Answer: a monoclonal antibody $\Rightarrow$ B

Answer: (B) Go Back to Q43

Q44.

Solution

Concept – the reducing agent in SDS–PAGE: Under *reducing* conditions the sample buffer contains a thiol reagent such as β-mercaptoethanol or DTT in addition to SDS.

Step 1 – what SDS does: SDS denatures the proteins and coats them with negative charge, but it cannot break covalent disulphide bonds.

Step 2 – what the reducing agent adds: β-mercaptoethanol **reduces (breaks) the disulphide bonds** that hold subunits or looped chains together.

Step 3 – the consequence: With the disulphides broken, a multi-subunit protein separates into its individual polypeptide chains, each of which then migrates according to its own size.

Why the other options are wrong:

- A: the negative charge is supplied by SDS, not by the reducing agent.
- B: staining is done afterward with a dye such as Coomassie blue.
- D: cross-linking the gel is the job of the acrylamide/bis and catalysts, not of β-mercaptoethanol.

Final Answer: to break disulphide bonds so subunits separate $\Rightarrow$ C

Answer: (C) Go Back to Q44

Q45.

Solution

Concept – reading a molecular weight from an SDS–PAGE standard curve: On SDS–PAGE, $\log_{10}(\text{MW})$ varies linearly with the relative migration distance R_f.

Step 1 – write the calibration line: $\log_{10}(\text{MW in kDa}) = -1.5\,R_f + 2.4$.

Step 2 – insert the measured R_f: $\log_{10}(\text{MW}) = -1.5(0.4) + 2.4$

Step 3 – evaluate the product: $-1.5 \times 0.4 = -0.6$

Step 4 – add the intercept: $\log_{10}(\text{MW}) = -0.6 + 2.4 = 1.8$

Step 5 – take the antilog: $\text{MW} = 10^{1.8}$

Step 6 – evaluate: $10^{1.8} \approx 63$ kDa.

Final Answer: MW ≈ 63 kDa $\Rightarrow$ B

Answer: (B) Go Back to Q45

Q46.

Solution

Concept – why SDS-treated proteins migrate toward the anode: In SDS–PAGE the direction of migration is set by the charge that SDS imparts.

Step 1 – effect of SDS on charge: SDS is an anionic detergent that binds along the polypeptide in proportion to its length, swamping the protein's own charge and giving it a large *net negative* charge.

Step 2 – response to the field: Negatively charged molecules are pulled toward the positive electrode, the **anode**.

Step 3 – combine with sieving: As they all move toward the anode, the gel matrix sorts them by size, so smaller proteins travel farther, exactly as the migrating band in the figure shows.

Why the other options are wrong:

- A: a net positive charge (movement to the cathode) is the opposite of what SDS produces.
- B: the proteins are far from neutral; SDS makes them strongly negative.
- C: SDS masks the native charge, so migration no longer depends on the protein's own pI.

Final Answer: a uniform net negative charge, so they run toward the anode $\Rightarrow$ D

Answer: (D) Go Back to Q46

Answer Key

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