GATE Biotechnology

Sample Paper – 2

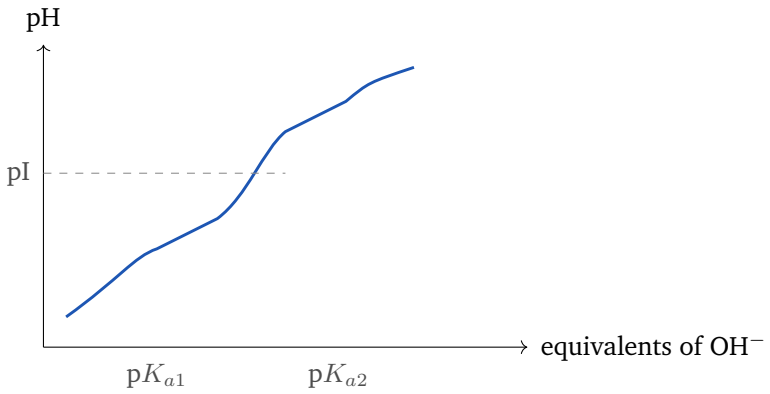
Duration: 128 Minutes **Maximum Marks: 72**

Instructions

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

Biochemistry

Q1. The titration curve of the amino acid glycine is sketched below. Glycine has two ionisable groups with p$K_{a1} = 2.34$ (the α-carboxyl group) and p$K_{a2} = 9.60$ (the α-amino group). Its isoelectric point (pI), the pH at which glycine carries no net charge, is: **[1 mark]**



(A) 2.34

(B) 9.60

(C) 11.94

(D) 5.97

Q2. Among the twenty standard amino acids, one has only a hydrogen atom as its side chain, so its α-carbon is attached to two identical groups and is therefore *not* a chiral (asymmetric) centre. This optically inactive amino acid is: **[1 mark]**

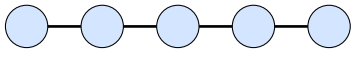
(A) alanine

(B) threonine

(C) cysteine

(D) glycine

Q3. A single polypeptide chain is made up of 200 amino-acid residues joined in a row, as sketched below. Taking the average mass of one residue in a protein as about 110 daltons, the approximate molecular weight of this polypeptide is: **[1 mark]**



$n = 200$ residues, $\sim$110 Da each

(A) 2.2 kDa

(B) 11 kDa

(C) 22 kDa

(D) 44 kDa

Q4. The regular local folding of a polypeptide backbone into α-helices and β-pleated sheets, stabilised mainly by hydrogen bonds between backbone amide and carbonyl groups, is described as the protein's: **[1 mark]**

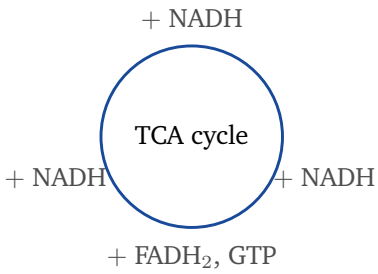
(A) primary structure

(B) tertiary structure

(C) secondary structure

(D) quaternary structure

Q5. One complete turn of the citric acid (Krebs) cycle oxidises one acetyl-CoA, releasing reducing equivalents as summarised below. The number of *NADH* molecules generated in a single turn of the cycle is: **[1 mark]**



(A) 1

(B) 3

(C) 4

(D) 12

Q6. Several coenzymes are derived from water-soluble vitamins. The flavin coenzyme that is derived from vitamin B_2 (riboflavin) and serves as a tightly bound electron carrier in many oxidoreductases is: **[1 mark]**

(A) NAD^+ (from niacin)

(B) coenzyme A (from pantothenate)

(C) thiamine pyrophosphate (from B_1)

(D) FAD (flavin adenine dinucleotide)

Microbiology

Q7. The acid-fast (Ziehl–Neelsen) staining technique is used to identify bacteria such as *Mycobacterium tuberculosis* whose walls are rich in waxy mycolic acids. The *primary* stain, driven into the cell with heat, is: **[1 mark]**

(A) crystal violet

(B) safranin

(C) methylene blue

(D) carbol fuchsin

Q8. An exponentially growing bacterial culture increases from 1.0×10^4 cells to 1.6×10^5 cells during a 4-hour period. The number of generations (doublings) that the population has undergone is: **[1 mark]**

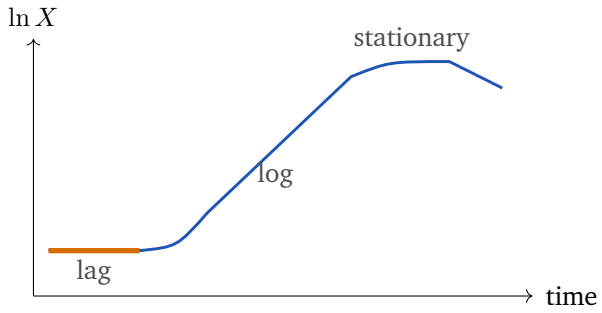
(A) 2

(B) 4

(C) 8

(D) 16

Q9. The batch growth curve of a bacterial culture, plotted as $\ln X$ against time, is shown below with one segment highlighted. The highlighted early phase, during which the cells adapt to the new medium and synthesise enzymes but do *not* increase in number, is the: **[1 mark]**



(A) exponential (log) phase

(B) lag phase

(C) stationary phase

(D) death (decline) phase

Q10. The Schaeffer–Fulton method is a differential stain used to demonstrate bacterial endospores, which are highly resistant to ordinary staining. In this method the *primary* stain that is steamed into the spore is: [1 mark]

(A) malachite green

(B) crystal violet

(C) safranin

(D) carbol fuchsin

Q11. Some bacteria are killed by molecular oxygen because they cannot detoxify its reactive by-products, and so they grow only in its complete absence. Such organisms are classified as: [1 mark]

(A) obligate anaerobes

(B) obligate aerobes

(C) facultative anaerobes

(D) microaerophiles

Cell Biology and Molecular Biology

Q12. As the replication fork advances, the unwinding of the parental duplex introduces positive supercoils (torsional strain) ahead of it. The enzyme that relieves this strain by transiently cutting and rejoining the DNA backbone is: [1 mark]

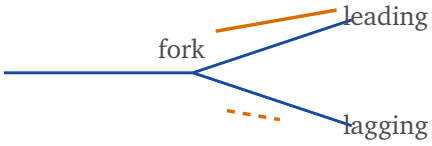
(A) helicase

(B) DNA topoisomerase (gyrase)

(C) primase

(D) DNA ligase

Q13. The replication fork below shows a leading strand made continuously and a lagging strand made as short pieces, each begun from a short RNA primer. The enzyme that lays down these RNA primers to start new DNA synthesis is: **[1 mark]**



(A) helicase

(B) DNA polymerase III

(C) primase

(D) DNA ligase

Q14. A DNA polymerase adds each incoming deoxynucleotide to the free hydroxyl group at the end of the growing strand. Consequently, the new DNA strand is always synthesised in the direction: **[1 mark]**

(A) $3' \rightarrow 5'$

(B) $5' \rightarrow 3'$

(C) both $5' \rightarrow 3'$ and $3' \rightarrow 5'$ equally

(D) $3' \rightarrow 3'$

Q15. In a sample of double-stranded DNA, chemical analysis shows that adenine makes up 30% of the total bases, as illustrated by the base-pairing scheme below. Applying Chargaff's rules, the percentage of guanine in this DNA is: **[1 mark]**

$$\begin{array}{c} \text{A} = \text{T}, \quad \text{G} \equiv \text{C} \\ \hline \text{A} - - - - - - - \text{T} \\ \text{G} - - - - - - - \text{C} \\ \text{A} - - - - - - - \text{T} \\ \hline \end{array}$$

(A) 20%

(B) 30%

(C) 40%

(D) 70%

Q16. The classic experiment that proved DNA replication is semiconservative, by following the density of DNA labelled with heavy (^{15}N) and light (^{14}N) nitrogen across successive generations, was performed by: **[1 mark]**

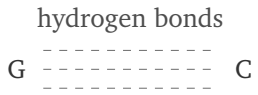
(A) Watson and Crick

(B) Hershey and Chase

(C) Meselson and Stahl

(D) Griffith

Q17. The complementary bases guanine and cytosine pair with each other in the DNA double helix, as shown below. The number of hydrogen bonds formed between a G and a C in a G≡C base pair is: **[1 mark]**



(A) 2

(B) 3

(C) 1

(D) 4

Q18. Besides adding nucleotides, DNA polymerase can recognise a wrongly inserted base, remove it and then continue. This built-in proofreading is carried out by the enzyme's: **[1 mark]**

(A) $3' \rightarrow 5'$ exonuclease activity

(B) $5' \rightarrow 3'$ polymerase activity

(C) $5' \rightarrow 3'$ exonuclease activity

(D) endonuclease activity

Genetics, Immunology and Evolution

Q19. In garden pea, tallness (T) is completely dominant over dwarfness (t). Two heterozygous tall plants are crossed, $Tt \times Tt$. The *genotypic* ratio expected among the F_2 offspring is: **[1 mark]**

(A) $3:1$

(B) $1:1$

(C) $1:2:1$

(D) $9:3:3:1$

Q20. During a primary immune response the first antibody class to be secreted is a large molecule that circulates as a pentamer and is very efficient at agglutination and complement activation. This antibody class is: **[1 mark]**

(A) IgM

(B) IgG

(C) IgA

(D) IgE

Genetics, Immunology and Evolution (continued)

Q21. A tall pea plant of unknown genotype is crossed with a dwarf plant (tt) in a test cross, and the offspring are 50% tall and 50% dwarf, as shown in the Punnett square. The genotype of the unknown tall parent must be: **[2 marks]**

	T	t
t	Tt	tt
t	Tt	tt

(A) TT (homozygous dominant)

(B) Tt (heterozygous)

(C) tt (homozygous recessive)

(D) cannot be determined from a test cross

Q22. Red–green colour blindness is an X-linked recessive trait. A woman who is a carrier (X^CX^c) marries a man with normal colour vision (X^CY). The probability that any given *son* of this couple is colour blind is: [2 marks]

(A) $\frac{1}{2}$

(B) $\frac{1}{4}$

(C) 0

(D) 1

Q23. An antibody molecule can be cleaved into fragments. The stem region formed by the paired constant domains of the two heavy chains, which determines the antibody's class and mediates effector functions such as complement fixation and binding to Fc receptors, is the: [2 marks]

(A) Fab region

(B) Fc (constant) region

(C) hypervariable (CDR) region

(D) hinge region

Q24. A population is described by the Hardy–Weinberg principle. According to this principle, one can conclude that the population is *evolving* at a given locus when: [2 marks]

(A) the allele frequencies satisfy $p + q = 1$

(B) the genotype frequencies are $p^2 : 2pq : q^2$

(C) the allele frequencies change from one generation to the next

(D) mating in the population is random

Recombinant DNA Technology and Bioinformatics

Q25. A *linear* DNA molecule of total length 10 kb carries two recognition sites for *Eco*RI, located at the 3 kb and 7 kb positions measured from the left end, as shown. Complete digestion of this DNA with *Eco*RI produces fragments of: [2 marks]

(A) 3 kb, 4 kb and 3 kb

(B) 3 kb and 7 kb

(C) 4 kb and 6 kb

(D) 10 kb only (single uncut piece)

Q26. The restriction enzyme *Eco*RI recognises the palindromic sequence 5′-GAATTC-3′ and cleaves between the G and the first A on each strand. Because the two staggered cuts are offset, the fragments generated carry: **[2 marks]**

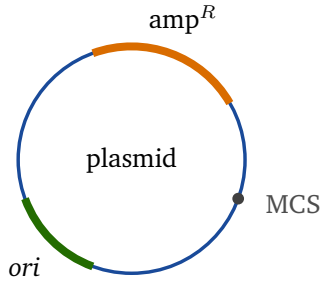
(A) blunt ends

(B) 5′ single-stranded (cohesive/sticky) overhangs

(C) 3′ overhangs of four bases

(D) no free ends at all

Q27. The map of a simple cloning plasmid is shown below, marking an ampicillin-resistance gene, a multiple cloning site and one further element. For the plasmid to be maintained and copied autonomously inside the bacterial host, the essential element is the: **[2 marks]**



(A) ampicillin-resistance gene

(B) multiple cloning site

(C) *lacZ* reporter gene

(D) origin of replication (*ori*)

Q28. To physically map and sequence a genome, researchers often need vectors that can accept very large DNA inserts, of the order of 100–300 kb, and maintain them stably in *Escherichia coli*. The cloning vector best suited to inserts of this size is a: **[2 marks]**

(A) standard high-copy plasmid

(B) phagemid

(C) cosmid

(D) bacterial artificial chromosome (BAC)

Q29. Some restriction enzymes cut both strands at the centre of their palindromic recognition site and therefore leave flush, double-stranded ends with no overhangs. An enzyme that generates such *blunt* ends is: **[2 marks]**

(A) *Sma*I (cuts CCC↓GGG)

(B) *Eco*RI (cuts G↓AATTC)

(C) *Hind*III (cuts A↓AGCTT)

(D) *Bam*HI (cuts G↓GATCC)

Q30. When the results of a protein BLAST search are ranked, each hit is reported with an associated E-value. A hit with a very *low* E-value (for example 10^{-40}) should be interpreted as: **[2 marks]**

(A) an alignment likely to have arisen purely by chance

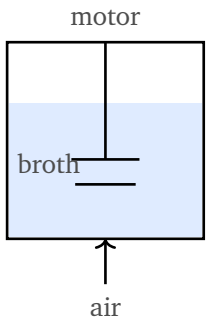
(B) a match with poor sequence coverage

(C) a statistically significant, biologically meaningful match

(D) a sign of high sequence divergence

Bioprocess Engineering and Process Biotechnology

Q31. In the batch stirred-tank bioreactor shown, an organism grows exponentially and the biomass concentration rises from 2 g L^{-1} to 16 g L^{-1} over a period of 4 hours. The specific growth rate μ during this exponential phase is nearest to: **[2 marks]**



(A) $0.17\ \text{h}^{-1}$

(B) $0.35\ \text{h}^{-1}$

(C) $0.69\ \text{h}^{-1}$

(D) $0.52\ \text{h}^{-1}$

Q32. In a batch fermentation, 60 g of glucose is consumed as the carbon and energy source and 15 g of dry cell biomass is formed. The biomass yield coefficient on substrate, $Y_{X/S}$, is: **[2 marks]**

(A) $0.25\ \text{g g}^{-1}$

(B) $4.0\ \text{g g}^{-1}$

(C) $0.75\ \text{g g}^{-1}$

(D) $0.15\ \text{g g}^{-1}$

Q33. For a culture in balanced exponential growth, the doubling time is related to the specific growth rate by $t_d = \dfrac{\ln 2}{\mu}$. If the specific growth rate is $\mu = 0.693\ \text{h}^{-1}$, the doubling time of the culture is: **[2 marks]**

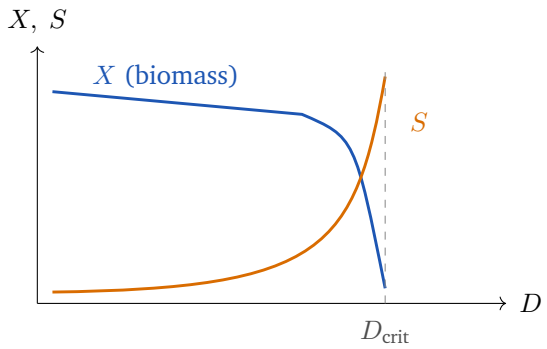
(A) 0.5 h

(B) 2 h

(C) 1 h

(D) 0.693 h

Q34. In a chemostat obeying Monod kinetics, the steady-state residual substrate concentration is $S = \dfrac{K_s\, D}{\mu_{\max} - D}$, and the biomass and substrate vary with the dilution rate D as plotted below. As the dilution rate D is raised towards $\mu_{\max}$, the residual substrate concentration S: **[2 marks]**



(A) approaches zero

(B) stays exactly constant

(C) increases sharply towards the feed value as washout is approached

(D) becomes negative

Q35. In a fed-batch fermentation, the limiting substrate is fed slowly so that its concentration in the broth is deliberately kept very low throughout the run. The main reason for operating in this way is to: **[2 marks]**

(A) increase the working volume as fast as possible

(B) dilute the product to keep it stable

(C) wash the cells out of the reactor

(D) avoid substrate (or catabolite) inhibition and overflow metabolism

Q36. The mixing performance of a stirred-tank bioreactor is characterised by a dimensionless group that expresses the ratio of inertial forces to viscous forces in the agitated fluid. For an impeller of diameter D_i turning at N revolutions per second in a broth of density ρ and viscosity μ, this group is: **[2 marks]**

(A) the Reynolds number, $\dfrac{\rho N D_i^2}{\mu}$

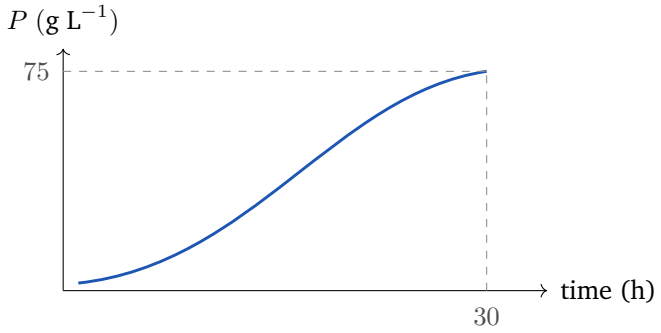
(B) the Damköhler number

(C) the Peclet number

(D) the Schmidt number

Q37. In the batch fermentation whose product-formation curve is shown, the product concentration reaches its final value of 75 g L^{-1} at the end of 30

hours of operation. The overall volumetric productivity of the product for this batch is: [2 marks]



(A) 0.4 g L^{-1}h^{-1}

(B) 2250 g L^{-1}h^{-1}

(C) 2.5 g L^{-1}h^{-1}

(D) 30 g L^{-1}h^{-1}

Q38. In a chemostat there is a critical dilution rate, D_{crit}, above which the cells are removed faster than they can grow and the culture is completely washed out. For a feed substrate concentration far above K_s, this critical dilution rate is approximately equal to: [2 marks]

(A) zero

(B) $\mu_{\max}$

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

(D) the saturation constant K_s

Plant and Animal Biotechnology

Q39. When an explant is placed on a nutrient medium supplemented with suitable auxins and cytokinins, it often first proliferates into an unorganised, dedifferentiated mass of parenchyma-like cells. This mass, from which shoots and roots can later be regenerated, is called: [2 marks]

(A) a protoplast

(B) a callus

(C) an apical meristem

(D) a somatic embryo

Q40. In plant tissue culture the balance of two classes of growth regulator in the medium directs organ formation. A medium with a *high auxin-to-cytokinin ratio* generally promotes: [2 marks]

(A) root initiation (rhizogenesis)

(B) shoot bud initiation (caulogenesis)

(C) continued callus growth only

(D) early flowering

Q41. The most widely used basal medium for the *in vitro* culture of plant tissues, notable for its high concentrations of nitrate and ammonium salts, is: [2 marks]

(A) Luria–Bertani (LB) medium

(B) Dulbecco's Modified Eagle Medium (DMEM)

(C) Murashige and Skoog (MS) medium

(D) yeast extract–peptone–dextrose (YEPD) medium

Q42. Culturing immature pollen grains or whole anthers on a suitable medium can regenerate plants that contain only a single set of chromosomes. This route to *haploid* plants is known as: [2 marks]

(A) somatic hybridisation

(B) micropropagation from shoot tips

(C) protoplast fusion

(D) anther (pollen) culture, i.e. androgenesis

Q43. Before animal cell lines are stored in liquid nitrogen at about $-196\ ^\circ\text{C}$, a cryoprotectant is added to the freezing medium to prevent ice-crystal damage to the cells. The cryoprotectant most commonly used for this purpose is: [2 marks]

(A) dimethyl sulfoxide (DMSO)

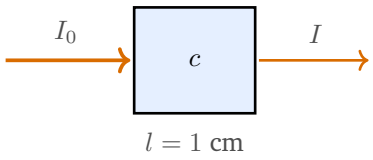
(B) sodium chloride

(C) trypsin

(D) EDTA

Analytical Techniques

Q44. In the spectrophotometric measurement sketched below, monochromatic light passes through a 1 cm cuvette holding a coloured solution. The absorbing species has a molar absorptivity $\varepsilon = 5000\ \text{M}^{-1}\text{cm}^{-1}$ and a concentration $c = 4 \times 10^{-5}$ M. Using the Beer–Lambert law $A = \varepsilon\, c\, l$, the absorbance recorded is: **[2 marks]**



(A) 0.02

(B) 2.0

(C) 0.05

(D) 0.20

Q45. When nucleic acids are quantified on a UV spectrophotometer, the concentration of DNA or RNA is estimated from its absorbance at the wavelength where the purine and pyrimidine bases absorb most strongly. That wavelength is: **[2 marks]**

(A) 280 nm

(B) 595 nm

(C) 340 nm

(D) 260 nm

Q46. The purity of a DNA preparation is judged from the ratio of its absorbance at 260 nm to that at 280 nm. For a preparation of reasonably

pure, protein-free double-stranded DNA, this A_{260}/A_{280} ratio is close to: **[2 marks]**

(A) 1.0

(B) 1.8

(C) 0.5

(D) 2.6

Detailed Solutions

Q1.

Solution

Concept – the isoelectric point of an amino acid: For an amino acid with only two ionisable groups, the pI is the pH midway between the two pK_a values that bracket the zwitterionic (net-neutral) form.

Step 1 – list the data: p$K_{a1} = 2.34$ (the α-COOH group) and p$K_{a2} = 9.60$ (the α-NH_3^+ group).

Step 2 – identify the neutral species: The zwitterion, with COO^- and NH_3^+, is bracketed by these two ionisations.

Step 3 – write the pI formula: $\text{pI} = \dfrac{\text{p}K_{a1} + \text{p}K_{a2}}{2}$

Step 4 – substitute: $\text{pI} = \dfrac{2.34 + 9.60}{2}$

Step 5 – add the numerator: $2.34 + 9.60 = 11.94$

Step 6 – divide: $\text{pI} = \dfrac{11.94}{2} = 5.97$

Why the other options are wrong:

- A (2.34) and B (9.60): these are the individual pK_a values, not their average.
- C (11.94): this is only the numerator (their sum), not the pI.

Final Answer: $\text{pI} = 5.97 \Rightarrow$ D

Answer: (D) Go Back to Q1

Q2.

Solution

Concept – chirality of the α-carbon: A carbon is a chiral (asymmetric) centre only when it carries four *different* substituents.

Step 1 – the general amino-acid α-carbon: It bears an amino group, a carboxyl group, a hydrogen and a side chain (R); with four different groups it is chiral.

Step 2 – the special case of glycine: In glycine the side chain is simply another hydrogen atom (R = H).

Step 3 – count the distinct groups: The α-carbon of glycine then carries $-NH_2$, $-COOH$ and *two* identical H atoms, so it has only three distinct groups.

Step 4 – conclude: With two identical substituents the α-carbon is not asymmet-

ric, so glycine is achiral and optically inactive.

Why the other options are wrong:

- A, alanine (R = CH_3): its α-carbon has four different groups and is chiral.
- B, threonine: it in fact has *two* chiral centres.
- C, cysteine: its α-carbon is chiral.

Final Answer: glycine $\Rightarrow$ D

Answer: (D) Go Back to Q2

Q3.

Solution

Concept – estimating protein mass from residue count: Because water is lost at each peptide bond, the mean mass of an amino-acid *residue* in a protein is about 110 Da, and the protein mass is roughly (number of residues) $\times 110$ Da.

Step 1 – list the data: Number of residues $n = 200$; average residue mass ≈ 110 Da.

Step 2 – write the estimate: Molecular weight $\approx n \times 110$ Da

Step 3 – substitute: $\approx 200 \times 110$ Da

Step 4 – multiply: $= 22000$ Da

Step 5 – convert to kilodaltons: 22000 Da $= 22$ kDa

Why the other options are wrong:

- A (2.2 kDa): off by a factor of ten (as if 11 Da per residue).
- B (11 kDa): used 55 Da per residue, about half the true average.
- D (44 kDa): double the correct value.

Final Answer: ≈ 22 kDa $\Rightarrow$ C

Answer: (C) Go Back to Q3

Q4.

Solution

Concept – the four levels of protein structure: Primary is the sequence; secondary is local backbone folding; tertiary is the overall 3D fold of one chain; quaternary is the assembly of several chains.

Step 1 – read the description: Regular local patterns, α-helix and β-sheet, held by backbone hydrogen bonds.

Step 2 – match to the level: These repeating local motifs define the **secondary** structure.

Step 3 – note the stabilising force: The hydrogen bonds are between the backbone carbonyl (C=O) and amide (N−H) groups, not between side chains.

Why the other options are wrong:

- A, primary: just the linear order of residues, with no folding implied.
- B, tertiary: the full 3D shape of the whole chain, stabilised largely by side-chain interactions.
- D, quaternary: how multiple folded subunits come together.

Final Answer: secondary structure $\Rightarrow$ $\boxed{\text{C}}$

Answer: (C) Go Back to Q4

Q5.

Solution

Concept – reducing equivalents from one turn of the TCA cycle: Each acetyl-CoA fully oxidised in the cycle generates a fixed, well-known set of energy carriers.

Step 1 – list the NADH-producing steps: NADH is made at three oxidative decarboxylation/oxidation steps: isocitrate dehydrogenase, α-ketoglutarate dehydrogenase and malate dehydrogenase.

Step 2 – count them: That gives 3 NADH per turn.

Step 3 – note the other carriers (aside): The same turn also yields 1 $FADH_2$ (at succinate dehydrogenase) and 1 GTP (at succinyl-CoA synthetase), but the question asks only about NADH.

Step 4 – state the answer: NADH per turn $= 3$.

Why the other options are wrong:

- A (1): counts only one dehydrogenase step.

- C (4): would wrongly count $FADH_2$ as NADH.
- D (12): confuses this with the ATP tally from oxidative phosphorylation.

Final Answer: 3 NADH per turn $\Rightarrow$ B

Answer: (B) Go Back to Q5

Q6.

Solution

Concept – vitamin-derived coenzymes: Many redox coenzymes are built on B-vitamins; the flavins come specifically from riboflavin (vitamin B_2).

Step 1 – link the vitamin to its coenzyme: Riboflavin is the precursor of the flavin nucleotides FMN and FAD.

Step 2 – identify the electron carrier: FAD (flavin adenine dinucleotide) accepts two electrons and two protons to become $FADH_2$ in many oxidoreductases (for example succinate dehydrogenase).

Why the other options are wrong:

- A, NAD^+: is derived from niacin (vitamin B_3), not riboflavin.
- B, coenzyme A: comes from pantothenate (vitamin B_5).
- C, thiamine pyrophosphate: comes from thiamine (vitamin B_1).

Final Answer: FAD $\Rightarrow$ D

Answer: (D) Go Back to Q6

Q7.

Solution

Concept – the acid-fast (Ziehl–Neelsen) stain: Acid-fast bacteria have a waxy, mycolic-acid-rich wall that resists ordinary staining but retains a strong lipophilic dye when heat is applied.

Step 1 – name the primary stain: The primary dye is **carbol fuchsin** (basic fuchsin in phenol), driven in by steaming the slide.

Step 2 – the decolouriser: Acid-alcohol is then used; acid-fast cells retain the red carbol fuchsin while non-acid-fast cells lose it.

Step 3 – the counterstain: Methylene blue counterstains the decolourised (non-acid-fast) background, so acid-fast bacilli appear red against blue.

Why the other options are wrong:

- A, crystal violet: is the primary stain of the *Gram* procedure.
- B, safranin: is the Gram counterstain.
- C, methylene blue: here it is the counterstain, not the primary stain.

Final Answer: carbol fuchsin $\Rightarrow$ D

Answer: (D) Go Back to Q7

Q8.

Solution

Concept – number of generations in exponential growth: The number of doublings is $n = \log_2 \frac{X}{X_0}$, i.e. how many times the population has doubled.

Step 1 – list the data: $X_0 = 1.0 \times 10^4$ cells and $X = 1.6 \times 10^5$ cells.

Step 2 – form the fold increase: $\frac{X}{X_0} = \frac{1.6 \times 10^5}{1.0 \times 10^4} = 16$

Step 3 – express as a power of two: $16 = 2^4$

Step 4 – read off the number of generations: $n = \log_2(16) = 4$

Step 5 – interpret: Over the 4-hour period the culture doubled four times (and the doubling time happens to be 1 h), but the question asks only for the number of generations, which is 4.

Final Answer: $n = 4$ generations $\Rightarrow$ B

Answer: (B) Go Back to Q8

Q9.

Solution

Concept – the phases of a batch growth curve: On a $\ln X$ plot the slope equals the specific growth rate; the first, flat segment has essentially zero slope.

Step 1 – read the highlighted segment: The highlighted part is the initial flat region, before the curve begins to rise.

Step 2 – interpret it biologically: Here the freshly inoculated cells are adapting, synthesising enzymes and building up metabolic machinery, without net cell division.

Step 3 – name the phase: A flat $\ln X$ with cells adapting but not dividing is the **lag phase**.

Why the other options are wrong:

- A, log phase: is the steep rising segment, not the flat start.
- C, stationary phase: is the later plateau where growth balances death.
- D, death phase: is the final falling segment.

Final Answer: the lag phase $\Rightarrow$ B

Answer: (B) Go Back to Q9

Q10.

Solution

Concept – the endospore (Schaeffer–Fulton) stain: Endospores have a tough, impermeable coat, so a strongly penetrating dye must be forced in with heat.

Step 1 – name the primary stain: The primary stain steamed into the spore is **malachite green**.

Step 2 – decolourise: Washing with water removes malachite green from the vegetative cell body but not from the heat-fixed spore.

Step 3 – counterstain: Safranin then stains the vegetative cells pink, so spores appear green within pink cells.

Why the other options are wrong:

- B, crystal violet: is the Gram primary stain.
- C, safranin: here acts as the counterstain, not the primary stain.
- D, carbol fuchsin: is the acid-fast primary stain.

Final Answer: malachite green $\Rightarrow$ A

Answer: (A) Go Back to Q10

Q11.

Solution

Concept – classifying bacteria by oxygen requirement: Organisms differ in whether oxygen is required, tolerated or toxic, depending on the protective enzymes (catalase, superoxide dismutase) they possess.

Step 1 – read the description: Oxygen is toxic and growth occurs only in its complete absence.

Step 2 – match the category: Cells that are poisoned by O_2 and grow only anaer-

obically are **obligate (strict) anaerobes**.

Step 3 – explain the biology: They typically lack superoxide dismutase and/or catalase, so toxic oxygen radicals accumulate in air.

Why the other options are wrong:

- B, obligate aerobes: *require* oxygen to grow.
- C, facultative anaerobes: grow with or without oxygen.
- D, microaerophiles: need oxygen but only at low tension.

Final Answer: obligate anaerobes $\Rightarrow$ A

Answer: (A) Go Back to Q11

Q12.

Solution

Concept – relieving torsional strain at the replication fork: Unwinding the duplex overwinds the DNA ahead of the fork; a special enzyme must remove this strain so replication can continue.

Step 1 – describe the problem: Helicase separates the strands, generating positive supercoils just ahead of the fork.

Step 2 – name the enzyme that relieves it: DNA topoisomerase (in bacteria, DNA gyrase) transiently cuts one or both strands, lets the DNA rotate or pass through, and reseals it.

Step 3 – result: This removes the supercoils and prevents the DNA ahead of the fork from becoming knotted.

Why the other options are wrong:

- A, helicase: *creates* the strain by unwinding; it does not relieve it.
- C, primase: synthesises RNA primers.
- D, DNA ligase: seals nicks between fragments.

Final Answer: DNA topoisomerase (gyrase) $\Rightarrow$ B

Answer: (B) Go Back to Q12

Q13.

Solution

Concept – priming of new DNA strands: DNA polymerases cannot start a chain from scratch; they can only extend a base-paired $3'$-OH, so a short primer must be made first.

Step 1 – identify what is needed: Each new strand (and every Okazaki fragment on the lagging strand) must begin from a short RNA primer.

Step 2 – name the enzyme: The RNA primers are synthesised by **primase**, a specialised RNA polymerase.

Step 3 – what happens next: DNA polymerase III then extends from the primer's $3'$-OH; later the primers are removed and replaced with DNA.

Why the other options are wrong:

- A, helicase: unwinds the duplex; it makes no primer.
- B, DNA polymerase III: extends an existing primer but cannot initiate one.
- D, DNA ligase: joins fragments after the primers are replaced.

Final Answer: primase $\Rightarrow$ $\boxed{\text{C}}$

Answer: (C) Go Back to Q13

Q14.

Solution

Concept – direction of DNA synthesis: A new nucleotide is added only to the $3'$-hydroxyl at the growing end, which fixes the direction of synthesis.

Step 1 – see where the bond forms: The incoming dNTP's $5'$-phosphate joins the free $3'$-OH of the last residue.

Step 2 – deduce the direction: The chain therefore grows by adding to its $3'$ end, i.e. in the $5' \rightarrow 3'$ direction.

Step 3 – consistency check: Since the new strand runs $5' \rightarrow 3'$ and is antiparallel to its template, the template is read $3' \rightarrow 5'$.

Why the other options are wrong:

- A, $3' \rightarrow 5'$: no known DNA polymerase synthesises in this direction.
- C: synthesis is strictly $5' \rightarrow 3'$, not both ways.
- D, $3' \rightarrow 3'$: is not a valid chemical direction for the chain.

Final Answer: $5' \rightarrow 3' \Rightarrow \boxed{\text{B}}$

Answer: (B) Go Back to Q14

Q15.

Solution

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

Step 1 – use the pairing rule for A: $\%\text{A} = \%\text{T} = 30\%$.

Step 2 – add the A–T pair: $\%\text{A} + \%\text{T} = 30 + 30 = 60\%$.

Step 3 – find the G–C total: $\%\text{G} + \%\text{C} = 100 - 60 = 40\%$.

Step 4 – split G and C equally: Since $\%\text{G} = \%\text{C}$, $\%\text{G} = \dfrac{40}{2} = 20\%$.

Step 5 – check the total: $30+30+20+20 = 100\%$, so the accounting is consistent.

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

Answer: (A) Go Back to Q15

Q16.

Solution

Concept – the experiment proving semiconservative replication: Density-gradient centrifugation of DNA labelled with heavy and light nitrogen isotopes distinguishes conservative, semiconservative and dispersive models.

Step 1 – recall the design: Cells grown in ^{15}N (heavy) were shifted to ^{14}N (light) and the DNA density was followed over successive generations.

Step 2 – name the workers: This classic experiment was carried out by **Meselson and Stahl** (1958).

Step 3 – the key result: After one round the DNA was of uniform intermediate density (one heavy + one light strand), ruling out the conservative model and supporting the semiconservative model.

Why the other options are wrong:

- A, Watson and Crick: proposed the double-helix structure, not this experiment.
- B, Hershey and Chase: showed DNA (not protein) is the genetic material of phage.
- D, Griffith: demonstrated bacterial transformation.

Final Answer: Meselson and Stahl $\Rightarrow$ C

Answer: (C) Go Back to Q16

Q17.

Solution

Concept – hydrogen bonding in base pairs: Watson–Crick base pairs are held together by a specific number of hydrogen bonds: A–T by two and G–C by three.

Step 1 – identify the pair: The pair in question is guanine with cytosine (G≡C).

Step 2 – count the hydrogen bonds: A G–C pair forms **three** hydrogen bonds, shown by the triple bond symbol ≡.

Step 3 – note the consequence: Because G–C has one more hydrogen bond than A–T, DNA rich in G–C is more thermally stable and has a higher melting temperature.

Why the other options are wrong:

- A (2): is the number of hydrogen bonds in an A–T pair.
- C (1) and D (4): neither matches any standard Watson–Crick base pair.

Final Answer: 3 hydrogen bonds ⇒ B

Answer: (B) Go Back to Q17

Q18.

Solution

Concept – proofreading by DNA polymerase: High-fidelity DNA polymerases have a second active site that removes a newly added, mispaired nucleotide.

Step 1 – what proofreading requires: After a wrong base is added, the enzyme must excise it from the $3'$ end of the growing strand.

Step 2 – name the activity: This is the $3' \to 5'$ **exonuclease** activity, which chews back from the $3'$ end.

Step 3 – the outcome: The mismatched nucleotide is removed, the correct one is inserted, and synthesis resumes, raising replication fidelity by orders of magnitude.

Why the other options are wrong:

- B, $5' \to 3'$ polymerase activity: *adds* nucleotides; it is what makes the error.
- C, $5' \to 3'$ exonuclease activity: removes RNA primers/DNA ahead of it (nick

translation), not proofreading.

- D, endonuclease activity: cuts internally and is not the proofreading function.

Final Answer: $3' \to 5'$ exonuclease activity $\Rightarrow$ A

Answer: (A) Go Back to Q18

Q19.

Solution

Concept – genotypic versus phenotypic ratio of a monohybrid cross: A cross of two heterozygotes gives a $1:2:1$ *genotypic* ratio, even though the phenotypic ratio is $3:1$ under complete dominance.

Step 1 – set up the cross: $Tt \times Tt$; each parent forms gametes T and t in equal proportion.

Step 2 – combine the gametes: The 2×2 Punnett square gives TT, Tt, Tt, tt.

Step 3 – tally the genotypes: $1\ TT : 2\ Tt : 1\ tt$.

Step 4 – state the genotypic ratio: $1:2:1$.

Step 5 – distinguish from phenotype: The corresponding phenotypic ratio (tall : dwarf) would be $3:1$, but the question asks for the genotypic ratio, which is $1:2:1$.

Final Answer: $1:2:1 \Rightarrow$ C

Answer: (C) Go Back to Q19

Q20.

Solution

Concept – the first antibody of the primary response: The five immunoglobulin classes appear at different times; one is made earliest and exists as a pentamer.

Step 1 – recall the kinetics: On first exposure to an antigen, **IgM** is the first class secreted.

Step 2 – note its structure: Secreted IgM is a pentamer of five monomers, giving it ten antigen-binding sites and high avidity.

Step 3 – functional consequence: Its many binding sites make IgM very effective at agglutination and at activating the complement cascade.

Why the other options are wrong:

- B, IgG: dominates the *secondary* response and is a monomer.
- C, IgA: is the main antibody of mucosal secretions (a dimer there).
- D, IgE: is present in trace amounts and mediates allergy.

Final Answer: IgM $\Rightarrow$ A

Answer: (A) Go Back to Q20

Q21.

Solution

Concept – the logic of a test cross: Crossing an individual of dominant phenotype with a homozygous recessive reveals the unknown genotype from the offspring ratio.

Step 1 – read the result: The offspring are 50% tall and 50% dwarf, i.e. a $1:1$ ratio.

Step 2 – test the homozygous possibility: If the tall parent were TT, then $TT \times tt$ would give *all* Tt (all tall); no dwarf offspring would appear. This is ruled out by the data.

Step 3 – test the heterozygous possibility: If the tall parent were Tt, then $Tt \times tt$ gives $\frac{1}{2}\,Tt$ (tall) and $\frac{1}{2}\,tt$ (dwarf), a $1:1$ ratio, exactly matching the Punnett square shown.

Step 4 – conclude: The unknown tall parent must therefore be heterozygous, Tt.

Why the other options are wrong:

- A, TT: would give all tall offspring.
- C, tt: would be dwarf, contradicting its tall phenotype.
- D: a test cross is designed precisely to determine this genotype, so it can be determined.

Final Answer: Tt (heterozygous) $\Rightarrow$ B

Answer: (B) Go Back to Q21

Q22.

Solution

Concept – inheritance of an X-linked recessive trait: A son receives his single X chromosome from his mother, so his phenotype for an X-linked gene depends only on which maternal X he inherits.

Step 1 – write the parents' genotypes: Mother is a carrier X^CX^c; father is X^CY (normal).

Step 2 – see what a son inherits: A son gets the Y from his father and one X from his mother.

Step 3 – list the maternal X options: The mother passes X^C (normal) with probability $\frac{1}{2}$ and X^c (colour-blind allele) with probability $\frac{1}{2}$.

Step 4 – identify the affected son: A son receiving X^cY is colour blind; this occurs with probability $\frac{1}{2}$.

Step 5 – state the result: $P(\text{son is colour blind}) = \dfrac{1}{2}$.

Why the other options are wrong:

- B ($\frac{1}{4}$): would be the fraction of *all* children (both sexes) affected, not of sons.
- C (0): ignores that the mother can pass the X^c allele.
- D (1): would require the mother to be homozygous affected.

Final Answer: $P = \dfrac{1}{2} \Rightarrow \boxed{\text{A}}$

Answer: (A) Go Back to Q22

Q23.

Solution

Concept – the fragments of an antibody: Proteolytic cleavage of an antibody separates the two antigen-binding arms (Fab) from the stem (Fc); each region has distinct roles.

Step 1 – locate the stem: The stem is formed by the paired constant domains of the two heavy chains.

Step 2 – name it: This crystallisable stem is the **Fc region**.

Step 3 – state its functions: The Fc region defines the antibody's class (isotype) and mediates effector functions, binding complement (C1q) and Fc receptors on phagocytes and other immune cells.

Why the other options are wrong:

- A, Fab region: is the arm that *binds antigen*, not the effector stem.
- C, hypervariable (CDR) region: forms the antigen-binding site within the Fab.
- D, hinge region: gives the arms flexibility but is not the effector stem itself.

Final Answer: the Fc (constant) region $\Rightarrow$ B

Answer: (B) Go Back to Q23

Q24.

Solution

Concept – what Hardy–Weinberg equilibrium means: The Hardy–Weinberg principle describes a *non-evolving* population in which allele frequencies stay constant across generations; a change in those frequencies is the signature of evolution.

Step 1 – state the equilibrium condition: At equilibrium the allele frequencies p and q do not change from one generation to the next.

Step 2 – state the criterion for evolution: Therefore the population is *evolving* at that locus precisely when the allele frequencies **do change** between generations.

Step 3 – link to causes: Such a change is produced by evolutionary forces such as selection, mutation, migration (gene flow), genetic drift or non-random mating.

Why the other options are wrong:

- A ($p + q = 1$): is just the definition that the two allele frequencies sum to one; it is always true and says nothing about change.
- B ($p^2 : 2pq : q^2$): is the equilibrium genotype distribution, i.e. the *non-evolving* state.
- D, random mating: is one of the *assumptions* for equilibrium, not evidence of evolution.

Final Answer: allele frequencies change from generation to generation $\Rightarrow$ C

Answer: (C) Go Back to Q24

Q25.

Solution

Concept – fragments from cutting a linear DNA: On a *linear* molecule, k cuts produce $k+1$ fragments; the fragment sizes are the distances between successive cut points (including the two ends).

Step 1 – list the data: Total length $= 10$ kb; *Eco*RI sites at the 3 kb and 7 kb positions from the left end.

Step 2 – first fragment (left end to first site): $3 - 0 = 3$ kb.

Step 3 – middle fragment (between the two sites): $7 - 3 = 4$ kb.

Step 4 – last fragment (second site to right end): $10 - 7 = 3$ kb.

Step 5 – list the fragments: 3 kb, 4 kb and 3 kb (two cuts on a linear molecule $\Rightarrow$ three pieces).

Step 6 – check the sum: $3 + 4 + 3 = 10$ kb, the full length, so the accounting is complete.

Final Answer: 3 kb, 4 kb and 3 kb $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q25

Q26.

Solution

Concept – staggered cuts give cohesive ends: When a restriction enzyme cuts the two strands at positions offset from the axis of symmetry, each fragment is left with a short single-stranded tail.

Step 1 – write the sequence and cut sites: $5'$-G↓AATTC-$3'$ on top and $3'$-CTTAA↑G-$5'$ on the bottom; the cuts are between G and A on each strand.

Step 2 – see the offset: Because the two cuts are staggered, each end keeps a protruding single strand $5'$-AATT.

Step 3 – name the ends: These are $5'$ single-stranded overhangs, i.e. **cohesive (sticky) ends**.

Step 4 – why it matters: The AATT overhangs are complementary, so any two *Eco*RI-cut fragments can base-pair and be ligated together, which is central to cloning.

Why the other options are wrong:

- A, blunt ends: arise only when the enzyme cuts on the symmetry axis.
- C, $3'$ overhangs of four bases: *Eco*RI leaves $5'$, not $3'$, overhangs.

- D, no free ends: cutting necessarily creates free ends.

Final Answer: $5'$ cohesive (sticky) overhangs $\Rightarrow$ B

Answer: (B) Go Back to Q26

Q27.

Solution

Concept – essential features of a cloning vector: A vector needs, at minimum, an origin of replication, a selectable marker and a site to insert DNA; of these, only one lets the plasmid copy itself.

Step 1 – identify what allows autonomous replication: Autonomous copying requires the **origin of replication (*ori*)**, where host replication machinery initiates.

Step 2 – confirm it is indispensable: Without an *ori* the plasmid cannot be replicated and would be lost as the cells divide, no matter what else it carries.

Why the other options are wrong:

- A, ampicillin-resistance gene: is a *selectable marker*; useful, but it does not replicate the plasmid.
- B, multiple cloning site: is only a cluster of restriction sites for inserting DNA.
- C, *lacZ* reporter gene: enables blue–white screening but is not required for replication.

Final Answer: the origin of replication (*ori*) $\Rightarrow$ D

Answer: (D) Go Back to Q27

Q28.

Solution

Concept – matching insert size to vector capacity: Different vectors have different maximum insert sizes; large-insert cloning needs a special vector.

Step 1 – state the target insert size: The inserts are 100–300 kb, far beyond the capacity of ordinary plasmids.

Step 2 – pick the right vector: Inserts of this size are carried stably in *E. coli* by a **bacterial artificial chromosome (BAC)**, based on the single-copy F-plasmid replicon.

Step 3 – why a BAC works: Its low copy number and stable maintenance make it well suited to very large fragments, so BACs were the workhorse of genome-mapping and sequencing projects.

Why the other options are wrong:

- A, standard plasmid: typically holds only up to about 10 kb.
- B, phagemid: holds a few kb.
- C, cosmid: holds roughly 35–45 kb, still far below 100 kb.

Final Answer: bacterial artificial chromosome (BAC) $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q28

Q29.

Solution

Concept – blunt-cutting restriction enzymes: An enzyme leaves blunt ends when it cuts both strands at the same position, right on the axis of symmetry of its recognition site.

Step 1 – examine *Sma*I: *Sma*I recognises CCCGGG and cuts as CCC↓GGG on both strands, at the centre of the palindrome.

Step 2 – see the result: Both strands are cut at the same point, leaving no overhang, i.e. **blunt ends**.

Why the other options are wrong:

- B, *Eco*RI (G↓AATTC): staggered cut $\Rightarrow 5'$ sticky ends.
- C, *Hind*III (A↓AGCTT): staggered cut $\Rightarrow 5'$ sticky ends.
- D, *Bam*HI (G↓GATCC): staggered cut $\Rightarrow 5'$ sticky ends.

Final Answer: *Sma*I $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q29

Q30.

Solution

Concept – meaning of the BLAST E-value: The E-value is the number of alignments as good as the observed one that would be expected by chance in a database of that size; smaller means less likely to be random.

Step 1 – interpret a very small E-value: An E-value of 10^{-40} means such a match

would essentially never occur by chance.

Step 2 – draw the conclusion: The alignment is therefore **statistically significant** and, in practice, indicates a genuine biological relationship (homology).

Step 3 – rule of thumb: Hits with E-values below about 10^{-5} are usually treated as significant; the lower the E-value, the stronger the hit.

Why the other options are wrong:

- A: a *high* E-value (near 1 or more), not a low one, signals a chance alignment.
- B and D: the E-value reflects significance, not coverage or divergence directly, and a low value indicates a strong, well-conserved match.

Final Answer: a statistically significant, meaningful match $\Rightarrow$ C

Answer: (C) 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: $X_0 = 2$ g L^{-1}, $X = 16$ g L^{-1}, $t = 4$ h.

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

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

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

Step 5 – evaluate: $\mu \approx 0.52$ h^{-1}

Final Answer: $\mu \approx 0.52$ 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 $= 15$ g; glucose consumed $= 60$ g.

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 yields 0.25 g of cells; the remaining carbon goes to products, CO_2 and maintenance energy.

Why the other options are wrong:

- B (4.0 g g^{-1}): is the inverted ratio $60/15$.
- C (0.75) and D (0.15): do not match $15/60$.

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

Answer: (A) Go Back to Q32

Q33.

Solution

Concept – doubling time and specific growth rate: For exponential growth the doubling time is $t_d = \dfrac{\ln 2}{\mu}$.

Step 1 – list the data: $\mu = 0.693$ h^{-1} and $\ln 2 = 0.693$.

Step 2 – substitute: $t_d = \dfrac{0.693}{0.693}$

Step 3 – evaluate: $t_d = 1$ h

Step 4 – check the units: $\dfrac{\text{(dimensionless)}}{\text{h}^{-1}} = \text{h}$, so the answer correctly has units of time.

Final Answer: $t_d = 1$ h $\Rightarrow$ C

Answer: (C) Go Back to Q33

Q34.

Solution

Concept – steady-state substrate in a chemostat near washout: The residual substrate is $S = \dfrac{K_s\, D}{\mu_{\max} - D}$; its behaviour is governed by the denominator $(\mu_{\max} - D)$.

Step 1 – examine the denominator: As D is raised towards $\mu_{\max}$, the term $(\mu_{\max} - D)$ shrinks towards zero.

Step 2 – effect on S: With a vanishing denominator, $S = \dfrac{K_s D}{\mu_{\max} - D}$ grows without bound, so the residual substrate rises steeply.

Step 3 – physical picture: The cells can no longer grow fast enough to keep up

with the feed, so they are progressively washed out and unconsumed substrate accumulates towards the feed concentration S_0.

Step 4 – match the plot: This is exactly what the graph shows: X collapses while S climbs sharply as $D \to D_{\text{crit}}$.

Why the other options are wrong:

- A: S is smallest at low D, not as washout is approached.
- B: S clearly varies with D; it is not constant.
- D: a concentration cannot be negative.

Final Answer: S increases sharply towards the feed value near washout $\Rightarrow$ C

Answer: (C) Go Back to Q34

Q35.

Solution

Concept – why fed-batch keeps substrate low: In fed-batch operation the feed rate is chosen so the limiting substrate stays at a low, controlled level throughout the run.

Step 1 – state the problem being avoided: A high substrate concentration can inhibit growth or trigger overflow metabolism (for example ethanol from yeast under the Crabtree effect, or acetate from *E. coli*), and can cause catabolite repression of desired product genes.

Step 2 – see how low substrate helps: By keeping the substrate low, these substrate/catabolite-inhibition effects are avoided while still supplying enough carbon for growth and product formation.

Step 3 – conclude the purpose: Hence the main reason is to **avoid substrate (catabolite) inhibition and overflow metabolism**.

Why the other options are wrong:

- A: volume does rise slowly in fed-batch, but rapid volume increase is not the aim.
- B: the strategy controls the substrate, not product dilution.
- C: fed-batch has no outflow, so cells are not washed out.

Final Answer: to avoid substrate/catabolite inhibition $\Rightarrow$ D

Answer: (D) Go Back to Q35

Q36.

Solution

Concept – the impeller Reynolds number: Mixing in a stirred tank is characterised by a dimensionless group comparing inertial to viscous forces.

Step 1 – write the group: For a stirred bioreactor, $\text{Re} = \dfrac{\rho N D_i^2}{\mu}$, where ρ is density, N the impeller speed (rev s^{-1}), D_i the impeller diameter and μ the viscosity.

Step 2 – interpret the terms: The numerator represents inertial forces and the denominator viscous forces, so their ratio sets the flow regime.

Step 3 – use the value: High Re ($\gtrsim 10^4$) indicates turbulent, well-mixed flow, while low Re indicates laminar flow with poor mixing.

Why the other options are wrong:

- B, Damköhler number: compares reaction rate with transport rate.
- C, Peclet number: compares convective with diffusive transport.
- D, Schmidt number: compares momentum with mass diffusivity.

Final Answer: the Reynolds number, $\dfrac{\rho N D_i^2}{\mu} \Rightarrow \boxed{\text{A}}$

Answer: (A) Go Back to Q36

Q37.

Solution

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

Step 1 – list the data: Final product concentration $= 75$ g L^{-1}; batch time $= 30$ h.

Step 2 – substitute: Productivity $= \dfrac{75}{30}$

Step 3 – evaluate: $= 2.5$ g $\text{L}^{-1}\text{h}^{-1}$

Step 4 – interpret: On average the process makes 2.5 g of product per litre of broth each hour over the whole run.

Why the other options are wrong:

- A (0.4): is the inverted ratio $30/75$.
- B (2250): is the product 75×30, not the quotient.
- D (30): is just the batch time, not a rate.

Final Answer: 2.5 g $\text{L}^{-1}\text{h}^{-1} \Rightarrow \boxed{\text{C}}$

Answer: (C) Go Back to Q37

Q38.

Solution

Concept – the critical (washout) dilution rate: In a chemostat the cells wash out once the dilution rate exceeds the maximum growth rate the feed can support.

Step 1 – recall the balance: At steady state $\mu = D$; the cells can match D only up to their maximum achievable growth rate.

Step 2 – write D_{crit}: $D_{\text{crit}} = \dfrac{\mu_{\max} S_0}{K_s + S_0}$.

Step 3 – simplify for a rich feed: When the feed substrate $S_0 \gg K_s$, the factor $\dfrac{S_0}{K_s + S_0} \to 1$, so $D_{\text{crit}} \approx \mu_{\max}$.

Step 4 – conclude: Raising D above about $\mu_{\max}$ washes the culture out, because the cells cannot grow fast enough to replace those removed.

Why the other options are wrong:

- A (0): washout occurs at a *high* D, not zero.
- C $(2\mu_{\max})$: no organism can sustain a growth rate above $\mu_{\max}$.
- D (K_s): is a concentration, not a dilution rate.

Final Answer: $D_{\text{crit}} \approx \mu_{\max} \Rightarrow$ B

Answer: (B) Go Back to Q38

Q39.

Solution

Concept – callus in plant tissue culture: On a balanced auxin/cytokinin medium many explants first form an unorganised mass of dividing cells before any organ is regenerated.

Step 1 – read the description: An unorganised, dedifferentiated mass of parenchyma-like cells forms from the explant.

Step 2 – name it: This mass is a **callus**.

Step 3 – its significance: By later adjusting the hormone balance, the callus can be induced to regenerate shoots and roots (organogenesis) or somatic embryos, making it central to micropropagation.

Why the other options are wrong:

- A, protoplast: is a single wall-less cell, not a tissue mass.
- C, apical meristem: is an organised, pre-existing growth region of the plant.
- D, somatic embryo: is an organised bipolar structure, more advanced than undifferentiated callus.

Final Answer: a callus $\Rightarrow$ B

Answer: (B) Go Back to Q39

Q40.

Solution

Concept – hormone ratios direct organ formation (Skoog–Miller): In tissue culture the auxin-to-cytokinin ratio decides whether roots, shoots or callus form.

Step 1 – state the rule for high auxin: A *high* auxin-to-cytokinin ratio favours **root** initiation (rhizogenesis).

Step 2 – state the complementary rule: A *high* cytokinin-to-auxin ratio favours shoot-bud initiation, and roughly balanced levels favour callus proliferation.

Step 3 – apply it here: Since the medium has a high auxin-to-cytokinin ratio, the expected response is root formation.

Why the other options are wrong:

- B, shoot initiation: needs a high *cytokinin*-to-auxin ratio.
- C, callus only: corresponds to a roughly balanced ratio.
- D, flowering: is not the primary response controlled by this ratio in culture.

Final Answer: root initiation (rhizogenesis) $\Rightarrow$ A

Answer: (A) Go Back to Q40

Q41.

Solution

Concept – the standard plant tissue-culture medium: Plant, animal and microbial cultures each use characteristic media; the plant workhorse is rich in inorganic nitrogen.

Step 1 – identify the plant medium: The **Murashige and Skoog (MS)** medium, formulated in 1962, is by far the most widely used basal medium for plant tissue culture.

Step 2 – note its hallmark: It is distinguished by high levels of nitrate and ammonium salts, plus a defined mix of micronutrients, vitamins and a carbon source (sucrose).

Why the other options are wrong:

- A, LB medium: is used to grow *bacteria*.
- B, DMEM: is a mammalian *cell-culture* medium.
- D, YEPD: is used to grow *yeast*.

Final Answer: Murashige and Skoog (MS) medium $\Rightarrow$ C

Answer: (C) Go Back to Q41

Q42.

Solution

Concept – producing haploids from male gametophytes: Culturing the haploid pollen lineage can regenerate whole plants that carry only one chromosome set.

Step 1 – read the method: Immature pollen grains or whole anthers are cultured *in vitro*.

Step 2 – name the technique: Regenerating plants from pollen/anthers is **anther (pollen) culture**, also called *androgenesis*.

Step 3 – the outcome and its use: The regenerants are haploid; doubling their chromosome number (for example with colchicine) yields homozygous doubled-haploid lines valued in plant breeding.

Why the other options are wrong:

- A, somatic hybridisation: fuses somatic protoplasts and gives (poly)ploid hybrids, not haploids.
- B, micropropagation from shoot tips: gives normal (diploid) clones.
- C, protoplast fusion: combines whole genomes rather than reducing to a haploid.

Final Answer: anther (pollen) culture, androgenesis $\Rightarrow$ D

Answer: (D) Go Back to Q42

Q43.

Solution

Concept – cryoprotection of animal cells: Freezing cells forms ice crystals that rupture membranes; a cryoprotectant limits this damage by controlling water and ice behaviour.

Step 1 – identify the standard cryoprotectant: For freezing mammalian cell lines, **dimethyl sulfoxide (DMSO)** is the most commonly added cryoprotectant, typically at about 5–10%.

Step 2 – how it works: DMSO permeates the cells and reduces the formation of damaging intracellular ice during slow, controlled cooling to -196 °C.

Why the other options are wrong:

- B, sodium chloride: is a salt, not a cryoprotectant, and high concentrations are harmful.
- C, trypsin: is a protease used to detach adherent cells.
- D, EDTA: is a chelating agent, not a cryoprotectant.

Final Answer: dimethyl sulfoxide (DMSO) $\Rightarrow$ A

Answer: (A) Go Back to Q43

Q44.

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: $\varepsilon = 5000\ \text{M}^{-1}\text{cm}^{-1}$, $c = 4 \times 10^{-5}$ M, $l = 1$ cm.

Step 2 – substitute into the law: $A = 5000 \times (4 \times 10^{-5}) \times 1$

Step 3 – multiply the coefficients: $5000 \times 4 = 20000 = 2 \times 10^{4}$

Step 4 – combine the powers of ten: $A = (2 \times 10^{4}) \times 10^{-5} = 2 \times 10^{-1}$

Step 5 – write the value: $A = 0.20$

Step 6 – check the units: $\text{M}^{-1}\text{cm}^{-1} \times \text{M} \times \text{cm}$ cancels to a dimensionless number, as absorbance must be.

Final Answer: $A = 0.20 \Rightarrow$ D

Answer: (D) Go Back to Q44

Q45.

Solution

Concept – UV absorbance of nucleic acids: The aromatic purine and pyrimidine bases absorb ultraviolet light strongly at a characteristic wavelength, used for quantification.

Step 1 – recall the peak: DNA and RNA absorb maximally at 260 **nm**.

Step 2 – use it for quantitation: An A_{260} of 1.0 (1 cm path) corresponds to about $50\ \mu\text{g mL}^{-1}$ of double-stranded DNA (or $\sim 40\ \mu\text{g mL}^{-1}$ for RNA).

Why the other options are wrong:

- A, 280 nm: is where *proteins* absorb (aromatic residues), used as a contamination check.
- B, 595 nm: is the read wavelength of the Bradford protein assay.
- C, 340 nm: is used to follow NADH/NADPH in enzyme assays.

Final Answer: 260 nm $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q45

Q46.

Solution

Concept – the A_{260}/A_{280} purity ratio: Nucleic acids peak at 260 nm and proteins at 280 nm, so their absorbance ratio reports on DNA purity.

Step 1 – recall the target value: Reasonably pure, protein-free double-stranded DNA has an A_{260}/A_{280} ratio of about 1.8.

Step 2 – interpret deviations: A ratio well below 1.8 indicates protein (or phenol) contamination, since protein raises the A_{280}; pure RNA reads a little higher, around 2.0.

Why the other options are wrong:

- A (1.0) and C (0.5): are far too low and would signal heavy protein contamination.
- D (2.6): is unrealistically high for DNA and would suggest measurement or contamination problems.

Final Answer: $A_{260}/A_{280} \approx 1.8 \Rightarrow \boxed{\text{B}}$

Answer: (B) Go Back to Q46

Answer Key

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