GATE Biotechnology

Sample Paper – 3

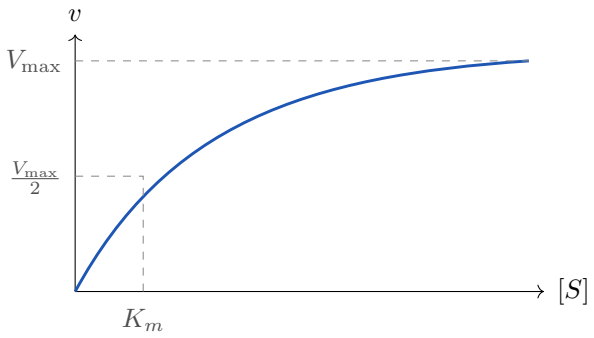
Duration: 128 Minutes **Maximum Marks: 72**

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 that follows Michaelis–Menten kinetics has a maximum velocity $V_{\max} = 80$ 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) 80 μmol min^{-1}

(B) 60 μmol min^{-1}

(C) 40 μmol min^{-1}

(D) 20 μmol min^{-1}

Q2. The first committed and rate-limiting step of glycolysis, at which the pathway is most tightly regulated, is the phosphorylation of fructose-6-phosphate to fructose-1,6-bisphosphate. This step is catalysed by: **[1 mark]**

(A) hexokinase

(B) pyruvate kinase

(C) aldolase

(D) phosphofructokinase-1 (PFK-1)

Q3. In glycolysis, the oxidation of glyceraldehyde-3-phosphate to 1,3-bisphosphoglycer is coupled to the reduction of a coenzyme derived from the vitamin niacin. The electron-accepting coenzyme used at this step is: **[1 mark]**

(A) FAD

(B) NADP$^+$

(C) coenzyme A

(D) NAD$^+$

Q4. In animal cells, excess glucose is stored as a branched polymer that can be rapidly mobilised by the liver and skeletal muscle. This storage polysaccharide of glucose is: **[1 mark]**

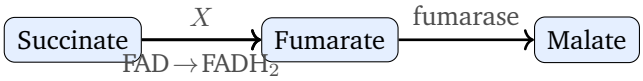
(A) starch

(B) cellulose

(C) glycogen

(D) chitin

Q5. A portion of the citric acid (TCA) cycle is shown below, where enzyme X oxidises succinate to fumarate and is also part of the electron-transport chain (Complex II). Enzyme X is: **[1 mark]**



(A) fumarase

(B) succinate dehydrogenase

(C) citrate synthase

(D) aconitase

Q6. For an enzyme working at saturating substrate, the turnover number k_{cat} is an important kinetic parameter. The turnover number is best defined as: **[1 mark]**

(A) the number of substrate molecules converted to product per active site per unit time

(B) the ratio $K_m/V_{\max}$

(C) the product $V_{\max} \times K_m$

(D) the substrate concentration giving half-maximal velocity

Microbiology

Q7. Lactic acid bacteria used in dairy fermentations carry out homolactic fermentation, in which pyruvate produced by glycolysis is reduced by NADH. The principal end product of this fermentation is: **[1 mark]**

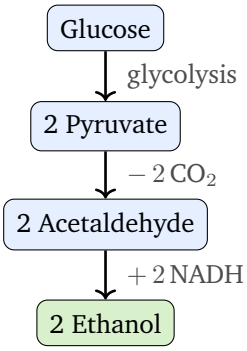
(A) ethanol and CO_2

(B) acetone and butanol

(C) lactic acid (lactate)

(D) acetic acid

Q8. In alcoholic fermentation by *Saccharomyces cerevisiae*, each pyruvate from glycolysis is first decarboxylated to acetaldehyde, which is then reduced by NADH, as summarised below. The end products formed per molecule of glucose are: **[1 mark]**



(A) 2 lactate

(B) 2 acetate and 2 CO_2

(C) 2 ethanol and 2 CO_2

(D) 1 ethanol and 1 CO_2

Q9. The industrial acetone–butanol–ethanol (ABE) solvent fermentation, historically important for producing these solvents from starch, is carried out by anaerobic, spore-forming bacteria of the genus: **[1 mark]**

(A) *Clostridium*

(B) *Saccharomyces*

(C) *Lactobacillus*

(D) *Escherichia*

Q10. Denitrifying bacteria growing in oxygen-depleted soil carry out anaerobic respiration, using an inorganic ion instead of oxygen as the terminal electron acceptor of their electron-transport chain. That terminal electron acceptor is: **[1 mark]**

(A) molecular oxygen (O_2)

(B) nitrate (NO_3^-)

(C) glucose

(D) water

Q11. A bacterium requires oxygen for growth but is harmed by the full atmospheric level of 21% O_2, growing best at reduced oxygen tensions of about 2–10%. Such an organism is classified as a: **[1 mark]**

(A) obligate aerobe

(B) obligate anaerobe

(C) microaerophile

(D) facultative anaerobe

Cell Biology and Molecular Biology

Q12. The bacterial RNA polymerase holoenzyme is made up of a core enzyme plus one dissociable subunit that directs the enzyme to the correct promoter and is released soon after transcription begins. This promoter-recognition subunit is the: **[1 mark]**

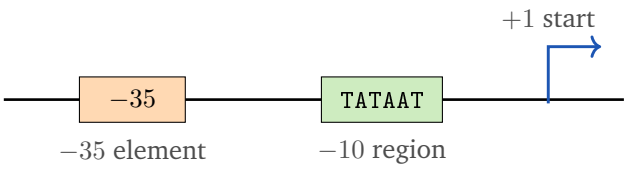
(A) β subunit

(B) σ (sigma) factor

(C) ω subunit

(D) α subunit

Q13. A typical *E. coli* promoter is shown below, with two conserved hexamer elements upstream of the transcription start site ($+1$). The consensus sequence `TATAAT`, centred about 10 base pairs upstream of $+1$, is called the: **[1 mark]**



(A) -10 (Pribnow) box

(B) -35 element

(C) operator

(D) Shine–Dalgarno sequence

Q14. Eukaryotic cells use three distinct nuclear RNA polymerases. The enzyme that transcribes protein-coding genes to produce messenger RNA (mRNA) precursors is: **[1 mark]**

(A) RNA polymerase I

(B) RNA polymerase II

(C) RNA polymerase III

(D) primase

Q15. During processing of a eukaryotic pre-mRNA, the non-coding intervening sequences (introns) are precisely removed and the flanking exons are joined together. This splicing reaction is carried out by a large ribonucleoprotein machine called the: **[1 mark]**

(A) ribosome

(B) spliceosome

(C) proteasome

(D) nucleosome

Q16. The tryptophan (*trp*) operon of *E. coli* is a repressible operon, mapped below. When tryptophan is abundant it acts as a corepressor, binding the inactive aporepressor and converting it to an active form. The immediate consequence for the operon is that: **[1 mark]**

(A) transcription of the operon increases

(B) the operator is deleted from the DNA

(C) transcription of the operon is switched off

(D) RNA polymerase moves twice as fast

Q17. Like DNA polymerases, RNA polymerase adds each new ribonucleotide to the free hydroxyl group at the growing end of the RNA chain. Therefore the RNA strand is synthesised in the direction: [1 mark]

(A) $5' \rightarrow 3'$

(B) $3' \rightarrow 5'$

(C) in both directions at once

(D) $5' \rightarrow 5'$

Q18. As part of eukaryotic mRNA maturation, a string of about 150–250 adenine nucleotides (the poly-A tail) is added to the $3'$ end of the transcript. The main functions of this poly-A tail are to: [1 mark]

(A) increase mRNA stability and assist nuclear export and translation

(B) encode a hydrophobic signal peptide

(C) act as the ribosome-binding site in prokaryotes

(D) remove the introns from the transcript

Genetics, Immunology and Evolution

Q19. A large, randomly mating population is at Hardy–Weinberg equilibrium for a gene with two alleles. The frequency of the dominant allele A is $p = 0.7$. The expected frequency of homozygous dominant (AA) individuals is: [1 mark]

(A) 0.21

(B) 0.09

(C) 0.42

(D) 0.49

Q20. On first exposure to an antigen (the primary immune response), one immunoglobulin class is secreted earliest and, as a pentamer, is especially good at agglutinating pathogens. The class that appears first is: **[1 mark]**

(A) IgM

(B) IgG

(C) IgA

(D) IgE

Q21. In a large randomly mating population at Hardy–Weinberg equilibrium, an autosomal recessive disorder affects 1 in 400 newborns, so that $q^2 = \frac{1}{400}$. The expected frequency of unaffected heterozygous carriers in the population is closest to: **[2 marks]**

(A) 0.095 (about 1 in 10.5)

(B) 0.0025

(C) 0.9025

(D) 0.05

Q22. In a small, isolated population, allele frequencies change from one generation to the next purely because only a limited, random sample of gametes forms the next generation, with no role for fitness differences. This evolutionary mechanism is called: **[2 marks]**

(A) natural selection

(B) gene flow

(C) genetic drift

(D) mutation pressure

Q23. The clonal selection theory is a cornerstone of modern immunology. It proposes that the specificity of an adaptive immune response arises because an antigen: **[2 marks]**

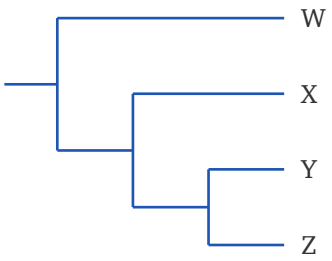
(A) instructs a lymphocyte to fold a new antibody around it

(B) is itself required to generate the diversity of receptors

(C) selects and stimulates only those lymphocytes whose pre-existing receptors already match it

(D) is engulfed and directly becomes the secreted antibody

Q24. The rooted phylogenetic tree below was inferred for four taxa (W, X, Y, Z) from sequence data. Based on the branching pattern, the pair of taxa that shares the most recent common ancestor (that is, the most closely related pair) is: **[2 marks]**



(A) Y and Z

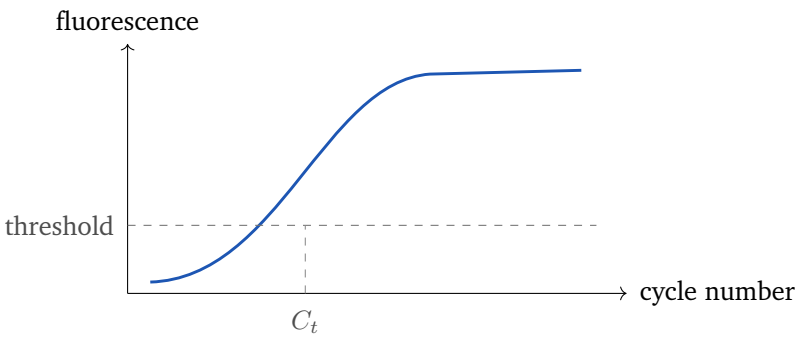
(B) W and X

(C) W and Z

(D) X and Y

Recombinant DNA Technology and Bioinformatics

Q25. In a real-time quantitative PCR (qPCR) run, the fluorescence of each reaction is followed cycle by cycle, giving the amplification curves shown. The cycle number at which a sample's fluorescence first rises above a fixed threshold line, set just above background, is the: **[2 marks]**



(A) melting temperature

(B) annealing cycle

(C) plateau cycle

(D) threshold cycle (C_t)

Q26. A TaqMan qPCR assay uses a hydrolysis probe that carries a reporter fluorophore at one end and a quencher at the other. During each cycle, fluorescence is generated because the $5' \to 3'$ exonuclease activity of Taq polymerase: **[2 marks]**

(A) denatures the double-stranded template

(B) cleaves the reporter fluorophore away from the quencher on the probe

(C) removes the primers from the product

(D) adds a poly-A tail to the amplicon

Q27. Two samples are compared in a qPCR assay operating at 100% efficiency (perfect doubling each cycle). Sample A crosses the threshold 3 cycles earlier than sample B ($\Delta C_t = 3$). The starting amount of target in sample A relative to sample B is approximately: **[2 marks]**

(A) 3 times

(B) 2 times

(C) 6 times

(D) 8 times

Q28. Standard PCR subjects the reaction to about 30 cycles that each include a $95\ ^\circ$C denaturation step. The DNA polymerase used stays active through this repeated heating because it is purified from a thermophilic bacterium. This enzyme is: **[2 marks]**

(A) *Taq* DNA polymerase (from *Thermus aquaticus*)

(B) *E. coli* DNA polymerase I

(C) T4 DNA ligase

(D) reverse transcriptase

Q29. To quantify a specific messenger RNA, reverse-transcription PCR (RT-PCR) is used. The very first enzymatic step, catalysed by reverse transcriptase acting on the RNA template, produces: [2 marks]

(A) complementary DNA (cDNA)

(B) a functional protein

(C) genomic double-stranded DNA directly

(D) ribosomal RNA

Q30. When designing a matched pair of PCR primers, the melting temperature (T_m) of each primer depends on its length and base composition. For primers of equal length, a higher T_m results from a greater content of: [2 marks]

(A) adenine and thymine

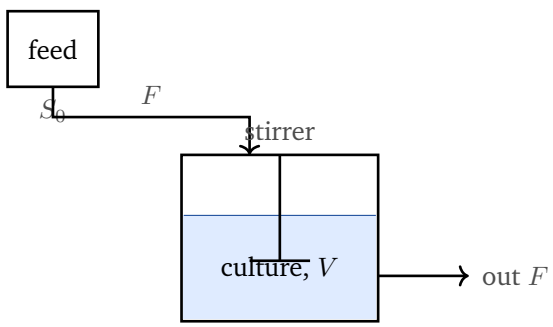
(B) adenine and uracil

(C) thymine only

(D) guanine and cytosine

Bioprocess Engineering and Process Biotechnology

Q31. The continuous stirred-tank bioreactor (chemostat) below has a constant working volume of 5 L and is fed with sterile medium at a volumetric flow rate of 1.5 L h^{-1}, with culture withdrawn at the same rate. The dilution rate at which it operates is: [2 marks]



(A) $0.15\ \text{h}^{-1}$

(B) $3.33\ \text{h}^{-1}$

(C) $0.60\ \text{h}^{-1}$

(D) $0.30\ \text{h}^{-1}$

Q32. In a steady-state chemostat the specific growth rate adjusts to equal the dilution rate. If the operator sets the dilution rate higher than a certain critical value, the cells are removed faster than they can grow and the culture is lost. Washout occurs when the dilution rate exceeds: **[2 marks]**

(A) the saturation constant K_s

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

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

(D) zero

Q33. At steady state in a chemostat, the residual limiting-substrate concentration is given by $S = \dfrac{K_s\, D}{\mu_{\max} - D}$. For an organism with $K_s = 0.2\ \text{g L}^{-1}$ and $\mu_{\max} = 0.8\ \text{h}^{-1}$, operated at a dilution rate $D = 0.4\ \text{h}^{-1}$, the residual substrate concentration S is: **[2 marks]**

(A) $0.2\ \text{g L}^{-1}$

(B) $0.4\ \text{g L}^{-1}$

(C) $0.1\ \text{g L}^{-1}$

(D) $0.8\ \text{g L}^{-1}$

Q34. The biomass output rate (productivity) of a chemostat is the product $D\,X$. This productivity is maximised at a dilution rate somewhat below $\mu_{\max}$. Operating the chemostat at a dilution rate too close to $\mu_{\max}$ is avoided mainly because it risks: **[2 marks]**

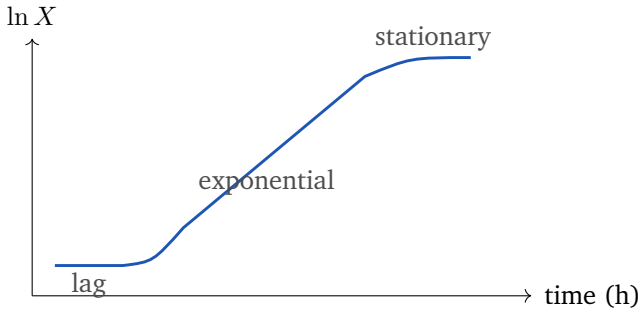
(A) excessive foaming

(B) medium contamination

(C) washout of the cells from the vessel

(D) substrate inhibition of growth

Q35. The batch growth of a culture is plotted below as $\ln X$ against time. During the exponential phase the biomass rises from 0.5 g L^{-1} to 4 g L^{-1} in 5 hours. The specific growth rate μ over this period is nearest to: **[2 marks]**



(A) $0.14\ h^{-1}$

(B) $0.21\ h^{-1}$

(C) $0.42\ h^{-1}$

(D) $0.69\ h^{-1}$

Q36. In modelling substrate utilisation, a fraction of the carbon source is consumed not for making new cells or product, but simply for keeping existing cells alive (maintaining ion gradients, motility and turnover). The maintenance coefficient m describes substrate used for: **[2 marks]**

(A) product formation only

(B) DNA replication only

(C) synthesis of new biomass

(D) non-growth (cell-maintenance) functions

Q37. Aerobic fermentations are often monitored through off-gas analysis. The respiratory quotient (RQ), a useful indicator of the metabolic state of the culture, is defined as: **[2 marks]**

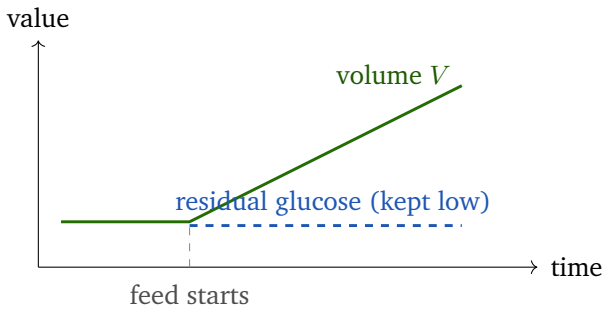
(A) moles of O_2 consumed ÷ moles of CO_2 produced

(B) moles of CO_2 produced ÷ moles of O_2 consumed

(C) mass of substrate consumed ÷ mass of biomass formed

(D) mass of biomass formed ÷ mass of product formed

Q38. In the high-cell-density production of baker's yeast, the sugar feed is deliberately supplied slowly in a fed-batch mode rather than all at once. The main reason for keeping the residual glucose concentration low throughout the feed is to: **[2 marks]**



(A) maximise the growth rate by saturating the cells with sugar

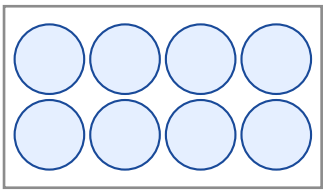
(B) keep glucose low enough to prevent overflow (ethanol) formation by the Crabtree effect

(C) stop the cells from consuming any oxygen

(D) hold the residual glucose at a constant saturating level

Plant and Animal Biotechnology

Q39. Normal (non-transformed) animal cells grown on a dish divide until they form a single continuous layer and then stop dividing once they are completely surrounded by neighbouring cells, as sketched below. This growth-regulating property is called: **[2 marks]**



confluent monolayer

(A) apoptosis

(B) malignant transformation

(C) contact inhibition

(D) anchorage independence

Q40. Most normal animal cells will grow and divide only when they are attached to and spread upon a solid surface such as the wall of a flask or a microcarrier bead. This requirement for a surface to grow on is termed: [2 marks]

(A) suspension growth

(B) immortalisation

(C) contact inhibition

(D) anchorage dependence

Q41. A primary culture of normal human fibroblasts is not immortal: after a fixed, limited number of population doublings it stops dividing and enters replicative senescence. This maximum number of divisions that a normal cell population can undergo is known as the: [2 marks]

(A) lag phase

(B) Hayflick limit

(C) log phase

(D) plateau phase

Q42. Classical animal cell culture media are usually supplemented with about 5–10% of a natural biological fluid that provides growth factors, hormones, attachment factors and transport proteins. The most widely used such supplement is: [2 marks]

(A) agar

(B) fetal bovine serum (FBS)

(C) yeast extract

(D) casein hydrolysate alone

Q43. In plant tissue culture, whether an explant or callus forms shoots, forms roots or remains as undifferentiated callus is governed largely by the balance of two classes of plant growth regulators in the medium. These two regulators are auxin and: [2 marks]

(A) gibberellin

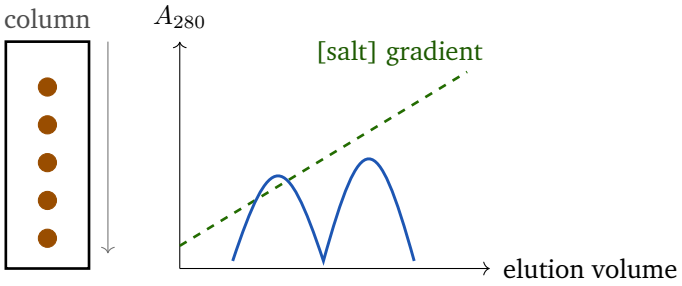
(B) ethylene

(C) abscisic acid

(D) cytokinin

Analytical Techniques

Q44. In the cation-exchange chromatography run sketched below, positively charged proteins bind to the negatively charged resin and are then eluted by a gradient. The bound proteins are released, in order of increasing net positive charge, by progressively increasing the: [2 marks]



(A) temperature of the column

(B) length of the column

(C) wavelength of the detector

(D) salt concentration (ionic strength) of the buffer

Q45. In anion-exchange chromatography the stationary phase carries positively charged functional groups, for example the diethylaminoethyl (DEAE) group. Under the loading conditions this resin binds molecules that are: [2 marks]

(A) electrically neutral

(B) positively charged

(C) negatively charged (acidic)

(D) only lipids

Q46. A protein has an isoelectric point of pI $= 5.0$. It is loaded onto a DEAE (anion-exchange) column equilibrated at pH $= 8.0$. At this loading pH the protein carries a net charge such that it: **[2 marks]**

(A) carries a net negative charge and therefore binds the anion exchanger

(B) carries a net positive charge and therefore flows straight through

(C) carries no net charge and elutes immediately in the void

(D) carries a net positive charge and binds a cation exchanger instead

Detailed Solutions

Q1.

Solution

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

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

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

Step 3 – evaluate the numerator: $80 \times 12 = 960$

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

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

Step 6 – sanity check: Here $[S] = 3K_m$, so $v = \dfrac{3}{4}V_{\max} = \dfrac{3}{4} \times 80 = 60$, which agrees.

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

Answer: (B) Go Back to Q1

Q2.

Solution

Concept – regulation of glycolysis: Glycolysis has three essentially irreversible, regulated steps, and one of them is the main control point of the whole pathway.

Step 1 – identify the committed step: The conversion of fructose-6-phosphate to fructose-1,6-bisphosphate is the first step committed solely to glycolysis.

Step 2 – name the enzyme: This step is catalysed by **phosphofructokinase-1 (PFK-1)**.

Step 3 – why it is rate-limiting: PFK-1 is allosterically inhibited by ATP and citrate and activated by AMP and fructose-2,6-bisphosphate, making it the pathway's principal control valve.

Why the other options are wrong:

- A, hexokinase: phosphorylates glucose at the entry step, but glucose-6-phosphate can still go to other pathways, so this is not the committed step.
- B, pyruvate kinase: catalyses the final glycolytic step, not the first committed one.
- C, aldolase: cleaves fructose-1,6-bisphosphate and is not a major regulatory

enzyme.

Final Answer: phosphofructokinase-1 (PFK-1) $\Rightarrow$ D

Answer: (D) Go Back to Q2

Q3.

Solution

Concept – the oxidation step of glycolysis: The only oxidation in glycolysis occurs when glyceraldehyde-3-phosphate is converted to 1,3-bisphosphoglycerate, and it needs an electron acceptor.

Step 1 – identify the enzyme: The step is catalysed by glyceraldehyde-3-phosphate dehydrogenase.

Step 2 – identify the coenzyme: The dehydrogenase transfers a hydride ion to **NAD^+**, reducing it to NADH.

Step 3 – link to the vitamin: NAD^+ is built from the vitamin niacin (nicotinic acid / nicotinamide, vitamin B3), matching the clue in the question.

Why the other options are wrong:

- A, FAD: is the acceptor in the succinate dehydrogenase and fatty-acid oxidation steps, not in glycolysis.
- B, $NADP^+$: is used mainly in biosynthesis and the pentose phosphate pathway.
- C, coenzyme A: carries acyl groups; it does not accept electrons here.

Final Answer: $NAD^+ \Rightarrow$ D

Answer: (D) Go Back to Q3

Q4.

Solution

Concept – glucose storage polymers: Different organisms store surplus glucose as different polysaccharides.

Step 1 – recall the animal store: Animals store glucose as **glycogen**, a highly branched polymer of glucose held in liver and skeletal muscle.

Step 2 – why the branches matter: The many non-reducing ends allow rapid mobilisation of glucose when blood sugar falls.

Why the other options are wrong:

- A, starch: is the glucose store of *plants*, not animals.
- B, cellulose: is a structural (not storage) polysaccharide of plant cell walls.
- D, chitin: is a structural polymer of N-acetylglucosamine in fungal walls and arthropod exoskeletons.

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

Answer: (C) Go Back to Q4

Q5.

Solution

Concept – the succinate-to-fumarate step of the TCA cycle: One TCA enzyme is unique in being embedded in the inner mitochondrial membrane and in also serving the electron-transport chain.

Step 1 – identify the reaction: Succinate is oxidised to fumarate, with the two removed hydrogens passed to FAD to give $FADH_2$.

Step 2 – name the enzyme: This is done by **succinate dehydrogenase**, enzyme X in the scheme.

Step 3 – note its dual role: Succinate dehydrogenase is also Complex II of the electron-transport chain, feeding electrons from $FADH_2$ into the ubiquinone pool.

Why the other options are wrong:

- A, fumarase: hydrates fumarate to malate, the *next* step.
- C, citrate synthase: makes citrate from acetyl-CoA and oxaloacetate.
- D, aconitase: interconverts citrate and isocitrate.

Final Answer: succinate dehydrogenase $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q5

Q6.

Solution

Concept – the turnover number k_{cat}: At saturating substrate every active site is working at full speed, and k_{cat} measures that speed.

Step 1 – write the relation: $k_{cat} = \dfrac{V_{max}}{[E]_{total}}$, where $[E]_{total}$ is the total enzyme (active-site) concentration.

Step 2 – interpret in words: This is the number of substrate molecules each active site converts to product per unit time when the enzyme is saturated.

Step 3 – match to the option: That description is exactly option A.

Why the other options are wrong:

- B, $K_m/V_{\max}$: is not a defined catalytic constant.
- C, $V_{\max} \times K_m$: has no standard meaning as a turnover number.
- D, the substrate concentration at half-maximal velocity: is the definition of K_m, not k_{cat}.

Final Answer: substrate molecules converted per active site per unit time $\Rightarrow$ A

Answer: (A) Go Back to Q6

Q7.

Solution

Concept – homolactic fermentation: When oxygen is absent, cells must reoxidise the NADH made in glycolysis by reducing pyruvate.

Step 1 – trace the electrons: In lactic acid bacteria, pyruvate is directly reduced by NADH, regenerating NAD^+ so glycolysis can continue.

Step 2 – name the product: The single reduced product is **lactic acid (lactate)**; this is why the fermentation is called homolactic.

Step 3 – link to application: This is the reaction that sours milk into yoghurt and curd.

Why the other options are wrong:

- A, ethanol and CO_2: is the product of yeast *alcoholic* fermentation.
- B, acetone and butanol: are products of the clostridial ABE fermentation.
- D, acetic acid: is made by aerobic oxidation of ethanol by *Acetobacter*, not by homolactic fermentation.

Final Answer: lactic acid (lactate) $\Rightarrow$ C

Answer: (C) Go Back to Q7

Q8.

Solution

Concept – alcoholic fermentation in yeast: Yeast reoxidises glycolytic NADH in two steps, releasing carbon dioxide and forming ethanol.

Step 1 – start from glycolysis: One glucose gives *two* pyruvate molecules.

Step 2 – decarboxylate each pyruvate: Pyruvate decarboxylase removes one CO_2 from each pyruvate, giving 2 acetaldehyde and $2\,CO_2$.

Step 3 – reduce the acetaldehyde: Alcohol dehydrogenase reduces each acetaldehyde with NADH, giving 2 ethanol and regenerating $2\,NAD^+$.

Step 4 – total the products: Per glucose the end products are 2 ethanol and $2\,CO_2$.

Why the other options are wrong:

- A, 2 lactate: is homolactic fermentation, not alcoholic.
- B, 2 acetate and 2 CO_2: describes a different oxidation.
- D, 1 ethanol and 1 CO_2: ignores that one glucose yields *two* pyruvate.

Final Answer: 2 ethanol and $2\,CO_2 \Rightarrow$ C

Answer: (C) Go Back to Q8

Q9.

Solution

Concept – the ABE (acetone–butanol–ethanol) fermentation: This classical solvent fermentation is run by strict anaerobes that form endospores.

Step 1 – recall the organism: The ABE fermentation is carried out by species of ***Clostridium***, chiefly *Clostridium acetobutylicum*.

Step 2 – note the two phases: These bacteria first make acids (acetate, butyrate) and then shift to producing the neutral solvents acetone, butanol and ethanol.

Step 3 – historical note: This was one of the first large-scale industrial fermentations, used to make butanol and acetone.

Why the other options are wrong:

- B, *Saccharomyces*: is the yeast used for ethanol, not the ABE process.
- C, *Lactobacillus*: carries out lactic-acid fermentation.
- D, *Escherichia*: is a facultative gut bacterium, not the ABE producer.

Final Answer: *Clostridium* $\Rightarrow$ A

Answer: (A) Go Back to Q9

Q10.

Solution

Concept – anaerobic respiration: In anaerobic respiration an inorganic molecule other than oxygen serves as the final electron acceptor of the electron-transport chain.

Step 1 – identify the process: Denitrifying bacteria in oxygen-poor soil respire using a nitrogen oxide.

Step 2 – name the acceptor: Their terminal electron acceptor is **nitrate (NO_3^-)**, which is progressively reduced through NO_2^-, NO and N_2O to N_2 gas.

Step 3 – note the significance: This denitrification returns fixed nitrogen to the atmosphere and is a key step of the nitrogen cycle.

Why the other options are wrong:

- A, O_2: is the acceptor in *aerobic* respiration, which the question excludes.
- C, glucose: is an electron *donor* (energy source), not the acceptor.
- D, water: is the fully reduced product of oxygen, not an acceptor here.

Final Answer: nitrate (NO_3^-) $\Rightarrow$ B

Answer: (B) Go Back to Q10

Q11.

Solution

Concept – oxygen classes of bacteria: Organisms differ in the oxygen level they need and can tolerate: obligate aerobes, obligate anaerobes, facultative anaerobes, aerotolerant anaerobes and microaerophiles.

Step 1 – read the requirement: The organism *needs* oxygen but is damaged by full atmospheric oxygen, thriving at only 2–10% O_2.

Step 2 – match the class: This describes a **microaerophile**.

Step 3 – give an example: *Helicobacter pylori* and *Campylobacter* are typical microaerophiles.

Why the other options are wrong:

- A, obligate aerobe: grows best at full atmospheric oxygen, not at reduced tension.

- B, obligate anaerobe: is killed by oxygen and cannot use it.
- D, facultative anaerobe: grows with or without oxygen and is not harmed by 21% O_2.

Final Answer: microaerophile $\Rightarrow$ C

Answer: (C) Go Back to Q11

Q12.

Solution

Concept – the bacterial RNA polymerase holoenzyme: The core enzyme ($\alpha_2\beta\beta'\omega$) can polymerise RNA but cannot by itself find a promoter.

Step 1 – identify the missing function: Promoter recognition requires an extra, dissociable subunit added to the core.

Step 2 – name the subunit: That subunit is the σ **(sigma) factor**, which together with core forms the holoenzyme.

Step 3 – note its fate: σ positions the enzyme at the -10 and -35 elements, and is released shortly after transcription initiation, leaving the core to elongate.

Why the other options are wrong:

- A, β subunit: forms part of the catalytic core but does not confer promoter specificity on its own.
- C, ω subunit: has a mainly assembly/stability role.
- D, α subunit: helps assembly and interacts with some activators, but σ is the promoter-recognition factor.

Final Answer: the σ (sigma) factor $\Rightarrow$ B

Answer: (B) Go Back to Q12

Q13.

Solution

Concept – the *E. coli* promoter: A typical bacterial promoter has two conserved hexamers upstream of the start site, near positions -10 and -35.

Step 1 – locate the element: The hexamer centred about 10 bp upstream of $+1$ has the consensus `TATAAT`.

Step 2 – name it: This is the -10 **box**, also called the Pribnow box.

Step 3 – note its role: Its AT-rich sequence is easy to melt, so it is where the DNA strands first separate to form the open complex.

Why the other options are wrong:

- B, -35 element: has the consensus `TTGACA` and lies further upstream.
- C, operator: is a regulatory (repressor-binding) site, not a core promoter element.
- D, Shine–Dalgarno sequence: lies in the mRNA and is the ribosome-binding site for *translation*, not a promoter element.

Final Answer: the -10 (Pribnow) box $\Rightarrow$ A

Answer: (A) Go Back to Q13

Q14.

Solution

Concept – the three eukaryotic RNA polymerases: Pol I makes most rRNA, Pol II makes mRNA precursors, and Pol III makes tRNA and 5S rRNA.

Step 1 – identify the product needed: Protein-coding genes must be copied into messenger RNA precursors (pre-mRNA).

Step 2 – match the polymerase: This job belongs to **RNA polymerase II**.

Step 3 – note a distinguishing fact: Pol II is specifically inhibited by low concentrations of α-amanitin, a feature used to tell the polymerases apart.

Why the other options are wrong:

- A, RNA polymerase I: transcribes the large ribosomal RNA precursor.
- C, RNA polymerase III: transcribes tRNAs and 5S rRNA.
- D, primase: makes short RNA primers for DNA replication, not mRNA.

Final Answer: RNA polymerase II $\Rightarrow$ B

Answer: (B) Go Back to Q14

Q15.

Solution

Concept – pre-mRNA splicing: Eukaryotic protein-coding genes are interrupted by introns that must be removed before translation.

Step 1 – describe the reaction: Introns are excised and the neighbouring exons are ligated together to make a continuous coding sequence.

Step 2 – name the machine: This is carried out by the **spliceosome**, a complex of small nuclear ribonucleoproteins (snRNPs U1, U2, U4, U5, U6) and proteins.

Step 3 – note the chemistry: Splicing proceeds through two transesterification reactions via a branch-point adenosine, forming a lariat intermediate.

Why the other options are wrong:

- A, ribosome: carries out translation of mRNA, not splicing.
- C, proteasome: degrades proteins.
- D, nucleosome: is the DNA–histone packaging unit, unrelated to splicing.

Final Answer: the spliceosome $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q15

Q16.

Solution

Concept – a repressible operon: In a repressible operon the end product of the pathway signals when transcription should stop.

Step 1 – state of the repressor: The *trp* repressor is made as an inactive aporepressor; it needs tryptophan as a corepressor to become active.

Step 2 – action when tryptophan is abundant: Plenty of tryptophan binds the aporepressor, converting it to the active DNA-binding form.

Step 3 – effect on the operon: The active repressor binds the operator and blocks RNA polymerase, so **transcription of the operon is switched off**.

Step 4 – biological logic: When tryptophan is plentiful the cell need not make the enzymes for its synthesis, so shutting the operon down conserves resources.

Why the other options are wrong:

- A, transcription increases: is the opposite of repression.
- B, the operator is deleted: the DNA sequence is unchanged; only binding changes.

- D, RNA polymerase moves faster: repression blocks initiation; it does not change elongation speed.

Final Answer: transcription of the operon is switched off $\Rightarrow$ C

Answer: (C) Go Back to Q16

Q17.

Solution

Concept – the direction of nucleic-acid synthesis: Nucleotides are added to the free $3'$-hydroxyl at the growing end of the chain.

Step 1 – locate the reactive group: RNA polymerase joins the incoming ribonucleotide's $5'$-phosphate to the $3'$-OH of the last nucleotide.

Step 2 – deduce the direction: Because growth is always at the $3'$ end, the new RNA strand is synthesised $5' \rightarrow 3'$.

Step 3 – relate to the template: The DNA template is therefore read in the antiparallel $3' \rightarrow 5'$ direction.

Why the other options are wrong:

- B, $3' \rightarrow 5'$: is the direction the template is read, not the direction of RNA growth.
- C, both directions: a single polymerase adds only at the $3'$ end.
- D, $5' \rightarrow 5'$: is not a valid polymerisation direction.

Final Answer: $5' \rightarrow 3' \Rightarrow$ A

Answer: (A) Go Back to Q17

Q18.

Solution

Concept – the $3'$ poly-A tail of eukaryotic mRNA: After transcription, most eukaryotic mRNAs are cleaved and given a long run of adenines at the $3'$ end.

Step 1 – how it is added: Poly-A polymerase adds ~ 150–250 adenines without a template, guided by the AAUAAA signal.

Step 2 – state the functions: The poly-A tail **increases mRNA stability, aids export from the nucleus, and enhances translation** (through poly-A-binding proteins).

Step 3 – link stability to lifetime: Gradual shortening of the tail is one trigger for eventual mRNA degradation, so a longer tail generally means a longer-lived message.

Why the other options are wrong:

- B, encode a signal peptide: the tail is non-coding.
- C, ribosome-binding site in prokaryotes: that is the Shine–Dalgarno sequence, and prokaryotic mRNAs are generally not polyadenylated for stability.
- D, remove introns: that is splicing, a separate step.

Final Answer: increases stability and assists export and translation $\Rightarrow$ A

Answer: (A) Go Back to Q18

Q19.

Solution

Concept – Hardy–Weinberg genotype frequencies: For two alleles with frequencies p and q ($p+q=1$), genotype frequencies are p^2 (homozygous dominant), $2pq$ (heterozygous) and q^2 (homozygous recessive).

Step 1 – list the data: $p = 0.7$ (dominant allele A).

Step 2 – select the right term: Homozygous dominant (AA) individuals occur at frequency p^2.

Step 3 – substitute: $p^2 = (0.7)^2$

Step 4 – evaluate: $= 0.49$

Step 5 – consistency check: $q = 1 - 0.7 = 0.3$, so $q^2 = 0.09$ and $2pq = 0.42$; total $= 0.49 + 0.42 + 0.09 = 1.00$.

Final Answer: $p^2 = 0.49 \Rightarrow$ D

Answer: (D) Go Back to Q19

Q20.

Solution

Concept – the primary immune response: On first contact with an antigen, one antibody class appears before the others.

Step 1 – identify the earliest class: The first antibody secreted is **IgM**.

Step 2 – explain its suitability: Secreted IgM is a pentamer with ten antigen-binding sites, making it very effective at agglutinating pathogens and activating complement early on.

Step 3 – contrast with later response: Later, class switching produces IgG, which dominates the secondary response.

Why the other options are wrong:

- B, IgG: dominates the *secondary* response and appears after IgM.
- C, IgA: is mainly a mucosal-secretion antibody.
- D, IgE: is a trace antibody involved in allergy and parasite defence.

Final Answer: IgM $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q20

Q21.

Solution

Concept – carriers from disease incidence under Hardy–Weinberg: The affected (recessive homozygote) frequency is q^2; from it we get q, then p, then the carrier frequency $2pq$.

Step 1 – read the incidence: $q^2 = \dfrac{1}{400} = 0.0025$.

Step 2 – find the recessive allele frequency: $q = \sqrt{0.0025} = 0.05$.

Step 3 – find the dominant allele frequency: $p = 1 - q = 1 - 0.05 = 0.95$.

Step 4 – compute the carrier frequency: $2pq = 2 \times 0.95 \times 0.05$

Step 5 – evaluate: $= 2 \times 0.0475 = 0.095$.

Step 6 – interpret: About 0.095, that is roughly 1 carrier in every 10.5 people, far more common than the affected 1 in 400.

Final Answer: carrier frequency $2pq \approx 0.095 \Rightarrow \boxed{\text{A}}$

Answer: (A) Go Back to Q21

Q22.

Solution

Concept – mechanisms that change allele frequencies: Evolution can proceed by natural selection, gene flow, mutation and random genetic drift.

Step 1 – read the description: Allele frequencies change only because a small, random sample of gametes founds the next generation, with no fitness differences involved.

Step 2 – name the mechanism: This purely chance sampling effect is **genetic drift**.

Step 3 – note its dependence on size: Drift is strongest in small populations and can fix or lose alleles by chance (for example, bottleneck and founder effects).

Why the other options are wrong:

- A, natural selection: acts through fitness differences, which the question explicitly excludes.
- B, gene flow: requires migration between populations.
- D, mutation pressure: is the slow input of new alleles, not random sampling of existing ones.

Final Answer: genetic drift $\Rightarrow$ C

Answer: (C) Go Back to Q22

Q23.

Solution

Concept – the clonal selection theory: Lymphocyte receptor diversity is generated *before* any encounter with antigen; the antigen then merely picks the matching cells.

Step 1 – the starting repertoire: Each lymphocyte already bears receptors of a single, randomly generated specificity, produced independently of antigen.

Step 2 – the role of the antigen: An incoming antigen binds only those cells whose pre-existing receptor fits it, and **selects and stimulates** them to proliferate.

Step 3 – the outcome: The selected cell expands into a clone of identical cells, giving a specific, amplified response and memory.

Why the other options are wrong:

- A, instructs a lymphocyte to fold an antibody around it: this is the old, dis-

credited instructional theory.

- B, required to generate diversity: diversity arises by gene rearrangement before antigen contact, not because of the antigen.
- D, becomes the antibody: antigens are not converted into antibodies.

Final Answer: the antigen selects and stimulates matching pre-existing lymphocytes $\Rightarrow$ C

Answer: (C) Go Back to Q23

Q24.

Solution

Concept – reading a phylogenetic tree: The pair of taxa joined at the node nearest the tips (the most recent common ancestor) is the most closely related.

Step 1 – find the deepest (most recent) node: In the tree, Y and Z join at the node closest to the tips.

Step 2 – identify the sister pair: Y and Z therefore form a clade, sharing the *most recent* common ancestor.

Step 3 – trace the earlier branches: X joins the (Y,Z) clade at an earlier node, and W branches off earliest of all, so W is the most distantly related.

Why the other options are wrong:

- B, W and X: these do not form a clade; W is the outermost branch.
- C, W and Z: their common ancestor is the deepest node, so they are distantly related.
- D, X and Y: X joins the Y–Z clade only at an older node, so X and Y are less closely related than Y and Z.

Final Answer: Y and Z $\Rightarrow$ A

Answer: (A) Go Back to Q24

Q25.

Solution

Concept – the threshold cycle in qPCR: Real-time PCR follows product accumulation cycle by cycle through a fluorescent signal.

Step 1 – define the threshold: A horizontal threshold line is set in the exponential region, just above background noise.

Step 2 – read off the cycle: The cycle at which a sample's fluorescence first crosses this line is the **threshold cycle (C_t)**, sometimes written C_q.

Step 3 – link to starting amount: The more template a sample starts with, the fewer cycles are needed to cross the threshold, so a smaller C_t means more starting target.

Why the other options are wrong:

- A, melting temperature: comes from a separate melt-curve analysis, not the amplification plot.
- B, annealing cycle: is not a defined qPCR quantity.
- C, plateau cycle: the plateau is where the reaction saturates and is not used for quantitation.

Final Answer: the threshold cycle (C_t) $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q25

Q26.

Solution

Concept – TaqMan (hydrolysis-probe) chemistry: While intact, the probe holds the reporter and quencher close together, so the reporter's fluorescence is quenched by FRET.

Step 1 – probe binding: During annealing the probe hybridises to the target between the two primers.

Step 2 – the key enzymatic action: As Taq polymerase extends the primer, its $5' \rightarrow 3'$ exonuclease activity **cleaves the probe, releasing the reporter fluorophore away from the quencher**.

Step 3 – the signal: Separated from the quencher, the reporter now fluoresces, and the signal rises in proportion to the amount of product made.

Why the other options are wrong:

- A, denatures the template: denaturation is caused by heat, not by the exonuclease.
- C, removes the primers: primers are incorporated, not removed.
- D, adds a poly-A tail: PCR does not add poly-A tails.

Final Answer: it cleaves the reporter from the quencher on the probe $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q26

Q27.

Solution

Concept – relating ΔC_t to fold difference: At 100% efficiency the amount of product doubles each cycle, so a difference of n cycles corresponds to a 2^n-fold difference in starting amount.

Step 1 – note the direction: Sample A crosses the threshold *earlier*, so A has *more* starting target than B.

Step 2 – write the relation: Fold difference $= 2^{\Delta C_t}$.

Step 3 – substitute $\Delta C_t = 3$: $= 2^3$

Step 4 – evaluate: $= 8$.

Step 5 – state the comparison: Sample A therefore started with about 8 times as much target as sample B.

Final Answer: about 8 times $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q27

Q28.

Solution

Concept – a thermostable polymerase for PCR: PCR repeatedly heats the reaction to about 95 °C, which would destroy an ordinary polymerase.

Step 1 – identify the requirement: The enzyme must survive many high-temperature denaturation steps and still be active.

Step 2 – name the enzyme: *Taq* DNA polymerase, purified from the hot-spring bacterium *Thermus aquaticus*, meets this need.

Step 3 – note its optimum: Taq works best near 72 °C, which is why extension is carried out at that temperature.

Why the other options are wrong:

- B, *E. coli* DNA polymerase I: is heat-labile and is inactivated at 95 °C.
- C, T4 DNA ligase: joins DNA ends; it does not polymerise a new strand.
- D, reverse transcriptase: makes DNA from RNA and is not thermostable.

Final Answer: *Taq* DNA polymerase $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q28

Q29.

Solution

Concept – reverse-transcription PCR (RT-PCR): To amplify from RNA, the RNA must first be copied into DNA.

Step 1 – the first enzymatic step: Reverse transcriptase reads the RNA template and synthesises a complementary DNA strand.

Step 2 – name the product: The product is **complementary DNA (cDNA)**.

Step 3 – what follows: The cDNA then serves as the template for ordinary PCR amplification (or for qPCR quantitation).

Why the other options are wrong:

- B, a protein: reverse transcriptase makes nucleic acid, not protein.
- C, genomic double-stranded DNA directly: the immediate product is a single cDNA strand from the RNA, not genomic DNA.
- D, ribosomal RNA: reverse transcriptase makes DNA, not RNA.

Final Answer: complementary DNA (cDNA) $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q29

Q30.

Solution

Concept – primer melting temperature: The T_m of a primer is the temperature at which half of it is duplexed with its target; it rises with base-pairing strength.

Step 1 – compare the base pairs: A G≡C pair has three hydrogen bonds, whereas an A=T pair has only two.

Step 2 – deduce the trend: More G≡C pairs mean stronger, more stable duplexes and thus a higher T_m for a primer of a given length.

Step 3 – identify the answer: A higher T_m therefore comes from a greater content of **guanine and cytosine**.

Why the other options are wrong:

- A, adenine and thymine: A=T pairs are weaker and *lower* the T_m.
- B, adenine and uracil: uracil belongs to RNA, not to DNA primers.
- C, thymine only: a single base type does not by itself raise T_m; the G+C fraction is what matters.

Final Answer: guanine and cytosine $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q30

Q31.

Solution

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

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

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

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

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

Step 5 – interpret: At steady state the culture's specific growth rate will settle to $\mu = D = 0.30\ \text{h}^{-1}$.

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

Answer: (D) Go Back to Q31

Q32.

Solution

Concept – washout in a chemostat: At steady state $\mu = D$, but the growth rate can only rise as far as its ceiling $\mu_{\max}$.

Step 1 – the steady-state condition: The cells match their growth rate to the imposed dilution rate, so $\mu = D$.

Step 2 – the ceiling on growth: Since μ can never exceed $\mu_{\max}$, the culture cannot keep up once $D > \mu_{\max}$.

Step 3 – the consequence: When $D > \mu_{\max}$, cells are removed faster than they can grow, so the biomass falls to zero: this is **washout**.

Step 4 – state the threshold: Washout therefore occurs when the dilution rate exceeds $\mu_{\max}$.

Why the other options are wrong:

- A, K_s: is a substrate-affinity constant, not the growth ceiling.
- C, $Y_{X/S}$: is the yield coefficient and does not set the washout point.
- D, zero: any positive D below $\mu_{\max}$ still gives a stable culture.

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

Answer: (B) Go Back to Q32

Q33.

Solution

Concept – residual substrate in a chemostat: Combining $\mu = D$ with the Monod equation gives $S = \dfrac{K_s D}{\mu_{\max} - D}$ at steady state.

Step 1 – list the data: $K_s = 0.2$ g L^{-1}, $\mu_{\max} = 0.8$ h^{-1}, $D = 0.4$ h^{-1}.

Step 2 – form the denominator: $\mu_{\max} - D = 0.8 - 0.4 = 0.4$ h^{-1}

Step 3 – form the numerator: $K_s D = 0.2 \times 0.4 = 0.08$ g L^{-1}h^{-1}

Step 4 – divide: $S = \dfrac{0.08}{0.4}$

Step 5 – evaluate: $S = 0.2$ g L^{-1}

Step 6 – sanity check: Here $D = \frac{1}{2}\mu_{\max}$, so from Monod $S = K_s$; indeed $S = 0.2 = K_s$, confirming the result.

Final Answer: $S = 0.2$ g L$^{-1} \Rightarrow$ A

Answer: (A) Go Back to Q33

Q34.

Solution

Concept – biomass productivity of a chemostat: Cell output rate is $D\,X$; it rises with D up to a peak and then collapses as washout is approached.

Step 1 – behaviour near $\mu_{\max}$: As $D \to \mu_{\max}$, the steady-state biomass X falls steeply toward zero.

Step 2 – the danger: Very close to $\mu_{\max}$ a small upward fluctuation in D (or a dip in $\mu_{\max}$) pushes the system past the critical point.

Step 3 – the result: The cells are then removed faster than they grow and the culture is **washed out**.

Step 4 – practical rule: Operators run the chemostat at a D safely below $\mu_{\max}$ (near the productivity peak) to avoid this.

Why the other options are wrong:

- A, foaming: is an aeration/agitation issue, not caused by high D.
- B, contamination: relates to sterility, not to the chosen dilution rate.

- D, substrate inhibition: is a property of the substrate concentration, not of operating near $\mu_{\max}$.

Final Answer: washout of the cells $\Rightarrow$ C

Answer: (C) Go Back to Q34

Q35.

Solution

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

Step 1 – list the data: $X_0 = 0.5$ g L^{-1}, $X = 4$ g L^{-1}, $t = 5$ h.

Step 2 – form the ratio: $\dfrac{X}{X_0} = \dfrac{4}{0.5} = 8$

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: $\mu = \dfrac{2.079}{5}$

Step 5 – evaluate: $\mu \approx 0.416$ h^{-1} ≈ 0.42 h^{-1}

Final Answer: $\mu \approx 0.42$ h^{-1} $\Rightarrow$ C

Answer: (C) Go Back to Q35

Q36.

Solution

Concept – the maintenance coefficient: Not all consumed substrate goes into new biomass or product; some is burned just to keep cells alive.

Step 1 – define the term: The maintenance coefficient m is the specific rate of substrate consumption used for **non-growth (maintenance) functions**.

Step 2 – give examples of maintenance: These include maintaining membrane ion gradients, cell motility, and the turnover of macromolecules.

Step 3 – place it in the substrate balance: Total substrate uptake = (substrate for growth) + (substrate for product) + (substrate for maintenance, $\propto m$).

Why the other options are wrong:

- A, product formation only: is a separate term in the substrate balance.
- B, DNA replication: is part of growth, not maintenance.
- C, new biomass synthesis: is captured by the yield term $Y_{X/S}$, not by m.

Final Answer: non-growth (cell-maintenance) functions $\Rightarrow$ D

Answer: (D) Go Back to Q36

Q37.

Solution

Concept – the respiratory quotient (RQ): RQ is obtained from off-gas analysis and reflects which substrate is being oxidised and the metabolic state of the culture.

Step 1 – write the definition: $\text{RQ} = \dfrac{\text{moles of } CO_2 \text{ produced}}{\text{moles of } O_2 \text{ consumed}}$.

Step 2 – interpret typical values: For carbohydrate oxidation RQ ≈ 1; values well above 1 signal fermentative (overflow) metabolism, and values below 1 suggest oxidation of more reduced substrates.

Step 3 – match to the option: CO_2 produced divided by O_2 consumed is option B.

Why the other options are wrong:

- A: inverts the ratio (O_2/CO_2).
- C: substrate over biomass is a yield-type ratio, not RQ.
- D: biomass over product is unrelated to gas exchange.

Final Answer: $\text{RQ} = \dfrac{CO_2 \text{ produced}}{O_2 \text{ consumed}} \Rightarrow$ B

Answer: (B) Go Back to Q37

Q38.

Solution

Concept – fed-batch culture of baker's yeast: Yeast shows the Crabtree effect: at high glucose it ferments to ethanol even when oxygen is available, wasting carbon and lowering cell yield.

Step 1 – identify the problem to avoid: A high residual glucose concentration triggers overflow metabolism to ethanol.

Step 2 – the fed-batch strategy: Feeding the sugar slowly keeps the residual glucose **low**, so respiration is favoured over fermentation.

Step 3 – the benefit: With glucose kept low, carbon is channelled into biomass, giving the high cell densities wanted for baker's yeast.

Why the other options are wrong:

- A, saturate the cells with sugar: high glucose is exactly what causes wasteful ethanol formation.
- C, stop oxygen consumption: the aim is to *favour* aerobic respiration, not stop it.
- D, hold glucose at a saturating level: this would again drive the Crabtree overflow.

Final Answer: keep glucose low to prevent overflow (ethanol) formation $\Rightarrow$ B

Answer: (B) Go Back to Q38

Q39.

Solution

Concept – growth control of normal animal cells: Normal cells sense their neighbours and stop dividing when the surface is covered.

Step 1 – describe the behaviour: Cells divide until they form one continuous layer (a confluent monolayer) and then stop once every cell touches its neighbours.

Step 2 – name the property: This is **contact inhibition** (of growth and of movement).

Step 3 – contrast with cancer cells: Transformed (cancerous) cells lose contact inhibition and pile up into multilayers, a hallmark used in culture to spot transformation.

Why the other options are wrong:

- A, apoptosis: is programmed cell death, not a stop-dividing-at-confluence response.
- B, malignant transformation: is the *loss* of this control, the opposite of what is described.
- D, anchorage independence: is the ability to grow without a surface, again a transformed trait.

Final Answer: contact inhibition $\Rightarrow$ C

Answer: (C) Go Back to Q39

Q40.

Solution

Concept – surface requirement of animal cells: Many animal cells need to attach and spread on a solid support to grow.

Step 1 – describe the requirement: Normal cells divide only when anchored to a surface such as the flask wall or a microcarrier bead.

Step 2 – name the property: This is **anchorage dependence**.

Step 3 – industrial relevance: Because of it, large-scale culture of such cells uses microcarrier beads or roller bottles to maximise attachment area.

Why the other options are wrong:

- A, suspension growth: is the ability to grow *without* attachment, the opposite property.
- B, immortalisation: refers to unlimited division, a different concept.
- C, contact inhibition: is stopping at confluence, not the need for a surface.

Final Answer: anchorage dependence $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q40

Q41.

Solution

Concept – replicative senescence of normal cells: Normal somatic cells can divide only a limited number of times in culture.

Step 1 – describe the observation: Normal human fibroblasts undergo a fixed number of population doublings and then permanently stop dividing (senescence).

Step 2 – name the limit: This maximum number of divisions is the **Hayflick limit**.

Step 3 – give the mechanism: It is linked to progressive telomere shortening at each division, until the cells can no longer replicate their DNA ends.

Why the other options are wrong:

- A, lag phase: is the early adaptation period of a culture, not a division ceiling.
- C, log phase: is the active growth phase, not a limit.
- D, plateau phase: describes confluence/stationary density, not the lifetime division count.

Final Answer: the Hayflick limit $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q41

Q42.

Solution

Concept – serum supplementation of culture media: Basal media supply salts, sugars, amino acids and vitamins, but usually not the growth factors cells need.

Step 1 – what is added: A natural fluid is added at about 5–10% to provide growth factors, hormones, attachment and transport proteins.

Step 2 – name the supplement: The most widely used such supplement is **fetal bovine serum (FBS)**, also called fetal calf serum.

Step 3 – note a limitation: FBS is chemically undefined and batch-variable, which is why defined, serum-free media are increasingly used for reproducible bioprocesses.

Why the other options are wrong:

- A, agar: is a gelling agent used for microbial plates, not a growth-factor source.
- C, yeast extract: is a nutrient for microbial media, not for animal cells.
- D, casein hydrolysate alone: supplies amino acids but not the growth factors and hormones that serum provides.

Final Answer: fetal bovine serum (FBS) $\Rightarrow \boxed{\text{B}}$

Answer: (B) Go Back to Q42

Q43.

Solution

Concept – hormonal control of organ formation in tissue culture: Skoog and Miller showed that the *ratio* of two growth regulators steers cultured plant tissue toward shoots or roots.

Step 1 – name the two regulators: The two are auxin and **cytokinin**.

Step 2 – state the effect of their ratio: A high cytokinin-to-auxin ratio promotes shoot formation; a high auxin-to-cytokinin ratio promotes root formation; balanced levels keep the tissue as undifferentiated callus.

Step 3 – link to practice: Media formulations adjust this ratio deliberately to regenerate whole plants in micropropagation.

Why the other options are wrong:

- A, gibberellin: mainly promotes stem elongation and germination, not the shoot/root switch.
- B, ethylene: is involved in ripening and senescence.
- C, abscisic acid: mediates stress responses and dormancy.

Final Answer: cytokinin $\Rightarrow$ D

Answer: (D) Go Back to Q43

Q44.

Solution

Concept – elution in ion-exchange chromatography: Proteins bind a charged resin electrostatically and are released by weakening that electrostatic attraction.

Step 1 – the binding step: On a cation exchanger (negatively charged resin), positively charged proteins bind.

Step 2 – the elution step: Raising the **salt concentration (ionic strength)** of the buffer supplies competing ions that displace the bound proteins from the resin.

Step 3 – the order of elution: Weakly bound proteins come off at low salt, and more strongly (more positively) charged proteins need higher salt, giving separation along the gradient shown.

Why the other options are wrong:

- A, temperature: is not the primary elution variable in ion exchange.
- B, column length: is fixed and does not elute bound proteins.
- C, detector wavelength: only changes what is detected, not what elutes.

Final Answer: salt concentration (ionic strength) $\Rightarrow$ D

Answer: (D) Go Back to Q44

Q45.

Solution

Concept – charge matching in ion-exchange chromatography: An ion exchanger binds molecules of the *opposite* charge to its own functional groups.

Step 1 – charge of an anion exchanger: A DEAE resin carries *positive* charges.

Step 2 – what it binds: It therefore binds oppositely charged, **negatively charged**

(acidic) molecules.

Step 3 – consistency with the name: It is called an "anion" exchanger because it exchanges and retains anions (negatively charged species).

Why the other options are wrong:

- A, neutral: uncharged molecules are not retained by ionic attraction.
- B, positively charged: like charges repel; positive proteins pass through an anion exchanger and instead bind a cation exchanger.
- D, only lipids: ion exchange separates by charge, not by lipid nature.

Final Answer: negatively charged (acidic) molecules $\Rightarrow$ C

Answer: (C) Go Back to Q45

Q46.

Solution

Concept – protein charge relative to its pI: A protein is negatively charged above its isoelectric point and positively charged below it.

Step 1 – compare pH with pI: Loading pH $= 8.0$ is above the protein's pI $= 5.0$.

Step 2 – deduce the net charge: Because pH $>$ pI, the protein carries a **net negative** charge at pH 8.0.

Step 3 – predict the binding: A negatively charged protein is attracted to the positively charged DEAE anion exchanger, so it **binds** the column.

Step 4 – how it would later elute: It can then be eluted by raising the salt concentration or by lowering the pH toward its pI.

Why the other options are wrong:

- B, net positive and flows through: positive charge would occur only *below* the pI (pH < 5).
- C, no net charge: zero net charge occurs only at the pI itself (pH $= 5.0$), not at pH 8.0.
- D, net positive, binds a cation exchanger: the sign of the charge is wrong at this pH.

Final Answer: net negative charge, so it binds the anion exchanger $\Rightarrow$ A

Answer: (A) Go Back to Q46

Answer Key

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