GATE Biotechnology

Sample Paper – 10

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. Phosphofructokinase-1 (PFK-1) catalyses the committed, rate-limiting step of glycolysis and is under tight allosteric control. In liver, the most potent allosteric *activator* of PFK-1, which signals that glucose is abundant, is: [1 mark]

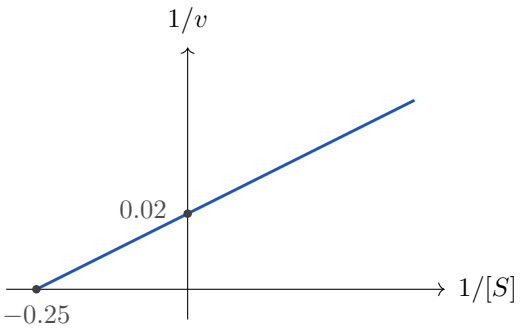
(A) fructose-2,6-bisphosphate

(B) citrate

(C) ATP at high concentration

(D) NADH

Q2. The Lineweaver–Burk (double-reciprocal) plot of an enzyme is shown below. Its intercept on the vertical ($1/v$) axis is 0.02 min μmol^{-1} and its intercept on the horizontal ($1/[S]$) axis is -0.25 mM^{-1}. The Michaelis constant K_m of this enzyme is: **[1 mark]**



(A) 50 mM

(B) 0.25 mM

(C) 0.02 mM

(D) 4 mM

Q3. In many amino-acid biosynthetic pathways, the final end product of the pathway binds to and inhibits the first, committed enzyme of that pathway. This mode of metabolic control is called: **[1 mark]**

(A) feedback (end-product) inhibition

(B) feed-forward activation

(C) substrate-level phosphorylation

(D) zymogen activation

Q4. Among the following phosphorylated intermediates of metabolism, the compound with the *most negative* standard free energy of hydrolysis, that is, the highest phosphoryl-group-transfer potential, is: **[1 mark]**

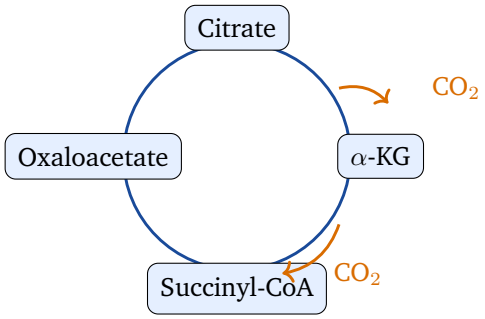
(A) glucose-6-phosphate

(B) ATP (hydrolysis of the terminal phosphate)

(C) glycerol-3-phosphate

(D) phosphoenolpyruvate (PEP)

Q5. One complete turn of the citric acid (Krebs) cycle is outlined below, starting from citrate. Counting only the two oxidative decarboxylation steps, the number of CO_2 molecules released per single turn of the cycle is: [1 mark]



(A) 1

(B) 2

(C) 3

(D) 6

Q6. The coenzyme derived from the vitamin niacin, which serves as the principal soluble electron carrier that accepts a hydride ion during the oxidative reactions of catabolism, is: [1 mark]

(A) NAD^+

(B) FAD

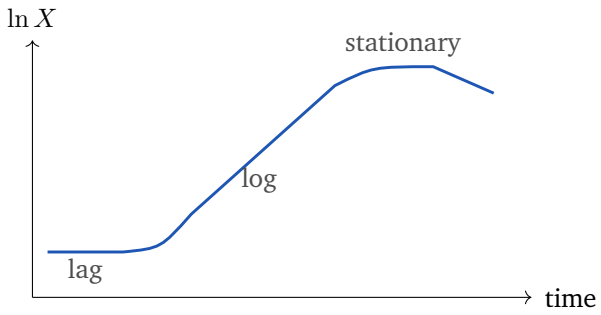
(C) coenzyme A

(D) thiamine pyrophosphate (TPP)

Microbiology

Q7. The batch growth curve of a bacterium, plotted as $\ln X$ against time, is shown below. Many secondary metabolites, including a large number

of antibiotics, are produced chiefly when active growth has slowed and nutrients become limiting. On this curve, that production occurs during the: **[1 mark]**



(A) exponential (log) phase

(B) stationary phase

(C) lag phase

(D) death (decline) phase

Q8. During exponential growth a bacterial population increases from 5×10^3 cells to 5×10^7 cells in exactly 4 hours. The generation (doubling) time of this culture is nearest to: **[1 mark]**

(A) 9 min

(B) 12 min

(C) 18 min

(D) 30 min

Q9. The large-scale industrial production of ethanol by the alcoholic fermentation of sugars (for both beverages and biofuel) is carried out mainly using the microorganism: **[1 mark]**

(A) *Lactobacillus bulgaricus*

(B) *Saccharomyces cerevisiae*

(C) *Acetobacter aceti*

(D) *Aspergillus niger*

Q10. Which microorganism is correctly matched with the principal commercial fermentation product it is used to manufacture? [1 mark]

(A) *Aspergillus niger* $\rightarrow$ citric acid

(B) *Penicillium chrysogenum* $\rightarrow$ lactic acid

(C) *Corynebacterium glutamicum* $\rightarrow$ ethanol

(D) *Clostridium acetobutylicum* $\rightarrow$ penicillin

Q11. An organism that obtains its energy from the oxidation of reduced inorganic compounds and fixes carbon from CO_2 is nutritionally classified as a: [1 mark]

(A) chemolithoautotroph

(B) photoautotroph

(C) chemoorganoheterotroph

(D) photoheterotroph

Cell Biology and Molecular Biology

Q12. In many hormone-triggered pathways, binding of the ligand to a G-protein-coupled receptor activates adenylyl cyclase, which raises the intracellular level of a small diffusible second messenger that in turn activates protein kinase A. This second messenger is: [1 mark]

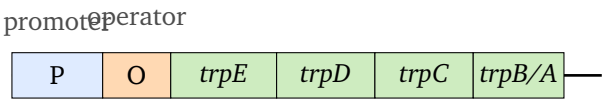
(A) inositol 1,4,5-trisphosphate (IP_3)

(B) diacylglycerol (DAG)

(C) calcium ion (Ca^{2+})

(D) cyclic AMP (cAMP)

Q13. The *trp* operon of *Escherichia coli* is shown below. Tryptophan acts as a co-repressor: when tryptophan is plentiful it binds the *trp* aporepressor, and the active complex switches transcription OFF by binding to the: [1 mark]



(A) structural genes *trpE–trpA*

(B) operator

(C) leader (attenuator) region

(D) transcription terminator

Q14. A receptor tyrosine kinase, such as the insulin receptor or the EGF receptor, is switched to its active signalling state on ligand binding by: **[1 mark]**

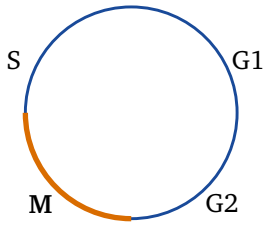
(A) hydrolysing GTP to GDP

(B) opening a transmembrane ion channel

(C) dimerising and autophosphorylating its tyrosine residues

(D) directly synthesising cAMP

Q15. The eukaryotic cell cycle is represented below, with one quadrant highlighted. Chromosome condensation, alignment at the metaphase plate and separation of sister chromatids all take place during the phase marked: **[1 mark]**



(A) G1 phase

(B) S phase

(C) G2 phase

(D) M (mitotic) phase

Q16. During bacterial translation, each incoming aminoacyl-tRNA is delivered to the A site of the ribosome by an elongation factor that uses the energy of GTP hydrolysis. That elongation factor is: **[1 mark]**

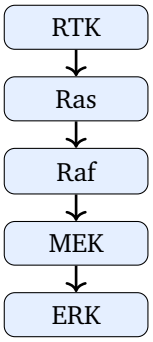
(A) EF-G

(B) IF-2

(C) RF-1

(D) EF-Tu

Q17. The Ras–MAPK signal-transduction cascade is outlined below. In this pathway the small GTPase Ras is switched to its ACTIVE, signalling state when it is bound to: **[1 mark]**



active when GTP-bound

(A) GDP

(B) cAMP

(C) GTP

(D) inorganic phosphate

Q18. During eukaryotic mRNA processing, the modification added to the $5'$ end of the primary transcript, which protects the transcript from exonucleases and helps the small ribosomal subunit to bind, is the: **[1 mark]**

(A) 7-methylguanosine cap

(B) poly-A tail

(C) retained intron

(D) Shine–Dalgarno sequence

Genetics, Immunology and Evolution

Q19. Human ABO blood groups are governed by the multiple alleles I^A, I^B and i. In a person of blood group AB, both the A and the B antigens are expressed fully and equally on the red cells. This pattern of allelic interaction is best described as: **[1 mark]**

(A) complete dominance

(B) epistasis

(C) X-linkage

(D) codominance

Q20. During a primary immune response the first antibody class to be secreted into the blood, existing as a pentamer with ten antigen-binding sites, is: **[1 mark]**

(A) IgM

(B) IgG

(C) IgA

(D) IgE

Genetics, Immunology and Evolution (continued)

Q21. A large randomly mating population is at Hardy–Weinberg equilibrium for a single gene with two alleles. The frequency of the recessive allele is $q = 0.3$. The expected frequency of *homozygous dominant* individuals in the population is: **[2 marks]**

(A) 0.09

(B) 0.49

(C) 0.42

(D) 0.21

Q22. A man of blood group O marries a woman of blood group AB. Considering only the ABO locus, the blood groups that can appear among their children are: **[2 marks]**

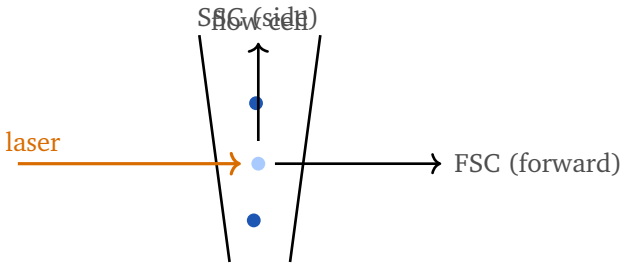
(A) only groups A and B

(B) only group AB

(C) groups A, B, AB and O

(D) only group O

Q23. The principle of a flow cytometer is shown below: cells in single file cross a laser beam and the scattered light is collected. The light scattered at a small *forward* angle (forward scatter, FSC) is used mainly as a measure of the: **[2 marks]**



(A) internal granularity (complexity) of the cell

(B) fluorescence of a bound labelled antibody

(C) DNA content of the cell

(D) relative size (diameter) of the cell

Q24. The enormous diversity of antibody antigen-binding sites is generated largely during B-lymphocyte development by a process that rearranges separate germline gene segments. This process is: **[2 marks]**

(A) alternative splicing of a single fixed gene

(B) V(D)J somatic recombination of gene segments

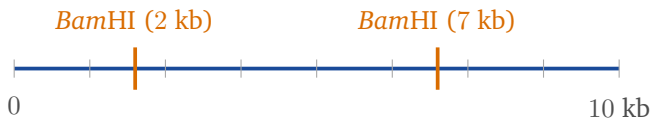
(C) point mutation of the germline promoter

(D) whole-genome polyploidisation of the B cell

Recombinant DNA Technology and Bioinformatics

Q25. A linear DNA fragment of total length 10 kb carries two recognition sites for *Bam*HI, at the 2 kb and 7 kb positions measured from the left end, as

shown. Complete digestion of this fragment with *Bam*HI produces pieces of: [2 marks]



(A) 2 kb, 5 kb and 3 kb

(B) 2 kb and 7 kb

(C) 5 kb and 5 kb

(D) 10 kb only (single piece)

Q26. In next-generation sequencing (NGS) by synthesis on the Illumina platform, the DNA fragments to be read are first amplified into dense clonal clusters on the surface of the flow cell by the process of: [2 marks]

(A) Sanger chain termination

(B) rolling-circle replication

(C) bridge amplification

(D) reverse transcription

Q27. In a two-colour DNA microarray experiment, cDNA from a test sample is labelled with the red dye Cy5 and cDNA from a control sample with the green dye Cy3; the two are mixed and hybridised to the array shown. A spot that fluoresces predominantly *red* indicates that the corresponding gene is: [2 marks]

(A) expressed equally in both samples

(B) over-expressed (up-regulated) in the test sample

(C) not expressed in either sample

(D) physically deleted from the test genome

Q28. In the analysis of high-throughput sequencing data, the standard plain-text file format that stores each short read together with its per-base quality (Phred) scores is: [2 marks]

(A) FASTA

(B) PDB

(C) FASTQ

(D) GenBank flat file

Q29. To express a eukaryotic protein in a bacterial host that cannot splice introns, the coding sequence is best cloned as an intron-free cDNA copy synthesised from the mature mRNA. The enzyme used to make this first-strand cDNA is: [2 marks]

(A) DNA polymerase I

(B) Taq polymerase

(C) reverse transcriptase

(D) RNA polymerase

Q30. A useful cloning vector must contain, as a minimum, an origin of replication, a selectable marker, and one further feature that provides a cluster of unique restriction sites for inserting foreign DNA. That feature is: [2 marks]

(A) a telomere

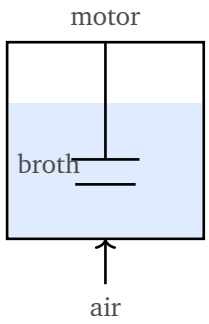
(B) a centromere

(C) a poly-A signal

(D) a multiple cloning site (polylinker)

Bioprocess Engineering and Process Biotechnology

Q31. In the batch stirred-tank bioreactor shown, an organism grows exponentially and the biomass concentration rises from 0.5 g L^{-1} to 4 g L^{-1} in 3 hours. The specific growth rate μ over this period is nearest to: [2 marks]



(A) $0.23\ \text{h}^{-1}$

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

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

(D) $1.39\ \text{h}^{-1}$

Q32. In a fermentation, 12 g of dry cell biomass and 4 g of a secreted product are formed while 60 g of glucose is consumed as the carbon and energy source. The biomass yield coefficient on substrate, $Y_{X/S}$, is: **[2 marks]**

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

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

(C) $0.07\ \text{g g}^{-1}$

(D) $5.0\ \text{g g}^{-1}$

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

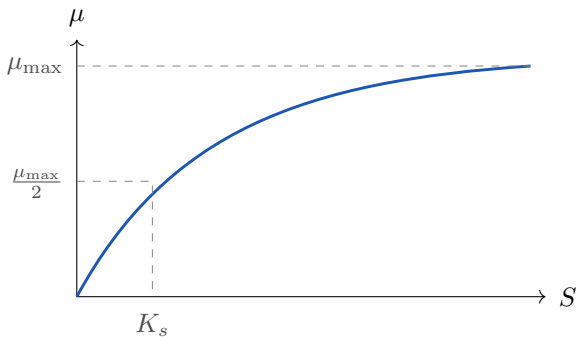
(A) $2.5\ \text{h}^{-1}$

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

(C) $0.4\ \text{h}^{-1}$

(D) $10\ \text{h}^{-1}$

Q34. An organism follows Monod kinetics, $\mu = \dfrac{\mu_{\max} S}{K_s + S}$, shown below, with $\mu_{\max} = 0.8\ \text{h}^{-1}$ and saturation constant $K_s = 2\ \text{g L}^{-1}$. When the limiting-substrate concentration is $S = 6\ \text{g L}^{-1}$, the specific growth rate μ is: **[2 marks]**



(A) $0.8\ \text{h}^{-1}$

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

(C) $0.2\ \text{h}^{-1}$

(D) $0.6\ \text{h}^{-1}$

Q35. During anaerobic fermentation, 0.46 g of ethanol is produced per gram of glucose consumed ($Y_{P/S} = 0.46\ \text{g g}^{-1}$). If 200 g of glucose is completely fermented, the mass of ethanol produced is: **[2 marks]**

(A) 46 g

(B) 200 g

(C) 108 g

(D) 92 g

Q36. In an aerobic bioreactor the volumetric oxygen transfer rate is OTR $= k_La\,(C^* - C_L)$. Given $k_La = 200\ \text{h}^{-1}$, a saturation dissolved-oxygen concentration $C^* = 8\ \text{mg L}^{-1}$ and an actual dissolved-oxygen level $C_L = 2\ \text{mg L}^{-1}$, the OTR is: **[2 marks]**

(A) $400\ \text{mg L}^{-1}\text{h}^{-1}$

(B) $1600\ \text{mg L}^{-1}\text{h}^{-1}$

(C) $1200\ \text{mg L}^{-1}\text{h}^{-1}$

(D) $2000\ \text{mg L}^{-1}\text{h}^{-1}$

Q37. In a batch fermentation the product concentration reaches its maximum of $60\ \text{g L}^{-1}$ at the end of 24 hours of total operation. The overall volu-

metric productivity of the product for this batch is: [2 marks]

(A) 15 g $L^{-1}h^{-1}$

(B) 2.5 g $L^{-1}h^{-1}$

(C) 0.4 g $L^{-1}h^{-1}$

(D) 60 g $L^{-1}h^{-1}$

Q38. A fermentation is run in a mode in which nutrient is added to the reactor continuously or in pulses, but no broth is removed until the end, so that the culture volume increases with time. This mode of operation is called: [2 marks]

(A) fed-batch operation

(B) simple batch operation

(C) continuous (chemostat) operation

(D) turbidostat operation

Plant and Animal Biotechnology

Q39. The most widely used microbial biopesticide, whose Cry proteins (δ-endotoxins) are lethal to insect larvae and whose genes have been engineered into Bt cotton and Bt maize, is produced by the bacterium: [2 marks]

(A) *Pseudomonas fluorescens*

(B) *Agrobacterium tumefaciens*

(C) *Bacillus thuringiensis*

(D) *Rhizobium leguminosarum*

Q40. A biofertilizer that fixes atmospheric nitrogen in a symbiotic association within the root nodules of leguminous crops is: [2 marks]

(A) *Rhizobium*

(B) *Bacillus thuringiensis*

(C) *Trichoderma viride*

(D) *Saccharomyces cerevisiae*

Q41. Arbuscular mycorrhizal fungi are applied as biofertilizers mainly because they greatly improve the plant's uptake of the poorly mobile soil nutrient: [2 marks]

(A) phosphorus

(B) atmospheric nitrogen

(C) potassium only

(D) carbon dioxide

Q42. 'Golden Rice' was genetically engineered to help combat vitamin-A deficiency. It was designed to accumulate in its endosperm the orange pro-vitamin-A precursor: [2 marks]

(A) ascorbic acid

(B) β-carotene

(C) folic acid

(D) cyanocobalamin

Q43. In the production of a transgenic animal by pronuclear microinjection, the foreign DNA construct is introduced by injecting it into the: [2 marks]

(A) somatic cell nucleus of an adult animal

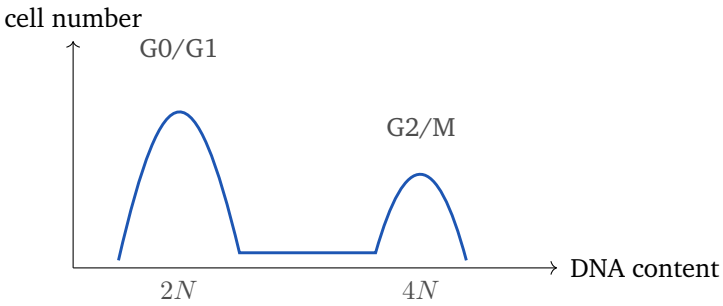
(B) mature red blood cell

(C) male pronucleus of a fertilised egg (zygote)

(D) mitochondrion of an unfertilised oocyte

Analytical Techniques

Q44. Cells stained with a stoichiometric DNA dye (such as propidium iodide) are analysed by flow cytometry, giving the DNA-content histogram shown. The peak that contains cells with *twice* the DNA content of the first (G0/G1) peak corresponds to cells in the: [2 marks]



(A) S phase

(B) G2/M phase

(C) sub-G1 (apoptotic) fraction

(D) G0 resting state

Q45. A coloured solution is analysed by spectrophotometry. Its absorbing species has a molar absorptivity of 1.5×10^4 $\mathrm{M^{-1}cm^{-1}}$. Measured in a cuvette of path length 1 cm, the solution shows an absorbance of 0.90. Using the Beer–Lambert law $A = \varepsilon\, c\, l$, the molar concentration of the solution is: **[2 marks]**

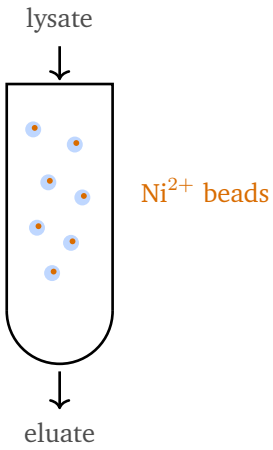
(A) 1.35×10^{-4} M

(B) 6×10^{-5} M

(C) 6×10^{-4} M

(D) 1.5×10^{4} M

Q46. A recombinant protein engineered with a six-histidine ($\mathrm{His_6}$) tag is purified in a single step by passing the cell lysate over a column of beads bearing immobilised $\mathrm{Ni^{2+}}$ ions, as sketched, and is then released with imidazole. This purification method is: **[2 marks]**



(A) size-exclusion chromatography

(B) ion-exchange chromatography

(C) reverse-phase chromatography

(D) affinity chromatography (IMAC)

Detailed Solutions

Q1.

Solution

Concept – allosteric control of glycolytic flux: PFK-1 catalyses the first committed step of glycolysis, so the cell regulates the whole pathway by tuning this one enzyme.

Step 1 – identify the signalling molecule of plenty: When glucose is abundant, the liver enzyme phosphofructokinase-2 makes fructose-2,6-bisphosphate.

Step 2 – its action on PFK-1: Fructose-2,6-bisphosphate binds an allosteric site and strongly *activates* PFK-1, pushing more substrate into glycolysis.

Step 3 – match to the option: The most potent activator listed is therefore fructose-2,6-bisphosphate.

Why the other options are wrong:

- B, citrate: signals a full Krebs cycle and *inhibits* PFK-1.
- C, high ATP: signals an energy surplus and *inhibits* PFK-1.
- D, NADH: is a reduced electron carrier, not an allosteric activator of PFK-1.

Final Answer: fructose-2,6-bisphosphate $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q1

Q2.

Solution

Concept – reading a Lineweaver–Burk plot: The double-reciprocal line is $\frac{1}{v} = \frac{K_m}{V_{\max}} \cdot \frac{1}{[S]} + \frac{1}{V_{\max}}$, so its y-intercept is $1/V_{\max}$ and its x-intercept is $-1/K_m$.

Step 1 – use the y-intercept to get $V_{\max}$: $\dfrac{1}{V_{\max}} = 0.02$

Step 2 – solve for $V_{\max}$: $V_{\max} = \dfrac{1}{0.02} = 50\ \mu\text{mol min}^{-1}$

Step 3 – use the x-intercept to get K_m: $-\dfrac{1}{K_m} = -0.25$

Step 4 – solve for K_m: $\dfrac{1}{K_m} = 0.25$

$K_m = \dfrac{1}{0.25} = 4$ mM

Step 5 – pick the answer: The question asks for K_m, which is 4 mM.

Why the other options are wrong:

- A, 50 mM: that is the value of $V_{\max}$, wrongly quoted as a concentration.
- B and C: 0.25 and 0.02 are the raw intercept readings, not K_m.

Final Answer: $K_m = 4$ mM $\Rightarrow$ D

Answer: (D) Go Back to Q2

Q3.

Solution

Concept – control of a biosynthetic pathway: Cells avoid wasting energy by shutting a pathway off once enough of its product has accumulated.

Step 1 – what the end product does: The final product acts as a signal of sufficiency and binds the first committed enzyme.

Step 2 – effect of that binding: Binding lowers the enzyme's activity, so flux through the whole pathway falls.

Step 3 – name the mechanism: Because the *end product* feeds back to inhibit an *earlier* step, this is feedback (end-product) inhibition.

Why the other options are wrong:

- B, feed-forward activation: an early metabolite *activates* a later enzyme, the opposite arrangement.
- C, substrate-level phosphorylation: is a way of making ATP, not a control mode.
- D, zymogen activation: is irreversible activation of an inactive precursor, unrelated to end-product control.

Final Answer: feedback (end-product) inhibition $\Rightarrow$ A

Answer: (A) Go Back to Q3

Q4.

Solution

Concept – phosphoryl-transfer potential: A more negative $\Delta G^{\circ\prime}$ of hydrolysis means a greater tendency to donate the phosphoryl group, that is, a higher transfer potential.

Step 1 – recall the standard values (kJ mol^{-1}): PEP ≈ -61.9; ATP ≈ -30.5;

glucose-6-phosphate ≈ -13.8; glycerol-3-phosphate ≈ -9.2.

Step 2 – rank them: PEP is the most negative of the four.

Step 3 – interpret: PEP therefore has the highest phosphoryl-transfer potential and can even phosphorylate ADP to ATP (as at the pyruvate-kinase step).

Why the other options are wrong:

- A and C: glucose-6-phosphate and glycerol-3-phosphate are low-energy phosphate esters.
- B, ATP: is intermediate, so it lies below PEP on the scale.

Final Answer: phosphoenolpyruvate (PEP) $\Rightarrow \boxed{\text{D}}$

Answer: (D) Go Back to Q4

Q5.

Solution

Concept – oxidative decarboxylations of the Krebs cycle: Carbon leaves the cycle only at the two decarboxylation steps, each releasing one CO_2.

Step 1 – first CO_2: Isocitrate dehydrogenase converts isocitrate to α-ketoglutarate, releasing one CO_2.

Step 2 – second CO_2: The α-ketoglutarate dehydrogenase complex converts α-ketoglutarate to succinyl-CoA, releasing a second CO_2.

Step 3 – total per turn: $1 + 1 = 2$ molecules of CO_2 per single turn of the cycle.

Why the other options are wrong:

- C and D: three or six CO_2 would count carbons from the whole glucose molecule or several turns, not one turn.
- A, 1: overlooks the second decarboxylation step.

Final Answer: 2 molecules of $CO_2 \Rightarrow \boxed{\text{B}}$

Answer: (B) Go Back to Q5

Q6.

Solution

Concept – vitamin-derived electron carriers: Several coenzymes are built from vitamins, and each has a defined role in metabolism.

Step 1 – link the vitamin to the coenzyme: Niacin (vitamin B_3) is the precursor of nicotinamide adenine dinucleotide, NAD^+.

Step 2 – describe its action: NAD^+ accepts a hydride ion during catabolic oxidations, becoming NADH.

Step 3 – conclude: So the niacin-derived hydride acceptor is NAD^+.

Why the other options are wrong:

- B, FAD: comes from riboflavin (vitamin B_2).
- C, coenzyme A: comes from pantothenate and carries acyl groups, not hydride.
- D, TPP: comes from thiamine and handles aldehyde-transfer, not hydride transfer.

Final Answer: $NAD^+ \Rightarrow \boxed{A}$

Answer: (A) Go Back to Q6

Q7.

Solution

Concept – primary versus secondary metabolism: Growth-associated (primary) products form during rapid growth, while many secondary metabolites form later, when growth slows.

Step 1 – describe the stationary phase: Here nutrients are limiting and the net growth rate is near zero, so the culture enters the idiophase.

Step 2 – link it to antibiotics: Antibiotics and other secondary metabolites are typically produced in this idiophase, that is, the stationary phase.

Step 3 – read the curve: On the plot this is the upper plateau after the steep log-phase rise.

Why the other options are wrong:

- A, log phase: is the growth-associated (trophophase) period, favouring primary metabolites and biomass.
- C, lag phase: cells are only adapting; little product forms.

- D, death phase: cells are lysing, and yields decline.

Final Answer: the stationary phase $\Rightarrow$ B

Answer: (B) Go Back to Q7

Q8.

Solution

Concept – generation time from a fold increase: The number of doublings is $n = \dfrac{\ln(X/X_0)}{\ln 2}$, and the generation time is $t_d = \dfrac{t}{n}$.

Step 1 – list the data: $X_0 = 5 \times 10^3$, $X = 5 \times 10^7$, $t = 4$ h $= 240$ min.

Step 2 – find the fold increase: $\dfrac{X}{X_0} = \dfrac{5 \times 10^7}{5 \times 10^3} = 10^4$

Step 3 – compute the number of generations: $n = \log_2(10^4) = \dfrac{\ln 10^4}{\ln 2} = \dfrac{9.210}{0.693}$

$n \approx 13.29$

Step 4 – compute the generation time: $t_d = \dfrac{240}{13.29}$

$t_d \approx 18.1$ min

Step 5 – round to the nearest option: $t_d \approx 18$ min.

Final Answer: $t_d \approx 18$ min $\Rightarrow$ C

Answer: (C) Go Back to Q8

Q9.

Solution

Concept – the workhorse of alcoholic fermentation: Industrial ethanol is made by yeast, which ferments sugars anaerobically to ethanol and CO_2.

Step 1 – identify the organism: The budding yeast *Saccharomyces cerevisiae* is used for beverage alcohol and bioethanol.

Step 2 – note the biochemistry: It converts glucose to two ethanol and two CO_2 molecules by glycolysis followed by pyruvate decarboxylation and alcohol dehydrogenase.

Why the other options are wrong:

- A, *Lactobacillus bulgaricus*: makes lactic acid (yoghurt), not ethanol.
- C, *Acetobacter aceti*: oxidises ethanol to acetic acid (vinegar).
- D, *Aspergillus niger*: is used chiefly to make citric acid.

Final Answer: *Saccharomyces cerevisiae* $\Rightarrow$ B

Answer: (B) Go Back to Q9

Q10.

Solution

Concept – classic microbe–product pairings: Each industrial organism is tied to a characteristic fermentation product.

Step 1 – check option A: *Aspergillus niger* is the standard producer of *citric acid* by submerged fermentation of molasses; this pairing is correct.

Step 2 – verify the others are mismatched: The remaining three swap the products around incorrectly.

Why the other options are wrong:

- B: *Penicillium chrysogenum* makes *penicillin*, not lactic acid.
- C: *Corynebacterium glutamicum* makes amino acids such as *glutamate/lysine*, not ethanol.
- D: *Clostridium acetobutylicum* makes *acetone and butanol* (the ABE fermentation), not penicillin.

Final Answer: *Aspergillus niger* $\rightarrow$ citric acid $\Rightarrow$ A

Answer: (A) Go Back to Q10

Q11.

Solution

Concept – naming nutritional types: The class name combines the energy source (*photo/chemo*), the electron-donor type (*litho* for inorganic, *organo* for organic) and the carbon source (*auto* for CO_2, *hetero* for organic).

Step 1 – energy source: Energy comes from oxidising inorganic compounds $\Rightarrow$ *chemo-* and *litho-*.

Step 2 – carbon source: Carbon comes from CO_2 fixation $\Rightarrow$ *-auto-*.

Step 3 – assemble the term: Putting the parts together gives chemolithoautotroph.

Why the other options are wrong:

- B, photoautotroph: uses light for energy, not inorganic oxidation.

- C, chemoorganoheterotroph: uses organic compounds for both energy and carbon.
- D, photoheterotroph: uses light for energy and organic carbon.

Final Answer: chemolithoautotroph $\Rightarrow$ A

Answer: (A) Go Back to Q11

Q12.

Solution

Concept – the cAMP second-messenger pathway: A hormone binds a GPCR, the activated G_s protein stimulates adenylyl cyclase, and the enzyme makes a small diffusible messenger from ATP.

Step 1 – product of adenylyl cyclase: Adenylyl cyclase converts ATP into cyclic AMP (cAMP).

Step 2 – downstream action: cAMP rises inside the cell and activates protein kinase A (PKA), which phosphorylates target proteins.

Step 3 – identify the messenger: The diffusible second messenger is therefore cAMP.

Why the other options are wrong:

- A and B: IP_3 and DAG are the second messengers of the *phospholipase-C* branch, not the adenylyl-cyclase branch.
- C, Ca^{2+}: is released downstream of IP_3; it is not the direct product of adenylyl cyclase.

Final Answer: cyclic AMP (cAMP) $\Rightarrow$ D

Answer: (D) Go Back to Q12

Q13.

Solution

Concept – repressible control of the *trp* operon: The *trp* operon is ON by default and is switched off when tryptophan is plentiful.

Step 1 – role of tryptophan: Tryptophan is the co-repressor; it binds the inactive aporepressor to form the active repressor.

Step 2 – where the active repressor binds: The active repressor binds the *oper-*

ator, which overlaps the promoter, and blocks RNA polymerase.

Step 3 – consequence: Transcription of *trpE–trpA* stops, so the cell stops making tryptophan it already has.

Why the other options are wrong:

- A, structural genes: are the transcribed genes, not the repressor's binding site.
- C, attenuator: fine-tunes output by premature termination but is not where the repressor protein binds.
- D, terminator: ends transcription and is unrelated to repressor binding.

Final Answer: the operator ⇒ B

Answer: (B) Go Back to Q13

Q14.

Solution

Concept – activation of a receptor tyrosine kinase (RTK): An RTK is a single-pass membrane receptor whose cytoplasmic domain has tyrosine-kinase activity.

Step 1 – ligand binding: The ligand (for example insulin or EGF) brings two receptor monomers together, causing dimerisation.

Step 2 – autophosphorylation: Within the dimer, the two kinase domains phosphorylate tyrosines on each other (trans-autophosphorylation).

Step 3 – outcome: These phosphotyrosines become docking sites that recruit downstream signalling proteins.

Why the other options are wrong:

- A, GTP hydrolysis: is how G proteins act, not RTKs.
- B, ion-channel opening: describes ligand-gated channels.
- D, making cAMP: is the job of adenylyl cyclase downstream of GPCRs.

Final Answer: dimerisation and tyrosine autophosphorylation ⇒ C

Answer: (C) Go Back to Q14

Q15.

Solution

Concept – events of the mitotic (M) phase: Chromosome condensation, metaphase-plate alignment and sister-chromatid separation are the defining events of mitosis.

Step 1 – match events to phase: All three events belong to the M phase (mitosis plus cytokinesis).

Step 2 – read the highlighted quadrant: The shaded quadrant is labelled M in the diagram.

Step 3 – conclude: The described events therefore occur in the M phase.

Why the other options are wrong:

- A, G1: is a growth gap before DNA synthesis.
- B, S: is when DNA is replicated, not when chromatids separate.
- C, G2: is a growth gap that prepares the cell for mitosis but is not mitosis itself.

Final Answer: the M (mitotic) phase $\Rightarrow$ D

Answer: (D) Go Back to Q15

Q16.

Solution

Concept – elongation factors in bacterial translation: Distinct elongation factors carry out distinct GTP-driven steps of the ribosome cycle.

Step 1 – delivery of aminoacyl-tRNA: EF-Tu, in its GTP-bound form, escorts each aminoacyl-tRNA into the ribosomal A site.

Step 2 – energy coupling: Correct codon–anticodon pairing triggers GTP hydrolysis, and EF-Tu·GDP leaves the ribosome.

Step 3 – conclude: The factor that delivers aminoacyl-tRNA to the A site is EF-Tu.

Why the other options are wrong:

- A, EF-G: drives translocation of the ribosome along the mRNA, a later step.
- B, IF-2: is an *initiation* factor for the first tRNA.
- C, RF-1: is a *release* factor that recognises stop codons.

Final Answer: EF-Tu $\Rightarrow$ D

Answer: (D) Go Back to Q16

Q17.

Solution

Concept – the GTPase switch in the Ras–MAPK cascade: Ras is a small G protein that cycles between an inactive GDP-bound state and an active GTP-bound state.

Step 1 – activation: A guanine-nucleotide exchange factor (SOS), recruited by the activated RTK, replaces GDP with GTP on Ras.

Step 2 – active state: Ras·GTP is the ON form; it binds and activates Raf, starting the Raf→MEK→ERK phosphorylation relay.

Step 3 – switch-off (aside): GTP hydrolysis (helped by a GAP) returns Ras to the inactive GDP form.

Why the other options are wrong:

- A, GDP: is the *inactive* state of Ras.
- B, cAMP: belongs to the GPCR/adenylyl-cyclase pathway, not to Ras.
- D, inorganic phosphate: is a hydrolysis by-product, not the activating ligand.

Final Answer: GTP-bound Ras is active ⇒ C

Answer: (C) Go Back to Q17

Q18.

Solution

Concept – $5'$ capping of eukaryotic mRNA: The first co-transcriptional modification of a eukaryotic transcript is addition of a cap at its $5'$ end.

Step 1 – what is added: A 7-methylguanosine is joined to the first nucleotide through an unusual $5'$–$5'$ triphosphate linkage.

Step 2 – functions of the cap: It protects the transcript from $5'$ exonucleases and is recognised by initiation factors, helping the small ribosomal subunit bind.

Step 3 – conclude: The $5'$ modification is the 7-methylguanosine cap.

Why the other options are wrong:

- B, poly-A tail: is added at the $3'$ end, not the $5'$ end.
- C, intron: is removed during splicing, not added as a protective feature.
- D, Shine–Dalgarno sequence: is a *bacterial* ribosome-binding site, absent

from eukaryotic mRNA.

Final Answer: the 7-methylguanosine cap $\Rightarrow$ A

Answer: (A) Go Back to Q18

Q19.

Solution

Concept – allelic interaction at the ABO locus: The way a heterozygote expresses two different alleles defines the type of dominance.

Step 1 – describe the AB phenotype: An $I^A I^B$ person makes *both* the A antigen and the B antigen, each fully.

Step 2 – define the term: When both alleles are expressed simultaneously and independently in the heterozygote, the relationship is codominance.

Step 3 – distinguish from blending: This is not an intermediate (blended) phenotype, so it is not incomplete dominance.

Why the other options are wrong:

- A, complete dominance: one allele would mask the other, but here neither is masked.
- B, epistasis: involves one *gene* masking a different gene, not two alleles of one gene.
- C, X-linkage: concerns the gene's chromosomal location, not the AB expression pattern.

Final Answer: codominance $\Rightarrow$ D

Answer: (D) Go Back to Q19

Q20.

Solution

Concept – the first antibody of a primary response: The immunoglobulin classes appear in a set order during an immune response.

Step 1 – earliest secreted class: IgM is the first antibody secreted after initial antigen exposure.

Step 2 – its structure: Secreted IgM is a pentamer of five monomers, giving ten antigen-binding sites, which makes it a strong agglutinator.

Step 3 – conclude: The first-secreted pentameric antibody is IgM.

Why the other options are wrong:

- B, IgG: dominates the *secondary* response and is the most abundant serum antibody, but appears later.
- C, IgA: guards mucosal surfaces as a dimer.
- D, IgE: mediates allergy and antiparasite responses, at very low serum levels.

Final Answer: IgM $\Rightarrow$ A

Answer: (A) Go Back to Q20

Q21.

Solution

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

Step 1 – list the data: $q = 0.3$.

Step 2 – find p: $p = 1 - q = 1 - 0.3 = 0.7$

Step 3 – homozygous dominant frequency: Homozygous dominant frequency $= p^2$

Step 4 – substitute: $p^2 = (0.7)^2$

Step 5 – evaluate: $p^2 = 0.49$

Why the other options are wrong:

- A, 0.09: that is q^2, the homozygous *recessive* frequency.
- C, 0.42: that is $2pq$, the heterozygote frequency.
- D, 0.21: is pq, not a Hardy–Weinberg genotype class.

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

Answer: (B) Go Back to Q21

Q22.

Solution

Concept – ABO genotypes of the parents: Work out each parent's genotype, then combine the gametes.

Step 1 – genotype of the group-O father: Group O is recessive, so his genotype is ii; every sperm carries i.

Step 2 – genotype of the group-AB mother: Group AB is I^AI^B; her eggs carry either I^A or I^B.

Step 3 – combine the gametes: i with I^A gives I^Ai (group A); i with I^B gives I^Bi (group B).

Step 4 – list the outcomes: The children can be group A or group B only, in a $1:1$ ratio.

Why the other options are wrong:

- B, only AB: would need an I^A from one parent and I^B from the other; the father gives only i.
- C, all four groups: AB and O cannot arise from this cross.
- D, only O: impossible, since the mother contributes no i allele.

Final Answer: only groups A and B $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q22

Q23.

Solution

Concept – forward versus side scatter in flow cytometry: When a cell crosses the laser, light scatters in different directions carrying different information.

Step 1 – forward scatter (FSC): Light scattered at a small angle in the forward direction increases with the cell's cross-sectional area, so FSC reports the cell's *size*.

Step 2 – side scatter (SSC): Light scattered at about 90° depends on internal structures and granularity, a separate parameter.

Step 3 – answer the question: Because FSC is asked for, the correct measure is the relative size (diameter) of the cell.

Why the other options are wrong:

- A, granularity: is read from *side* scatter, not forward scatter.

- B, antibody fluorescence: is detected in the fluorescence channels, not by scatter.
- C, DNA content: is measured with a DNA-binding fluorophore, again a fluorescence signal.

Final Answer: the relative size of the cell $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q23

Q24.

Solution

Concept – the genetic basis of antibody diversity: A limited genome must encode a vast repertoire of antibody specificities, achieved by rearranging gene segments.

Step 1 – the segment pools: The heavy-chain locus carries many V, D and J segments and the light-chain loci carry V and J segments.

Step 2 – somatic recombination: During B-cell development, the RAG recombinase joins one V, (one D) and one J segment, so each B cell assembles a unique variable region.

Step 3 – outcome: This combinatorial V(D)J recombination, added to junctional diversity, generates the enormous antibody repertoire.

Why the other options are wrong:

- A, alternative splicing: helps switch membrane versus secreted forms, but does not create the primary variable-region diversity.
- C, promoter mutation: does not rearrange the coding segments.
- D, polyploidisation: does not occur and would not diversify binding sites.

Final Answer: V(D)J somatic recombination $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q24

Q25.

Solution

Concept – cutting a linear DNA at two sites: Two internal cuts on a *linear* molecule produce three fragments; find their lengths from the cut positions.

Step 1 – mark the cut positions: The cuts fall at 2 kb and 7 kb from the left end of a 10 kb fragment.

Step 2 – left fragment: From 0 to 2 kb gives a 2 kb piece.

Step 3 – middle fragment: From 2 kb to 7 kb gives $7 - 2 = 5$ kb.

Step 4 – right fragment: From 7 kb to 10 kb gives $10 - 7 = 3$ kb.

Step 5 – check the total: $2 + 5 + 3 = 10$ kb, matching the starting length.

Why the other options are wrong:

- B, 2 and 7 kb: quotes the cut positions, not the fragment lengths.
- C, 5 and 5 kb: would need a single central cut.
- D, 10 kb only: applies if the enzyme did not cut at all.

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

Answer: (A) Go Back to Q25

Q26.

Solution

Concept – cluster generation in Illumina sequencing: Before sequencing-by-synthesis can be read, each fragment must be amplified into a local cluster of identical copies on the flow cell.

Step 1 – immobilisation: Adapter-ligated fragments anneal to complementary oligos grafted onto the flow-cell surface.

Step 2 – bridge amplification: Each fragment bends over to prime an adjacent surface oligo, and repeated arching-and-copying builds a dense clonal cluster.

Step 3 – why clusters matter: Thousands of identical strands per cluster give a fluorescent signal strong enough to detect at each cycle.

Why the other options are wrong:

- A, Sanger termination: is a different, low-throughput sequencing chemistry.
- B, rolling-circle: is used in some other platforms, not Illumina cluster generation.
- D, reverse transcription: converts RNA to cDNA and is a library-prep step, not the on-flow-cell amplification.

Final Answer: bridge amplification $\Rightarrow$ C

Answer: (C) Go Back to Q26

Q27.

Solution

Concept – reading a two-colour microarray: Spot colour reflects the ratio of bound test (Cy5, red) to control (Cy3, green) cDNA.

Step 1 – meaning of a red spot: More test cDNA than control cDNA has hybridised, so red dominates.

Step 2 – link to expression: More test transcript means that gene is expressed at a higher level in the test sample.

Step 3 – conclude: A predominantly red spot marks a gene that is up-regulated (over-expressed) in the test sample.

Why the other options are wrong:

- A, equal expression: would give a yellow (red+green) spot.
- C, no expression: would give a dark, signal-less spot.
- D, gene deletion: is not what a hybridisation-intensity ratio measures; a red spot means more, not absent, transcript.

Final Answer: over-expressed (up-regulated) in the test sample $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q27

Q28.

Solution

Concept – sequence file formats: Different plain-text formats store different information about sequences.

Step 1 – what NGS output needs: Each short read must be stored with a quality score for every base.

Step 2 – the matching format: FASTQ holds four lines per read: an identifier, the sequence, a separator, and a line of Phred quality characters.

Step 3 – conclude: The read-plus-quality format is FASTQ.

Why the other options are wrong:

- A, FASTA: stores only the sequence and a header, with *no* quality scores.
- B, PDB: stores three-dimensional *protein/nucleic-acid structures*, not reads.
- D, GenBank flat file: is an annotated single-record format, not a per-read quality store.

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

Answer: (C) Go Back to Q28

Q29.

Solution

Concept – making intron-free cDNA: Bacteria cannot splice introns, so a eukaryotic gene is expressed from a cDNA copied from the mature (spliced) mRNA.

Step 1 – start from mRNA: The mature mRNA already has its introns removed and a poly-A tail.

Step 2 – copy it to DNA: Reverse transcriptase, an RNA-dependent DNA polymerase, synthesises a first-strand DNA copy of the mRNA.

Step 3 – outcome: The resulting cDNA is intron-free and can be expressed in a bacterial host.

Why the other options are wrong:

- A, DNA polymerase I: uses a DNA template, not RNA.
- B, Taq polymerase: is a DNA-dependent DNA polymerase used in PCR.
- D, RNA polymerase: makes RNA from DNA, the opposite direction.

Final Answer: reverse transcriptase $\Rightarrow$ C

Answer: (C) Go Back to Q29

Q30.

Solution

Concept – essential features of a cloning vector: A vector must replicate, allow selection of transformed cells, and let DNA be inserted conveniently.

Step 1 – the first two features: The origin of replication lets it copy itself, and the selectable marker (for example an antibiotic-resistance gene) identifies cells that took up the plasmid.

Step 2 – the insertion feature: The multiple cloning site (polylinker) is a short stretch with many unique restriction sites for inserting foreign DNA.

Step 3 – conclude: The needed feature is the multiple cloning site.

Why the other options are wrong:

- A and B: telomeres and centromeres are needed only for large linear artificial chromosomes, not ordinary plasmid vectors.

- C, poly-A signal: is an mRNA-processing element for eukaryotic *expression*, not a minimal cloning requirement.

Final Answer: a multiple cloning site (polylinker) $\Rightarrow$ D

Answer: (D) Go Back to Q30

Q31.

Solution

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

Step 1 – list the data: $X_0 = 0.5$ g L^{-1}, $X = 4$ g L^{-1}, $t = 3$ h.

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

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

Step 4 – divide by time: $\mu = \frac{2.079}{3}$

$\mu \approx 0.693$ h^{-1}

Step 5 – round to the option: $\mu \approx 0.69$ h^{-1}.

Final Answer: $\mu \approx 0.69$ h^{-1} $\Rightarrow$ C

Answer: (C) Go Back to Q31

Q32.

Solution

Concept – biomass yield coefficient: $Y_{X/S}$ is the mass of cells formed per unit mass of substrate consumed, $Y_{X/S} = \frac{\Delta X}{\Delta S}$.

Step 1 – list the relevant data: Biomass formed $\Delta X = 12$ g; substrate consumed $\Delta S = 60$ g. (The 4 g of product is not part of $Y_{X/S}$.)

Step 2 – write the formula: $Y_{X/S} = \frac{\Delta X}{\Delta S}$

Step 3 – substitute: $Y_{X/S} = \frac{12}{60}$

Step 4 – evaluate: $Y_{X/S} = 0.2$ g g^{-1}

Why the other options are wrong:

- A, 0.4: would use 24 g of biomass, double the true value.
- C, 0.07: mistakenly divides the 4 g product by 60 g substrate.

- D, 5.0: inverts the ratio $(60/12)$.

Final Answer: $Y_{X/S} = 0.2$ g g$^{-1} \Rightarrow$ B

Answer: (B) Go Back to Q32

Q33.

Solution

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

Step 1 – list the data: $F = 2$ L h^{-1}, $V = 5$ L.

Step 2 – write the formula: $D = \dfrac{F}{V}$

Step 3 – substitute: $D = \dfrac{2}{5}$

Step 4 – evaluate: $D = 0.4$ h^{-1}

Step 5 – check the units: $\dfrac{\text{L h}^{-1}}{\text{L}} = \text{h}^{-1}$, a reciprocal time, as expected.

Why the other options are wrong:

- A, 2.5: inverts the ratio $(5/2)$.
- B, 0.5: uses a 4-L volume, not 5 L.
- D, 10: multiplies F and V instead of dividing.

Final Answer: $D = 0.4$ h$^{-1} \Rightarrow$ C

Answer: (C) Go Back to Q33

Q34.

Solution

Concept – the Monod equation: $\mu = \dfrac{\mu_{\max} S}{K_s + S}$ describes how growth rate rises with substrate and saturates at $\mu_{\max}$.

Step 1 – list the data: $\mu_{\max} = 0.8$ h^{-1}, $K_s = 2$ g L^{-1}, $S = 6$ g L^{-1}.

Step 2 – substitute: $\mu = \dfrac{0.8 \times 6}{2 + 6}$

Step 3 – evaluate the numerator: $0.8 \times 6 = 4.8$

Step 4 – evaluate the denominator: $2 + 6 = 8$

Step 5 – divide: $\mu = \dfrac{4.8}{8} = 0.6\ \text{h}^{-1}$

Why the other options are wrong:

- A, 0.8: is $\mu_{\max}$, reached only when $S \gg K_s$.
- B, 0.4: is the value at $S = K_s$ (half of $\mu_{\max}$), but here $S = 3K_s$.
- C, 0.2: uses a wrong denominator.

Final Answer: $\mu = 0.6\ \text{h}^{-1} \Rightarrow$ D

Answer: (D) Go Back to Q34

Q35.

Solution

Concept – product yield coefficient: $Y_{P/S}$ is the mass of product formed per unit mass of substrate consumed, so product mass $= Y_{P/S} \times S$.

Step 1 – list the data: $Y_{P/S} = 0.46\ \text{g g}^{-1}$; substrate consumed $S = 200\ \text{g}$.

Step 2 – write the relation: Ethanol mass $= Y_{P/S} \times S$

Step 3 – substitute: $= 0.46 \times 200$

Step 4 – evaluate: $= 92\ \text{g}$

Step 5 – sanity check: $0.46\ \text{g g}^{-1}$ is close to the theoretical maximum of $0.51\ \text{g g}^{-1}$ for ethanol from glucose, so 92 g is reasonable.

Why the other options are wrong:

- A, 46 g: uses 100 g of glucose, not 200 g.
- B, 200 g: is the glucose mass, not the ethanol produced.
- C, 108 g: exceeds even the theoretical yield and has no basis.

Final Answer: 92 g of ethanol $\Rightarrow$ D

Answer: (D) Go Back to Q35

Q36.

Solution

Concept – volumetric oxygen transfer rate: OTR $= k_L a\,(C^* - C_L)$, where $C^* - C_L$ is the driving concentration difference.

Step 1 – list the data: $k_L a = 200\ \text{h}^{-1}$, $C^* = 8\ \text{mg L}^{-1}$, $C_L = 2\ \text{mg L}^{-1}$.

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

Step 3 – substitute into the OTR formula: OTR $= 200 \times 6$

Step 4 – evaluate: OTR $= 1200$ mg $L^{-1}h^{-1}$

Why the other options are wrong:

- A, 400: uses a driving force of only 2 mg L^{-1}.
- B, 1600: uses $C^* = 8$ alone, ignoring C_L.
- D, 2000: uses a driving force of 10, not 6.

Final Answer: OTR $= 1200$ mg $L^{-1}h^{-1} \Rightarrow$ C

Answer: (C) Go Back to Q36

Q37.

Solution

Concept – overall volumetric productivity: Overall productivity is the final product concentration divided by the total batch time, $P_r = \frac{P}{t}$.

Step 1 – list the data: Final product $P = 60$ g L^{-1}; total time $t = 24$ h.

Step 2 – write the formula: $P_r = \frac{P}{t}$

Step 3 – substitute: $P_r = \frac{60}{24}$

Step 4 – evaluate: $P_r = 2.5$ g $L^{-1}h^{-1}$

Why the other options are wrong:

- A, 15: divides by 4 h (the lag) instead of the total 24 h.
- C, 0.4: inverts the ratio (24/60).
- D, 60: is the final concentration, not a rate.

Final Answer: $P_r = 2.5$ g $L^{-1}h^{-1} \Rightarrow$ B

Answer: (B) Go Back to Q37

Q38.

Solution

Concept – modes of bioreactor operation: The mode is defined by whether feed is added and broth removed during the run.

Step 1 – describe the given mode: Nutrient is added (continuously or in pulses) but nothing is withdrawn until the end, so the volume rises.

Step 2 – name it: This is fed-batch operation, widely used to avoid substrate inhibition and to prolong product formation.

Step 3 – contrast the alternatives: It differs from simple batch (no addition), and from continuous mode (constant volume with simultaneous feed and withdrawal).

Why the other options are wrong:

- B, batch: adds nothing after inoculation.
- C, continuous: keeps the volume constant by removing broth at the feed rate.
- D, turbidostat: is a continuous mode controlled by turbidity, again at constant volume.

Final Answer: fed-batch operation $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q38

Q39.

Solution

Concept – microbial biopesticides: Certain bacteria make insecticidal proteins that are exploited as environmentally friendly pest-control agents.

Step 1 – identify the organism: *Bacillus thuringiensis* (Bt) produces crystalline Cry proteins (δ-endotoxins) during sporulation.

Step 2 – mode of action: In the alkaline larval gut the Cry protein is activated and punches pores in the gut epithelium, killing the insect larva.

Step 3 – link to crops: The *cry* genes have been engineered into Bt cotton and Bt maize for built-in insect resistance.

Why the other options are wrong:

- A, *Pseudomonas fluorescens*: is used as a biocontrol/biofertilizer agent but is not the Cry-toxin source.
- B, *Agrobacterium tumefaciens*: is a gene-transfer vector, not a biopesticide.

- D, *Rhizobium*: is a nitrogen-fixing biofertilizer, not an insecticide.

Final Answer: *Bacillus thuringiensis* $\Rightarrow$ C

Answer: (C) Go Back to Q39

Q40.

Solution

Concept – symbiotic nitrogen-fixing biofertilizers: Some bacteria fix atmospheric N_2 inside legume root nodules, enriching the soil biologically.

Step 1 – identify the symbiont: *Rhizobium* infects legume roots and forms nodules where it fixes N_2 into ammonia.

Step 2 – benefit to the plant: The fixed nitrogen is supplied to the host legume, reducing the need for chemical nitrogen fertiliser.

Step 3 – conclude: The symbiotic nitrogen-fixing biofertilizer is *Rhizobium*.

Why the other options are wrong:

- B, *Bacillus thuringiensis*: is a biopesticide, not a nitrogen fixer.
- C, *Trichoderma viride*: is a fungal biocontrol agent against plant pathogens.
- D, *Saccharomyces cerevisiae*: is a fermentation yeast, not a soil symbiont.

Final Answer: *Rhizobium* $\Rightarrow$ A

Answer: (A) Go Back to Q40

Q41.

Solution

Concept – mycorrhizal biofertilizers: Arbuscular mycorrhizal (AM) fungi form a symbiosis with plant roots and extend the effective root surface with their hyphae.

Step 1 – the limiting nutrient: Phosphorus is poorly mobile in soil, so roots quickly deplete the phosphate around them.

Step 2 – role of the fungal hyphae: The fine hyphae reach beyond this depletion zone and absorb phosphate, delivering it to the plant.

Step 3 – conclude: AM fungi are valued mainly for improving *phosphorus* uptake.

Why the other options are wrong:

- B, atmospheric nitrogen: AM fungi do not fix N_2; that is done by *Rhizo-*

bium/cyanobacteria.

- C, potassium only: potassium is not their defining benefit.
- D, carbon dioxide: the fungus *receives* carbon from the plant, it does not supply CO_2.

Final Answer: phosphorus $\Rightarrow$ A

Answer: (A) Go Back to Q41

Q42.

Solution

Concept – the trait engineered into Golden Rice: Golden Rice was created to supply a vitamin-A precursor in the edible endosperm.

Step 1 – the introduced pathway: Transgenes (phytoene synthase and a carotene desaturase) reconstitute carotenoid synthesis in the endosperm.

Step 2 – the accumulated compound: The endosperm accumulates β-carotene, which gives the golden colour and is a pro-vitamin A.

Step 3 – nutritional benefit: The body converts β-carotene into vitamin A, helping prevent deficiency-related blindness.

Why the other options are wrong:

- A, ascorbic acid: is vitamin C, not a vitamin-A precursor.
- C, folic acid: is another B-vitamin, unrelated to the Golden Rice trait.
- D, cyanocobalamin: is vitamin B_{12}, not made by this engineering.

Final Answer: β-carotene $\Rightarrow$ B

Answer: (B) Go Back to Q42

Q43.

Solution

Concept – pronuclear microinjection: This classic method for making transgenic mammals injects DNA into a very early embryo.

Step 1 – the target cell: A freshly fertilised egg (zygote) still shows two visible pronuclei, the maternal and paternal ones.

Step 2 – where DNA goes: The transgene is injected into the larger *male pronucleus* before the two pronuclei fuse.

Step 3 – outcome: Injected DNA may integrate into the genome, so all cells of the resulting animal can carry the transgene.

Why the other options are wrong:

- A, adult somatic nucleus: that describes *nuclear transfer* cloning, a different technique.
- B, red blood cell: mammalian erythrocytes lack a nucleus and cannot form an embryo.
- D, oocyte mitochondrion: injecting a mitochondrion would not give stable nuclear transgene integration.

Final Answer: the male pronucleus of a fertilised egg $\Rightarrow$ C

Answer: (C) Go Back to Q43

Q44.

Solution

Concept – DNA-content histogram in flow cytometry: A stoichiometric DNA dye gives a fluorescence signal proportional to the amount of DNA per cell.

Step 1 – the first peak: Cells in G0/G1 have the unreplicated $(2N)$ amount of DNA and form the first, tallest peak.

Step 2 – the second peak: After S-phase replication, cells in G2 and M have $4N$ DNA, exactly twice the G0/G1 content, forming the second peak.

Step 3 – identify the double-DNA peak: The peak at twice the G0/G1 content is therefore the G2/M peak.

Why the other options are wrong:

- A, S phase: cells lie *between* the two peaks with intermediate DNA content.
- C, sub-G1: is an apoptotic peak with *less* than $2N$ DNA, to the left.
- D, G0 resting: sits within the first $(2N)$ peak, not at double DNA.

Final Answer: the G2/M phase $\Rightarrow$ B

Answer: (B) Go Back to Q44

Q45.

Solution

Concept – the Beer–Lambert law: $A = \varepsilon\, c\, l$, so concentration is $c = \dfrac{A}{\varepsilon\, l}$.

Step 1 – list the data: $A = 0.90$, $\varepsilon = 1.5 \times 10^4\ \text{M}^{-1}\text{cm}^{-1}$, $l = 1$ cm.

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

Step 3 – substitute: $c = \dfrac{0.90}{1.5 \times 10^4 \times 1}$

Step 4 – evaluate: $c = \dfrac{0.90}{1.5 \times 10^4} = 6 \times 10^{-5}\ \text{M}$

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

Why the other options are wrong:

- A, 1.35×10^{-4}: multiplies instead of dividing where it should divide.
- C, 6×10^{-4}: is ten times too large, an exponent slip.
- D, 1.5×10^4: is ε itself, not a concentration.

Final Answer: $c = 6 \times 10^{-5}\ \text{M} \Rightarrow$ B

Answer: (B) Go Back to Q45

Q46.

Solution

Concept – purification by specific molecular recognition: When a protein is captured on a column through a specific, reversible interaction, the method is affinity chromatography.

Step 1 – the specific interaction here: The His_6 tag chelates the immobilised Ni^{2+} ions, so only the tagged protein is retained while other proteins wash through.

Step 2 – elution: Imidazole, which competes with the histidine side chains for the Ni^{2+}, releases the bound protein in pure form.

Step 3 – name the method: This tag-and-metal approach is immobilised-metal affinity chromatography (IMAC), a form of affinity chromatography.

Why the other options are wrong:

- A, size-exclusion: separates purely by molecular size, using no specific binding.
- B, ion-exchange: separates by net surface charge, not by a tag.

- C, reverse-phase: separates by hydrophobicity on a nonpolar matrix.

Final Answer: affinity chromatography (IMAC) $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q46

Answer Key

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