GATE Biotechnology

Sample Paper – 6

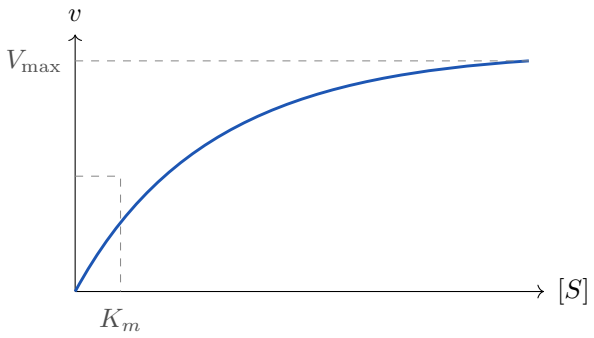
Duration: 128 Minutes **Maximum Marks: 72**

Instructions

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

Biochemistry

Q1. An enzyme following Michaelis–Menten kinetics has a maximum velocity $V_{\max} = 80\ \mu$mol min^{-1} and a Michaelis constant $K_m = 2$ mM, as sketched below. The initial reaction velocity when the substrate concentration $[S] = 6$ mM is: **[1 mark]**



(A) $80\ \mu$mol min^{-1}

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

(C) $40\ \mu$mol min^{-1}

(D) $20\ \mu$mol min^{-1}

Q2. A sample of double-stranded DNA is found to contain 30% adenine among its bases. Using Chargaff's base-pairing rules, the percentage of guanine in this DNA is: **[1 mark]**

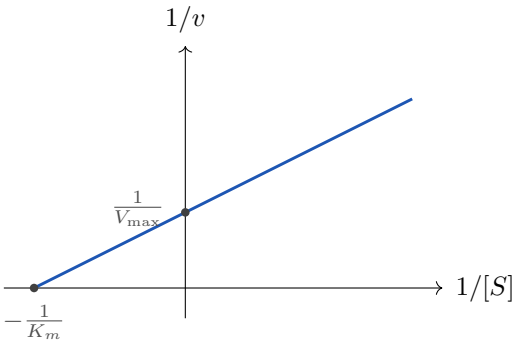
(A) 30%

(B) 70%

(C) 20%

(D) 40%

Q3. The Lineweaver–Burk (double-reciprocal) plot of an enzyme-catalysed reaction is shown below. The line cuts the vertical $(1/v)$ axis at a value of $0.01\ (\mu\text{mol min}^{-1})^{-1}$. The maximum velocity $V_{\max}$ of the enzyme is therefore: **[1 mark]**



(A) $100\ \mu$mol min^{-1}

(B) $0.01\ \mu$mol min^{-1}

(C) $50\ \mu$mol min^{-1}

(D) $10\ \mu$mol min^{-1}

Q4. One complete turn of the citric acid (Krebs) cycle oxidises one molecule of acetyl-CoA. The number of ATP (or GTP) molecules produced directly by substrate-level phosphorylation within a single turn of the cycle is: **[1 mark]**

(A) 3

(B) 12

(C) 2

(D) 1

Q5. Many oxidation–reduction reactions of metabolism use a flavin coenzyme as an electron carrier. The coenzyme flavin adenine dinucleotide (FAD) is derived from which water-soluble vitamin? **[1 mark]**

(A) niacin (vitamin B3)

(B) pantothenic acid (vitamin B5)

(C) thiamine (vitamin B1)

(D) riboflavin (vitamin B2)

Q6. An acetate buffer is prepared from acetic acid and sodium acetate. The pK_a of acetic acid is 4.76, and the buffer contains the conjugate base (acetate) and the acid in a ratio $[\mathrm{A}^-]/[\mathrm{HA}] = 10$. Using the Henderson–Hasselbalch equation, the pH of the buffer is: **[1 mark]**

(A) 5.76

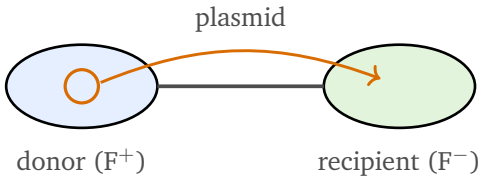
(B) 4.76

(C) 3.76

(D) 6.76

Microbiology

Q7. The process sketched below shows a plasmid being transferred from a donor bacterium to a recipient through a physical mating bridge (sex pilus) formed by direct cell-to-cell contact. This mode of horizontal gene transfer is called: **[1 mark]**



(A) transformation

(B) conjugation

(C) transduction

(D) transfection

Q8. A plasmid that is able either to replicate autonomously in the cytoplasm or to integrate reversibly into the host bacterial chromosome and replicate along with it is best described as a(n): **[1 mark]**

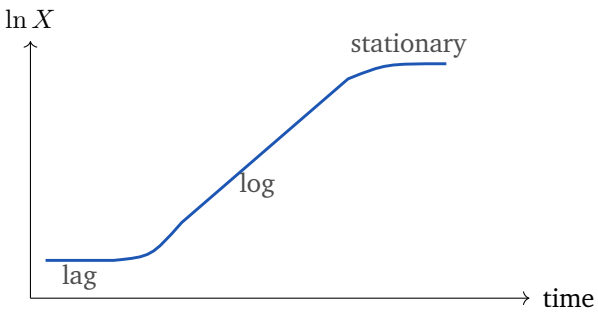
(A) episome

(B) transposon

(C) cosmid

(D) prophage

Q9. During exponential growth a bacterial culture increases from 5×10^2 cells to 5×10^8 cells in exactly 10 hours, as shown on the semi-log growth plot. The generation (doubling) time of this culture is nearest to: **[1 mark]**



(A) 20 min

(B) 15 min

(C) 30 min

(D) 60 min

Q10. In one mode of horizontal gene transfer, a fragment of bacterial DNA is accidentally packaged inside a bacteriophage and is then carried into a new bacterial cell during infection. This bacteriophage-mediated transfer of host genes is known as: [1 mark]

(A) conjugation

(B) transformation

(C) binary fission

(D) transduction

Q11. An Hfr (high-frequency recombination) strain of *Escherichia coli* is able to transfer chromosomal genes to a recipient at high frequency during conjugation. In an Hfr cell, the F (fertility) factor is: [1 mark]

(A) completely absent from the cell

(B) present only as a free autonomous plasmid

(C) present as many small cytoplasmic copies

(D) integrated into the bacterial chromosome

Cell Biology and Molecular Biology

Q12. In the Watson–Crick model of B-form DNA, the two polynucleotide strands are antiparallel and wound into a right-handed double helix. The number of base pairs contained in one complete turn of the B-DNA helix is approximately: [1 mark]

(A) 3.4

(B) 10.5

(C) 20

(D) 34

Q13. A linear stretch of double-stranded B-DNA is 120 base pairs long. Taking the helix to make one complete turn every 10 base pairs, the number of complete helical turns in this stretch is: **[1 mark]**

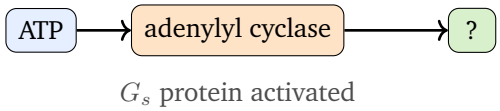
(A) 120

(B) 240

(C) 12

(D) 6

Q14. The signalling pathway summarised below is triggered when a hormone binds a G-protein-coupled receptor and activates the membrane enzyme adenylyl cyclase. The intracellular second messenger produced by adenylyl cyclase from ATP is: **[1 mark]**



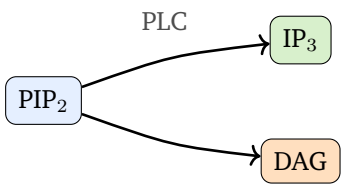
(A) inositol trisphosphate (IP_3)

(B) cyclic AMP (cAMP)

(C) diacylglycerol (DAG)

(D) cyclic GMP (cGMP)

Q15. In another signalling branch, the membrane enzyme phospholipase C (PLC) hydrolyses the membrane lipid phosphatidylinositol-4,5-bisphosphate (PIP_2), splitting it into two second messengers, as shown. These two second messengers are: **[1 mark]**



(A) cAMP and GTP

(B) cGMP and calcium ions

(C) IP_3 and DAG

(D) ATP and inorganic phosphate

Q16. In the eukaryotic nucleus, three distinct RNA polymerases transcribe different classes of RNA. The enzyme responsible for transcribing protein-coding genes into messenger RNA (pre-mRNA) is: [1 mark]

(A) RNA polymerase I

(B) RNA polymerase III

(C) RNA polymerase II

(D) DNA polymerase III

Q17. During the maturation of a eukaryotic messenger RNA, a chain of about 200 adenine nucleotides is enzymatically added to the $3'$ end of the transcript. This particular post-transcriptional modification is called: [1 mark]

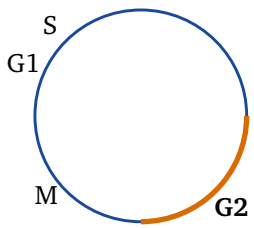
(A) $5'$ capping with 7-methylguanosine

(B) polyadenylation (addition of a poly(A) tail)

(C) splicing out of introns

(D) RNA editing of individual bases

Q18. The eukaryotic cell cycle is drawn below with one interphase quadrant highlighted. This phase follows DNA replication and is the gap during which the cell continues to grow and synthesises proteins in preparation for mitosis. The highlighted phase is: [1 mark]



(A) G1 phase

(B) G2 phase

(C) S phase

(D) M phase

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 recessive allele is $q = 0.3$. The expected frequency of homozygous recessive individuals in this population is: **[1 mark]**

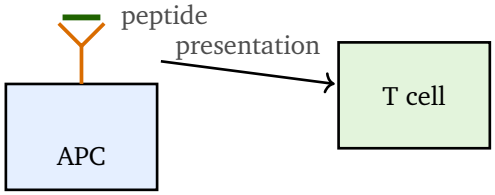
(A) 0.30

(B) 0.42

(C) 0.09

(D) 0.49

Q20. The diagram shows an antigen-presenting cell displaying a peptide on an MHC class II molecule to a T lymphocyte. MHC class II molecules present processed *exogenous* antigenic peptides to which class of T cells? **[1 mark]**



(A) $CD4^+$ helper T cells

(B) $CD8^+$ cytotoxic T cells

(C) B lymphocytes

(D) natural killer (NK) cells

Q21. Unlike the more restricted MHC class II molecules, MHC class I molecules are able to display endogenous peptides to cytotoxic T cells on nearly every body cell. MHC class I molecules are therefore expressed on the surface of: **[2 marks]**

(A) only professional antigen-presenting cells

(B) only B and T lymphocytes

(C) mature red blood cells only

(D) essentially all nucleated cells of the body

Q22. A plant heterozygous for a single gene, genotype Aa, with complete dominance, is crossed with a homozygous recessive plant of genotype aa (a test cross). The phenotypic ratio expected among the offspring of this cross is: **[2 marks]**

(A) $3:1$

(B) $1:1$

(C) $9:7$

(D) $1:2:1$

Q23. On a cytotoxic T cell, the CD8 co-receptor strengthens the interaction with the MHC class I molecule during antigen recognition. CD8 does this by binding to a specific, non-polymorphic part of the MHC class I heavy chain, namely the: **[2 marks]**

(A) peptide-binding cleft formed by $\alpha 1$ and $\alpha 2$

(B) conserved $\alpha 3$ (Ig-like) domain of the heavy chain

(C) variable region of β_2-microglobulin

(D) polymorphic $\alpha 1$ domain

Q24. In a two-point cross, two genes located on the same pair of chromosomes are found to recombine with a frequency of 50%, the same value expected for genes on different chromosomes. This recombination frequency indicates that the two genes are: **[2 marks]**

(A) very tightly linked

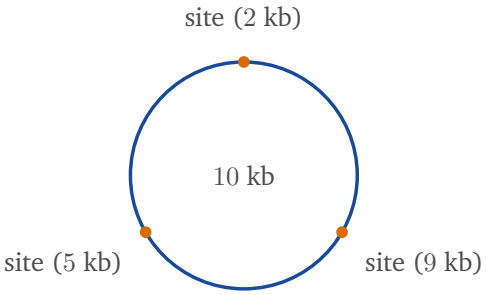
(B) exactly 50 centimorgan apart and always inherited together

(C) effectively unlinked (assorting independently)

(D) alleles of the very same gene

Recombinant DNA Technology and Bioinformatics

Q25. A circular plasmid of total length 10 kb carries three recognition sites for a restriction enzyme, located at the 2 kb, 5 kb and 9 kb positions around the circle, as shown. When this plasmid is completely digested with the enzyme, the number of linear DNA fragments produced is: **[2 marks]**



(A) 6

(B) 1

(C) 2

(D) 3

Q26. To build a library that represents only the genes actually expressed (transcribed) in a tissue, the messenger RNA is first copied into complementary DNA. The enzyme that synthesises this complementary DNA (cDNA) strand using the mRNA as a template is: **[2 marks]**

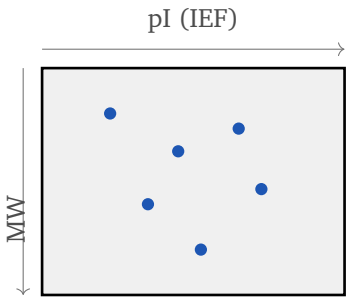
(A) reverse transcriptase

(B) DNA ligase

(C) a restriction endonuclease

(D) RNA polymerase II

Q27. In proteomics a protein mixture is spread out over a two-dimensional gel: it is first separated in one direction by isoelectric point and then, at right angles, by molecular weight, giving a pattern of spots as sketched. This separation method is called: **[2 marks]**



(A) Western blotting

(B) two-dimensional gel electrophoresis

(C) Southern blotting

(D) Northern blotting

Q28. In a proteomics workflow, purified protein spots are digested into peptides and identified by measuring the mass-to-charge ratio of those peptides very accurately. The analytical instrument that performs this measurement is the: [2 marks]

(A) X-ray crystallograph

(B) mass spectrometer

(C) ELISA plate reader

(D) thermal cycler (PCR machine)

Q29. When a query sequence is compared against a genomic database with the BLAST algorithm, each alignment is assigned a statistic that estimates how many hits of that quality would be expected by pure chance. A highly significant (biologically meaningful) match is indicated by a very *low* value of the: [2 marks]

(A) bit score

(B) percent identity

(C) query coverage

(D) E-value (expect value)

Q30. The Human Genome Project produced the first near-complete reference sequence of human DNA. Although the human genome contains about 3 billion base pairs, the number of *protein-coding genes* it was finally estimated to contain is closest to: **[2 marks]**

(A) $100{,}000$

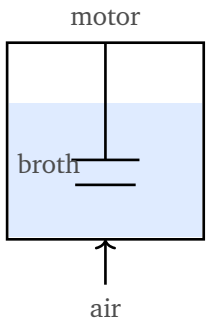
(B) $20{,}000$

(C) 3 billion

(D) 500

Bioprocess Engineering and Process Biotechnology

Q31. In the batch stirred-tank bioreactor shown, an organism grows exponentially with a measured doubling (generation) time of 2 hours. Taking $\ln 2 = 0.693$, the specific growth rate μ of the culture is: **[2 marks]**



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

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

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

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

Q32. In a fermentation, 45 g of dry cell biomass is produced while 90 g of glucose is consumed as the sole carbon and energy source. The biomass yield coefficient on substrate, $Y_{X/S}$, for this process is: **[2 marks]**

(A) $0.5\ \text{g g}^{-1}$

(B) $2.0\ \text{g g}^{-1}$

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

(D) 1.35 g g^{-1}

Q33. In analytical ultracentrifugation the rate at which a particle sediments is expressed by its sedimentation coefficient, measured in Svedberg (S) units. One Svedberg unit corresponds to a sedimentation coefficient of: [2 marks]

(A) 10^{-9} s

(B) 10^{-6} s

(C) 10^{-13} s

(D) 1 s

Q34. After a fermentation is complete, downstream processing begins with the removal of the cells from the culture broth. The unit operation typically used *first*, to achieve this solid–liquid separation of biomass from the spent medium, is: [2 marks]

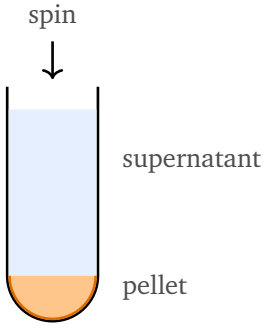
(A) centrifugation or filtration (solid–liquid separation)

(B) ion-exchange chromatography

(C) crystallisation of the product

(D) freeze-drying (lyophilisation)

Q35. A cell homogenate is fractionated by differential centrifugation, in which the sample is spun at successively higher speeds and the pellet is collected at each stage, as sketched. At the *lowest* centrifugal speed, the first (heaviest) cell component to sediment as a pellet is the: [2 marks]



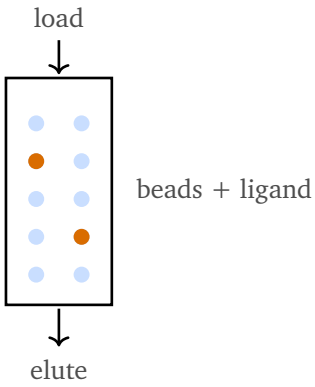
(A) free ribosomes

(B) microsomal vesicles

(C) nuclei

(D) soluble cytosolic proteins

Q36. The chromatography column drawn below is packed with beads carrying an immobilised ligand that binds one target protein very specifically, while all other proteins flow straight through. This highly selective purification method, in which separation depends on specific biological binding, is: **[2 marks]**



(A) size-exclusion (gel-filtration) chromatography

(B) ion-exchange chromatography

(C) reverse-phase chromatography

(D) affinity chromatography

Q37. A widely used strategy for purifying a recombinant protein is to fuse it to a short tag of six consecutive histidine residues, which then binds tightly to a nickel-charged (Ni-NTA) resin. This purification tag is the: **[2 marks]**

(A) glutathione-S-transferase (GST) tag

(B) FLAG epitope tag

(C) polyhistidine (His_6) tag

(D) maltose-binding protein (MBP) tag

Q38. In a batch fermentation the product concentration climbs steadily and reaches its maximum value of 60 g L^{-1} at the end of 15 hours of opera-

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

(A) 0.25 g $L^{-1}h^{-1}$

(B) 900 g $L^{-1}h^{-1}$

(C) 45 g $L^{-1}h^{-1}$

(D) 4 g $L^{-1}h^{-1}$

Plant and Animal Biotechnology

Q39. Plant cell and tissue cultures are an important commercial source of pharmaceutical secondary metabolites. The valuable anticancer alkaloid obtained from the Madagascar periwinkle, *Catharanthus roseus*, is: [2 marks]

(A) vincristine (a vinca alkaloid)

(B) morphine

(C) nicotine

(D) caffeine

Q40. When a small piece of plant tissue (an explant) is placed on a nutrient medium containing suitable auxins and cytokinins, it often gives rise to an unorganised, dividing mass of cells that can later be used to regenerate plants or to produce secondary metabolites. This proliferating cell mass is called: [2 marks]

(A) a protoplast

(B) an explant

(C) a meristem

(D) a callus

Q41. Insect-resistant Bt cotton has been engineered to carry a gene from the soil bacterium *Bacillus thuringiensis* that encodes an insecticidal crystal (Cry) protein. The gene introduced into Bt cotton is the: [2 marks]

(A) *cry* gene (Bt δ-endotoxin)

(B) *nptII* (kanamycin-resistance) gene

(C) *gus* (reporter) gene

(D) *gfp* (green fluorescent protein) gene

Q42. Dolly the sheep, the first mammal cloned from an adult cell, was created by transferring the nucleus of a somatic (udder) cell into an enucleated egg cell, which was then implanted to develop. The technique used to produce Dolly was: **[2 marks]**

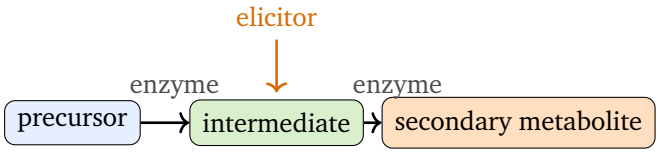
(A) somatic cell nuclear transfer (SCNT)

(B) ordinary in vitro fertilisation (IVF)

(C) hybridoma cell fusion

(D) embryo splitting (twinning)

Q43. In a plant cell suspension culture the biosynthetic route shown converts a simple precursor into a valuable secondary metabolite. A signal molecule (an elicitor), often derived from a fungal cell wall, is deliberately added to the culture. The main purpose of adding such an elicitor is to: **[2 marks]**



(A) induce callus formation from the explant

(B) reduce microbial contamination of the culture

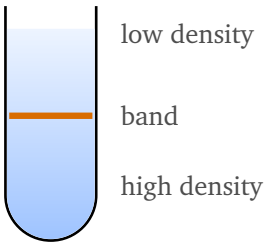
(C) sterilise the culture medium

(D) enhance (boost) the production of the secondary metabolite

Analytical Techniques

Q44. In equilibrium (isopycnic) density-gradient centrifugation, a caesium chloride gradient is spun to equilibrium and a macromolecule forms a sharp

band at a fixed level in the tube, as shown. A given macromolecule comes to rest at the position where: **[2 marks]**



(A) it reaches the very bottom of the tube

(B) the density of the gradient equals the molecule's own buoyant density

(C) the net centrifugal force acting on it becomes zero

(D) it rises to the meniscus at the top of the tube

Q45. A coloured solution is analysed by spectrophotometry. The absorbing species has a molar absorptivity of $5000\ \text{M}^{-1}\text{cm}^{-1}$. Measured in a 1 cm cuvette, the solution shows an absorbance of 0.75. Using the Beer–Lambert law $A = \varepsilon\, c\, l$, the molar concentration of the solution is: **[2 marks]**

(A) 1.5×10^{-4} M

(B) 1.5×10^{-3} M

(C) 3.0×10^{-4} M

(D) 7.5×10^{-4} M

Q46. A mixture of proteins is loaded onto a *cation*-exchange column, whose resin carries fixed *negatively* charged groups. Under the chosen buffer conditions, the proteins that will bind to and be retained by this column are those that are: **[2 marks]**

(A) positively charged (net cationic) proteins

(B) negatively charged (net anionic) proteins

(C) electrically neutral proteins

(D) all proteins, retained equally regardless of charge

Detailed Solutions

Q1.

Solution

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

Step 1 – list the data: $V_{\max} = 80\ \mu\text{mol min}^{-1}$, $K_m = 2$ mM and $[S] = 6$ mM.

Step 2 – substitute into the equation: $v = \dfrac{80 \times 6}{2 + 6}$

Step 3 – evaluate the numerator: $80 \times 6 = 480$

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

Step 5 – complete the arithmetic: $v = \dfrac{480}{8} = 60\ \mu\text{mol min}^{-1}$

Step 6 – sanity check: Since $[S] = 6$ mM is $3K_m$, the velocity should be $\frac{3}{4}V_{\max} = 0.75 \times 80 = 60$, which agrees.

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

Answer: (B) Go Back to Q1

Q2.

Solution

Concept – Chargaff's base-pairing rules: In double-stranded DNA adenine pairs with thymine and guanine pairs with cytosine, so $\%A = \%T$ and $\%G = \%C$.

Step 1 – use the given value: $\%A = 30\%$, therefore $\%T = 30\%$.

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

Step 3 – find the remaining G–C fraction: The four bases total 100%, so $\%G + \%C = 100 - 60 = 40\%$.

Step 4 – split the G–C fraction equally: Since $\%G = \%C$, each is $\dfrac{40}{2} = 20\%$.

Step 5 – state the guanine value: $\%G = 20\%$.

Why the other options are wrong:

- A, 30%: that is the value of adenine (and thymine), not guanine.
- B, 70%: this would be $\%G + \%C + \ldots$, an impossible single-base value here.
- D, 40%: that is the *combined* G+C content, not guanine alone.

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

Answer: (C) Go Back to Q2

Q3.

Solution

Concept – the Lineweaver–Burk equation: Taking reciprocals of the Michaelis–Menten equation gives $\frac{1}{v} = \frac{K_m}{V_{\max}} \cdot \frac{1}{[S]} + \frac{1}{V_{\max}}$, a straight line whose y-intercept is $\frac{1}{V_{\max}}$.

Step 1 – identify what the intercept gives: The intercept on the $1/v$ axis equals $\frac{1}{V_{\max}}$.

Step 2 – read the value from the plot: $\frac{1}{V_{\max}} = 0.01\ (\mu\text{mol min}^{-1})^{-1}$.

Step 3 – invert to find $V_{\max}$: $V_{\max} = \frac{1}{0.01}$

Step 4 – evaluate: $V_{\max} = 100\ \mu\text{mol min}^{-1}$.

Why the other options are wrong:

- B, 0.01: that is the intercept value itself, not its reciprocal.
- C, 50, and D, 10: neither is the reciprocal of 0.01.

Final Answer: $V_{\max} = 100\ \mu\text{mol min}^{-1} \Rightarrow \boxed{\text{A}}$

Answer: (A) Go Back to Q3

Q4.

Solution

Concept – substrate-level phosphorylation in the TCA cycle: Within one turn of the citric acid cycle, a high-energy nucleoside triphosphate is generated directly (not through the electron-transport chain) at one specific step.

Step 1 – locate the substrate-level step: The conversion of succinyl-CoA to succinate, catalysed by succinyl-CoA synthetase, is coupled to the direct synthesis of one GTP (or ATP).

Step 2 – count such steps per turn: There is exactly one such step in a single turn of the cycle.

Step 3 – separate this from the ETC yield: The 3 NADH and 1 $FADH_2$ made per turn feed the electron-transport chain and are *not* counted as direct (substrate-level) ATP.

Step 4 – state the direct yield: Direct substrate-level product $= 1$ GTP/ATP per turn.

Why the other options are wrong:

- A, 3: this is the number of NADH per turn, made by dehydrogenases, not direct ATP.
- B, 12: an old estimate of the *total* ATP yield per turn including oxidative phosphorylation.
- C, 2: no turn of the cycle makes two substrate-level phosphates.

Final Answer: 1 GTP/ATP by substrate-level phosphorylation $\Rightarrow$ D

Answer: (D) Go Back to Q4

Q5.

Solution

Concept – flavin coenzymes come from riboflavin: Both FMN and FAD are built on a riboflavin core, and they carry electrons as hydride/hydrogen acceptors in redox reactions.

Step 1 – recall the origin of FAD: FAD is synthesised from riboflavin (vitamin B2) by adding one AMP-derived nucleotide unit.

Step 2 – confirm the vitamin: The functional isoalloxazine ring that accepts electrons is the riboflavin part.

Why the other options are wrong:

- A, niacin (B3): gives rise to NAD^+ and $NADP^+$, not FAD.
- B, pantothenic acid (B5): is the precursor of coenzyme A.
- C, thiamine (B1): forms thiamine pyrophosphate (TPP), a decarboxylation coenzyme.

Final Answer: FAD is derived from riboflavin (vitamin B2) $\Rightarrow$ D

Answer: (D) Go Back to Q5

Q6.

Solution

Concept – the Henderson–Hasselbalch equation: $\text{pH} = \text{p}K_a + \log_{10}\dfrac{[\text{A}^-]}{[\text{HA}]}$, relating buffer pH to the ratio of conjugate base to acid.

Step 1 – list the data: $\text{p}K_a = 4.76$ and $\dfrac{[\text{A}^-]}{[\text{HA}]} = 10$.

Step 2 – evaluate the log term: $\log_{10}(10) = 1$.

Step 3 – substitute into the equation: $\text{pH} = 4.76 + 1$

Step 4 – complete the arithmetic: $\text{pH} = 5.76$.

Step 5 – interpret: Because there is ten times more conjugate base than acid, the buffer sits one pH unit *above* its $\text{p}K_a$.

Final Answer: $\text{pH} = 5.76 \Rightarrow \boxed{\text{A}}$

Answer: (A) Go Back to Q6

Q7.

Solution

Concept – horizontal gene transfer by cell contact: Bacteria can exchange genes by three routes: transformation (uptake of free DNA), transduction (phage-mediated) and conjugation (direct contact).

Step 1 – read the diagram: Two cells are joined by a sex pilus and a plasmid is passing from the donor (F^+) to the recipient (F^-).

Step 2 – match the feature to the mechanism: Transfer that needs a physical mating bridge and cell-to-cell contact is conjugation.

Step 3 – confirm the players: The donor carries the F (fertility) plasmid that encodes the pilus; the recipient becomes F^+ after transfer.

Why the other options are wrong:

- A, transformation: uptake of naked DNA from the surroundings, with no pilus.
- C, transduction: DNA is carried by a bacteriophage, not through a bridge.
- D, transfection: introduction of nucleic acid into *eukaryotic* cells.

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

Answer: (B) Go Back to Q7

Q8.

Solution

Concept – episomes: An episome is a genetic element that can exist in two states, either replicating freely in the cytoplasm or integrated into the host chromosome.

Step 1 – match the description: The element described switches reversibly between autonomous and integrated replication, which is the defining property of an episome.

Step 2 – give the classic example: The F (fertility) plasmid of *E. coli* is the textbook episome; when integrated it produces Hfr strains.

Why the other options are wrong:

- B, transposon: a mobile element that jumps within/between DNA molecules, not an autonomously replicating plasmid.
- C, cosmid: an engineered cloning vector, not a natural integrating element.
- D, prophage: specifically integrated *viral* DNA, not a plasmid that also replicates freely.

Final Answer: an episome $\Rightarrow$ A

Answer: (A) Go Back to Q8

Q9.

Solution

Concept – generation time from exponential growth: The number of doublings is $n = \log_2 \frac{X}{X_0}$ and the generation time is $t_d = \frac{t}{n}$.

Step 1 – list the data: $X_0 = 5 \times 10^2$, $X = 5 \times 10^8$, total time $t = 10$ h $= 600$ min.

Step 2 – find the fold increase: $\frac{X}{X_0} = \frac{5 \times 10^8}{5 \times 10^2} = 10^6$.

Step 3 – compute the number of generations: $n = \log_2(10^6) = 6 \log_2 10 = 6 \times 3.322$

$n \approx 19.93$

Step 4 – compute the generation time: $t_d = \frac{600}{19.93}$

$t_d \approx 30.1$ min

Step 5 – round to the nearest option: $t_d \approx 30$ min.

Final Answer: $t_d \approx 30$ min $\Rightarrow$ C

Answer: (C) Go Back to Q9

Q10.

Solution

Concept – transduction: Transduction is horizontal gene transfer in which bacterial DNA is moved from one cell to another inside a bacteriophage particle.

Step 1 – read the description: Host DNA is mistakenly packaged into a phage and delivered to a new bacterium on infection.

Step 2 – name the mechanism: A phage acting as the vehicle for bacterial genes defines transduction.

Step 3 – note the two forms: Generalised transduction packages random host DNA; specialised transduction transfers genes next to the prophage integration site.

Why the other options are wrong:

- A, conjugation: needs cell-to-cell contact through a pilus, not a phage.
- B, transformation: uptake of free DNA from the medium.
- C, binary fission: is simple cell division, not gene transfer between cells.

Final Answer: transduction $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q10

Q11.

Solution

Concept – the F factor in Hfr strains: An Hfr cell arises when the free F plasmid integrates into the bacterial chromosome by recombination.

Step 1 – define Hfr: "High-frequency recombination" strains transfer chromosomal genes efficiently because the F factor is now part of the chromosome.

Step 2 – locate the F factor: In an Hfr cell the F factor is *integrated into the bacterial chromosome*, so it drags adjacent chromosomal genes into the recipient during conjugation.

Step 3 – contrast the states: An ordinary F^+ cell keeps F as a free plasmid and transfers mainly the plasmid; integration is what makes a cell Hfr.

Why the other options are wrong:

- A: an Hfr cell certainly contains the F factor.
- B: a free autonomous F factor describes an F^+ cell, not an Hfr cell.
- C: F is a single-copy element, not present as many cytoplasmic copies.

Final Answer: the F factor is integrated into the chromosome $\Rightarrow$ D

Answer: (D) Go Back to Q11

Q12.

Solution

Concept – geometry of the B-DNA double helix: B-DNA is a right-handed helix with a rise of about 0.34 nm per base pair and a helical repeat close to 3.4 nm per turn.

Step 1 – relate turn length to rise: Number of base pairs per turn $= \dfrac{\text{length of one turn}}{\text{rise per base pair}} = \dfrac{3.4 \text{ nm}}{0.34 \text{ nm}}$.

Step 2 – evaluate: $\dfrac{3.4}{0.34} \approx 10$, and the accepted refined value is about 10.5 base pairs per turn.

Step 3 – state the answer: B-DNA has roughly 10.5 base pairs per complete helical turn.

Why the other options are wrong:

- A, 3.4: this is the pitch (length of one turn) in nanometres, not a base-pair count.
- C, 20: about twice the correct value.
- D, 34: this is the pitch expressed in angstroms (34 Å), not a base-pair count.

Final Answer: ≈ 10.5 base pairs per turn $\Rightarrow$ B

Answer: (B) Go Back to Q12

Q13.

Solution

Concept – counting helical turns: If a helix repeats every fixed number of base pairs, the number of turns is the total base pairs divided by the base pairs per turn.

Step 1 – list the data: Length $= 120$ base pairs; helical repeat $= 10$ base pairs per turn.

Step 2 – set up the division: Number of turns $= \dfrac{120}{10}$.

Step 3 – evaluate: $= 12$ complete turns.

Why the other options are wrong:

- A, 120: that is the base-pair count, not the number of turns.
- B, 240: this would count individual nucleotides (2×120), not turns.
- D, 6: this uses 20 bp per turn, which is not the given repeat.

Final Answer: 12 complete helical turns $\Rightarrow$ C

Answer: (C) Go Back to Q13

Q14.

Solution

Concept – adenylyl cyclase makes cyclic AMP: When a stimulatory G-protein-coupled receptor activates the G_s protein, its α subunit switches on adenylyl cyclase.

Step 1 – identify the reaction: Adenylyl cyclase converts ATP into cyclic AMP by forming a cyclic phosphodiester bond, releasing pyrophosphate.

Step 2 – name the product: The intracellular second messenger produced is cyclic AMP (cAMP).

Step 3 – trace the downstream effect: cAMP then activates protein kinase A, which phosphorylates target proteins.

Why the other options are wrong:

- A, IP_3, and C, DAG: are products of phospholipase C acting on PIP_2, a different pathway.
- D, cGMP: is made by guanylyl cyclase from GTP, not by adenylyl cyclase.

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

Answer: (B) Go Back to Q14

Q15.

Solution

Concept – the phospholipase C pathway: Phospholipase C cleaves the membrane lipid PIP_2 into two second messengers that act on different targets.

Step 1 – name the two products: PLC splits PIP_2 into inositol-1,4,5-trisphosphate (IP_3) and diacylglycerol (DAG).

Step 2 – describe their roles: IP_3 is water-soluble and releases Ca^{2+} from the endoplasmic reticulum; DAG stays in the membrane and activates protein kinase C.

Step 3 – match to the option: The pair produced is IP_3 and DAG.

Why the other options are wrong:

- A: cAMP and GTP belong to the adenylyl-cyclase and G-protein systems.
- B: cGMP and Ca^{2+} are downstream or unrelated messengers, not the direct PLC products.
- D: ATP and inorganic phosphate are not second messengers here.

Final Answer: IP_3 and DAG $\Rightarrow$ C

Answer: (C) Go Back to Q15

Q16.

Solution

Concept – the three eukaryotic RNA polymerases: Eukaryotes use RNA polymerase I for most rRNA, RNA polymerase II for mRNA, and RNA polymerase III for tRNA and 5S rRNA.

Step 1 – match the task to the enzyme: Transcription of protein-coding genes into pre-mRNA is carried out by RNA polymerase II.

Step 2 – confirm with a hallmark: RNA polymerase II is the one sensitive to α-amanitin and whose largest subunit bears the CTD tail used for capping and processing.

Why the other options are wrong:

- A, RNA polymerase I: transcribes the large ribosomal RNA precursor.
- B, RNA polymerase III: transcribes tRNA and 5S rRNA.
- D, DNA polymerase III: is a bacterial *DNA*-replicating enzyme, not a transcriptase.

Final Answer: RNA polymerase II $\Rightarrow$ C

Answer: (C) Go Back to Q16

Q17.

Solution

Concept – $3'$ processing of eukaryotic mRNA: After cleavage at the poly(A) signal, poly(A) polymerase adds a long stretch of adenine residues to the $3'$ end.

Step 1 – identify the modification: Adding about 200 adenines to the $3'$ end is polyadenylation, producing the poly(A) tail.

Step 2 – state its purpose: The poly(A) tail increases mRNA stability, aids nuclear export and promotes efficient translation.

Why the other options are wrong:

- A, $5'$ capping: happens at the *other* end with 7-methylguanosine.
- C, splicing: removes introns from the middle of the transcript, not the $3'$ tail.
- D, RNA editing: changes individual bases and does not add a tail of adenines.

Final Answer: addition of a poly(A) tail $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q17

Q18.

Solution

Concept – the phases of interphase: Interphase runs G1 $\rightarrow$ S $\rightarrow$ G2; DNA is replicated in S, and G2 is the growth gap that follows replication and precedes mitosis.

Step 1 – use the clue in the question: The highlighted phase comes *after* DNA replication and prepares the cell for mitosis.

Step 2 – identify it: The gap after S phase and before M phase is the G2 phase, matching the highlighted quadrant.

Step 3 – note G2 activity: During G2 the cell keeps growing, synthesises proteins such as tubulin, and checks the replicated DNA for damage.

Why the other options are wrong:

- A, G1: is the gap *before* DNA replication.
- C, S: is when DNA is replicated, not the phase after it.
- D, M: is mitosis itself, which follows G2.

Final Answer: the G2 phase $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q18

Q19.

Solution

Concept – Hardy–Weinberg genotype frequencies: With allele frequencies p (dominant) and q (recessive), genotype frequencies are p^2 (homozygous dominant), $2pq$ (heterozygous) and q^2 (homozygous recessive).

Step 1 – pick the right term: Homozygous recessive individuals occur at frequency q^2.

Step 2 – substitute the given value: $q = 0.3$, so $q^2 = (0.3)^2$.

Step 3 – evaluate: $q^2 = 0.09$.

Why the other options are wrong:

- A, 0.30: that is q itself, not q^2.
- B, 0.42: that is the heterozygote frequency $2pq = 2(0.7)(0.3)$.
- D, 0.49: that is $p^2 = (0.7)^2$, the homozygous *dominant* frequency.

Final Answer: $q^2 = 0.09 \Rightarrow$ C

Answer: (C) Go Back to Q19

Q20.

Solution

Concept – MHC class II and the CD4 helper T cell: MHC class II molecules present peptides derived from *exogenous* antigens (taken up and processed in endosomes) and are read by $CD4^+$ helper T cells.

Step 1 – match the pathway: Exogenous antigen $\rightarrow$ processed in the endocytic pathway $\rightarrow$ loaded on MHC class II.

Step 2 – identify the responding T cell: The CD4 co-receptor binds a conserved region of MHC class II, so $CD4^+$ helper T cells recognise these complexes.

Step 3 – recall the mnemonic: "CD4 with class II, CD8 with class I" ($4 \times 2 = 8 \times 1$).

Why the other options are wrong:

- B, $CD8^+$ cytotoxic T cells: read MHC class I, not class II.
- C, B lymphocytes: recognise native antigen through their B-cell receptor, not via MHC-II presentation to themselves.
- D, NK cells: are inhibited by MHC class I and are not the primary readers of MHC class II.

Final Answer: $CD4^+$ helper T cells $\Rightarrow$ A

Answer: (A) Go Back to Q20

Q21.

Solution

Concept – tissue distribution of MHC class I: MHC class I displays endogenous (cytosolic) peptides so that cytotoxic T cells can survey virtually every cell for infection or malignancy.

Step 1 – reason from function: For immune surveillance to work everywhere, class I must be present on essentially every cell that has a nucleus.

Step 2 – state the distribution: MHC class I is expressed on essentially all nucleated cells of the body.

Step 3 – note the exception: Mature red blood cells lack a nucleus and express little or no MHC class I, which is why "all nucleated cells" is the precise wording.

Why the other options are wrong:

- A: restricting class I to professional APCs describes class II expression, not class I.
- B: class I is far more widespread than just lymphocytes.
- C: mature red blood cells are exactly the cells that essentially lack class I.

Final Answer: essentially all nucleated cells $\Rightarrow$ D

Answer: (D) Go Back to Q21

Q22.

Solution

Concept – the test cross: Crossing a heterozygote Aa with a homozygous recessive aa reveals the heterozygote's gametes directly in the offspring ratio.

Step 1 – list the gametes: Aa produces $\frac{1}{2}A$ and $\frac{1}{2}a$; aa produces only a.

Step 2 – combine the gametes: Offspring are $\frac{1}{2}\,Aa$ and $\frac{1}{2}\,aa$.

Step 3 – convert to phenotypes: Aa shows the dominant phenotype and aa shows the recessive phenotype.

Step 4 – state the ratio: Dominant : recessive $= 1:1$.

Why the other options are wrong:

- A, $3:1$: is the F_2 ratio from $Aa \times Aa$, not a test cross.

- C, $9:7$: reflects complementary gene interaction in a dihybrid cross.
- D, $1:2:1$: is a *genotypic* ratio (from $Aa \times Aa$), not this phenotypic outcome.

Final Answer: $1:1 \Rightarrow$ B

Answer: (B) Go Back to Q22

Q23.

Solution

Concept – how CD8 docks onto MHC class I: The MHC class I heavy chain has three domains: $\alpha 1$ and $\alpha 2$ form the peptide-binding groove, while $\alpha 3$ is a conserved immunoglobulin-like domain.

Step 1 – identify the CD8 contact: CD8 binds the non-polymorphic $\alpha 3$ domain, well away from the bound peptide.

Step 2 – explain why this matters: Because $\alpha 3$ is conserved (non-polymorphic), CD8 can stabilise the interaction with any class I allele while the T-cell receptor reads the variable peptide-groove region.

Why the other options are wrong:

- A: the $\alpha 1/\alpha 2$ groove holds the peptide and is read by the T-cell receptor, not by CD8.
- C: β_2-microglobulin supports the fold but is not the CD8-binding domain.
- D: the $\alpha 1$ domain is polymorphic and part of the peptide-binding surface, not the CD8 site.

Final Answer: the conserved $\alpha 3$ domain $\Rightarrow$ B

Answer: (B) Go Back to Q23

Q24.

Solution

Concept – recombination frequency and linkage: Recombination frequency ranges from 0% (completely linked) up to a maximum of 50%, which is the value expected when alleles assort independently.

Step 1 – interpret the 50% value: A recombination frequency of 50% means parental and recombinant offspring are equally frequent.

Step 2 – draw the conclusion: Genes so far apart on the same chromosome that crossing over occurs between them in essentially every meiosis behave as if

unlinked (independent assortment).

Step 3 – note the cap: Because multiple crossovers reset the count, observed recombination frequency never exceeds 50%, so 50% cannot be turned into a reliable map distance.

Why the other options are wrong:

- A: tightly linked genes show a *low* recombination frequency, near 0%.
- B: at 50% the genes are *not* inherited together; they behave independently.
- D: alleles of the same gene do not recombine to give 50% new combinations.

Final Answer: effectively unlinked (independent assortment) $\Rightarrow$ C

Answer: (C) Go Back to Q24

Q25.

Solution

Concept – cutting a circular molecule: On a circular DNA molecule, each restriction site is one cut, and the number of linear fragments equals the number of cuts.

Step 1 – count the sites: There are three recognition sites, at 2 kb, 5 kb and 9 kb.

Step 2 – apply the circular rule: For a circle, fragments $=$ number of cuts $= 3$.

Step 3 – verify by adding fragment sizes: $5 - 2 = 3$ kb, $9 - 5 = 4$ kb, and wrapping around $10 - 9 + 2 = 3$ kb.

Step 4 – check the total: $3 + 4 + 3 = 10$ kb, which matches the plasmid length, confirming exactly three fragments.

Why the other options are wrong:

- A, 6: double-counts; three cuts give three, not six, pieces.
- B, 1: a single cut would only linearise the circle.
- C, 2: two cuts on a circle give two fragments, but here there are three sites.

Final Answer: 3 fragments $\Rightarrow$ D

Answer: (D) Go Back to Q25

Q26.

Solution

Concept – making cDNA from mRNA: A cDNA library represents only expressed genes, and it is built by copying mRNA back into DNA.

Step 1 – identify the required activity: Synthesising DNA using an RNA template is RNA-dependent DNA polymerase activity.

Step 2 – name the enzyme: Reverse transcriptase carries out this RNA $\rightarrow$ DNA synthesis, generating the first cDNA strand.

Step 3 – note the origin: Reverse transcriptase is obtained from retroviruses, whose life cycle depends on this activity.

Why the other options are wrong:

- B, DNA ligase: seals nicks; it does not synthesise a strand from an RNA template.
- C, restriction endonuclease: cuts DNA at specific sites, not a polymerase.
- D, RNA polymerase II: makes RNA from a DNA template, the opposite direction.

Final Answer: reverse transcriptase $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q26

Q27.

Solution

Concept – resolving a proteome in two dimensions: Complex protein mixtures are spread out by combining two independent separation principles at right angles.

Step 1 – read the two axes: First dimension: isoelectric focusing separates by isoelectric point (pI). Second dimension: SDS-PAGE separates by molecular weight.

Step 2 – name the method: Combining IEF and SDS-PAGE gives two-dimensional gel electrophoresis, yielding a scatter of protein spots.

Step 3 – state the advantage: Because two unrelated properties are used, thousands of proteins can be resolved as individual spots.

Why the other options are wrong:

- A, Western blotting: detects specific proteins with antibodies *after* electrophoresis; it is not itself a 2-D separation.

- C, Southern blotting: detects specific *DNA* sequences.
- D, Northern blotting: detects specific *RNA* molecules.

Final Answer: two-dimensional gel electrophoresis $\Rightarrow$ B

Answer: (B) Go Back to Q27

Q28.

Solution

Concept – identifying proteins by mass: Modern proteomics identifies proteins by digesting them into peptides and measuring peptide masses very precisely.

Step 1 – identify the measured quantity: The instrument measures the mass-to-charge ratio (m/z) of ionised peptides.

Step 2 – name the instrument: A mass spectrometer performs this measurement; matching the peptide-mass fingerprint to databases identifies the protein.

Step 3 – note common formats: Techniques such as MALDI-TOF and electrospray-ionisation tandem MS are the workhorses of protein identification.

Why the other options are wrong:

- A, X-ray crystallograph: determines three-dimensional structure, not peptide masses for identification.
- C, ELISA plate reader: measures colour/absorbance in immunoassays.
- D, thermal cycler: runs PCR on DNA and does not measure mass.

Final Answer: the mass spectrometer $\Rightarrow$ B

Answer: (B) Go Back to Q28

Q29.

Solution

Concept – the BLAST E-value: The expect value (E-value) estimates the number of alignments as good as the observed one that would arise by chance in a database of the given size.

Step 1 – interpret small versus large E: A very small E-value means such a match would almost never occur by chance, so the hit is highly significant.

Step 2 – match to the question: A biologically meaningful (significant) match corresponds to a very *low* E-value.

Step 3 – contrast with the score: The bit score rises for better alignments, while the E-value falls; both track quality but in opposite directions.

Why the other options are wrong:

- A, bit score: a *high* (not low) bit score signals a good hit, so "low value" does not fit.
- B, percent identity: useful but not the chance-based significance statistic asked for.
- C, query coverage: describes how much of the query aligns, not statistical significance.

Final Answer: a very low E-value $\Rightarrow$ D

Answer: (D) Go Back to Q29

Q30.

Solution

Concept – gene number versus genome size: Genome *size* (base pairs) and *gene count* are different things; much of the human genome is non-coding.

Step 1 – recall the surprising finding: The Human Genome Project revised the protein-coding gene count sharply downward from early guesses.

Step 2 – state the accepted figure: The human genome contains roughly $20{,}000$ protein-coding genes (about $20{,}000$–$25{,}000$).

Step 3 – keep the two numbers distinct: The ~ 3 billion figure is the number of base pairs, not the number of genes.

Why the other options are wrong:

- A, $100{,}000$: an early over-estimate that the project overturned.
- C, 3 billion: that is the base-pair count of the genome, not the gene count.
- D, 500: far too few for a complex mammal.

Final Answer: about $20{,}000$ protein-coding genes $\Rightarrow$ B

Answer: (B) Go Back to Q30

Q31.

Solution

Concept – specific growth rate from doubling time: During exponential growth the specific growth rate and the doubling time are linked by $\mu = \dfrac{\ln 2}{t_d}$.

Step 1 – list the data: Doubling time $t_d = 2$ h and $\ln 2 = 0.693$.

Step 2 – substitute into the relation: $\mu = \dfrac{0.693}{2}$

Step 3 – evaluate: $\mu = 0.3465\ \text{h}^{-1}$

Step 4 – round to the option: $\mu \approx 0.35\ \text{h}^{-1}$.

Why the other options are wrong:

- A, $0.69\ \text{h}^{-1}$: this is $\ln 2$ divided by 1 h, i.e. a 1-hour doubling time.
- B, $1.39\ \text{h}^{-1}$: about $\ln 2$ times 2, the inverse mistake.
- D, $0.17\ \text{h}^{-1}$: this uses a 4-hour doubling time.

Final Answer: $\mu \approx 0.35\ \text{h}^{-1} \Rightarrow \boxed{\text{C}}$

Answer: (C) Go Back to Q31

Q32.

Solution

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

Step 1 – list the data: Biomass formed $= 45$ g; glucose consumed $= 90$ g.

Step 2 – substitute into the definition: $Y_{X/S} = \dfrac{45}{90}$

Step 3 – evaluate: $Y_{X/S} = 0.5\ \text{g g}^{-1}$

Step 4 – interpret: About half a gram of cells is produced for every gram of glucose used, a realistic aerobic value.

Why the other options are wrong:

- B, 2.0: this is the inverted ratio $90/45$, i.e. substrate per biomass.
- C, 0.25: uses the wrong numbers.
- D, 1.35: a yield above $1\ \text{g g}^{-1}$ is not physically reasonable on glucose alone.

Final Answer: $Y_{X/S} = 0.5\ \text{g g}^{-1} \Rightarrow \boxed{\text{A}}$

Answer: (A) Go Back to Q32

Q33.

Solution

Concept – the Svedberg unit: The sedimentation coefficient s measures how fast a particle sediments per unit centrifugal field; it is quoted in Svedberg (S) units.

Step 1 – recall the definition: One Svedberg unit is defined as $1\ \text{S} = 10^{-13}$ seconds.

Step 2 – give a familiar example: The prokaryotic ribosome sediments at 70S, made of 50S and 30S subunits (S values are not additive).

Step 3 – note what s depends on: The sedimentation coefficient increases with particle mass and compactness and decreases with drag.

Why the other options are wrong:

- A, 10^{-9} s, and B, 10^{-6} s: wrong by several orders of magnitude.
- D, 1 s: far too large; a coefficient of 1 s is enormous compared with real particles.

Final Answer: $1\ \text{S} = 10^{-13}$ s $\Rightarrow$ C

Answer: (C) Go Back to Q33

Q34.

Solution

Concept – the first step of downstream processing: Downstream processing usually proceeds as: cell separation $\rightarrow$ cell disruption (if intracellular) $\rightarrow$ purification $\rightarrow$ polishing/formulation.

Step 1 – identify the goal of the first step: The immediate need after fermentation is to separate the solid cells from the liquid broth.

Step 2 – choose the unit operation: Centrifugation or (micro)filtration performs this solid–liquid separation efficiently at large scale.

Step 3 – place it in the sequence: Only after the biomass is removed do purification steps such as chromatography follow.

Why the other options are wrong:

- B, chromatography: is a later high-resolution purification step, not the first bulk separation.
- C, crystallisation: is a downstream polishing step for the purified product.
- D, freeze-drying: is a final formulation step for the finished product.

Final Answer: centrifugation or filtration $\Rightarrow$ A

Answer: (A) Go Back to Q34

Q35.

Solution

Concept – differential centrifugation: Spinning a homogenate at increasing speeds pellets organelles in order of decreasing size and density.

Step 1 – recall the sedimentation order: Heaviest first: nuclei $\rightarrow$ mitochondria (and chloroplasts) $\rightarrow$ microsomes/membrane vesicles $\rightarrow$ ribosomes; soluble proteins stay in the final supernatant.

Step 2 – apply to the lowest speed: At the lowest centrifugal speed the largest, densest structures pellet first, which are the nuclei.

Step 3 – conclude: The first pellet contains the nuclei.

Why the other options are wrong:

- A, ribosomes: are small and need very high speeds; they pellet last.
- B, microsomal vesicles: sediment at intermediate-to-high speed, after nuclei and mitochondria.
- D, soluble cytosolic proteins: do not pellet at all and remain in the supernatant.

Final Answer: the nuclei $\Rightarrow$ C

Answer: (C) Go Back to Q35

Q36.

Solution

Concept – affinity chromatography: Separation here relies not on size or charge but on a specific, reversible biological interaction between the target and an immobilised ligand.

Step 1 – read the column design: The beads carry a ligand that binds one target protein; everything else washes through.

Step 2 – name the method: Using specific ligand binding to capture a single protein is affinity chromatography.

Step 3 – describe elution: The bound protein is later released by adding free ligand or by changing pH/salt, giving a highly purified product in one step.

Why the other options are wrong:

- A, size-exclusion: separates purely by molecular size, with no specific binding.
- B, ion-exchange: separates by net charge, not specific ligand recognition.
- C, reverse-phase: separates by hydrophobicity on a non-polar matrix.

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

Answer: (D) Go Back to Q36

Q37.

Solution

Concept – the polyhistidine purification tag: A short run of histidine residues chelates transition-metal ions, allowing capture on a metal-charged resin.

Step 1 – match the description: Six consecutive histidines that bind a nickel (Ni-NTA) column define the polyhistidine (His_6) tag.

Step 2 – explain the chemistry: The imidazole side chains of histidine coordinate the immobilised Ni^{2+}; the protein is then eluted with a high concentration of free imidazole.

Why the other options are wrong:

- A, GST tag: binds glutathione resin, not nickel.
- B, FLAG tag: is a short epitope purified with an anti-FLAG antibody column.
- D, MBP tag: binds an amylose (maltose) resin.

Final Answer: the polyhistidine (His_6) tag $\Rightarrow$ $\boxed{\text{C}}$

Answer: (C) Go Back to Q37

Q38.

Solution

Concept – overall volumetric productivity: For a batch, the overall volumetric productivity is the final product concentration divided by the total batch time.

Step 1 – list the data: Final product concentration $= 60\ \text{g L}^{-1}$; batch time $= 15\ \text{h}$.

Step 2 – set up the ratio: $\text{Productivity} = \dfrac{60\ \text{g L}^{-1}}{15\ \text{h}}$

Step 3 – evaluate: $= 4\ \text{g L}^{-1}\text{h}^{-1}$.

Why the other options are wrong:

- A, 0.25: this is the inverted ratio $15/60$.
- B, 900: this multiplies the two numbers instead of dividing.
- C, 45: this subtracts $(60 - 15)$ and has the wrong units.

Final Answer: 4 g $L^{-1}h^{-1} \Rightarrow$ D

Answer: (D) Go Back to Q38

Q39.

Solution

Concept – secondary metabolites from plant cultures: Cultured plant cells are exploited to make high-value alkaloids, terpenoids and glycosides that are hard to synthesise chemically.

Step 1 – recall the source plant: *Catharanthus roseus* (Madagascar periwinkle) is famous for its anticancer vinca alkaloids.

Step 2 – name the metabolite: Vincristine (and the related vinblastine) is the anticancer alkaloid obtained from this plant.

Step 3 – note its action: Vincristine binds tubulin and blocks mitotic spindle formation, arresting dividing cancer cells.

Why the other options are wrong:

- B, morphine: comes from the opium poppy, *Papaver somniferum*.
- C, nicotine: is from tobacco, *Nicotiana tabacum*.
- D, caffeine: is from coffee and tea plants, and is not an anticancer vinca alkaloid.

Final Answer: vincristine (a vinca alkaloid) $\Rightarrow$ A

Answer: (A) Go Back to Q39

Q40.

Solution

Concept – callus in plant tissue culture: On a medium with the right balance of auxin and cytokinin, an explant dedifferentiates into an unorganised, actively dividing cell mass.

Step 1 – match the description: An unorganised proliferating mass of cells aris-

ing from an explant is a callus.

Step 2 – state its uses: A callus can be induced to form shoots and roots (regeneration) or grown in suspension to yield secondary metabolites.

Why the other options are wrong:

- A, protoplast: a plant cell whose wall has been enzymatically removed, not a cell mass.
- B, explant: the original starting piece of tissue placed on the medium, before proliferation.
- C, meristem: an organised region of dividing cells within the intact plant, not an unorganised mass.

Final Answer: a callus $\Rightarrow$ D

Answer: (D) Go Back to Q40

Q41.

Solution

Concept – Bt crops and the *cry* gene: Insect resistance in Bt crops comes from a bacterial gene encoding an insecticidal crystal protein.

Step 1 – identify the source and product: *Bacillus thuringiensis* produces Cry (δ-endotoxin) proteins, encoded by *cry* genes.

Step 2 – state what is transferred: The *cry* gene is introduced into cotton so the plant makes the Bt toxin itself.

Step 3 – explain the mechanism: In the alkaline gut of susceptible insect larvae the Cry protein is activated and punctures the gut lining, killing the pest, while remaining harmless to mammals.

Why the other options are wrong:

- B, *nptII*: is a selectable marker for kanamycin resistance, not the insecticidal gene.
- C, *gus*: is a reporter gene used to visualise expression.
- D, *gfp*: is a fluorescent reporter, not an insecticide.

Final Answer: the *cry* gene (Bt δ-endotoxin) $\Rightarrow$ A

Answer: (A) Go Back to Q41

Q42.

Solution

Concept – reproductive cloning of Dolly: Dolly showed that the nucleus of a differentiated adult cell can be reprogrammed to direct development of a whole organism.

Step 1 – describe the procedure: The nucleus of an adult somatic (udder) cell was inserted into an egg cell whose own nucleus had been removed.

Step 2 – name the technique: This is somatic cell nuclear transfer (SCNT).

Step 3 – complete the story: The reconstructed egg was stimulated to divide and implanted into a surrogate ewe, producing a lamb genetically identical to the udder-cell donor.

Why the other options are wrong:

- B, IVF: fertilises an egg with sperm and does not clone an adult.
- C, hybridoma fusion: makes antibody-producing cell lines, not whole animals.
- D, embryo splitting: divides an early embryo to make identical twins, but does not use an adult somatic nucleus.

Final Answer: somatic cell nuclear transfer (SCNT) $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q42

Q43.

Solution

Concept – elicitors and secondary metabolism: Elicitors mimic a stress or pathogen attack and switch on the plant's defensive biosynthetic pathways.

Step 1 – read the pathway: The precursor is converted through enzyme-catalysed steps into a secondary metabolite, and an elicitor is added at the branch point.

Step 2 – state the elicitor's effect: By activating the biosynthetic genes and enzymes, the elicitor *enhances* the yield of the secondary metabolite in the culture.

Step 3 – give an example: A fungal cell-wall fragment added to a cell suspension can markedly raise the output of defence alkaloids or phenolics.

Why the other options are wrong:

- A: callus induction is driven by plant growth regulators (auxin/cytokinin), not elicitors.

- B and C: elicitors are signalling molecules, not antimicrobial agents or sterilants.

Final Answer: to boost secondary-metabolite production $\Rightarrow$ D

Answer: (D) Go Back to Q43

Q44.

Solution

Concept – isopycnic (equilibrium) density-gradient centrifugation: In a density gradient, a particle moves up or down only until it reaches the level whose density matches its own.

Step 1 – describe the force balance: A particle denser than the surrounding medium sinks; one less dense floats up; motion stops where the two densities are equal.

Step 2 – define the banding position: The particle forms a sharp band where the gradient density equals the particle's own buoyant density.

Step 3 – note the classic use: This is how DNA of different GC content (or the Meselson–Stahl heavy/light DNA) separates into distinct bands in a CsCl gradient.

Why the other options are wrong:

- A: the particle does not reach the bottom; it stops at its buoyant density.
- C: at equilibrium the *net* force is zero, but banding is defined by density matching, and a truly zero field would give no separation.
- D: it does not rise to the meniscus unless its density is lower than the whole gradient.

Final Answer: where gradient density equals the molecule's buoyant density $\Rightarrow$ B

Answer: (B) Go Back to Q44

Q45.

Solution

Concept – the Beer–Lambert law: $A = \varepsilon\, c\, l$, where A is absorbance, ε the molar absorptivity, c the concentration and l the path length.

Step 1 – list the data: $A = 0.75$, $\varepsilon = 5000\ \text{M}^{-1}\text{cm}^{-1}$, $l = 1$ cm.

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

Step 3 – substitute: $c = \dfrac{0.75}{5000 \times 1}$

Step 4 – evaluate: $c = \dfrac{0.75}{5000} = 1.5 \times 10^{-4}$ 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:

- B, 1.5×10^{-3}: off by a factor of ten.
- C, 3.0×10^{-4}: uses $\varepsilon = 2500$, not 5000.
- D, 7.5×10^{-4}: divides by 1000 instead of 5000.

Final Answer: $c = 1.5 \times 10^{-4}$ M $\Rightarrow$ A

Answer: (A) Go Back to Q45

Q46.

Solution

Concept – ion-exchange chromatography: A charged resin binds proteins carrying the opposite net charge, so separation depends on the protein's net charge at the working pH.

Step 1 – read the resin charge: A cation-exchange resin carries fixed *negative* groups.

Step 2 – decide which proteins bind: Opposite charges attract, so positively charged (net cationic) proteins bind to the negative resin, while it exchanges cations.

Step 3 – describe elution: Bound proteins are released by raising the salt concentration or by changing the pH toward or past their isoelectric points.

Why the other options are wrong:

- B: negatively charged proteins are repelled by the negative resin and flow through (they bind an *anion* exchanger instead).
- C: neutral proteins have no net charge to be retained.
- D: retention clearly depends on charge, so not all proteins bind equally.

Final Answer: positively charged (net cationic) proteins $\Rightarrow$ A

Answer: (A) Go Back to Q46

Answer Key

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