

IIT JAM Biotechnology

Sample Paper – 3

Collegedunia Practice Series | Exam Date: 14 February 2027

Instructions

- This paper contains **60 questions** carrying a maximum of **100 marks**. Duration: **3 hours (180 minutes)**.
- **Section A (Q1–Q30, MCQ)**: Q1–Q10 carry **+1 mark** each; wrong response: $-\frac{1}{3}$ mark. Q11–Q30 carry **+2 marks** each; wrong response: $-\frac{2}{3}$ mark. Choose the **single best** option.
- **Section B (Q31–Q40, MSQ)**: Each carries **+2 marks**. **No negative marking**. One or more options may be correct; full marks only if *all* correct options are selected; no partial credit.
- **Section C (Q41–Q60, NAT)**: Q41–Q50 carry **+1 mark**; Q51–Q60 carry **+2 marks**. **No negative marking**. Enter the numerical answer using the virtual keypad.
- **No calculators, log tables, or electronic devices**. A virtual scientific calculator is provided in the CBT interface.

Section A — Multiple Choice Questions (MCQ)

Q1–Q10: 1 mark each ($-\frac{1}{3}$ for wrong). Choose the **single** correct option.

Q1. Which of the following best describes **facilitated diffusion**?

- (A) Primary active transport using direct ATP hydrolysis
- (B) Secondary active transport driven by an established ion gradient
- (C) Movement of solutes down their concentration gradient through specific transport proteins, with no energy input required
- (D) Uptake of large extracellular molecules by membrane vesicle formation (endocytosis)

Q2. HIV (Human Immunodeficiency Virus) belongs to the viral family:

- (A) Paramyxoviridae
- (B) Retroviridae
- (C) Orthomyxoviridae
- (D) Adenoviridae

Q3. Genetic drift is best described as:

- (A) Random changes in allele frequencies due to chance events, especially pronounced in small populations
- (B) Directed changes in allele frequencies caused by differential reproductive success (natural selection)
- (C) Movement of alleles between populations through migration (gene flow)
- (D) Heritable changes in DNA sequence caused by mutagens or replication errors

Q4. Which enzyme catalyses the *first* committed step of glycolysis by phosphorylating glucose to glucose-6-phosphate?

- (A) Phosphofructokinase-1 (PFK-1)
- (B) Aldolase
- (C) Glucose-6-phosphatase
- (D) Hexokinase

Q5. Proteins targeted for degradation by the **26S proteasome** are covalently tagged with multiple copies of which small protein?

- (A) Phosphate groups added by protein kinases
- (B) Methyl groups added by methyltransferases
- (C) Polyubiquitin chains (multiple ubiquitin molecules)
- (D) SUMO (Small Ubiquitin-related Modifier)

Q6. In transamination reactions, the amino group of an amino acid is transferred to:

- (A) Pyruvate exclusively (forming alanine)
- (B) An α -keto acid (most commonly α -ketoglutarate, forming glutamate)
- (C) ATP, forming AMP and pyrophosphate
- (D) NAD^+ , forming NADH

Q7. The competitive exclusion principle (Gause's law) states that:

- (A) Two species competing for a completely identical ecological niche cannot coexist stably; one will be competitively excluded



- (B) Competition always leads inevitably to the extinction of the weaker competitor
- (C) Co-evolution always reduces competition between interacting species over time
- (D) Competitive species invariably have higher intrinsic birth rates than non-competitive species

Q8. During the **denaturation** step of a standard PCR thermal cycle, the reaction mixture is heated to approximately:

- (A) 37°C
- (B) 55–65°C
- (C) 72°C
- (D) 94–98°C

Q9. Peroxisomes play a key role in detoxifying hydrogen peroxide (H_2O_2) because they contain the enzyme:

- (A) ATP synthase (Complex V), which drives oxidative phosphorylation
- (B) Steroidogenic enzymes responsible for steroid hormone synthesis
- (C) Catalase, which converts H_2O_2 to water and molecular oxygen
- (D) Ryanodine receptors that store and release Ca^{2+} for signalling

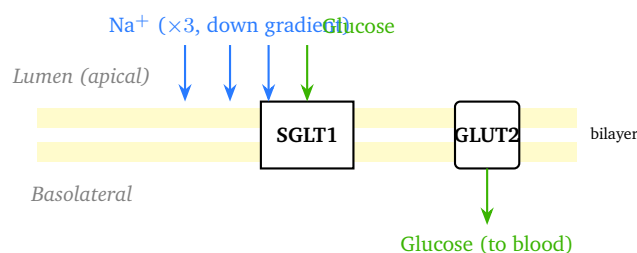
Q10. In the **glucose-alanine cycle**, which amino acid serves as the primary carrier of amino-nitrogen from skeletal muscle to the liver for disposal?

- (A) Glycine
- (B) Alanine
- (C) Glutamate
- (D) Arginine

Q11–Q30: 2 marks each ($-\frac{2}{3}$ for wrong). Choose the **single** correct option.

Q11. The intestinal Na^+ -glucose co-transporter (SGLT1) mediates glucose absorption across the apical membrane of enterocytes by:





- (A) Secondary active transport driven by the inward Na^+ electrochemical gradient maintained by Na^+/K^+ -ATPase
- (B) Passive facilitated diffusion requiring no ion gradient or energy
- (C) Primary active transport using direct ATP hydrolysis by SGLT1
- (D) Uniport mechanism transporting only glucose across the membrane

Q12. Lysogeny in bacteriophage λ (lambda) is **maintained** when:

- (A) Cro protein accumulates and represses both the P_L and P_R promoters
- (B) Integration host factor (IHF) is absent from the bacterial cell
- (C) RecA-mediated cleavage of CI repressor occurs in response to DNA damage (SOS induction)
- (D) CI repressor is bound at O_{R1} and O_{R2} , repressing lytic genes while stimulating its own transcription via O_{R2}

Q13. A population bottleneck is defined as:

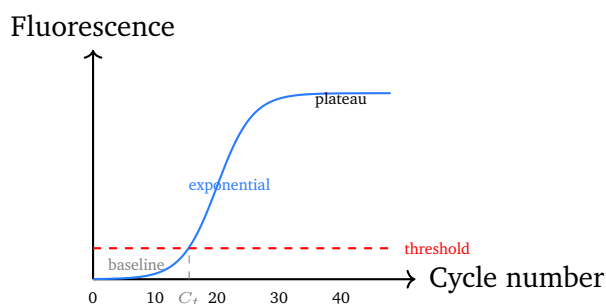
- (A) A large founding population colonising a new, previously unoccupied habitat
- (B) Two related species interbreeding to produce viable hybrid offspring
- (C) A drastic and sudden reduction in population size that substantially reduces genetic diversity
- (D) An elevated mutation rate caused by environmental genotoxic agents

Q14. In the **urea cycle**, which enzyme catalyses the hydrolysis of arginine to yield ornithine and **urea** in the hepatic cytosol?

- (A) Arginase II (the mitochondrial isoform, involved in different metabolic contexts)
- (B) Arginase I (the cytosolic liver isoform, the terminal enzyme of the urea cycle)

- (C) Carbamoyl phosphate synthetase I (CPS-I, the first step of the urea cycle)
- (D) Ornithine transcarbamylase (OTC, an inner mitochondrial membrane enzyme)

Q15. SYBR Green is used as a fluorescent reporter in quantitative real-time PCR (qPCR). Which statement correctly describes its mechanism?



- (A) It intercalates into double-stranded DNA and emits fluorescence proportional to the amount of dsDNA synthesised
 - (B) It binds to single-stranded DNA templates and fluoresces only when free in solution
 - (C) It inhibits primer-dimer formation, thereby increasing assay specificity
 - (D) It is covalently linked to sequence-specific primers and fluoresces only after primer extension
- Q16.** Protein kinase C (PKC) is activated by which combination of second messengers?
- (A) Cyclic AMP (cAMP) and the transcription factor CREB
 - (B) Inositol-1,4,5-trisphosphate (IP₃) acting directly on PKC
 - (C) Cyclic GMP (cGMP) acting through protein kinase G (PKG)
 - (D) Diacylglycerol (DAG) together with elevated cytosolic Ca²⁺
- Q17.** Which family of transcription factors specifies **anterior-to-posterior body axis identity** along the main body axis in animals?
- (A) Wnt signalling pathway transcriptional effectors (β -catenin/TCF)
 - (B) Notch–Delta pathway target genes



- (C) Hox genes (homeodomain-containing transcription factors)
 (D) Sonic Hedgehog (Shh) pathway effectors (Gli proteins)

Q18. In the Lotka–Volterra predator–prey model, when the prey population increases substantially, what happens to the predator population?

- (A) It decreases due to intensified intraspecific competition for territory
 (B) It subsequently increases, as greater food availability supports higher predator reproduction
 (C) It remains constant at its intrinsic carrying capacity, independent of prey density
 (D) It immediately doubles within the same generation time as the prey

Q19. The **committed step** of fatty acid biosynthesis is the carboxylation reaction catalysed by **acetyl-CoA carboxylase (ACC)**, which produces:



- (A) Malonyl-CoA from acetyl-CoA and CO_2 , requiring ATP hydrolysis (biotin cofactor)
 (B) Acetyl-CoA from malonyl-CoA by decarboxylation during chain elongation
 (C) Palmitoyl-CoA directly from eight acetyl-CoA molecules in a single step
 (D) NADPH from NADP^+ using isocitrate dehydrogenase for reductive biosynthesis

Q20. The inverse of the matrix $A = \begin{pmatrix} 3 & 1 \\ 5 & 2 \end{pmatrix}$ is:

- (A) $\begin{pmatrix} 2 & 1 \\ 5 & 3 \end{pmatrix}$
 (B) $\begin{pmatrix} -2 & 1 \\ 5 & -3 \end{pmatrix}$



(C) $\begin{pmatrix} 2 & -1 \\ 5 & 3 \end{pmatrix}$

(D) $\begin{pmatrix} 2 & -1 \\ -5 & 3 \end{pmatrix}$

Q21. For efficient expression of a recombinant protein in *E. coli*, an expression vector must contain:

- (A) A centromere sequence to ensure plasmid segregation in mammalian dividing cells
- (B) Splice-donor and splice-acceptor sequences flanking the coding insert
- (C) A strong prokaryotic promoter (such as T7 or tac) and a Shine–Dalgarno ribosome-binding sequence
- (D) A nuclear localisation signal (NLS) peptide sequence for nuclear import

Q22. The **classical pathway** of complement activation is initiated by:

- (A) Mannose-binding lectin (MBL) recognising microbial surface carbohydrate patterns
- (B) Antigen–antibody immune complexes (IgG or IgM) binding and activating C1q
- (C) Spontaneous low-level hydrolysis of C3 in plasma (tick-over)
- (D) Toll-like receptor (TLR) signalling cascades in innate immune cells

Q23. Newly synthesised secretory proteins and integral membrane proteins are targeted cotranslationally to the **endoplasmic reticulum** (ER) by:

- (A) An N-terminal signal peptide that is recognised by the Signal Recognition Particle (SRP) and directs the ribosome to the ER membrane
- (B) A C-terminal KDEL tetrapeptide retention signal that retrieves escaped ER-resident proteins from the Golgi
- (C) A glycosylphosphatidylinositol (GPI) lipid anchor that is added to the protein in the ER lumen
- (D) A SNARE protein domain that mediates vesicle docking and membrane fusion at the ER



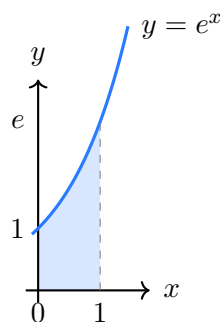
Q24. Epistasis in genetics refers to a situation in which:

- (A) A point mutation alters the coding sequence of a structural gene
- (B) Two alleles at the *same* locus interact through dominance and recessiveness
- (C) The physical chromosomal position of a gene as determined by linkage mapping
- (D) One gene at a given locus masks or modifies the phenotypic expression of a gene at a *different* locus

Q25. The first stage of **primary ecological succession** on barren, lifeless rock (for example after glacial retreat) involves:

- (A) Immediate establishment of the climax community without earlier colonisation stages
- (B) Pioneer species such as lichens and mosses colonising bare substrate and initiating soil formation
- (C) Fire-adapted plant communities replacing existing forest after a disturbance
- (D) Competitive invasion by new tree species into an already-established mature forest

Q26. The value of $\int_0^1 e^x dx$ is:

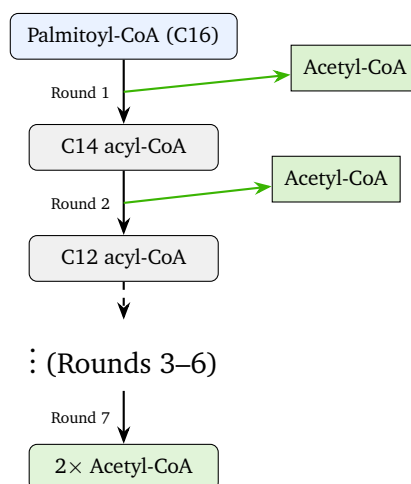


- (A) 1
- (B) e
- (C) $e - 1$
- (D) $e + 1$



- Q27.** In vertebrates, cytosine methylation (an epigenetic mark associated with gene silencing and chromatin compaction) occurs primarily at:
- (A) Any cytosine residue regardless of the surrounding sequence context
 - (B) GGC trinucleotide sequences at specific genomic regions
 - (C) TATA box elements located in the core promoters of active genes
 - (D) CpG dinucleotides (5'-C-G-3' sequence context)
- Q28.** The BLAST (Basic Local Alignment Search Tool) algorithm is primarily used in bioinformatics to:
- (A) Identify regions of sequence similarity between a query sequence and sequences in a database
 - (B) Predict the three-dimensional folded structure of a protein from its primary amino acid sequence
 - (C) Simulate the molecular dynamics trajectories of protein folding in silico
 - (D) Determine the GC content and codon usage bias of a gene sequence
- Q29.** The carbon skeletons of **glutamate** and **glutamine** enter the TCA cycle as:
- (A) Fumarate and acetoacetate (produced by Phe and Tyr catabolism)
 - (B) Succinyl-CoA (produced by Thr, Met and Val catabolism)
 - (C) α -Ketoglutarate (via glutamate dehydrogenase or aminotransferases)
 - (D) Acetyl-CoA (produced by Lys and Leu catabolism)
- Q30.** Palmitoyl-CoA (a C16 saturated fatty acyl-CoA) undergoes β -oxidation in the mitochondrial matrix. The **number of β -oxidation cycles** required to completely convert palmitoyl-CoA to acetyl-CoA units is:



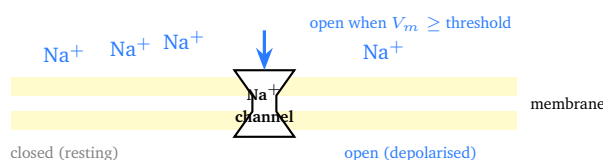


- (A) 6
- (B) 7
- (C) 8
- (D) 9

Section B — Multiple Select Questions (MSQ)

Q31–Q40: 2 marks each. **No negative marking.** One or more options may be correct. Full marks only if all correct options are selected.

Q31. Which of the following statements about **voltage-gated ion channels** are correct?



- (A) They open in response to changes in membrane potential (depolarisation)
- (B) They use ATP hydrolysis to maintain electrochemical gradients across membranes
- (C) Voltage-gated Na⁺ channels are responsible for the rapid rising phase of the action potential
- (D) They are permanently open pores that allow continuous ion flow regardless of membrane potential

Q32. Which of the following roles does the **liver** play in amino acid metabolism?



- (A) It is the primary site of the urea cycle, converting toxic ammonia to urea for urinary excretion
- (B) It is a major site of gluconeogenesis, utilising carbon skeletons derived from amino acids
- (C) It stores excess dietary amino acids directly as glycogen granules
- (D) It performs extensive transamination reactions to interconvert amino acid pools

Q33. Which of the following RNA species are transcribed by **RNA Polymerase III** in eukaryotes?

- (A) 5S ribosomal RNA (5S rRNA)
- (B) Transfer RNA (tRNA)
- (C) Messenger RNA (mRNA)
- (D) U6 small nuclear RNA (U6 snRNA)

Q34. Which of the following statements about the **CRISPR-Cas9** system for genome editing are correct?

- (A) Cas9 nuclease is guided to its target DNA sequence by a single guide RNA (sgRNA) containing a spacer complementary to the target
- (B) Cas9 creates a precise double-strand break (DSB) at the target site in the DNA
- (C) CRISPR-Cas9 functions exclusively in eukaryotic cells and cannot edit prokaryotic genomes
- (D) The PAM sequence (e.g., 5'-NGG-3' for *S. pyogenes* Cas9) is encoded within the sgRNA sequence itself

Q35. Which of the following correctly describe the **mitochondrial genome** (mtDNA) of most animals?

- (A) It is a closed circular double-stranded DNA molecule (typically 16–17 kb in mammals)
- (B) Its protein-coding genes contain numerous introns, similar to nuclear genes
- (C) It is maternally inherited in most animal species



- (D) It encodes all proteins required for mitochondrial function including those imported from the cytoplasm

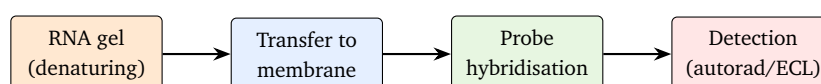
Q36. Which of the following mechanisms contribute to β -lactam antibiotic resistance in bacteria?

- (A) Production of β -lactamase enzymes that hydrolyse the β -lactam ring, inactivating the antibiotic
- (B) Mutation or acquisition of altered penicillin-binding proteins (PBPs) with reduced drug affinity
- (C) Increased outer membrane permeability, allowing greater antibiotic uptake
- (D) Active efflux of the antibiotic out of the cell via membrane-associated efflux pump systems

Q37. Which of the following correctly describe functions of **molecular chaperone proteins** (e.g., Hsp70, Hsp90)?

- (A) They prevent the aberrant aggregation of misfolded or partially folded polypeptide chains
- (B) They catalyse the formation of disulfide bonds between cysteine residues in secretory proteins
- (C) They assist newly synthesised polypeptides in achieving their correct three-dimensional native fold
- (D) Their intrinsic ATPase activity drives repeated cycles of substrate polypeptide binding and release

Q38. Which of the following steps are part of a standard **Northern blot** procedure for detecting specific RNA sequences?

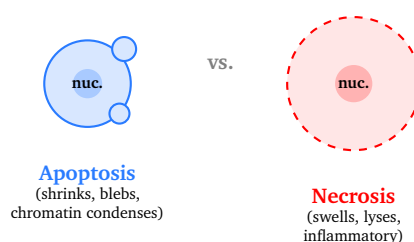


- (A) RNA samples are separated by gel electrophoresis under denaturing conditions (e.g., formaldehyde gels)
- (B) RNA is transferred from the gel to a nitrocellulose or nylon membrane by capillary or electroblotting



- (C) A labelled DNA or RNA probe is hybridised to the membrane to detect specific RNA bands
- (D) RNA is first digested with restriction endonucleases before electrophoresis to generate specific fragments

Q39. Which of the following features are characteristic of **apoptosis** (regulated/programmed cell death)?



- (A) Cell shrinkage and plasma membrane blebbing (outward protrusions)
- (B) Release of intracellular contents into surrounding tissue, triggering an inflammatory response
- (C) Chromatin condensation and nuclear fragmentation (karyorrhexis)
- (D) Formation of membrane-bound apoptotic bodies that are recognised and engulfed by phagocytes

Q40. Which of the following **enzyme–substrate** pairings are *correct*?

- (A) Amylase — starch (hydrolyses α -1,4-glycosidic bonds in polysaccharides)
- (B) Lipase — proteins (cleaves peptide bonds in polypeptide chains)
- (C) Lysozyme — peptidoglycan (cleaves β -1,4-glycosidic bonds in bacterial cell walls, releasing NAG-NAM fragments)
- (D) Proteases — peptide bonds (catalyse the hydrolysis of peptide bonds in polypeptides and proteins)

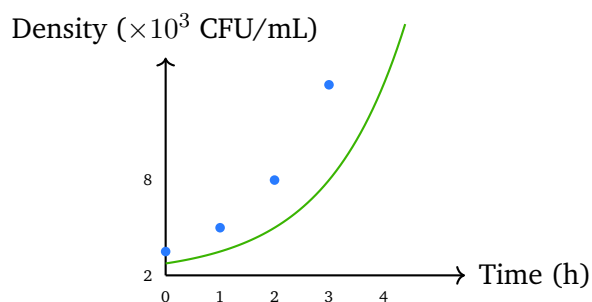
Section C — Numerical Answer Type (NAT)

Q41–Q50: 1 mark each. No negative marking.

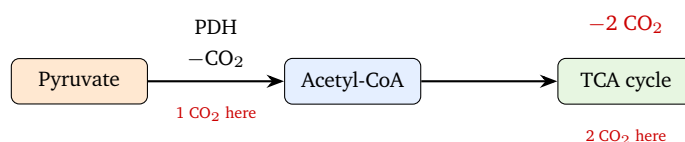
Q41. A bacterial culture has an initial density of 2×10^3 CFU/mL. The doubling time is **60 min**. The cell density (in units of $\times 10^3$ CFU/mL) after exactly **4 hours** is:



32



- Q42.** How many **peptide bonds** are present in a polypeptide chain consisting of **100 amino acid** residues?
- Q43.** A double-stranded DNA fragment contains **25% Adenine (A)** bases. The total **G+C content** (percentage of G and C residues combined) of this fragment is:
- Q44.** The number of codons in the standard genetic code that specify the amino acid **Serine** is:
- Q45.** In a randomly mating population, the frequency of allele $B = 0.6$ and allele $b = 0.4$. Under Hardy–Weinberg equilibrium, the expected frequency of **heterozygotes (Bb)** is:
- Q46.** The number of **CO₂ molecules** released when **one molecule of pyruvate** is completely oxidised via the pyruvate dehydrogenase (PDH) reaction followed by one complete turn of the TCA cycle is:



- Q47.** In one complete turn of the TCA cycle, the number of **GTP molecules** produced by substrate-level phosphorylation (via the succinyl-CoA synthetase reaction) is:
- Q48.** A radioactive isotope has a **half-life of 8 days**. Starting with **320 units** of radioactivity, the activity remaining after **32 days** is:

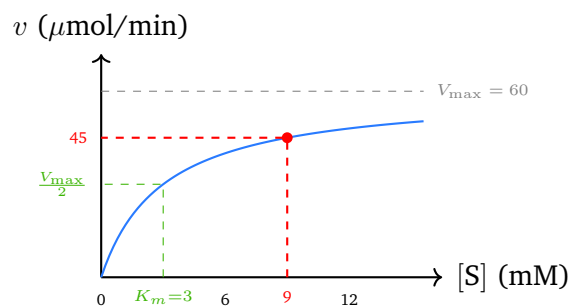


Q49. Given $pK_a = 2.14$ for phosphoric acid (H_3PO_4), at a **pH of 2.14**, the ratio $\frac{[H_2PO_4^-]}{[H_3PO_4]}$ is:

Q50. A circular plasmid is cut with restriction enzyme **A**, generating **2 fragments**. The same plasmid is cut with enzyme **B**, generating **3 fragments**. When both enzymes are used simultaneously (no overlapping recognition sites), the **maximum number of fragments** generated is:

Q51–Q60: 2 marks each. No negative marking.

Q51. An enzyme has $K_m = 3 \text{ mM}$ and $V_{\max} = 60 \mu\text{mol/min}$. The initial velocity v (in $\mu\text{mol/min}$) at a substrate concentration $[S] = 9 \text{ mM}$ is:

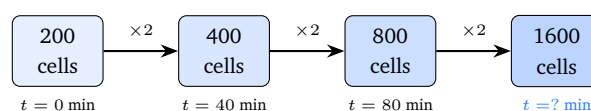


Q52. In a **dihybrid testcross** ($AaBb \times aabb$), the expected number of offspring showing **at least one dominant phenotype** (i.e., having at least one functional A or B allele) out of **200 total offspring** is:

Q53. The value of $\int_0^{\pi/2} \cos x \, dx$ is:

Q54. The mean of 5 numbers is 10. If the sum of 4 of them is 38, the **fifth number** is:

Q55. A microbial culture grows from **200 cells** to **1600 cells** by successive doublings. If each doubling takes **40 minutes**, the total elapsed time (in minutes) for this growth is:



- Q56.** The value of $\int_1^4 (2x - 1) dx$ is:
- Q57.** In a co-dominant genetic system, the genotype frequencies in a population are: $A^1A^1 = 0.36$, $A^1A^2 = 0.48$, $A^2A^2 = 0.16$. The frequency of allele A^1 (to 2 decimal places) is:
- Q58.** A crude enzyme extract has a total activity of **500 U** and total protein of **100 mg** (specific activity = 5 U/mg). After purification, the fraction has total activity = **250 U** and total protein = **5 mg**. The **fold purification** achieved is:
- Q59.** A linear double-stranded DNA molecule is **850 nm** long. Given that each base pair spans **0.34 nm** along the helix axis, the number of **base pairs** in this molecule is:
- Q60.** In a standard **dihybrid cross** ($AaBb \times AaBb$), **320 offspring** are expected. The number of offspring showing the **dominant phenotype for both traits** (the 9/16 phenotypic class) is:



Answer Key — IIT JAM Biotechnology Sample Paper 3

Section A — MCQ (Q1–Q30)

Q	Ans	Q	Ans	Q	Ans	Q	Ans	Q	Ans
1	C	2	B	3	A	4	D	5	C
6	B	7	A	8	D	9	C	10	B
11	A	12	D	13	C	14	B	15	A
16	D	17	C	18	B	19	A	20	D
21	C	22	B	23	A	24	D	25	B
26	C	27	D	28	A	29	C	30	B

Section B — MSQ (Q31–Q40)

Q	Correct options	Q	Correct options
31	(A) and (C)	36	(A), (B) and (D)
32	(A), (B) and (D)	37	(A), (C) and (D)
33	(A), (B) and (D)	38	(A), (B) and (C)
34	(A) and (B)	39	(A), (C) and (D)
35	(A) and (C)	40	(A), (C) and (D)

Section C — NAT (Q41–Q60)

Q	Answer	Q	Answer	Q	Answer	Q	Answer
41	32	46	3	51	45	56	12
42	99	47	1	52	150	57	0.60
43	50	48	20	53	1	58	10
44	6	49	1	54	12	59	2500
45	0.48	50	5	55	120	60	180

Detailed Solutions

SECTION A — MCQ

Q1. Answer: (C)

Solution

Facilitated diffusion moves solutes *down* their concentration gradient through specific carrier proteins or channels. It requires no ATP or ion gradient — it is thermodynamically spontaneous but still requires a specific transport protein. (C)

Q2. Answer: (B)

Solution

HIV is a lentivirus, a genus within the family **Retroviridae**. Retroviruses carry a positive-sense ssRNA genome and use reverse transcriptase to produce a dsDNA intermediate that integrates into the host genome. (B)

Q3. Answer: (A)

Solution

Genetic drift refers to random, stochastic fluctuations in allele frequencies caused by chance sampling events rather than natural selection. Its effect is most pronounced in small populations, where chance deviations from expected ratios are proportionally larger. (A)

Q4. Answer: (D)

Solution

Hexokinase (and glucokinase in the liver) phosphorylates glucose to glucose-6-phosphate using one ATP. This is the first committed step of glycolysis — glucose-6-phosphate cannot freely cross the plasma membrane and is therefore trapped inside the cell. (D)

Q5. Answer: (C)

Solution

The 26S proteasome degrades proteins tagged with polyubiquitin chains. Ubiquitin is a 76-amino acid protein that is covalently attached to lysine residues of target proteins by a cascade of E1, E2, and E3 enzymes. Multiple ubiquitin molecules form an isopeptide-linked chain that signals proteasomal degradation. (C)



Q6. Answer: (B)

Solution

In transamination, the amino group of an amino acid is transferred to an α -keto acid. The most common acceptor is α -ketoglutarate (α -KG), which is converted to glutamate while the donor amino acid becomes its corresponding α -keto acid. The reaction is catalysed by aminotransferases using PLP (pyridoxal phosphate) as a cofactor. (B)

Q7. Answer: (A)

Solution

Gause's competitive exclusion principle states that two species occupying the *identical* ecological niche (using the same resources in the same way) cannot coexist indefinitely in stable equilibrium. One species will outcompete the other, leading to exclusion. Coexistence requires niche differentiation. (A)

Q8. Answer: (D)

Solution

The denaturation step of PCR requires heating to 94–98°C to break hydrogen bonds between the two DNA strands, producing single-stranded templates for primer annealing. Lower temperatures are insufficient to fully denature double-stranded DNA templates. (D)

Q9. Answer: (C)

Solution

Peroxisomes contain high concentrations of **catalase**, which catalyses the reaction: $2\text{H}_2\text{O}_2 \rightarrow 2\text{H}_2\text{O} + \text{O}_2$. Peroxisomes are the primary organelle for H_2O_2 detoxification; H_2O_2 is generated as a byproduct of many oxidative reactions (e.g., fatty acid β -oxidation in peroxisomes, amino acid oxidase reactions). (C)

Q10. Answer: (B)

Solution

In the glucose-alanine cycle, muscle cells transaminate pyruvate with glutamate to produce **alanine** (via alanine aminotransferase, ALT). Alanine is exported to the blood, taken up by the liver, and transaminated back to pyruvate, which enters gluconeogenesis. The amino group is disposed of via the urea cycle. (B)



Q11. Answer: (A)

Solution

SGLT1 is a **secondary active transporter** (symporter). It co-transport 2–3 Na^+ ions down their electrochemical gradient alongside one glucose molecule against its concentration gradient. The Na^+ gradient is generated and maintained by the basolateral Na^+/K^+ -ATPase (primary active transport). SGLT1 itself hydrolyses no ATP directly. (A)

Q12. Answer: (D)

Solution

Lysogeny in phage λ is *maintained* by the CI repressor protein binding at operator sites O_{R1} and O_{R2} . This represses transcription from P_R and P_L (preventing lytic gene expression) while CI binding at O_{R2} also activates CI's own synthesis from P_{RM} , creating a positive-feedback loop that stabilises the lysogenic state. (D)

Q13. Answer: (C)

Solution

A population bottleneck is a drastic, sudden reduction in population size (e.g., due to a catastrophic event). Because only a small subset of individuals survive, much of the original genetic diversity is lost by random sampling. The surviving population has reduced heterozygosity and allelic richness compared to the original population. (C)

Q14. Answer: (B)

Solution

Arginase I (the cytosolic isoform expressed at high levels in hepatocytes) is the terminal enzyme of the urea cycle. It hydrolyses arginine to ornithine + urea: $\text{Arginine} + \text{H}_2\text{O} \rightarrow \text{Ornithine} + \text{Urea}$. Ornithine is recycled back into the mitochondrion to continue the cycle. (B)

Q15. Answer: (A)

Solution

SYBR Green I is a cyanine dye that intercalates into the minor groove of double-stranded DNA. When intercalated, its fluorescence increases approximately 1000-fold compared to the free dye in solution. Fluorescence therefore increases pro-



portionally with the amount of dsDNA synthesised during each PCR cycle, allowing quantification. (A)

Q16. Answer: (D)

Solution

Protein kinase C (PKC) is activated by two second messengers generated downstream of phospholipase C (PLC): **diacylglycerol (DAG)**, which recruits PKC to the membrane, and elevated cytosolic Ca^{2+} (released from the ER by IP_3), which is required for the conformational activation of classical PKC isoforms. IP_3 acts on the ER Ca^{2+} channel, not directly on PKC. (D)

Q17. Answer: (C)

Solution

Hox genes encode homeodomain-containing transcription factors that specify segment/positional identity along the anterior-to-posterior body axis in animals. They are conserved across bilaterians and expressed in overlapping domains with an anterior boundary that reflects their chromosomal order (colinearity). Mutations cause homeotic transformations (e.g., Antennapedia in *Drosophila*). (C)

Q18. Answer: (B)

Solution

In the Lotka-Volterra predator-prey model, an increase in prey abundance provides more food for predators, increasing predator reproduction and survival. The predator population therefore grows in response, with a characteristic time lag. This produces the classic oscillating population cycles seen in systems such as the Canadian lynx and snowshoe hare. (B)

Q19. Answer: (A)

Solution

Acetyl-CoA carboxylase (ACC) catalyses: $\text{Acetyl-CoA} + \text{HCO}_3^- + \text{ATP} \rightarrow \text{Malonyl-CoA} + \text{ADP} + \text{P}_i$. ACC uses a biotin prosthetic group to carry and transfer the carboxyl group. Malonyl-CoA is the two-carbon donor in all elongation steps of fatty acid synthesis and is the committed intermediate of de novo fatty acid biosynthesis. (A)

Q20. Answer: (D)



Solution

For $A = \begin{pmatrix} 3 & 1 \\ 5 & 2 \end{pmatrix}$: $\det(A) = (3)(2) - (1)(5) = 6 - 5 = 1$. Since $\det(A) = 1$,
 $A^{-1} = \frac{1}{1} \begin{pmatrix} 2 & -1 \\ -5 & 3 \end{pmatrix} = \begin{pmatrix} 2 & -1 \\ -5 & 3 \end{pmatrix}$. (D)

Q21. Answer: (C)

Solution

For recombinant protein expression in *E. coli*, the vector must contain: (1) a strong **prokaryotic promoter** (e.g., T7, tac, lac) to drive high-level transcription, (2) a **Shine-Dalgarno (ribosome-binding) sequence** upstream of the ATG start codon for efficient prokaryotic translation initiation, (3) a multiple cloning site, (4) a selectable marker, and (5) an origin of replication. Splice sites and centromeres are eukaryotic features irrelevant to bacterial expression. (C)

Q22. Answer: (B)

Solution

The **classical complement pathway** is initiated when C1q binds to the Fc regions of IgG or IgM antibodies in antigen-antibody immune complexes. This activates C1r and C1s serine proteases, which then cleave C4 and C2 to form the classical pathway C3 convertase (C4b2a). The lectin pathway uses MBL; the alternative pathway uses spontaneous C3 hydrolysis. (B)

Q23. Answer: (A)

Solution

Co-translational targeting to the ER is directed by the **N-terminal signal peptide** of the nascent polypeptide. As the signal peptide emerges from the ribosome, the **Signal Recognition Particle (SRP)** recognises and binds it, pausing translation. The SRP-ribosome complex then docks with the SRP receptor on the ER membrane, and translation resumes with the polypeptide threaded into the translocon (Sec61 channel). (A)

Q24. Answer: (D)



Solution

Epistasis describes a gene interaction where an allele (or alleles) at one locus *masks or modifies* the phenotypic expression of alleles at a *different, non-allelic locus*. This is distinct from dominance (interaction between alleles at the *same locus*). Examples include the Bombay phenotype (H gene is epistatic to the ABO blood group locus) and coat colour in Labrador retrievers. **(D)**

Q25. **Answer: (B)****Solution**

Primary succession on bare rock (e.g., after glacial retreat or volcanic lava solidification) begins when **pioneer species**, primarily lichens and mosses, colonise the substrate. Lichens (fungal-algal/cyanobacterial symbioses) secrete acids that physically and chemically weather rock, initiating soil formation. Organic matter accumulates, allowing subsequent colonisation by herbaceous plants, shrubs, and eventually trees. **(B)**

Q26. **Answer: (C)****Solution**

$$\int_0^1 e^x dx = [e^x]_0^1 = e^1 - e^0 = e - 1 \approx 1.718. \text{ (C)}$$

Q27. **Answer: (D)****Solution**

In vertebrates, DNA methylation occurs predominantly at cytosine residues within **CpG dinucleotides** (5'-CG-3'), producing 5-methylcytosine (5mC). This is carried out by DNA methyltransferases (DNMT1, DNMT3a, DNMT3b). Methylation at CpG islands in promoter regions is associated with transcriptional silencing, heterochromatin formation, and genomic imprinting. **(D)**

Q28. **Answer: (A)****Solution**

BLAST (Basic Local Alignment Search Tool) uses a heuristic algorithm to **identify regions of local sequence similarity** between a query sequence (nucleotide or protein) and sequences in a database. It reports alignments with statistical significance scores (E-values). It does not predict 3D structure (that is AlphaFold/Rosetta) or run molecular dynamics simulations. **(A)**



Q29. Answer: (C)

Solution

Glutamate undergoes oxidative deamination by glutamate dehydrogenase (GDH) to yield α -ketoglutarate (α -KG) + NH_4^+ . Glutamine is first hydrolysed by glutaminase to glutamate + NH_4^+ , and the glutamate is then converted to α -KG. Thus α -KG is the TCA cycle entry point for both amino acids, entering at the α -ketoglutarate step. (C)

Q30. Answer: (B)

Solution

Palmitoyl-CoA is a C16 acyl-CoA. Each round of β -oxidation removes one 2-carbon acetyl-CoA unit. Starting from C16: $\text{C16} \xrightarrow{\times 7} 8 \times \text{Acetyl-CoA}$. The last round produces 2 acetyl-CoA simultaneously from the C4 intermediate. Number of cycles $= \frac{16}{2} - 1 = 7$. (B)

SECTION B — MSQ

Q31. Answer: (A,C)

Solution

(A) **Correct:** Voltage-gated channels open in response to depolarisation (change in membrane potential). (B) **Wrong:** Voltage-gated channels are passive pores; they do NOT hydrolyse ATP — that is the function of ion pumps (e.g., Na^+/K^+ -ATPase). (C) **Correct:** Voltage-gated Na^+ channels open rapidly upon depolarisation, allowing Na^+ influx that drives the rising phase of the action potential. (D) **Wrong:** These channels are gated (not permanently open); they cycle between closed, open, and inactivated states depending on membrane potential. **Correct: (A) and (C)**

Q32. Answer: (A,B,D)

Solution

(A) **Correct:** The liver is the primary (and essentially exclusive) site of the urea cycle, converting toxic NH_4^+ to urea for renal excretion. (B) **Correct:** The liver is a major gluconeogenic organ, converting amino acid carbon skeletons (via pyruvate, oxaloacetate, α -KG etc.) to glucose during fasting. (C) **Wrong:** Amino acids are NOT stored as glycogen. Glycogen is a polymer of glucose. Excess amino acids are either oxidised for energy or converted to glucose/fatty acids/ketone bodies. (D) **Correct:** The liver has high activity of ALT, AST, and other aminotransferases for interconversion of amino acid pools and for gluconeogenic precursor production.



Correct: (A), (B) and (D)

Q33. Answer: (A,B,D)

Solution

(A) **Correct:** 5S rRNA is transcribed by RNA Pol III from an internal promoter within the 5S rRNA gene. (B) **Correct:** All tRNA genes are transcribed by RNA Pol III using internal promoter elements (A- and B-boxes). (C) **Wrong:** mRNA (pre-mRNA) is transcribed by **RNA Pol II**, not Pol III. (D) **Correct:** U6 snRNA (involved in the spliceosome) is transcribed by RNA Pol III, unlike U1, U2, U4, and U5 snRNAs which are transcribed by RNA Pol II. **Correct: (A), (B) and (D)**

Q34. Answer: (A,B)

Solution

(A) **Correct:** Cas9 is a programmable endonuclease guided to its genomic target by a **single guide RNA (sgRNA)**, which contains a ~20 nt spacer sequence complementary to the target DNA strand. (B) **Correct:** Cas9 (a bilobed protein with RuvC and HNH nuclease domains) creates a **blunt-ended double-strand break** 3 bp upstream of the PAM sequence. (C) **Wrong:** CRISPR-Cas9 systems are naturally found in **prokaryotes** (bacteria and archaea) as adaptive immune defence. The technology has been adapted for use in eukaryotes but it functions in both. (D) **Wrong:** The PAM sequence (e.g., 5'-NGG for *S. pyogenes* Cas9) is present in the **genomic target DNA**, not in the sgRNA. The sgRNA spacer is complementary to the non-PAM (protospacer) strand. **Correct: (A) and (B)**

Q35. Answer: (A,C)

Solution

(A) **Correct:** Animal mtDNA is a **closed circular double-stranded DNA** molecule; human mtDNA is 16,569 bp (≈ 16.6 kb). (B) **Wrong:** Animal mtDNA genes are **intron-free**; the genome is extremely compact, with little non-coding sequence. (C) **Correct:** mtDNA is **maternally inherited** in most animal species because mitochondria are contributed almost exclusively by the egg (oocyte) cytoplasm; paternal mitochondria from sperm are typically eliminated. (D) **Wrong:** mtDNA encodes only 13 proteins (all components of the oxidative phosphorylation machinery), 22 tRNAs, and 2 rRNAs. The vast majority (>1000) of mitochondrial proteins are encoded by nuclear genes, translated in the cytoplasm, and imported. **Correct: (A) and (C)**



Q36. Answer: (A,B,D)

Solution

(A) **Correct:** β -lactamase enzymes (e.g., TEM-1, CTX-M ESBLs) hydrolyse the β -lactam ring, opening it and inactivating the antibiotic before it can inhibit penicillin-binding proteins (PBPs). (B) **Correct:** Altered PBPs with reduced affinity for β -lactam antibiotics (e.g., PBP2a encoded by *mecA* in MRSA, PBP2x/2b mutations in *S. pneumoniae*) prevent drug binding while retaining transpeptidase function. (C) **Wrong:** DECREASED outer membrane permeability (via loss of porins such as OprD in *P. aeruginosa*) *increases* resistance by preventing antibiotic entry — increased permeability would increase susceptibility. (D) **Correct:** Active efflux pumps (e.g., AcrAB-TolC in *E. coli*, MexAB-OprM in *P. aeruginosa*) expel β -lactams from the periplasm/cytoplasm, reducing intracellular drug concentration. **Correct: (A), (B) and (D)**

Q37. Answer: (A,C,D)

Solution

(A) **Correct:** A key chaperone function is to bind exposed hydrophobic regions of unfolded or partially folded polypeptides, preventing aberrant intermolecular interactions that lead to **aggregation**. (B) **Wrong:** Disulfide bond formation is catalysed by **protein disulfide isomerase (PDI)** in the ER lumen — this is not a chaperone function. Hsp70/Hsp90 do not form or isomerise disulfide bonds. (C) **Correct:** Chaperones actively assist polypeptides in achieving their correct **native three-dimensional conformation**, both during translation (co-translational folding) and post-translationally. (D) **Correct:** Chaperones such as Hsp70 have an intrinsic **ATPase activity**. ATP hydrolysis drives conformational changes that regulate substrate binding (high-affinity ADP-bound state) and release (low-affinity ATP-bound state), allowing iterative folding cycles. **Correct: (A), (C) and (D)**

Q38. Answer: (A,B,C)

Solution

(A) **Correct:** RNA samples are separated by size using **denaturing gel electrophoresis** (commonly formaldehyde-agarose or glyoxal gels) to eliminate RNA secondary structure and ensure migration based on molecular weight. (B) **Correct:** After electrophoresis, RNA is **transferred** from the gel to a solid support membrane (nitrocellulose or positively-charged nylon) by capillary action (standard Northern) or electrophoretic transfer. RNA is then UV-crosslinked to the membrane. (C) **Correct:** The membrane is incubated with a **labelled probe** (radioactive ^{32}P , DIG-labelled, or biotinylated DNA/RNA oligonucleotide complementary to the



target RNA) which hybridises to specific RNA bands, detected by autoradiography or chemiluminescence. **(D) Wrong:** RNA is NOT cut with restriction endonucleases. Restriction enzymes cleave double-stranded DNA at specific recognition sequences; they do not act on RNA. **Correct: (A), (B) and (C)**

Q39. **Answer: (A,C,D)**

Solution

(A) Correct: Apoptotic cells undergo **cell shrinkage** (condensation of cytoplasm) and **plasma membrane blebbing** (formation of protrusions), in contrast to the swelling seen in necrosis. **(B) Wrong:** Release of intracellular contents causing inflammation is a hallmark of **necrosis** (accidental/passive cell death), not apoptosis. In apoptosis, the plasma membrane remains intact throughout, preventing leakage of pro-inflammatory cytoplasmic contents. **(C) Correct:** Activated caspases and CAD/DFF40 DNase cause **chromatin condensation** (pyknosis) and inter-nucleosomal DNA fragmentation, followed by nuclear fragmentation (**karyorrhexis**). **(D) Correct:** The cell breaks into membrane-enclosed **apoptotic bodies** containing intact organelles and nuclear fragments. These express “eat-me” signals (e.g., phosphatidylserine on the outer leaflet) and are rapidly recognised and engulfed by macrophages and neighbouring cells, preventing inflammation. **Correct: (A), (C) and (D)**

Q40. **Answer: (A,C,D)**

Solution

(A) Correct: Amylase (salivary α -amylase and pancreatic amylase) hydrolyses α -1,4-glycosidic bonds in **starch** (amylose and amylopectin), yielding maltose, maltotriose, and dextrans. **(B) Wrong:** **Lipase** acts on **lipids** (triacylglycerols), not proteins. The enzyme that cleaves peptide bonds in proteins is a protease. **(C) Correct:** Lysozyme (muramidase) cleaves the β -1,4 glycosidic bond between NAM and NAG in **bacterial cell-wall peptidoglycan**, causing lysis. This is why lysozyme is bactericidal and is found in tears, saliva, and mucus. **(D) Correct:** **Proteases** (serine proteases, cysteine proteases, metalloproteases, aspartic proteases) catalyse hydrolysis of **peptide bonds** in polypeptides and proteins. **Correct: (A), (C) and (D)**

SECTION C — NAT

Q41. **Answer: (32)**



Solution

4 hours = 240 min; number of doublings = $240 \text{ min} \div 60 \text{ min/doubling} = 4$. $N = N_0 \times 2^n = 2 \times 10^3 \times 2^4 = 2 \times 10^3 \times 16 = 32 \times 10^3 \text{ CFU/mL}$. Answer: **32** (in units of $\times 10^3 \text{ CFU/mL}$).

Q42. Answer: (99)

Solution

Each peptide bond is formed between consecutive amino acid residues. A chain of n amino acids contains $n - 1$ peptide bonds. For 100 residues: $100 - 1 = 99$ peptide bonds.

Q43. Answer: (50)

Solution

By Chargaff's rules, in dsDNA: $[A] = [T]$ and $[G] = [C]$. Given $A = 25\%$, then $T = 25\%$. Therefore $G + C = 100\% - 25\% - 25\% = 50\%$.

Q44. Answer: (6)

Solution

The six codons for serine (Ser, S) in the standard genetic code are: UCU, UCC, UCA, UCG (the UCN family) and AGU, AGC (the AGY family). Total = $4 + 2 = 6$ codons. Serine is one of the most degenerate amino acids, encoded by two separate codon families.

Q45. Answer: (0.48)

Solution

Under Hardy-Weinberg equilibrium, the frequency of heterozygotes (Bb) is $2pq$, where $p = \text{freq}(B) = 0.6$ and $q = \text{freq}(b) = 0.4$. $2pq = 2 \times 0.6 \times 0.4 = 0.48$.

Q46. Answer: (3)

Solution

PDH reaction: Pyruvate $\rightarrow$ Acetyl-CoA + 1 CO_2 (decarboxylation). **TCA cycle** (one turn with one acetyl-CoA): isocitrate dehydrogenase releases 1 CO_2 ; α -ketoglutarate dehydrogenase releases 1 CO_2 . Total = $1 + 1 + 1 = 3 \text{ CO}_2$ molecules per pyruvate.

Q47. Answer: (1)



Solution

In one turn of the TCA cycle, substrate-level phosphorylation occurs at the succinyl-CoA synthetase (succinate thiokinase) step: Succinyl-CoA + GDP + $P_i \rightarrow$ Succinate + GTP + CoA. This produces exactly **1 GTP** (or ATP, depending on the isoform) per turn.

Q48. **Answer: (20)**

Solution

Number of half-lives = 32 days $\div$ 8 days/half-life = 4. Remaining activity = $320 \times \left(\frac{1}{2}\right)^4 = 320 \times \frac{1}{16} = \mathbf{20}$ units.

Q49. **Answer: (1)**

Solution

Using the Henderson-Hasselbalch equation: $\text{pH} = \text{p}K_a + \log \frac{[A^-]}{[HA]}$. At $\text{pH} = \text{p}K_a$:
 $\text{p}K_a = \text{p}K_a + \log \frac{[\text{H}_2\text{PO}_4^-]}{[\text{H}_3\text{PO}_4]}$, so $\log \frac{[\text{H}_2\text{PO}_4^-]}{[\text{H}_3\text{PO}_4]} = 0$, hence $\frac{[\text{H}_2\text{PO}_4^-]}{[\text{H}_3\text{PO}_4]} = 10^0 = \mathbf{1}$.

Q50. **Answer: (5)**

Solution

Enzyme A makes 2 cuts in the circular plasmid $\Rightarrow$ 2 fragments. Enzyme B makes 3 cuts $\Rightarrow$ 3 fragments. When both are used simultaneously with no overlapping recognition sites, the total number of cuts = $2+3 = 5$. For a circular DNA molecule, n cuts produce exactly n fragments. Therefore, 5 cuts produce **5** fragments.

Q51. **Answer: (45)**

Solution

Michaelis-Menten equation: $v = \frac{V_{\max}[\text{S}]}{K_m + [\text{S}]} = \frac{60 \times 9}{3 + 9} = \frac{540}{12} = \mathbf{45} \mu\text{mol/min}$. Note:
 $[\text{S}] = 9 \text{ mM} = 3K_m$, so $v = \frac{3}{4}V_{\max} = \mathbf{45} \mu\text{mol/min}$.

Q52. **Answer: (150)**



Solution

Dihybrid testcross ($AaBb \times aabb$) produces four equally frequent classes: $AaBb : Aabb : aaBb : aabb = 1 : 1 : 1 : 1$. Offspring with *at least one dominant allele* include all classes *except* $aabb$ (double recessive). Probability (at least one dominant) = $1 - \frac{1}{4} = \frac{3}{4}$. Expected number = $200 \times \frac{3}{4} = 150$.

Q53. **Answer: (1)****Solution**

$$\int_0^{\pi/2} \cos x \, dx = [\sin x]_0^{\pi/2} = \sin\left(\frac{\pi}{2}\right) - \sin(0) = 1 - 0 = 1.$$

Q54. **Answer: (12)****Solution**

Mean of 5 numbers = 10 $\Rightarrow$ total sum = $5 \times 10 = 50$. Sum of 4 known numbers = 38. Fifth number = $50 - 38 = 12$.

Q55. **Answer: (120)****Solution**

$200 \xrightarrow{\times 2} 400 \xrightarrow{\times 2} 800 \xrightarrow{\times 2} 1600$: this requires **3 doublings**. Time = $3 \times 40 \text{ min} = 120$ minutes.

Q56. **Answer: (12)****Solution**

$$\int_1^4 (2x - 1) \, dx = [x^2 - x]_1^4 = (16 - 4) - (1 - 1) = 12 - 0 = 12.$$

Q57. **Answer: (0.60)****Solution**

For a co-dominant system, each allele is counted directly from genotype frequencies. $\text{freq}(A^1) = [\text{freq}(A^1A^1)] + \frac{1}{2}[\text{freq}(A^1A^2)] = 0.36 + \frac{1}{2}(0.48) = 0.36 + 0.24 = 0.60$. (Check: $\text{freq}(A^2) = 0.16 + 0.24 = 0.40$; total = $0.60 + 0.40 = 1.00$. ✓)

Q58. **Answer: (10)**

Solution

Specific activity (crude extract) = $\frac{500 \text{ U}}{100 \text{ mg}} = 5 \text{ U/mg}$. Specific activity (purified fraction) = $\frac{250 \text{ U}}{5 \text{ mg}} = 50 \text{ U/mg}$. Fold purification = $\frac{50 \text{ U/mg}}{5 \text{ U/mg}} = 10\text{-fold}$.

Q59. **Answer: (2500)**

Solution

In B-form DNA, the axial rise per base pair is 0.34 nm. Number of bp = $\frac{\text{length}}{\text{rise per bp}} = \frac{850 \text{ nm}}{0.34 \text{ nm/bp}} = 2500 \text{ bp}$.

Q60. **Answer: (180)**

Solution

Standard dihybrid cross ($AaBb \times AaBb$) produces the classical 9 : 3 : 3 : 1 phenotypic ratio. The dominant phenotype for *both* traits ($A_B_$ class) has probability $\frac{9}{16}$. Expected number = $320 \times \frac{9}{16} = 20 \times 9 = 180$.

