IIT JAM Biotechnology

Sample Paper – 5

Collegedunia Practice Series | Exam Date: 14 February 2027

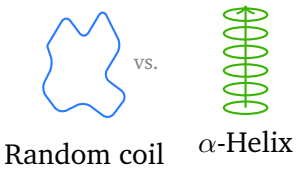
Instructions

- 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 statement about **random coil** protein conformation is correct?



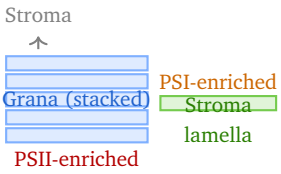
(A) It has a regular i→i+4 hydrogen-bond pattern like an α-helix

(B) It forms interstrand hydrogen bonds like a β-sheet

(C) It has no regular secondary structure and maximum conformational flexibility

(D) It is stabilised by disulfide bonds between non-adjacent residues

Q2. In the chloroplast thylakoid membrane system, which statement about the spatial distribution of Photosystem I (PSI) and Photosystem II (PSII) is correct?



(A) PSI is enriched in grana stacks; PSII is enriched in stroma lamellae
(B) PSII is enriched in grana stacks; PSI is enriched in stroma lamellae
(C) Both PSI and PSII are equally distributed throughout grana and stroma lamellae
(D) PSII is found exclusively in stroma lamellae; PSI only in the envelope membrane

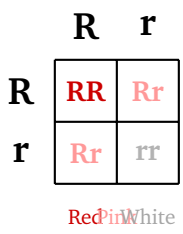
Q3. The Golgi apparatus receives vesicles from the rough endoplasmic reticulum (RER) at its *cis* face. Which function is performed by the Golgi?

(A) Performs O-linked glycosylation of proteins in transit and sorts them to lysosomes, plasma membrane, or secretory vesicles
(B) Synthesises integral membrane phospholipids de novo
(C) Generates ATP via oxidative phosphorylation within its lumen
(D) Performs N-linked glycosylation initiation using dolichol-PP oligosaccharide

Q4. Respiratory chain **Complex III** (cytochrome bc_1 complex) transfers electrons from:

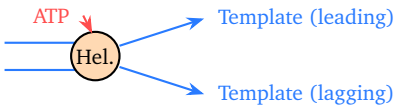
(A) NADH to ubiquinone (CoQ)
(B) Succinate to ubiquinone (CoQ)
(C) Ubiquinol ($CoQH_2$) to molecular oxygen (O_2)
(D) Ubiquinol ($CoQH_2$) to cytochrome c, pumping protons via the Q-cycle

Q5. **Incomplete dominance** is illustrated by which cross?



(A) Red (RR) $\times$ Red (RR) $\rightarrow$ all Red offspring
(B) Red (RR) $\times$ White (rr) $\rightarrow$ Pink (Rr) offspring in F1
(C) Red (RR) $\times$ White (rr) $\rightarrow$ both Red and White offspring in F1
(D) Red (Rr) $\times$ Red (Rr) $\rightarrow$ 3 Red : 1 White in F2

Q6. DNA helicase unwinds the double helix at the replication fork. Which statement is correct?



(A) Helicase forms phosphodiester bonds on the new strand
(B) Helicase moves only in the $3' \rightarrow 5'$ direction on the leading-strand template
(C) Helicase unwinds dsDNA by breaking hydrogen bonds between base pairs; movement requires ATP hydrolysis
(D) Helicase adds RNA primers to prime DNA synthesis

Q7. In the **lytic cycle** of a bacteriophage, the immediate outcome after phage infection is:

(A) Rapid phage DNA replication, assembly of new phage particles, and lysis of the host cell
(B) Integration of phage DNA into the host chromosome as a prophage
(C) Repression of phage genes by the CI repressor
(D) Long-term maintenance of phage genome as an episome without replication

Q8. *Mycoplasma* species are unique among bacteria because they:

(A) Have an exceptionally thick peptidoglycan cell wall
(B) Possess a Gram-negative outer membrane with LPS
(C) Are obligate intracellular parasites that cannot be cultured
(D) Completely **lack** a cell wall and are therefore resistant to penicillin and lysozyme

Q9. A **Northern blot** is used to detect:

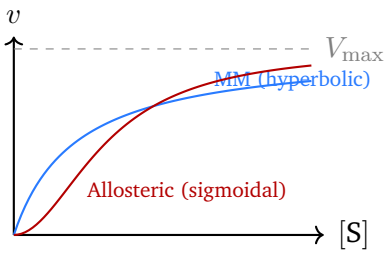
(A) Specific DNA sequences after restriction enzyme digestion
(B) Specific RNA sequences using a labelled nucleic acid probe
(C) Specific proteins using antibodies
(D) Single-nucleotide polymorphisms (SNPs) in genomic DNA

Q10. **Receptor-mediated endocytosis** of LDL (low-density lipoprotein) involves:

(A) Direct diffusion of LDL across the plasma membrane
(B) Active transport of LDL using an ABC transporter
(C) LDL binding to its receptor, internalisation via clathrin-coated pits, delivery to endosomes/lysosomes, and receptor recycling
(D) Phagocytosis of LDL particles by neutrophils only

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

Q11. **Allosteric enzymes** differ from Michaelis–Menten enzymes in that they:



(A) Show sigmoidal (S-shaped) v-vs.-[S] kinetics with Hill coefficient $n > 1$, reflecting positive cooperativity
(B) Always follow hyperbolic Michaelis–Menten kinetics
(C) Cannot be inhibited by products
(D) Have a single catalytic subunit with no regulatory sites

Q12. RFLP (Restriction Fragment Length Polymorphism) is used in DNA fingerprinting. The basis of this technique is:

(A) Amplification of short tandem repeats (STRs) by PCR, which produces size differences between individuals
(B) Fluorescent labelling of chromosomes with intercalating dyes to detect large chromosomal translocations

(C) Whole-genome sequencing to identify all single-nucleotide polymorphisms (SNPs) simultaneously

(D) Naturally occurring sequence polymorphisms at restriction enzyme recognition sites causing different-sized DNA fragments after restriction digestion and gel electrophoresis

Q13. Anfinsen's classic experiment with ribonuclease A demonstrated that:

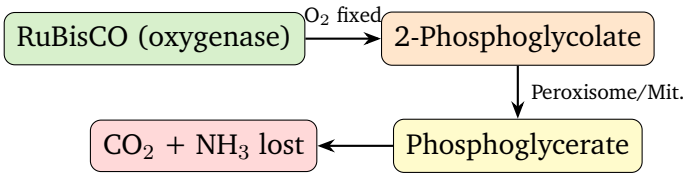
(A) Chaperone proteins are absolutely required for all protein folding in vivo

(B) The three-dimensional structure of a protein is determined by its amino acid sequence (primary structure) alone

(C) Disulfide bonds form before the polypeptide chain is released from the ribosome

(D) Denatured proteins cannot regain enzymatic activity under any conditions

Q14. **Photorespiration** in C_3 plants involves:



(A) Fixation of CO_2 by RuBisCO in the bundle-sheath cells of C_4 plants

(B) Production of ATP and NADPH without CO_2 release

(C) Fixation of O_2 instead of CO_2 by RuBisCO (oxygenase activity), leading to 2-phosphoglycolate and net loss of fixed carbon and energy

(D) The light-independent (dark) reactions that regenerate RuBP in the Calvin cycle

Q15. The restriction enzyme **HindIII** recognises 5′-AAGCTT-3′ and cuts between the two A residues. The overhangs produced are:

(A) 4-nucleotide 5′ overhangs (5′-AGCT-3′)

(B) 4-nucleotide 3′ overhangs

(C) Blunt ends (no overhangs)

(D) 2-nucleotide 5′ overhangs

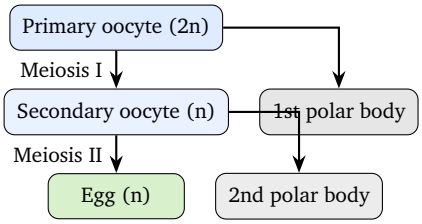
Q16. **B cell activation** by a T-dependent antigen requires, in addition to BCR crosslinking:

(A) Recognition of MHC class I by $CD8^+$ T cells
(B) Contact inhibition from dendritic cells
(C) Natural killer (NK) cell cytotoxicity
(D) Costimulation from T_H cells via CD40L–CD40 interaction and cytokines (IL-4, IL-21)

Q17. After translation termination in bacteria, the **ribosome recycling factor (RRF)** acts together with **EF-G** to:

(A) Recognise the stop codon and release the nascent polypeptide
(B) Dissociate the 70S ribosome into 50S and 30S subunits, freeing them for a new round of translation
(C) Degrade the mRNA after the ribosome encounters a stop codon
(D) Catalyse peptide bond formation at the ribosomal A site

Q18. During **oogenesis**, asymmetric meiotic division ensures that most cytoplasm is retained in the egg. Which sequence correctly describes oogenesis?



(A) Primary oocyte $\rightarrow$ 4 equal haploid cells after meiosis II
(B) Secondary oocyte $\rightarrow$ primary oocyte after fertilisation
(C) Primary oocyte $\rightarrow$ (Meiosis I) $\rightarrow$ secondary oocyte + 1st polar body $\rightarrow$ (Meiosis II) $\rightarrow$ egg + 2nd polar body
(D) Meiosis II in oocytes completes before fertilisation in all mammals

Q19. **Ketone bodies** (acetoacetate, β-hydroxybutyrate, acetone) are:

(A) Synthesised in liver mitochondria from acetyl-CoA during fasting/starvation and exported as alternative fuel to brain, heart, and skeletal muscle
(B) Produced in adipose tissue and transported directly to muscle as fatty acids
(C) Exclusively used by red blood cells under anaerobic conditions
(D) Synthesised in the cytoplasm from glucose via glycolysis

Q20. If P(success) $= \frac{1}{2}$ in a binomial trial, the probability of obtaining **exactly 3 successes in 5 trials** is:

(A) $\frac{3}{32}$
(B) $\frac{1}{4}$
(C) $\frac{3}{16}$
(D) $\frac{5}{16}$

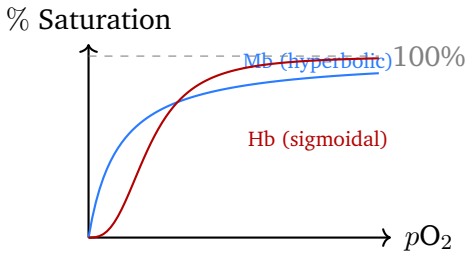
Q21. In the *E. coli* **his operon** attenuation mechanism, transcription of the operon *continues* (antitermination) when:

(A) His-tRNA is abundant and ribosomes translate the leader peptide without stalling
(B) His-tRNA is limiting, the ribosome stalls at tandem His codons in the leader, and the antiterminator hairpin forms in the leader mRNA
(C) The HisR repressor protein is inactivated by histidine
(D) cAMP-CRP binds upstream of the his operon promoter

Q22. **JAK–STAT signalling** is activated by cytokines. The correct sequence of events is:

(A) Cytokine binds receptor $\rightarrow$ receptor-associated JAKs transphosphorylate each other $\rightarrow$ JAKs phosphorylate STAT proteins $\rightarrow$ STAT dimers translocate to nucleus and activate transcription
(B) Cytokine activates Ras $\rightarrow$ MAPK cascade $\rightarrow$ Erk phosphorylates STAT
(C) Cytokine binds GPCR $\rightarrow$ adenylyl cyclase activated $\rightarrow$ cAMP activates PKA $\rightarrow$ STAT phosphorylation
(D) Cytokine activates PLCβ $\rightarrow$ IP_3 releases Ca^{2+} $\rightarrow$ calmodulin activates STAT

Q23. Compared to myoglobin, haemoglobin shows a **sigmoidal** oxygen-binding curve because:



(A) Myoglobin has four subunits that show negative cooperativity

(B) Haemoglobin has a lower affinity for oxygen than myoglobin at all pO_2 values

(C) Haemoglobin has four subunits; binding of O_2 to one subunit increases O_2 affinity of the others (positive cooperativity), producing a sigmoidal curve

(D) The Bohr effect increases haemoglobin affinity for O_2 in exercising muscle

Q24. **Confocal immunofluorescence microscopy** differs from conventional fluorescence microscopy in that it:

(A) Uses radioactive probes instead of fluorophores to detect proteins

(B) Requires no primary or secondary antibodies

(C) Measures protein size by gel electrophoresis

(D) Uses a pinhole aperture to eliminate out-of-focus light, enabling optical sectioning and three-dimensional reconstruction of fluorescently labelled structures

Q25. **Biomagnification** of persistent lipophilic toxins (e.g., DDT, methylmercury) means:

(A) Concentration of the toxin increases at each successive trophic level, reaching maximum levels in top predators

(B) The toxin is rapidly excreted by all organisms, preventing accumulation

(C) The toxin is converted to non-toxic forms by UV radiation in the atmosphere

(D) The toxin accumulates only in aquatic organisms and not in terrestrial food chains

Q26. The value of $\int_0^{\pi} \sin x \, dx$ is:

(A) 0
(B) 2
(C) π
(D) -2

Q27. The **baculovirus expression system** (using *Autographa californica* MNPV in Sf9/Sf21 insect cells) is preferred over *E. coli* expression for certain recombinant proteins because it:

(A) Produces high yields of recombinant protein and allows eukaryotic post-translational modifications (glycosylation, phosphorylation, proper folding)
(B) Integrates the recombinant gene permanently into the host chromosome via Ti plasmid
(C) Requires no viral infection and uses a stable plasmid vector
(D) Expresses proteins only as fusion proteins with glutathione S-transferase (GST)

Q28. Repair of **double-strand DNA breaks (DSBs)** by **Non-Homologous End Joining (NHEJ)**:

(A) Uses the sister chromatid as a template and is highly accurate; active in S/G2 phase
(B) Requires MSH2/MLH1 proteins to recognise mismatches at the break site
(C) Removes a 12–30 nucleotide oligomer containing the damaged site
(D) Is rapid but error-prone (may cause small insertions/deletions); active predominantly in G1 phase

Q29. In the secretory pathway, **COPII** vesicles are responsible for:

(A) Retrograde transport from the Golgi back to the ER (retrieval of ER-resident proteins)

(B) Anterograde transport of newly synthesised proteins from the ER to the Golgi cis-face
(C) Transport from the trans-Golgi network (TGN) to lysosomes
(D) Endocytosis of ligand-receptor complexes from the plasma membrane

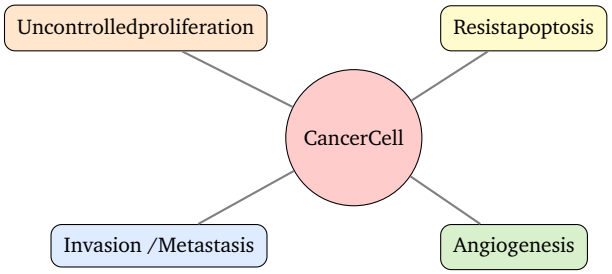
Q30. One complete turn of the TCA cycle starting from **acetyl-CoA** produces how many **NADH** molecules?

(A) 1
(B) 2
(C) 3
(D) 4

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 are recognised **hallmarks of cancer cells**?



(A) Sustained proliferative signalling and uncontrolled cell division
(B) Maintenance of contact inhibition (cells stop dividing at confluence)
(C) Resistance to apoptosis (evading programmed cell death)
(D) Induction of angiogenesis to supply tumour with nutrients and oxygen

Q32. Which of the following are types of **mutations classified by their effect on the protein**?

(A) Missense mutation: a single base change results in substitution of one amino acid for another

(B) Nonsense mutation: a single base change converts an amino-acid codon to a stop codon, causing premature translation termination

(C) Frameshift mutation: insertion or deletion of a number of nucleotides not divisible by 3 disrupts the reading frame

(D) Chromosomal translocation: a large segment of one chromosome moves to a non-homologous chromosome (a chromosomal, not point, mutation)

Q33. Which of the following correctly describe **types of cell signalling based on the distance between signalling cell and target cell**?

(A) Endocrine signalling: hormones secreted into the bloodstream and travel long distances to distant target cells

(B) Paracrine signalling: signalling molecules act on nearby cells within the same tissue or organ

(C) Juxtacrine signalling requires direct cell-cell contact via soluble ligands that diffuse across a gap junction

(D) Autocrine signalling: a cell secretes a signal that acts on itself or adjacent cells of the same type

Q34. Which of the following chromatography methods are **correctly paired with the molecular property** they exploit?

(A) Ion-exchange chromatography: separates proteins based on net surface charge

(B) Paper chromatography for protein purification separates proteins strictly by molecular weight

(C) Affinity chromatography: exploits specific non-covalent binding of a protein to an immobilised ligand (e.g., His-tag to Ni-NTA resin)

(D) Gel filtration (size-exclusion) chromatography: separates proteins by hydrodynamic size; larger molecules elute first

Q35. Which of the following are established **mechanisms of antibiotic resistance** in bacteria?

(A) Enzymatic inactivation of the antibiotic (e.g., β-lactamase hydrolyses the β-lactam ring of penicillin)

(B) Modification of the antibiotic target (e.g., altered PBPs in MRSA confer resistance to methicillin)
(C) Increased membrane permeability allowing greater drug uptake
(D) Active efflux pumps that expel the antibiotic from the bacterial cell

Q36. Which of the following **bioinformatics databases and their primary content** are correctly matched?

(A) GenBank (NCBI) / EMBL / DDBJ: primary repositories for nucleotide sequence data
(B) UniProt/Swiss-Prot: curated database of protein sequences with functional annotation
(C) Protein Data Bank (PDB): repository of experimentally determined three-dimensional structures of proteins and nucleic acids
(D) Google Scholar: a bioinformatics database that stores protein sequences for BLAST searches

Q37. Which of the following statements about the *E. coli* **lac operon** are correct?

(A) The operon contains the structural genes *lacZ* (β-galactosidase), *lacY* (permease), and *lacA* (transacetylase)
(B) The *lacI* gene is a structural gene encoded within the lacZYA operon cluster
(C) The true inducer is allolactose, which binds the lac repressor and prevents it from binding the operator
(D) Full transcriptional activation requires cAMP–CRP complex binding to the CAP site upstream of the promoter

Q38. Which of the following statements about **biogeochemical cycles** are correct?

(A) Biological nitrogen fixation is carried out by prokaryotes such as *Rhizobium* (symbiotic) and *Azotobacter* (free-living) converting N_2 to NH_3
(B) Denitrification by bacteria (e.g., *Pseudomonas denitrificans*) converts nitrate back to N_2, returning it to the atmosphere

(C) The sulfur cycle has no effect on climate or atmospheric chemistry

(D) Unlike the carbon and nitrogen cycles, the phosphorus cycle has no significant gaseous phase; phosphorus cycles mainly between rocks, soils, water, and living organisms

Q39. Which of the following are examples of **mutualistic symbiosis**?

(A) Mycorrhizal fungi and plant roots: fungi supply mineral nutrients (phosphate) to the plant; the plant supplies photosynthetically fixed carbon to the fungi

(B) *Rhizobium* and legume root nodules: bacteria fix atmospheric N_2 for the plant; the plant supplies carbohydrates to the bacteria

(C) Cleaner fish (e.g., wrasse) and large fish: cleaner fish remove parasites from larger fish; both partners benefit

(D) Predator–prey relationships (e.g., lion hunting zebra) are a form of mutualism

Q40. Which of the following correctly describe **statistical tests and their appropriate applications**?

(A) Chi-square (χ^2) test: used to assess goodness-of-fit to expected ratios (e.g., Mendelian segregation ratios) or to test independence between categorical variables

(B) Student's t-test: used to compare the means of two groups and determine whether the difference is statistically significant

(C) A significant correlation coefficient (r) between two variables implies that one variable causes changes in the other

(D) ANOVA (Analysis of Variance): used to compare means across three or more groups simultaneously

Section C — Numerical Answer Type (NAT)

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

Q41. A bacterial culture starts with 5×10^4 CFU/mL. The doubling time is 30 min. The number of cells (in $\times 10^4$ CFU/mL) after exactly 3 hours (180 minutes) is:

Q42. How many water molecules are released during the synthesis of a **tripeptide** from three free amino acids?

Q43. A double-stranded DNA molecule contains 15% Adenine. By Chargaff's rules, the percentage of **Guanine** in this DNA is:

Q44. How many **stop codons** are present in the standard genetic code?

Q45. In a randomly mating population in Hardy–Weinberg equilibrium, the frequency of allele A is 0.4. The expected frequency of **homozygous recessive** (aa) individuals is:

Q46. A double-stranded DNA fragment has 500 base pairs. The base composition is 30% G+C (i.e., 150 G·C pairs and 350 A·T pairs). The total number of **hydrogen bonds** in this dsDNA fragment is (A·T pairs have 2 H-bonds; G·C pairs have 3 H-bonds):

Q47. How many **$FADH_2$** molecules are produced per complete turn of the TCA cycle starting from one acetyl-CoA?

Q48. A radioactive sample has an initial activity of 1000 counts per minute (cpm). The half-life of the isotope is 10 days. The activity (in cpm) remaining after 30 days is:

Q49. The pH of a solution prepared by dissolving NaOH to give $[\mathrm{OH}^-] = 10^{-3}$ M at 25°C is:

Q50. A linear dsDNA fragment of 10,000 bp is digested with a restriction enzyme that recognises a 4-bp sequence. Assuming a random sequence with equal base frequencies, the expected number of **fragments** generated is approximately (use: 4-cutter cuts every $4^4 = 256$ bp on average):

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

Q51. An enzyme has $K_m = 2$ mM and $V_{\max} = 100\ \mu$mol/min. Using the Michaelis–Menten equation, the reaction velocity v (in μmol/min) at $[\mathrm{S}] = K_m = 2$ mM is:

Q52. In a monohybrid cross Aa $\times$ Aa producing **360** total offspring, the expected number showing the **homozygous recessive** (aa) phenotype is:

Q53. The value of $\displaystyle\int_0^3 x^2\,dx$ is:

Q54. The mean of a set of 6 numbers is 8 (sum = 48). If one of the numbers is found to be 20, the mean of the **remaining 5** numbers is:

Q55. A population grows logistically with intrinsic rate $r = 0.5\ \text{h}^{-1}$ and carrying capacity $K = 1000$ cells. When the population size $N = 500 = K/2$, the instantaneous growth rate dN/dt (cells/h) is:

Q56. The value of $\dfrac{d}{dx}\left[\ln(x^2+1)\right]$ evaluated at $x = 2$ is:

Q57. A population has allele frequencies $f(I^A) = 0.3$, $f(I^B) = 0.1$, $f(i) = 0.6$ (ABO blood group locus). Assuming Hardy–Weinberg equilibrium, the expected frequency of **blood type O** (genotype ii) is:

Q58. Using the relationship $S \propto M^{2/3}$ for globular proteins, if a monomeric subunit of 50 kDa has a sedimentation coefficient of 4 S, the approximate sedimentation coefficient (in S) of a complex of 10 identical subunits (total mass 500 kDa) is (round to nearest integer):

Q59. The approximate molecular weight (in Daltons) of a protein consisting of **250 amino acid residues**, assuming an average residue mass of 110 Da, is:

Q60. In a population of 10,000 individuals, 900 have blood type O (genotype ii). Assuming Hardy–Weinberg equilibrium with only two alleles (I and i), the expected number of **heterozygotes** (Ii) in the population is:

Answer Key — IIT JAM Biotechnology Sample Paper 5

Section A — MCQ (Q1–Q30)

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

Section B — MSQ (Q31–Q40)

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

Section C — NAT (Q41–Q60)

Q	Answer	Q	Answer	Q	Answer	Q	Answer
41	320	46	1150	51	50	56	0.8
42	2	47	3	52	90	57	0.36
43	35	48	125	53	9	58	18
44	3	49	11	54	5.6	59	27500
45	0.36	50	40	55	125	60	4200

Detailed Solutions

SECTION A — MCQ

Q1. **Answer: (C)**

Solution

A random coil has no regular secondary structure and maximum conformational flexibility because backbone dihedral angles (ϕ, ψ) are not constrained to narrow regions of the Ramachandran plot. Unlike an α-helix (i→i+4 intrastrand H-bonds) or a β-sheet (interstrand H-bonds), a random coil has no regular H-bond pattern. Disulfide bonds stabilise tertiary structure, not random coils. **(C)**

Q2. **Answer: (B)**

Solution

Lateral heterogeneity in the thylakoid: PSII is enriched in the stacked *grana* regions (appressed membranes), while PSI and the ATP synthase are enriched in the unstacked *stroma lamellae*. This segregation is maintained by the sizes of the antenna complexes and facilitates regulated energy distribution. **(B)**

Q3. **Answer: (A)**

Solution

The Golgi (cis → medial → trans cisternae) performs **O-linked** glycosylation (addition of sugars to Ser/Thr residues) and sorts cargo proteins into vesicles destined for lysosomes, the plasma membrane, or secretory vesicles. N-linked glycosylation is *initiated* in the RER (transfer of $Glc_3Man_9GlcNAc_2$ from dolichol-PP); its trimming/modification continues in the Golgi. ATP synthesis occurs in mitochondria, not the Golgi lumen. **(A)**

Q4. **Answer: (D)**

Solution

Complex III (cytochrome bc_1 complex) accepts electrons from ubiquinol ($CoQH_2$) and passes them to the soluble carrier cytochrome c (reduced). The Q-cycle mechanism pumps 4 H^+ from matrix to intermembrane space per 2 electrons. Complex I: NADH → CoQ; Complex II (succinate DH): $FADH_2$ → CoQ; Complex IV: cytochrome c → O_2. **(D)**

Q5. **Answer: (B)**

Solution

Incomplete dominance: neither allele is fully dominant; the heterozygote (Rr) shows an *intermediate* phenotype (pink flower) between the two homozygotes (RR = red; rr = white). In the F_1 cross of red $\times$ white, all offspring are Rr (pink). This is distinct from complete dominance (where Rr would look red) or co-dominance (where both colours would appear simultaneously). **(B)**

Q6. **Answer: (C)**

Solution

Replicative helicases (DnaB in *E. coli*; MCM2–7 complex in eukaryotes) unwind the double helix by **breaking hydrogen bonds** between complementary base pairs. This reaction requires ATP hydrolysis (each step driven by ATP $\rightarrow$ ADP + P_i). DnaB tracks $5' \rightarrow 3'$ on the lagging-strand template. Primers are added by primase (not helicase); phosphodiester bonds are formed by DNA polymerase. **(C)**

Q7. **Answer: (A)**

Solution

In the **lytic cycle**: phage injects DNA $\rightarrow$ immediate transcription of early/late genes $\rightarrow$ phage DNA replication $\rightarrow$ assembly of capsid and packaging of phage DNA $\rightarrow$ lysis of host cell releasing $\sim$100–200 progeny phage. The lysogenic cycle involves DNA integration as a prophage, repression by the CI repressor, and long-term coexistence with the host. **(A)**

Q8. **Answer: (D)**

Solution

Mycoplasma (e.g., *M. pneumoniae*, *M. genitalium*) are the smallest self-replicating bacteria and are unique among bacteria in completely **lacking a cell wall**. The absence of peptidoglycan makes them naturally resistant to β-lactam antibiotics (penicillin, ampicillin) and lysozyme, which target peptidoglycan. They can be cultured on specialised media (unlike obligate intracellular parasites). **(D)**

Q9. **Answer: (B)**

Solution

Northern blot: RNA is denatured and separated by size on a formaldehyde-agarose gel $\rightarrow$ transferred to a nitrocellulose or nylon membrane $\rightarrow$ hybridised with a labelled (radioactive or fluorescent) nucleic acid probe complementary to the target

RNA. Southern blot detects DNA; Western blot detects proteins using antibodies. SNP detection uses techniques such as allele-specific PCR or SNP microarrays, not Northern blot. **(B)**

Q10. **Answer: (C)**

Solution

Receptor-mediated endocytosis of LDL: (1) LDL binds LDL receptor (LDLR) on the cell surface $\rightarrow$ (2) receptor–LDL complexes cluster in clathrin-coated pits $\rightarrow$ (3) pit invaginates and pinches off to form a clathrin-coated vesicle $\rightarrow$ (4) endosome acidifies (via V-ATPase), releasing LDL from the receptor $\rightarrow$ (5) receptor recycled to plasma membrane; LDL delivered to lysosomes where cholesteryl esters are hydrolysed. **(C)**

Q11. **Answer: (A)**

Solution

Allosteric enzymes (e.g., ATCase, phosphofructokinase-1, haemoglobin as an allosteric O_2-binding protein) show **sigmoidal** v-vs.-[S] kinetics. Binding of the first substrate molecule increases the affinity of remaining binding sites (positive cooperativity). The Hill equation $v = V_{\max}[\mathrm{S}]^n/(K_{0.5}^n + [\mathrm{S}]^n)$ with $n > 1$ describes this behaviour. Michaelis–Menten kinetics are hyperbolic ($n = 1$, no cooperativity). **(A)**

Q12. **Answer: (D)**

Solution

RFLP exploits naturally occurring DNA sequence differences at restriction enzyme recognition sites. When a site is present in one individual but absent in another (due to a SNP), restriction digestion produces different-sized fragments that are separated by gel electrophoresis and detected by Southern blotting with a probe. Option (A) describes STR/microsatellite profiling (PCR-based), a distinct technique. **(D)**

Q13. **Answer: (B)**

Solution

Anfinsen denatured RNase A with 8 M urea (unfolds the protein) and β-mercaptoethanol (reduces the 4 disulfide bonds, yielding 8 free cysteines). Upon removing these denaturants by dialysis, the protein spontaneously refolded to its native structure and regained full enzymatic activity. Conclusion: the **primary**

amino acid sequence encodes all information necessary to determine the three-dimensional fold (thermodynamic hypothesis). **(B)**

Q14. **Answer: (C)**

Solution

RuBisCO has both carboxylase and **oxygenase** activities. When O_2 competes with CO_2, RuBisCO fixes O_2 to RuBP, producing one molecule of 3-phosphoglycerate and one molecule of 2-phosphoglycolate. 2-Phosphoglycolate is metabolised through the photorespiratory pathway in peroxisomes and mitochondria, releasing CO_2 and NH_3 and consuming ATP and NADPH — reducing photosynthetic efficiency in C_3 plants. C_4 plants concentrate CO_2 around RuBisCO to suppress oxygenase activity. **(C)**

Q15. **Answer: (A)**

Solution

HindIII cuts 5′-A↓AGCTT-3′ / 3′-TTCGA↑A-5′. This produces **4-nucleotide 5′ overhangs** with the sequence 5′-AGCT-3′. These are *sticky ends* that can base-pair with any other HindIII-cut end. Compare: EcoRI produces 4-nt 5′ overhangs (5′-AATT-3′); SmaI produces blunt ends; KpnI produces 3′ overhangs. **(A)**

Q16. **Answer: (D)**

Solution

For T-dependent antigens, B cells require two signals: (1) BCR crosslinking by native antigen; (2) costimulation from T_H cells via **CD40L (CD154) on T_H binding CD40 on B cells**, plus cytokines (IL-4 for IgG1/IgE class switching; IL-21 for plasma cell differentiation). This T–B cell conjugate leads to germinal centre formation, somatic hypermutation, clonal expansion, and plasma cell differentiation. MHC class I–CD8 interactions involve cytotoxic T cells, not B cell activation. **(D)**

Q17. **Answer: (B)**

Solution

After release factor-mediated termination, the 70S ribosome stalls on the mRNA. **RRF** mimics a tRNA structurally and occupies the A site, while **EF-G** uses GTP hydrolysis to translocate RRF, disrupting intersubunit contacts and splitting the 70S into the 50S and 30S subunits. IF3 then prevents reassociation of the 30S with the 50S. The free subunits can enter a new round of translation. **(B)**

Q18. **Answer: (C)**

Solution

Oogenesis undergoes asymmetric cytokinesis to preserve cytoplasm and nutrients in the egg: (1) Primary oocyte (2n) undergoes **Meiosis I** $\rightarrow$ secondary oocyte (n, large) + 1st polar body (n, small); (2) Secondary oocyte undergoes **Meiosis II** (completed only after fertilisation in most mammals) $\rightarrow$ egg (n, large) + 2nd polar body (n, small). Thus meiosis is not complete before fertilisation in humans (the egg is arrested at metaphase II). **(C)**

Q19. **Answer: (A)**

Solution

During fasting/starvation, free fatty acid β-oxidation in the liver generates excess acetyl-CoA that exceeds the capacity of the TCA cycle (oxaloacetate is diverted to gluconeogenesis). Acetyl-CoA is converted to **ketone bodies** (acetoacetate, β-hydroxybutyrate, acetone) in liver mitochondria via HMG-CoA synthase and HMG-CoA lyase. Ketone bodies are water-soluble and transported in the blood to extrahepatic tissues (brain, heart, skeletal muscle) where they are reconverted to acetyl-CoA and oxidised. **(A)**

Q20. **Answer: (D)**

Solution

Binomial probability: $P(X = k) = \binom{n}{k} p^k (1-p)^{n-k}$. $P(X = 3,\ n = 5,\ p = 1/2) = \binom{5}{3}\left(\frac{1}{2}\right)^3\left(\frac{1}{2}\right)^2 = 10 \times \frac{1}{8} \times \frac{1}{4} = \frac{10}{32} = \frac{5}{16}$. Answer: $\frac{5}{16}$. **(D)**

Q21. **Answer: (B)**

Solution

In his operon attenuation: the leader peptide contains two consecutive His codons. When **histidyl-tRNA is scarce**, the ribosome translating the leader mRNA **stalls** at the tandem His codons $\rightarrow$ ribosome stalling exposes complementary sequences in the mRNA that form the **antiterminator hairpin** (pairing of regions 2 and 3) instead of the terminator hairpin (regions 3 and 4) $\rightarrow$ RNA polymerase read-through and transcription of the his structural genes continues. When His-tRNA is abundant, the ribosome translates without stalling, the terminator hairpin forms, and transcription terminates. **(B)**

Q22. **Answer: (A)**

Solution

JAK–STAT pathway: cytokine (e.g., IFN-γ, IL-6, erythropoietin) binds to its receptor $\rightarrow$ receptor dimerisation/conformational change $\rightarrow$ receptor-associated **JAKs** (Janus kinases) transphosphorylate each other (activation) $\rightarrow$ phosphorylated JAKs phosphorylate specific tyrosine residues on the cytoplasmic receptor tail $\rightarrow$ **STAT** proteins (Signal Transducers and Activators of Transcription) dock via SH2 domains and are phosphorylated by JAKs $\rightarrow$ phospho-STAT dimers translocate to the nucleus $\rightarrow$ bind STAT-response elements and activate target gene transcription. **(A)**

Q23. **Answer: (C)**

Solution

Myoglobin is a monomer: one haem, hyperbolic O_2-binding curve (no cooperativity, $n = 1$). Haemoglobin has four subunits ($\alpha_2\beta_2$): O_2 binding to one subunit induces a conformational change (T$\rightarrow$R state shift) that increases O_2 affinity of adjacent subunits (positive cooperativity, Hill coefficient $n \approx 2.8$), producing a **sigmoidal** curve. The Bohr effect (H^+, CO_2) *decreases* Hb affinity for O_2 in active tissues (shifts curve right). **(C)**

Q24. **Answer: (D)**

Solution

In confocal fluorescence microscopy, a **pinhole aperture** placed in the optical path at the conjugate focal plane blocks out-of-focus fluorescence from above and below the focal plane. This gives sharper images and allows the acquisition of thin optical sections ($\sim$0.5 μm) through the sample, which can be reconstructed into a 3D image. Conventional epifluorescence microscopes lack this pinhole and collect fluorescence from the entire depth of the sample, resulting in blurred images for thick specimens. **(D)**

Q25. **Answer: (A)**

Solution

Biomagnification (biological magnification): lipophilic (fat-soluble) compounds such as DDT, PCBs, and methylmercury are not metabolised or excreted efficiently and accumulate in adipose tissue. Because each trophic level must consume large biomasses of the level below, the toxin **concentrates at each successive trophic level**. Top predators (e.g., ospreys, bald eagles, killer whales) accumulate the highest concentrations. DDT-induced eggshell thinning in raptors is a classic example. **(A)**

Q26. **Answer: (B)**

Solution

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

Q27. **Answer: (A)**

Solution

The **baculovirus expression vector system (BEVS)** uses recombinant *Autographa californica* multiple nucleopolyhedrovirus (AcMNPV) to infect insect cell lines (Sf9, Sf21). The polyhedrin promoter drives very high-level recombinant protein expression. Unlike *E. coli*, insect cells perform eukaryotic post-translational modifications including N- and O-linked glycosylation, phosphorylation, and proper disulfide bond formation, making BEVS suitable for complex eukaryotic proteins. It does not use a Ti plasmid (plant transformation) and does not require GST fusions. **(A)**

Q28. **Answer: (D)**

Solution

NHEJ (Non-Homologous End Joining): Ku70/Ku80 heterodimer binds DSB ends $\rightarrow$ recruits DNA-PKcs $\rightarrow$ ends are processed (sometimes with small deletions/insertions) $\rightarrow$ ligated by XRCC4–LigIV complex. NHEJ is **rapid but error-prone** because it does not use a homologous template and can introduce small indels. It is the dominant DSB repair pathway in G1 (when no sister chromatid is available). Homologous Recombination (HR) is accurate, uses the sister chromatid template, and is active in S/G2. Options (A) describes HR; (B) describes MMR; (C) describes NER. **(D)**

Q29. **Answer: (B)**

Solution

COPII vesicles (coat proteins Sec23/24 + Sec13/31, small GTPase Sar1) bud from the ER exit sites (ERES) and carry newly synthesised secretory and membrane proteins **anterograde to the cis-Golgi** (via ER–Golgi intermediate compartment, ERGIC). **COPI** vesicles perform retrograde transport (Golgi $\rightarrow$ ER), retrieving escaped ER-resident proteins (KDEL, KKXX motifs). Clathrin-coated vesicles mediate TGN $\rightarrow$ endosome and plasma membrane $\rightarrow$ endosome transport. **(B)**

Q30. **Answer: (C)**

Solution

Per complete turn of the TCA cycle from one acetyl-CoA, NADH is generated at three steps: (1) isocitrate dehydrogenase (isocitrate $\rightarrow$ α-ketoglutarate), (2) α-ketoglutarate dehydrogenase (α-KG $\rightarrow$ succinyl-CoA), (3) malate dehydrogenase (malate $\rightarrow$ oxaloacetate). Total = **3 NADH**. Additionally, 1 $FADH_2$ (succinate DH) and 1 GTP (succinyl-CoA synthetase) are produced. **(C)**

SECTION B — MSQ

Q31. **Answer: (A,C,D)**

Solution

Hallmarks of cancer (Hanahan & Weinberg): (A) Sustained proliferative signalling — cancer cells produce their own growth signals or constitutively activate downstream pathways (e.g., KRAS mutations). (C) Resistance to apoptosis — anti-apoptotic proteins (Bcl-2, Bcl-xL) are overexpressed; pro-apoptotic proteins (Bax, p53) are mutated. (D) Induction of angiogenesis — tumours secrete VEGF to grow new blood vessels beyond 1–2 mm. Cancer cells *lose* contact inhibition (B is a normal cell property, not a cancer hallmark). **Correct: (A), (C), and (D)**

Q32. **Answer: (A,B,C)**

Solution

(A) Missense: single nucleotide substitution $\rightarrow$ different amino acid (e.g., sickle cell: Glu$\rightarrow$Val). (B) Nonsense: substitution creates a UAA, UAG, or UGA stop codon $\rightarrow$ premature termination. (C) Frameshift: insertion/deletion of 1, 2 (or any number not divisible by 3) nucleotides $\rightarrow$ reading frame shift $\rightarrow$ completely different downstream amino acid sequence and usually a premature stop. (D) Chromosomal translocation is a *chromosomal structural rearrangement*, not a point mutation (not classified by effect on a single codon/protein). **Correct: (A), (B), and (C)**

Q33. **Answer: (A,B,D)**

Solution

(A) Endocrine: hormone secreted into bloodstream, acts on distant target cells (e.g., insulin from pancreatic β-cells). (B) Paracrine: signal diffuses locally to adjacent cells (e.g., prostaglandins, growth factors at a wound site). (D) Autocrine: cell responds to its own secreted signal (e.g., many cancer cells secrete and respond to their own growth factors; IL-2 autocrine loop in activated T cells). (C) is incorrect: juxtacrine signalling requires *direct cell-cell contact* via membrane-anchored ligands (e.g., Notch–Delta) or gap junctions, *not* soluble ligands. **Correct: (A), (B), and**

(D)

Q34. **Answer: (A,C,D)**

Solution

(A) Ion-exchange chromatography: proteins bind to a charged resin (anion-exchange or cation-exchange) based on their net surface charge at a given pH; eluted by increasing salt concentration. (C) Affinity chromatography: exploits specific, reversible non-covalent binding (e.g., His_6-tag to Ni-NTA, GST to glutathione, antibody to Protein A). (D) Gel filtration (size-exclusion): molecules enter pores based on size; large molecules excluded from pores, elute first (shorter retention time). (B) Paper chromatography is a partition/adsorption technique used for small molecules (amino acids, sugars), not for protein purification by molecular weight. **Correct: (A), (C), and (D)**

Q35. **Answer: (A,B,D)**

Solution

(A) Enzymatic inactivation: β-lactamase cleaves the β-lactam ring of penicillins/cephalosporins; aminoglycoside-modifying enzymes inactivate aminoglycosides. (B) Target modification: MRSA produces PBP2a (altered penicillin-binding protein) with low affinity for methicillin; mutations in DNA gyrase/topoisomerase IV confer fluoroquinolone resistance; ribosomal methylation confers aminoglycoside/macrolide resistance. (D) Efflux pumps: membrane transporters (e.g., AcrAB-TolC in *E. coli*; MexAB-OprM in *P. aeruginosa*) actively expel antibiotics. (C) *Decreased* outer membrane permeability (loss of OmpF porins) is a resistance mechanism, not increased permeability. **Correct: (A), (B), and (D)**

Q36. **Answer: (A,B,C)**

Solution

(A) GenBank (NCBI), EMBL-Bank, and DDBJ form the International Nucleotide Sequence Database Collaboration (INSDC) — primary repositories for nucleotide sequences. (B) UniProt/Swiss-Prot: manually curated protein sequence database with functional annotation, subcellular localisation, post-translational modifications, and disease associations. (C) PDB (Protein Data Bank, `rcsb.org`): stores experimentally determined 3D structures of macromolecules obtained by X-ray crystallography, NMR, and cryo-EM. (D) Google Scholar is a literature search engine, not a bioinformatics sequence/structure database. **Correct: (A), (B), and (C)**

Q37. **Answer: (A,C,D)**

Solution

(A) The lac operon structural genes are *lacZ* (β-galactosidase, cleaves lactose to glucose + galactose), *lacY* (lactose permease, transports lactose into cell), and *lacA* (thiogalactoside transacetylase; minor role). (C) Allolactose (an isomer of lactose formed by basal β-galactosidase) is the true inducer — it binds the LacI repressor, inducing a conformational change that releases the repressor from the operator. (D) Full activation of the lac operon requires cAMP–CRP (catabolite activator protein) binding to the CAP site upstream of the promoter — this occurs only when glucose is absent (high cAMP). (B) is incorrect: *lacI* is a separate regulatory gene with its own promoter, *not* part of the *lacZYA* operon structural cluster. **Correct: (A), (C), and (D)**

Q38. **Answer: (A,B,D)**

Solution

(A) Nitrogen fixation: prokaryotes reduce N_2 to NH_3 using nitrogenase (e.g., symbiotic *Rhizobium* in legume nodules; free-living *Azotobacter*, *Cyanobacteria*). (B) Denitrification: anaerobic bacteria (*Pseudomonas denitrificans*, *Paracoccus*) reduce nitrate (NO_3^-) $\rightarrow N_2$ (and N_2O), returning nitrogen gas to the atmosphere — completing the nitrogen cycle. (D) The phosphorus cycle lacks a significant gaseous phase; phosphorus is released from rocks/minerals by weathering and cycles through soil $\rightarrow$ plants $\rightarrow$ animals $\rightarrow$ decomposers, with long-term storage in ocean sediments. (C) is false: SO_2 (from volcanic activity and combustion) and H_2S contribute to acid rain and do affect climate/atmospheric chemistry. **Correct: (A), (B), and (D)**

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

Solution

(A) Mycorrhizae: arbuscular mycorrhizal fungi (AMF) colonise plant roots, dramatically increasing the surface area for mineral absorption (especially phosphate); in return, the plant supplies up to 20% of its photosynthate to the fungus. (B) *Rhizobium*–legume: bacteria housed in root nodules fix N_2 for the plant; plant provides carbohydrates (malate, succinate). (C) Cleaner fish (e.g., *Labroides dimidiatus*) remove ectoparasites and dead tissue from larger client fish; both benefit. (D) Predator–prey is **not** mutualism — it is **predation** (+/- relationship where the predator benefits and the prey is harmed). **Correct: (A), (B), and (C)**

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

Solution

(A) χ^2 test: compares observed vs. expected frequencies in categorical data (e.g., Mendelian 3:1 ratios); also tests independence in contingency tables. (B) Student's t-test: compares means of two groups (one-sample, two-sample independent, or paired); assesses whether the difference is greater than expected by chance. (D) ANOVA (Analysis of Variance): extends the t-test to ≥ 3 groups simultaneously (one-way ANOVA); avoids inflating Type I error from multiple pairwise comparisons. (C) is incorrect: a significant correlation coefficient shows *association* between two variables but does not imply causation (correlation $\neq$ causation; confounding variables, reverse causation, and coincidence are alternative explanations). **Correct: (A), (B), and (D)**

SECTION C — NAT

Q41. **Answer: (320)**

Solution

$t = 3\,\text{h} = 180\,\text{min}$. Number of doublings $= 180/30 = 6$. $N = 5 \times 10^4 \times 2^6 = 5 \times 10^4 \times 64 = 320 \times 10^4$. Answer in $\times 10^4$ units: **320**.

Q42. **Answer: (2)**

Solution

Formation of a peptide bond between two amino acids releases one water molecule. For a *tripeptide* (3 amino acids joined by 2 peptide bonds), $n - 1 = 3 - 1 = \mathbf{2}$ water molecules are released.

Q43. **Answer: (35)**

Solution

By Chargaff's rules: $[\text{A}] = [\text{T}] = 15\%$. Therefore $[\text{G}] + [\text{C}] = 100\% - 30\% = 70\%$, and since $[\text{G}] = [\text{C}]$: $[\text{G}] = \mathbf{35}\%$.

Q44. **Answer: (3)**

Solution

The standard genetic code has three stop (nonsense) codons: **UAA** (ochre), **UAG** (amber), and **UGA** (opal/umber). Total = **3**.

Q45. **Answer: (0.36)**

Solution

Hardy–Weinberg: $p = f(A) = 0.4$, $q = f(a) = 1 - 0.4 = 0.6$. Frequency of homozygous recessive $aa = q^2 = (0.6)^2 = \mathbf{0.36}$.

Q46. **Answer: (1150)**

Solution

A·T base pairs: $350 \times 2 = 700$ H-bonds. G·C base pairs: $150 \times 3 = 450$ H-bonds. Total $= 700 + 450 = \mathbf{1150}$ H-bonds.

Q47. **Answer: (1)**

Solution

$FADH_2$ is generated at only one step in the TCA cycle: the **succinate dehydrogenase** reaction (succinate $\rightarrow$ fumarate). All other oxidation steps in the cycle (isocitrate DH, α-KG DH, and malate DH) produce NADH. Therefore, one complete turn of the TCA cycle from one acetyl-CoA yields **1** $FADH_2$.

Q48. **Answer: (125)**

Solution

$30\,\text{d}/10\,\text{d} = 3$ half-lives. Activity $= 1000 \times (1/2)^3 = 1000/8 = \mathbf{125}$ cpm.

Q49. **Answer: (11)**

Solution

$[OH^-] = 10^{-3}$ M. pOH $= -\log(10^{-3}) = 3$. pH $= 14 -$ pOH $= 14 - 3 = \mathbf{11}$.

Q50. **Answer: (40)**

Solution

A 4-cutter recognises a 4-bp sequence; expected cut frequency $= (1/4)^4 = 1/256$ bp. Expected number of cuts $= 10{,}000/256 \approx 39$. A linear DNA with 39 cuts yields $39 + 1 = \mathbf{40}$ fragments.

Q51. **Answer: (50)**

Solution

Michaelis–Menten: $v = \dfrac{V_{\max}[\mathrm{S}]}{K_m + [\mathrm{S}]} = \dfrac{100 \times 2}{2+2} = \dfrac{200}{4} = \mathbf{50}\,\mu$mol/min. At $[\mathrm{S}] = K_m$, $v = V_{\max}/2$ always.

Q52. **Answer: (90)**

Solution

From Aa $\times$ Aa: offspring ratio = AA : Aa : aa = 1 : 2 : 1. Frequency of $aa = 1/4$. Expected number $= 360 \times 1/4 = \mathbf{90}$.

Q53. **Answer: (9)**

Solution

$$\int_0^3 x^2\,dx = \left[\frac{x^3}{3}\right]_0^3 = \frac{27}{3} - 0 = \mathbf{9}.$$

Q54. **Answer: (5.6)**

Solution

Sum of all 6 numbers $= 6 \times 8 = 48$. Sum of remaining 5 $= 48 - 20 = 28$. Mean of remaining 5 $= 28/5 = \mathbf{5.6}$.

Q55. **Answer: (125)**

Solution

Logistic growth: $\dfrac{dN}{dt} = rN\left(1 - \dfrac{N}{K}\right) = 0.5 \times 500 \times \left(1 - \dfrac{500}{1000}\right) = 0.5 \times 500 \times 0.5 =$ **125** cells/h.

Q56. **Answer: (0.8)**

Solution

$\dfrac{d}{dx}[\ln(x^2+1)] = \dfrac{2x}{x^2+1}$. At $x = 2$: $\dfrac{2 \times 2}{4+1} = \dfrac{4}{5} = \mathbf{0.8}$.

Q57. **Answer: (0.36)**

Solution

Hardy–Weinberg with 3 alleles. Blood type O has genotype ii. Frequency $= [f(i)]^2 = (0.6)^2 = \mathbf{0.36}$.

Q58. **Answer: (18)**

Solution

$S \propto M^{2/3}$. $S_{\text{complex}}/S_{\text{monomer}} = (M_{\text{complex}}/M_{\text{monomer}})^{2/3} = (500/50)^{2/3} = 10^{2/3}$. $10^{2/3} = (10^2)^{1/3} = 100^{1/3} \approx 4.642$. $S_{\text{complex}} = 4 \times 4.642 \approx 18.6\,\text{S} \approx \mathbf{18\,S}$.

Q59. **Answer: (27500)**

Solution

MW $= 250$ residues $\times\ 110$ Da/residue $= \mathbf{27{,}500}$ Da.

Q60. **Answer: (4200)**

Solution

$f(ii) = q^2 = 900/10{,}000 = 0.09 \Rightarrow q = 0.3$. $p = 1 - 0.3 = 0.7$. Frequency of heterozygotes $(Ii) = 2pq = 2 \times 0.7 \times 0.3 = 0.42$. Expected number $= 0.42 \times 10{,}000 = \mathbf{4200}$.