IIT JAM Biotechnology

Sample Paper – 4

Collegedunia Practice Series | Exam Date: 14 February 2027

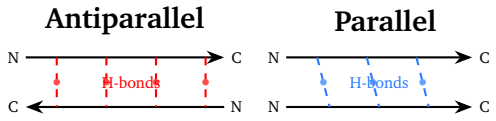
Instructions

- 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. Beta-pleated sheets are stabilized by hydrogen bonds between backbone groups of adjacent polypeptide strands. Which statement *correctly* describes the difference between parallel and antiparallel beta-sheets?



(A) Beta-sheet hydrogen bonds form between R-group side chains of residues on adjacent strands

(B) Parallel beta-sheets are thermodynamically more stable than antiparallel sheets because their H-bonds are perfectly linear

(C) Beta-sheets can only form between strands within the same polypeptide chain (intramolecular only)

(D) In antiparallel beta-sheets, adjacent strands run in opposite directions and the inter-strand H-bonds are more linear and stronger, while in parallel sheets the H-bonds are skewed

Q2. Which statement about Photosystem I (PSI) in oxygenic photosynthesis is correct?

(A) PSI (P700) uses electrons delivered via ferredoxin to reduce $NADP^+$ to NADPH through ferredoxin-$NADP^+$ reductase (FNR)
(B) PSI directly oxidizes water to produce O_2 and H^+ ions
(C) PSI is also called P680 because it absorbs light maximally at 680 nm
(D) PSI transfers electrons directly to plastoquinone, which carries them to the cytochrome b_6f complex

Q3. The Golgi apparatus is a central organelle of the eukaryotic secretory pathway. Which statement correctly describes its primary function?

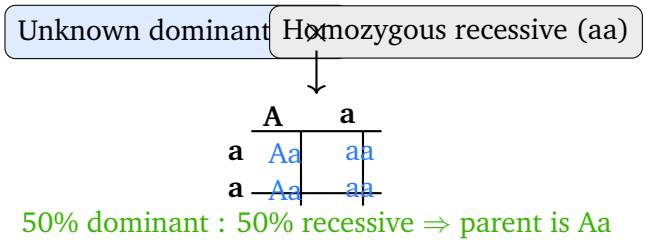
(A) The Golgi apparatus synthesizes ATP through an electron transport chain embedded in its cisternal membranes
(B) The Golgi apparatus is the primary site of ribosome assembly and rRNA processing in eukaryotic cells
(C) The Golgi apparatus receives proteins from the rough endoplasmic reticulum, modifies them (including glycosylation and proteolytic processing), sorts them, and packages them into vesicles directed to their final destinations such as the plasma membrane, secretory vesicles, or lysosomes
(D) The Golgi apparatus directly replicates chromosomal DNA and distributes copies to daughter cells during cell division

Q4. Succinate dehydrogenase (Complex II) of the mitochondrial electron transport chain catalyzes the oxidation of succinate to fumarate. Which of the following correctly describes the electron acceptor in this reaction?

(A) NAD^+ is reduced to NADH as the electron acceptor in the succinate dehydrogenase reaction
(B) FMN (flavin mononucleotide) is the final electron acceptor that transfers electrons directly to cytochrome c
(C) FAD (flavin adenine dinucleotide) serves as the electron acceptor, being reduced to $FADH_2$, which then transfers electrons to ubiquinone (CoQ)

(D) Cytochrome b is the immediate electron acceptor from succinate in Complex II

Q5. A test cross is used to determine the unknown genotype of an organism displaying a dominant phenotype. The diagram below shows the outcome of such a cross. Which correctly describes the design of a test cross?



(A) The organism with the dominant phenotype is crossed with a homozygous recessive individual (e.g., aabb) to determine the unknown genotype from the offspring ratios

(B) A test cross is a cross between two heterozygous individuals to observe dominant-to-recessive phenotype ratios

(C) The organism with the dominant phenotype is crossed with another organism of the same dominant phenotype to confirm homozygosity

(D) A test cross uses only molecular (DNA) markers and does not rely on phenotypic ratios to infer genotype

Q6. Telomeres protect the ends of linear eukaryotic chromosomes from degradation and end-fusion. Which statement best describes the role of telomerase in maintaining chromosome integrity?

(A) Telomerase is a DNA-dependent DNA polymerase that copies existing telomeric sequences using the lagging strand as a template

(B) Telomerase uses a protein subunit template to add random nucleotide sequences that cap chromosome ends

(C) Telomerase shortens telomeres by removing oxidatively damaged bases through a base-excision mechanism

(D) Telomerase is a ribonucleoprotein enzyme that carries its own integral RNA template (containing the sequence AAUCCC) to synthesize

TTAGGG repeats at chromosome ends, counteracting telomere shortening

Q7. Horizontal gene transfer (HGT) in bacteria can occur by conjugation, transformation, or transduction. Which statement correctly describes *transduction*?

(A) Transduction involves the direct transfer of DNA between bacteria through a pilus established by cell-to-cell contact
(B) In transduction, a bacteriophage accidentally packages a portion of host bacterial DNA during its lytic cycle and transfers it to a new bacterial host upon infection
(C) Transduction requires the uptake of free exogenous DNA from the surrounding medium by a naturally competent bacterium
(D) Transduction is mediated by conjugative plasmids and requires the tra gene products to form a mating pair

Q8. Gram-negative bacteria differ structurally from Gram-positive bacteria in a key way that is clinically significant. Which statement correctly identifies this structural difference?

(A) Gram-negative bacteria have a much thicker peptidoglycan layer than Gram-positive bacteria, retaining crystal violet dye after decolourization
(B) Gram-negative bacteria contain teichoic acids and lipoteichoic acids embedded in and anchored to their thick peptidoglycan wall
(C) Gram-negative bacteria possess an outer membrane containing lipopolysaccharide (LPS), which acts as an endotoxin; this outer membrane is absent in Gram-positive bacteria
(D) Gram-negative bacteria completely lack peptidoglycan in their cell wall, relying solely on the outer membrane for structural support

Q9. Blotting techniques are used to detect specific biological molecules after gel electrophoresis and membrane transfer. Which description correctly defines a *Western blot* (immunoblot)?

(A) A Western blot separates proteins by SDS-PAGE, transfers them to a

nitrocellulose or PVDF membrane, and detects specific proteins using enzyme-linked antibodies

(B) A Western blot detects specific DNA sequences using a labeled complementary nucleic acid probe after agarose gel electrophoresis

(C) A Western blot is used to detect specific RNA molecules after separation on a denaturing gel and transfer to a membrane

(D) A Western blot relies on hybridization with a complementary oligonucleotide probe to identify protein sequences after transfer to a nylon membrane

Q10. Movement of molecules across biological membranes can be passive or active. Which statement correctly defines *primary active transport*?

(A) Primary active transport uses a concentration gradient to move molecules from regions of high concentration to low concentration without energy input

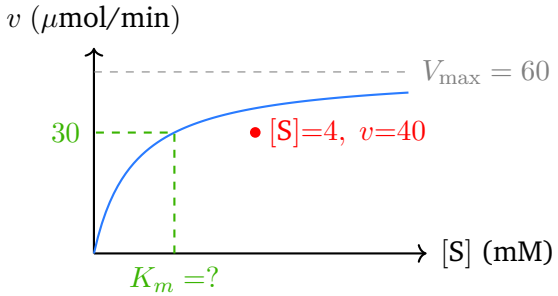
(B) Primary active transport is a type of facilitated diffusion that uses integral membrane carrier proteins but requires no ATP expenditure

(C) Primary active transport is the movement of water molecules across a semipermeable membrane along an osmotic gradient

(D) Primary active transport moves solutes against their electrochemical gradient by directly coupling transport to ATP hydrolysis, as exemplified by the Na^+/K^+-ATPase

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

Q11. An enzyme has $V_{\max} = 60\,\mu$mol/min. At [S] $= 4$ mM, the measured velocity is $v = 40\,\mu$mol/min. Calculate the Michaelis constant K_m for this enzyme.



(A) $4\,\text{mM}$
(B) $2\,\text{mM}$
(C) $8\,\text{mM}$
(D) $1\,\text{mM}$

Q12. In agarose gel electrophoresis of DNA, fragments are separated based on their size. Which statement correctly describes the migration behaviour of DNA fragments?

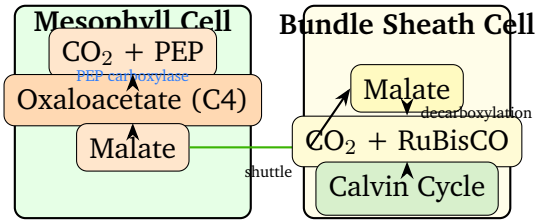
(A) Larger DNA fragments migrate farther from the wells toward the positive electrode because they carry more negative charges
(B) DNA fragments migrate toward the negative electrode because DNA is positively charged at neutral pH
(C) Smaller DNA fragments migrate faster and travel farther from the wells toward the positive electrode because they experience less frictional resistance in the agarose matrix
(D) Agarose gel electrophoresis separates DNA based on nucleotide base composition (GC content) rather than fragment length

Q13. Hsp70 is a molecular chaperone involved in protein quality control and folding. Which statement best describes the mechanism of Hsp70-assisted protein folding?

(A) Hsp70 recognizes exposed hydrophobic segments in unfolded polypeptides and uses ATP binding and hydrolysis cycles to facilitate repeated substrate binding and release, enabling correct folding
(B) Hsp70 forms a barrel-shaped cavity that completely encloses and isolates the substrate protein during folding, shielding it from the cytoplasm
(C) Hsp70 functions exclusively in the endoplasmic reticulum lumen (as BiP/GRP78) and is not found in the cytoplasm or mitochondria
(D) Hsp70 is a constitutively expressed, non-inducible protein whose expression level does not change in response to cellular stress or heat shock

Q14. C4 photosynthesis is an adaptation that reduces photorespiration in plants

growing in hot, bright environments. Which statement correctly describes the initial CO_2 fixation step in C4 plants?



(A) In C4 plants, CO_2 is initially fixed by RuBisCO in mesophyll cells to produce the 3-carbon compound 3-phosphoglycerate (3-PGA) as the first stable product

(B) In C4 plants, CO_2 is first incorporated into a 3-carbon compound (pyruvate) by PEP carboxylase, which then moves to bundle sheath cells

(C) C4 photosynthesis avoids photorespiration by using a temperature-insensitive form of RuBisCO that operates optimally at lower temperatures

(D) In C4 plants, CO_2 is initially fixed by phosphoenolpyruvate (PEP) carboxylase in mesophyll cells to form oxaloacetate (a 4-carbon compound), which shuttles CO_2 to bundle sheath cells for fixation by RuBisCO in the Calvin cycle

Q15. The restriction endonuclease EcoRI is widely used in recombinant DNA technology. Which statement correctly describes its recognition sequence and the type of ends it generates?

(A) EcoRI recognizes 5′-GGATCC-3′ and generates blunt ends by cutting exactly in the middle of the sequence

(B) EcoRI recognizes 5′-AAGCTT-3′ and generates 5′ overhangs of two nucleotides

(C) EcoRI recognizes 5′-GAATTC-3′ and cuts between G and A on both strands, generating 4-nucleotide 5′ overhangs (sticky ends: 5′-AATT)

(D) EcoRI recognizes a degenerate 4-bp sequence and generates 3′ overhangs (3′-recessed ends)

Q16. Cytotoxic T lymphocytes (CTLs) are essential effectors of adaptive cellular immunity. Which statement correctly describes how CTLs recognize target cells?

(A) CTLs express the CD4 co-receptor and recognize peptide antigens displayed on MHC Class II molecules present on professional antigen-presenting cells

(B) $CD8^+$ CTLs recognize peptide antigens presented on MHC Class I molecules, which are expressed on virtually all nucleated cells, enabling the killing of virus-infected or tumour cells

(C) $CD8^+$ CTLs primarily exert their effector function by secreting interleukins that stimulate B cells to undergo class switching and produce IgG antibodies

(D) CTLs recognize and bind free antigens (not MHC-bound) in the extracellular space, triggering apoptosis of nearby cells

Q17. During translation in bacteria, the ribosome encounters a stop codon in the mRNA A-site. Which statement correctly describes the molecular mechanism of translation termination?

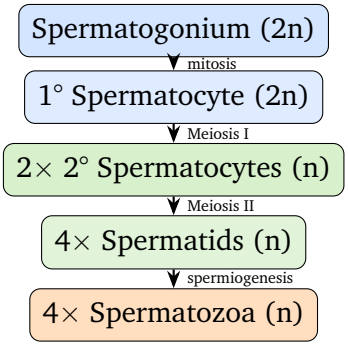
(A) In bacteria, stop codons (UAA, UAG, UGA) are recognized by protein release factors (RF1 and RF2)—not aminoacyl-tRNAs—which stimulate hydrolysis of the peptidyl-tRNA bond and release of the polypeptide

(B) Stop codons are decoded by specialized aminoacyl-tRNAs called release tRNAs that carry a water molecule in place of an amino acid and directly catalyse polypeptide release

(C) In bacteria, only a single release factor (RF3) is responsible for recognizing all three stop codons and cleaving the peptide chain

(D) Termination requires the Shine–Dalgarno sequence to base-pair with the $3'$ end of 16S rRNA, which causes the ribosome to dissociate

Q18. Spermatogenesis converts diploid spermatogonia into haploid spermatozoa through meiosis and differentiation. Which statement correctly describes the sequence of events?



(A) Spermatogonia undergo meiosis I directly to produce four primary spermatocytes, each already haploid (n)

(B) After meiosis II, two secondary spermatocytes together produce only two spermatids, yielding two spermatozoa per primary spermatocyte

(C) Secondary spermatocytes are diploid ($2n$) cells; they undergo meiosis I to produce haploid spermatids

(D) One primary spermatocyte ($2n$) completes meiosis I to form 2 secondary spermatocytes (n), which then complete meiosis II to yield 4 haploid spermatids, each maturing into a spermatozoon

Q19. Fatty acid biosynthesis (lipogenesis) and beta-oxidation (lipolysis) share intermediates but are distinct metabolic pathways. Which statement correctly contrasts fatty acid biosynthesis with beta-oxidation?

(A) Fatty acid biosynthesis occurs in the mitochondrial matrix and uses NADH as the reducing agent, mirroring beta-oxidation in the same compartment

(B) Fatty acid biosynthesis requires acetyl-CoA as the direct growing chain carrier and uses FAD as the electron donor throughout the elongation cycle

(C) Fatty acid biosynthesis occurs in the cytoplasm (cytosol), uses NADPH as the reductant, and employs acyl carrier protein (ACP) as the thioester intermediate carrier; beta-oxidation occurs in the mitochondrial matrix and produces NADH, $FADH_2$, and acetyl-CoA

(D) Fatty acid synthesis and beta-oxidation use the same set of enzymes but in opposite directions in the same subcellular compartment

Q20. Calculate the determinant of the 3×3 matrix

$$M = \begin{pmatrix} 2 & 1 & 0 \\ 1 & 3 & 1 \\ 0 & 1 & 2 \end{pmatrix}$$

(A) 5
(B) 8
(C) 10
(D) 12

Q21. The *trp* operon of *E. coli* encodes enzymes for tryptophan biosynthesis. Which statement correctly describes the role of tryptophan in regulating *trp* operon transcription?

(A) Tryptophan acts as a co-repressor: it binds to the otherwise inactive aporepressor protein and converts it into an active repressor that binds the *trp* operator, blocking transcription of the biosynthetic genes
(B) Tryptophan acts as an inducer: it binds to the active repressor and causes it to dissociate from the operator, allowing transcription of tryptophan biosynthetic genes
(C) The *trp* operon is constitutively expressed at maximum levels regardless of cellular tryptophan concentration; regulation occurs only at the translational level
(D) Tryptophan directly binds and activates RNA polymerase, stimulating enhanced transcription of the *trp* biosynthesis genes when tryptophan levels are low

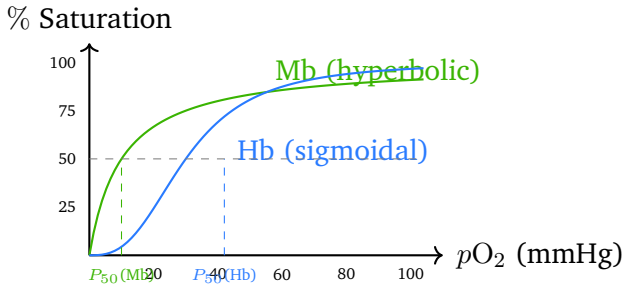
Q22. Receptor tyrosine kinases (RTKs) are key transducers of extracellular growth signals. Which statement correctly describes the initial events following ligand binding to an RTK?

(A) RTKs primarily signal through trimeric G-proteins that activate adenylyl cyclase to produce cAMP as a second messenger
(B) RTK signalling requires receptor internalization and translocation to the nucleus before kinase activity is triggered

(C) Ligand binding to RTKs induces receptor dimerization and transautophosphorylation of intracellular tyrosine residues, creating phosphotyrosine docking sites for SH2-domain-containing signalling proteins such as Grb2 and PI3K

(D) RTKs are constitutively active dimers that are negatively regulated by ligand binding, which causes receptor monomerization and kinase inactivation

Q23. Hemoglobin (Hb) and myoglobin (Mb) both bind oxygen, but their oxygen dissociation curves differ significantly. Which statement correctly describes the physiological significance of this difference?



(A) Hemoglobin shows a hyperbolic oxygen dissociation curve with a Hill coefficient $n = 1$, identical to that of myoglobin

(B) Myoglobin displays a sigmoidal oxygen binding curve due to cooperative interactions between its four subunits

(C) The cooperative binding of O_2 by hemoglobin reduces the efficiency of oxygen delivery to metabolically active peripheral tissues compared to myoglobin

(D) Hemoglobin displays a sigmoidal O_2 dissociation curve (Hill coefficient $n \approx 2.8$) due to cooperative interactions among its four subunits, enabling efficient O_2 loading in the lungs and efficient O_2 unloading in metabolically active tissues

Q24. ELISA (enzyme-linked immunosorbent assay) techniques differ in their design and sensitivity. Which statement correctly describes a *direct* ELISA?

(A) In a direct ELISA, a capture antibody is first coated on the plate, the antigen is then added and bound, and a second enzyme-conjugated detection antibody is used to quantify the antigen

(B) In a direct ELISA, the antigen is adsorbed directly onto the microplate well, and it is detected by a single enzyme-conjugated primary antibody that binds directly to the adsorbed antigen

(C) A direct ELISA uses an unlabeled primary antibody and a separate enzyme-conjugated secondary antibody to amplify the signal, making it more sensitive than other ELISA formats

(D) A direct ELISA is the most sensitive format because it uses three layers of antibodies (primary, secondary, and tertiary) for cascading signal amplification

Q25. Ecological succession describes directional changes in community composition over time. Which statement correctly distinguishes *secondary succession* from primary succession?

(A) Secondary succession begins on completely barren substrates (e.g., bare rock, newly formed volcanic islands) where soil must be built from scratch by pioneer organisms

(B) Secondary succession is always slower than primary succession because the original biological community must be entirely re-assembled from individual species dispersal

(C) Secondary succession occurs on previously occupied sites after disturbance (fire, logging, agriculture abandonment); it proceeds faster than primary succession because soil, nutrients, and seed banks are already present

(D) Secondary and primary succession always converge to identical climax communities regardless of the substrate or geographic location

Q26. Using the chain rule of differentiation, find $\frac{d}{dx}\left[e^{\sin x}\right]$:

(A) $e^{\sin x}\cos x$

(B) $e^{\cos x}$

(C) $e^{\sin x}(-\sin x)$

(D) $\cos x$

Q27. Agrobacterium tumefaciens harbours a Ti plasmid that is widely exploited as a plant transformation vector. Which statement correctly describes the

Ti plasmid system?

(A) The Ti plasmid is a large-insert cloning vector used to clone DNA fragments larger than 150 kb in Escherichia coli and is equivalent to a bacterial artificial chromosome (BAC)

(B) The Ti plasmid is a yeast episomal vector used to produce recombinant proteins in Saccharomyces cerevisiae via a galactose-inducible promoter

(C) The Ti plasmid's T-DNA integrates randomly into the Agrobacterium chromosome during tumorigenic infection, conferring enhanced virulence to the bacterium

(D) The T-DNA region of the Ti plasmid from Agrobacterium tumefaciens integrates stably and randomly into the nuclear genome of the host plant, making it a powerful vehicle for introducing transgenes into dicotyledonous plants

Q28. DNA repair pathways are specialized for different types of DNA damage. Which statement correctly describes *base excision repair* (BER)?

(A) BER is responsible for removing bulky helix-distorting lesions such as UV-induced cyclobutane pyrimidine dimers through a dual-incision mechanism that excises a 25–30 nucleotide oligomer

(B) BER removes small chemically modified bases, such as uracil (from cytosine deamination) and 8-oxoguanine (from oxidative damage), through the sequential action of a damage-specific DNA glycosylase followed by AP endonuclease

(C) BER corrects base-pair mismatches introduced during DNA replication by scanning newly synthesized strands for incorrectly paired bases and then excising and re-synthesizing a patch of DNA

(D) BER requires the XPC-RAD23B sensor complex to recognize DNA damage, followed by unwinding by TFIIH helicases and dual incision flanking the lesion

Q29. Lysosomes and late endosomes cooperate in the degradation of intracellular and endocytosed material. Which statement best describes lysosomal acidification?

(A) Lysosomal lumenal pH (∼7.4) is maintained at physiological levels by the Na^+/K^+-ATPase, which exchanges cytosolic Na^+ for K^+ and indirectly regulates proton concentration

(B) Lysosomal acid hydrolases are most active at neutral pH (7.0–7.4) and are irreversibly denatured at the low pH found in the lysosomal lumen

(C) The acidic lumenal pH of lysosomes (∼pH 5) is generated and maintained by the vacuolar-type H^+-ATPase (V-ATPase), which uses ATP to pump protons into the lumen, activating the resident acid hydrolases

(D) Late endosomes and lysosomes are entirely separate organelle populations that never fuse; degradation occurs exclusively in the late endosome

Q30. The TCA (Krebs) cycle generates both reduced cofactors (for the ETC) and one molecule synthesized by substrate-level phosphorylation. Which correctly identifies this substrate-level phosphorylation event?

(A) One GTP is produced per TCA cycle turn by substrate-level phosphorylation at the succinyl-CoA synthetase step (conversion of succinyl-CoA to succinate)

(B) Three ATP molecules are produced by substrate-level phosphorylation per turn of the TCA cycle

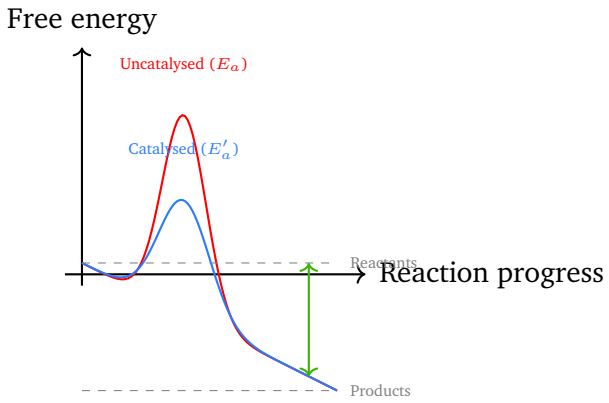
(C) Substrate-level phosphorylation in the TCA cycle occurs at the isocitrate dehydrogenase step, producing ATP directly from ADP + P_i

(D) No substrate-level phosphorylation occurs in the TCA cycle; all ATP synthesis from TCA metabolites proceeds exclusively through oxidative phosphorylation

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 correctly describe properties of enzyme catalysts?



(A) Enzymes lower the activation energy of a reaction, increasing the rate at which equilibrium is reached

(B) Enzymes are highly substrate-specific, typically binding only one or a small class of substrates due to complementarity of active site and substrate

(C) Enzymes change the equilibrium constant (K_{eq}) of the reaction they catalyse, shifting the thermodynamic balance toward products

(D) Enzymes are not consumed or permanently altered during catalysis and can participate in multiple reaction cycles

Q32. Which of the following are *essential* features required for a DNA molecule to function as a plasmid-based cloning vector in *E. coli*?

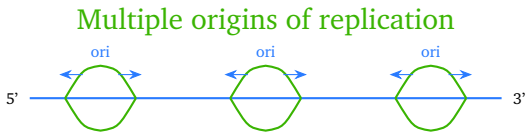
(A) An origin of replication (ori) that is functional in *E. coli*, allowing autonomous plasmid replication

(B) At least one selectable marker gene (e.g., an antibiotic resistance gene) to identify and select transformed colonies

(C) A multiple cloning site (MCS or polylinker) containing several unique restriction enzyme recognition sequences for insertion of foreign DNA

(D) Structural genes encoding viral capsid proteins required for packaging and delivering the vector DNA into host cells

Q33. Eukaryotic DNA replication differs from prokaryotic replication in several key features. Which of the following correctly describe features of *eukaryotic* DNA replication?



(A) Eukaryotic chromosomes fire replication from multiple origins of replication simultaneously, enabling rapid duplication of large genomes

(B) Eukaryotic DNA replication uses RNA-dependent DNA polymerase (reverse transcriptase) to initiate replication at origins

(C) The lagging strand is synthesised as discontinuous Okazaki fragments that are later joined by DNA ligase

(D) Telomerase uses its integral RNA template to extend the 3′ ends of linear chromosomes, preventing progressive telomere shortening

Q34. Which of the following statements correctly describe outcomes and features of anaerobic fermentation?

(A) In yeast under anaerobic conditions, pyruvate is decarboxylated to acetaldehyde, which is then reduced to ethanol with concomitant release of CO_2

(B) Anaerobic fermentation generates ATP through oxidative phosphorylation using O_2 as the terminal electron acceptor

(C) Fermentation regenerates NAD^+ from NADH, allowing glycolysis to continue and produce 2 ATP per glucose in the absence of O_2

(D) Anaerobic fermentation requires molecular oxygen (O_2) as the terminal electron acceptor for reoxidation of NADH

Q35. Which of the following RNA species are found in eukaryotic cells and play the stated roles?

(A) mRNA (messenger RNA) carries the genetic information transcribed from DNA to ribosomes, where it is translated into protein

(B) tRNA (transfer RNA) decodes mRNA codons at the ribosome and delivers the corresponding amino acid to the growing polypeptide chain

(C) Ribozymes (catalytic RNA molecules) catalyse *all* biochemical reactions in the cell, entirely replacing protein enzymes

(D) rRNA (ribosomal RNA) is both a structural component and a catalytic

component of ribosomes (e.g., 23S/28S rRNA catalyses peptide bond formation)

Q36. CRISPR-Cas9 has been adapted for a broad range of genome engineering applications beyond simple gene editing. Which of the following are validated applications of the CRISPR-Cas9 system?

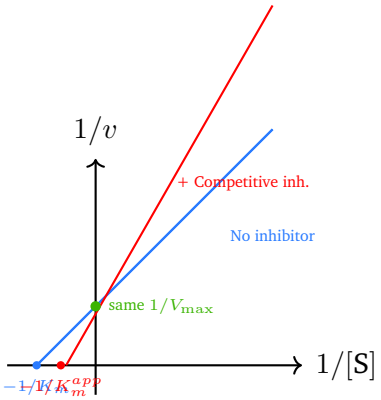
(A) Gene knockout via non-homologous end joining (NHEJ) repair of Cas9-induced double-strand breaks

(B) Precise gene correction by homology-directed repair (HDR) using a co-delivered donor DNA template

(C) Transcriptional activation of endogenous genes using catalytically dead dCas9 fused to transcriptional activator domains (CRISPRa)

(D) CRISPR-Cas9 can only function in human and mouse cell lines because it requires mammalian-specific nuclear import machinery

Q37. Competitive inhibition is a reversible form of enzyme inhibition. Which of the following statements about competitive inhibition are correct?



(A) Competitive inhibition increases the apparent K_m, reflecting decreased apparent affinity of the enzyme for its substrate

(B) Competitive inhibitors decrease the $V_{\max}$ of the enzyme by blocking the active site even at saturating substrate concentrations

(C) The $V_{\max}$ is unchanged in the presence of a competitive inhibitor because excess substrate can outcompete the inhibitor for the active site

(D) Competitive inhibition cannot be overcome by increasing the substrate concentration because the inhibitor binds irreversibly to the

active site

Q38. Agricultural biotechnology has produced several commercially significant crops. Which of the following are documented applications of agricultural biotechnology?

(A) Bt crops engineered to express insecticidal Cry proteins (from *Bacillus thuringiensis*) to control lepidopteran and coleopteran pests
(B) Herbicide-tolerant crops (e.g., Roundup Ready® soybean) generated by introducing a glyphosate-resistant EPSPS enzyme
(C) Golden Rice was developed to produce pharmacological insulin in the grain endosperm as a low-cost diabetes treatment
(D) Disease-resistant crops created using CRISPR-Cas9 to disrupt host susceptibility genes required for pathogen infection

Q39. The bacterial growth curve describes distinct phases of population dynamics in a closed batch culture. Which statements correctly describe these phases?

(A) During the lag phase, bacteria adapt metabolically to their new environment (synthesising new enzymes, repairing damage); there is no net increase in cell number
(B) During the exponential (log) phase, the growth rate is at its maximum and constant, following first-order kinetics with respect to cell number
(C) During the stationary phase, the rate of new cell formation equals the rate of cell death, resulting in no net change in viable cell count
(D) The stationary phase is characterized by the highest growth rate because bacteria have fully adapted to their environment

Q40. Chromosomal structural mutations involve changes to the organization of genetic material within chromosomes. Which of the following are types of chromosomal *structural* mutations?

(A) Deletion: loss of a chromosomal segment, resulting in reduced gene dosage

(B) Duplication: presence of an extra copy of a chromosomal segment, leading to increased gene dosage

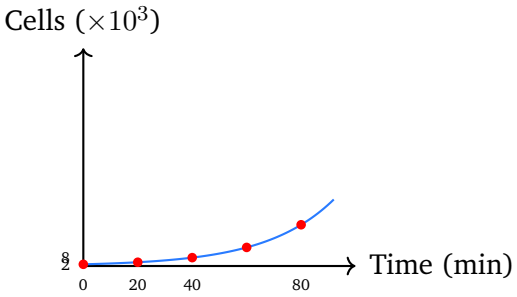
(C) Inversion: a chromosomal segment is excised and reinserted in the reverse orientation, altering gene order

(D) Aneuploidy: gain or loss of one or more whole chromosomes, as in trisomy ($2n+1$) or monosomy ($2n$-1)

Section C — Numerical Answer Type (NAT)

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

Q41. A bacterial culture starts at 2×10^3 CFU/mL. The doubling time is 20 minutes. The cell density (in units of $\times 10^3$ CFU/mL) after exactly 2 hours is:



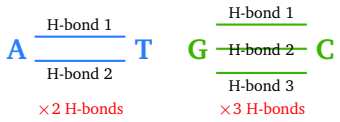
Q42. A linear polypeptide chain consists of 30 amino acid residues. How many peptide bonds are present in this polypeptide?

Q43. A sample of double-stranded DNA has an adenine (A) + thymine (T) content of 52%. What is the guanine + cytosine (G+C) content expressed as a percentage?

Q44. How many codons in the standard genetic code specify the amino acid **Arginine**? (Consider all sense codons from all codon families assigned to Arginine.)

Q45. In a large, randomly mating population the frequency of allele A is $p = 0.8$ and the frequency of allele a is $q = 0.2$. Under Hardy–Weinberg equilibrium, the expected frequency of homozygous dominant (AA) genotype as a decimal is:

Q46. A linear double-stranded DNA molecule of 300 bp has 60% AT content (180 AT base pairs) and 40% GC content (120 GC base pairs). Recall that A-T pairs are held by 2 hydrogen bonds and G-C pairs by 3 hydrogen bonds. The total number of hydrogen bonds in this molecule is:



Q47. How many net ATP molecules are produced by substrate-level phosphorylation during glycolysis starting from one molecule of glucose? (Do not count ATP produced by oxidative phosphorylation from NADH/$FADH_2$.)

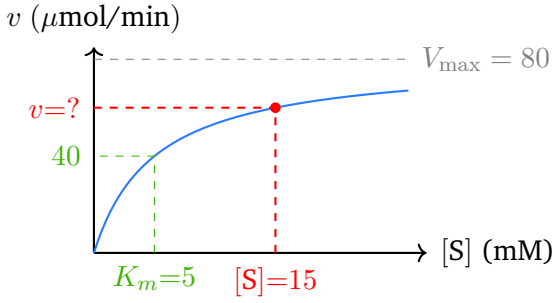
Q48. A radioactive isotope has a half-life ($t_{1/2}$) of 14 days. What fraction of the original radioactivity remains after 56 days? (Express as a decimal.)

Q49. A buffer solution contains 0.1 M NH_4Cl and 0.1 M NH_3 (pK_a of NH_4^+ = 9.25). Using the Henderson–Hasselbalch equation, the pH of this buffer is:

Q50. A circular plasmid of 5000 bp is digested separately with two restriction enzymes. HindIII cuts the plasmid into 3 fragments (3 cut sites) and EcoRI cuts it into 2 fragments (2 cut sites), with no overlapping recognition sites. When the plasmid is digested simultaneously with both HindIII and EcoRI, the maximum number of fragments expected is:

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

Q51. An enzyme has $K_m = 5\,\text{mM}$ and $V_{\max} = 80\,\mu\text{mol/min}$. Calculate the reaction velocity v (in μmol/min) at a substrate concentration of $[\text{S}] = 15\,\text{mM}$.



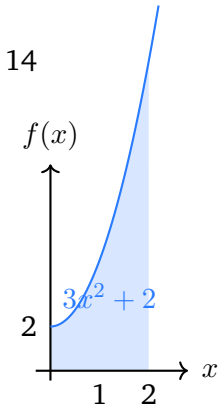
Q52. Starting with a single double-stranded DNA template molecule, how many double-stranded DNA molecules are present after 10 complete PCR cycles (assuming 100% efficiency at every cycle)?

Q53. Find the value of $f'(x)$ at $x = 1$, where $f(x) = 3x^4 - 2x^2 + 5x - 1$.

Q54. The following dataset contains 8 measurements: $\{2,\ 4,\ 4,\ 6,\ 8,\ 8,\ 10,\ 12\}$. What is the **median** of this dataset?

Q55. A bacterial population starts with 10^4 cells. The generation (doubling) time is 20 minutes. After exactly 1 hour, the number of cells (expressed in units of $\times 10^4$) is:

Q56. Evaluate the definite integral $\displaystyle\int_0^2 \left(3x^2 + 2\right) dx$.



Q57. In a large population, the frequency of allele A is $p = 0.3$ and of allele a is $q = 0.7$. Under Hardy–Weinberg equilibrium, the expected frequency of heterozygous individuals (Aa) is:

Q58. An enzyme preparation has a total activity of 300 Units (U) and a total protein content of 15 mg. The specific activity of the enzyme (in U/mg) is:

Q59. A protein consists of 180 amino acid residues. Assuming an average residue molecular mass of 110 Da, the approximate molecular weight of the protein (in Daltons) is:

Q60. In a randomly mating population of 400 individuals, 16 individuals display the albino phenotype (homozygous recessive, genotype aa). Assuming Hardy–Weinberg equilibrium, the expected number of heterozygous carriers (Aa) in the population is:

Answer Key — IIT JAM Biotechnology Sample Paper 4

Section A — MCQ (Q1–Q30)

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

Section B — MSQ (Q31–Q40)

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

Section C — NAT (Q41–Q60)

Q	Answer	Q	Answer	Q	Answer	Q	Answer
41	128	46	720	51	60	56	12
42	29	47	2	52	1024	57	0.42
43	48	48	0.0625	53	13	58	20
44	6	49	9.25	54	7	59	19800
45	0.64	50	5	55	8	60	128

Detailed Solutions

SECTION A — MCQ

Q1. **Answer: (D)**

Solution

Beta-sheet hydrogen bonds form between backbone carbonyl (C=O) and amide (N–H) groups of *adjacent* strands — not between side chains (R groups). In **antiparallel** beta-sheets the two strands run in opposite directions (N→C and C→N), so backbone groups face each other directly, producing *linear*, stronger H-bonds. In **parallel** beta-sheets both strands run N→C, forcing the H-bonds to be slightly skewed and therefore weaker. Option A is wrong (side chains); B is wrong (antiparallel, not parallel, has more linear bonds); C is wrong (inter-molecular beta-sheets are common). **(D)**

Q2. **Answer: (A)**

Solution

Photosystem I (PSI) is also called P700 (absorbs maximally at 700 nm). Excited electrons from PSI are passed to ferredoxin (Fd), and ferredoxin-NADP$^+$ reductase (FNR) then reduces NADP$^+$ to NADPH. PSI does *not* oxidize water (that is PSII/P680) and does not transfer electrons to plastoquinone (that is PSII). **(A)**

Q3. **Answer: (C)**

Solution

The **Golgi apparatus** (Golgi complex) is the central sorting and processing station of the secretory pathway. Proteins synthesized on the rough ER enter the cis-Golgi network and transit through the medial and trans cisternae, where enzymes carry out **post-translational modifications** such as N-linked and O-linked glycosylation, sulfation, and proteolytic trimming. At the trans-Golgi network (TGN), proteins are sorted and packaged into distinct vesicle populations destined for the plasma membrane (constitutive or regulated secretion), lysosomes (via mannose-6-phosphate receptors), or retention in the Golgi itself. ATP synthesis is a mitochondrial function (option A); ribosome assembly occurs in the nucleolus (option B); DNA replication is a nuclear function (option D). **(C)**

Q4. **Answer: (C)**

Solution

Succinate dehydrogenase (Complex II) catalyses: Succinate + FAD $\rightarrow$ Fumarate + $FADH_2$. The prosthetic group FAD (covalently bound) accepts the two electrons and two protons from succinate, becoming $FADH_2$. $FADH_2$ then passes its electrons directly to ubiquinone (CoQ). Complex II does *not* use NAD^+ (no NADH is produced) and does not pump protons across the inner mitochondrial membrane. **(C)**

Q5. **Answer: (A)**

Solution

A **test cross** (also called a back-cross) crosses an organism of unknown genotype (showing the dominant phenotype) with a homozygous recessive individual (e.g., *aa* or *aabb*). If all offspring show the dominant phenotype the unknown parent is homozygous dominant (AA); if 50% show dominant and 50% show recessive phenotypes, the unknown parent is heterozygous (Aa). The Punnett square in the question illustrates the Aa $\times$ aa cross giving a 1:1 ratio. **(A)**

Q6. **Answer: (D)**

Solution

Telomerase is a **ribonucleoprotein** reverse transcriptase. Its integral RNA component (TERC) contains the template sequence 3′-AAUCCC-5′, which is used to synthesize TTAGGG repeats onto the 3′ overhang of the leading-strand template. This counteracts the end-replication problem and prevents progressive telomere shortening. Telomerase is not a conventional DNA-dependent DNA polymerase and does not use a protein template. **(D)**

Q7. **Answer: (B)**

Solution

Transduction is the transfer of bacterial DNA mediated by a bacteriophage. During a lytic infection, the phage occasionally packages a fragment of host chromosomal DNA (generalised transduction) or integrates near host genes (specialised transduction). When this phage infects a new host, it delivers the bacterial DNA. This differs from **conjugation** (cell-to-cell contact via pilus) and **transformation** (uptake of free DNA). **(B)**

Q8. **Answer: (C)**

Solution

Gram-negative bacteria possess an **outer membrane** external to the thin peptidoglycan layer. The outer membrane's outer leaflet is composed of **lipopolysaccharide (LPS)**, also called endotoxin, which activates TLR4 and can cause septic shock. Gram-positive bacteria lack this outer membrane and have a much thicker peptidoglycan layer instead. Teichoic acids are characteristic of Gram-positive bacteria. **(C)**

Q9. **Answer: (A)**

Solution

A **Western blot** (immunoblot) detects specific proteins. Proteins are denatured and separated by SDS-PAGE, then transferred electrophoretically to a nitrocellulose or PVDF membrane. The membrane is blocked, incubated with a primary antibody specific to the target protein, and then with an enzyme-conjugated secondary antibody; the enzyme (e.g., HRP) produces a detectable signal. Southern blot detects DNA; Northern blot detects RNA. **(A)**

Q10. **Answer: (D)**

Solution

Primary active transport directly couples the uphill movement of solutes (against their electrochemical gradient) to ATP hydrolysis. The Na^+/K^+-ATPase is the classic example: it pumps 3 Na^+ out and 2 K^+ in per ATP hydrolysed. Facilitated diffusion and osmosis are passive processes that require no energy and move solutes/water down their gradients. **(D)**

Q11. **Answer: (B)**

Solution

Using the Michaelis–Menten equation:

$$v = \frac{V_{\max}[\mathrm{S}]}{K_m + [\mathrm{S}]}$$

$$40 = \frac{60 \times 4}{K_m + 4} \;\Rightarrow\; 40(K_m + 4) = 240 \;\Rightarrow\; 40K_m = 80 \;\Rightarrow\; K_m = 2\,\mathrm{mM}$$

(B)

Q12. **Answer: (C)**

Solution

DNA is negatively charged (phosphate backbone) and migrates toward the **positive electrode** (anode). **Smaller** fragments pass through the agarose pores more easily and travel farther in a given time, while larger fragments are retarded by the gel matrix. Separation is based on size (length in bp), not base composition. **(C)**

Q13. **Answer: (A)**

Solution

Hsp70 recognizes short hydrophobic peptide segments that are exposed in unfolded or partially folded proteins. On binding, Hsp70 is in the ATP-bound (low-affinity) state. ATP hydrolysis switches it to the ADP-bound (high-affinity, closed) conformation, clamping the substrate. Nucleotide exchange factors catalyse ADP→ATP exchange, reopening the binding cleft and releasing the substrate to try folding again. This cycle repeats until the protein folds correctly. The barrel-shaped cavity description refers to the GroEL/GroES (Hsp60) chaperonin, not Hsp70. Hsp70 is found in the cytoplasm, ER (as BiP), and mitochondria. **(A)**

Q14. **Answer: (D)**

Solution

In C4 plants, CO_2 is first fixed in **mesophyll cells** by **phosphoenolpyruvate (PEP) carboxylase**, which has a much higher affinity for CO_2 than RuBisCO and is not inhibited by O_2. PEP + CO_2 → oxaloacetate (a **4-carbon** compound). Oxaloacetate is converted to malate or aspartate, which diffuses to the **bundle sheath cells**. There, CO_2 is released by decarboxylation and re-fixed by RuBisCO in the Calvin cycle. This CO_2-concentrating mechanism suppresses photorespiration. **(D)**

Q15. **Answer: (C)**

Solution

EcoRI recognizes the palindromic sequence 5′-**GAATTC**-3′ and cuts between G and A on both strands:

5’-G ↓ AATTC-3’

3’-CTTAA ↑ G-5’

This generates a 4-nucleotide 5′ overhang (5′-AATT), called a sticky end. BamHI recognizes GGATCC; HindIII recognizes AAGCTT. **(C)**

Q16. **Answer: (B)**

Solution

CD8$^+$ cytotoxic T lymphocytes (CTLs) use their T-cell receptor (TCR) together with the CD8 co-receptor to recognize peptide antigens of 8–10 residues presented in the groove of **MHC Class I** molecules. MHC I is expressed on all nucleated cells, so CTLs can survey and eliminate virus-infected cells, tumour cells, or cells presenting foreign peptides. MHC Class II, in contrast, presents peptides to CD4$^+$ helper T cells. **(B)**

Q17. **Answer: (A)**

Solution

When a stop codon (UAA, UAG, or UGA) enters the ribosomal A-site, it is recognized by protein **release factors**, *not* by aminoacyl-tRNAs (there are no corresponding tRNAs). In bacteria, **RF1** recognizes UAA and UAG; **RF2** recognizes UAA and UGA. These factors mimic tRNA shape, enter the A-site, stimulate peptidyl transferase to catalyse hydrolysis of the ester bond between the polypeptide and the P-site tRNA, and the completed protein is released. **(A)**

Q18. **Answer: (D)**

Solution

During spermatogenesis: (1) Spermatogonia ($2n$) undergo mitosis to maintain the stem-cell pool, with some progeny differentiating into primary spermatocytes ($2n$). (2) Primary spermatocytes complete **meiosis I** to produce two secondary spermatocytes (n, but with duplicated chromatids). (3) Secondary spermatocytes complete **meiosis II** to produce four spermatids (n, single chromatids). (4) Each spermatid differentiates into a mature spermatozoon by spermiogenesis. Thus one primary spermatocyte ultimately yields four haploid spermatozoa. **(D)**

Q19. **Answer: (C)**

Solution

Fatty acid **synthesis** (de novo lipogenesis) occurs in the **cytosol**, uses **NADPH** as the reductant (from the pentose phosphate pathway), and the growing acyl chain is carried as a thioester on **acyl carrier protein (ACP)** within the fatty acid synthase (FAS) complex. Beta-oxidation occurs in the **mitochondrial matrix** and produces NADH, $FADH_2$, and acetyl-CoA. They use different enzymes, different co-factors, and different compartments—and are not simply the reverse of each other. **(C)**

Q20. **Answer: (B)**

Solution

Expanding along the first row:

$$\det(M) = 2\det\begin{pmatrix}3 & 1\\ 1 & 2\end{pmatrix} - 1\det\begin{pmatrix}1 & 1\\ 0 & 2\end{pmatrix} + 0$$

$$= 2(6-1) - 1(2-0) = 10 - 2 = \mathbf{8}$$

(B)

Q21. **Answer: (A)**

Solution

The *trp* operon encodes tryptophan biosynthetic enzymes. The repressor protein TrpR is synthesised in an inactive form (aporepressor) that cannot bind the operator on its own. When cellular tryptophan levels are high, tryptophan acts as a **co-repressor**: it binds the aporepressor, inducing a conformational change that gives the TrpR–Trp complex high affinity for the *trp* operator. This blocks RNA polymerase access, shutting down gene transcription. When tryptophan is scarce, the aporepressor is inactive and the operon is expressed. This is opposite to the lac operon, where allolactose *inactivates* (de-represses) the repressor. **(A)**

Q22. **Answer: (C)**

Solution

Ligand binding to an RTK induces **receptor dimerization** (or oligomerization). The two cytoplasmic kinase domains of the dimer cross-phosphorylate each other on specific tyrosine residues (**transautophosphorylation**). These phosphotyrosine motifs serve as docking sites for adapter proteins containing **SH2 domains** (e.g., Grb2, Shc, PI3K p85 subunit), which relay signals to downstream pathways such as Ras/MAPK and PI3K/Akt. GPCRs (not RTKs) signal via trimeric G-proteins. **(C)**

Q23. **Answer: (D)**

Solution

Hemoglobin (Hb) is a tetramer ($\alpha_2\beta_2$) that displays **cooperative** O_2 binding: binding of the first O_2 increases affinity for subsequent molecules. This gives a **sigmoidal** O_2 dissociation curve with a Hill coefficient $n \approx 2.8$. Myoglobin (Mb) is a monomer with a **hyperbolic** curve ($n = 1$, no cooperativity). The sigmoidal shape means Hb loads O_2 efficiently in the lungs (high pO_2, steep part of the sigmoid) and unloads it efficiently in active tissues (lower pO_2, steep part of the sigmoid), an

advantage over myoglobin's hyperbolic curve. **(D)**

Q24. **Answer: (B)**

Solution

In a **direct ELISA**: (1) the **antigen** is adsorbed directly onto the microplate well surface; (2) a single **enzyme-conjugated primary antibody** (specific to the antigen) is added and binds the antigen; (3) a substrate is added and the enzyme produces a colorimetric/fluorescent signal. A **sandwich ELISA** uses a capture antibody (coated on plate) + detection antibody (enzyme-labelled). An **indirect ELISA** uses unlabeled primary + enzyme-labelled secondary antibody. **(B)**

Q25. **Answer: (C)**

Solution

Secondary succession occurs on sites previously occupied by a community that was disrupted by disturbance (fire, flood, logging, agriculture). Critically, the **soil** is already present and may contain seed banks, spores, root networks, and organic matter. This allows rapid re-establishment ($\sim$decades to centuries vs. millennia for primary succession on bare rock). **Primary succession** starts on substrate that has never been colonized (volcanic rock, glacial till). **(C)**

Q26. **Answer: (A)**

Solution

By the chain rule, $\frac{d}{dx}[f(g(x))] = f'(g(x)) \cdot g'(x)$. Here $f(u) = e^u$ and $g(x) = \sin x$:

$$\frac{d}{dx}\left[e^{\sin x}\right] = e^{\sin x} \cdot \cos x$$

(A)

Q27. **Answer: (D)**

Solution

The **Ti (tumour-inducing) plasmid** of *Agrobacterium tumefaciens* carries a **T-DNA** (transferred DNA) region flanked by 25-bp border repeats. During infection, T-DNA is excised, transferred into the plant cell, and integrates randomly into the **plant nuclear genome**. For cloning purposes, the oncogenes on T-DNA are replaced with the gene of interest (disarmed Ti plasmid); virulence genes on the Ti plasmid still

supply the transfer machinery in trans. This system works best in dicots; monocot transformation uses particle bombardment or modified Agrobacterium strains. **(D)**

Q28. **Answer: (B)**

Solution

Base excision repair (BER) corrects *small*, non-helix-distorting base modifications: (1) a damage-specific **DNA glycosylase** cleaves the N-glycosidic bond, releasing the damaged base and creating an AP (abasic/apurinic/apyrimidinic) site; (2) **AP endonuclease** (APE1) nicks the phosphodiester backbone at the AP site; (3) DNA polymerase (Pol β) fills the single-nucleotide gap; (4) DNA ligase seals the nick. Common substrates: uracil (from C deamination), 8-oxoG (from oxidation), and alkylated bases. NER handles bulky lesions; MMR handles replication mismatches. **(B)**

Q29. **Answer: (C)**

Solution

The **V-type H^+-ATPase** (vacuolar ATPase) is an electrogenic proton pump present in the membranes of lysosomes and late endosomes. It uses ATP hydrolysis to pump H^+ ions *into* the lumen, establishing the acidic pH (≈4.5–5.5) essential for optimal activity of the resident acid hydrolases (cathepsins, acid lipase, etc.). Inhibition of V-ATPase with bafilomycin A1 or concanamycin raises lysosomal pH and blocks degradation. The Na^+/K^+-ATPase is a plasma membrane pump and does not acidify lysosomes. **(C)**

Q30. **Answer: (A)**

Solution

Per turn of the TCA cycle, substrate-level phosphorylation occurs at the **succinyl-CoA synthetase** step:

$$\text{Succinyl-CoA} + \text{GDP} + P_i \rightarrow \text{Succinate} + \text{GTP} + \text{CoA}$$

This produces **1 GTP** (equivalent to 1 ATP). All other energy-releasing steps of the TCA cycle produce NADH or $FADH_2$, which yield ATP via oxidative phosphorylation in the ETC. **(A)**

SECTION B — MSQ

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

Solution

(A) Correct: Enzymes lower the activation energy (E_a) by stabilizing the transition state, increasing the reaction rate. They do not change the overall ΔG of the reaction. **(B) Correct:** Enzyme active sites are precisely shaped by evolution to bind specific substrates with high specificity (lock-and-key / induced fit). **(C) WRONG:** Enzymes do *not* change the thermodynamic equilibrium constant (K_{eq}); they only accelerate the rate at which equilibrium is approached. **(D) Correct:** Enzymes emerge from the reaction unchanged and can catalyse many cycles — they are true catalysts. Correct options: **(A), (B), (D)**.

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

Solution

(A) Correct: An origin of replication (ori) allows the plasmid to replicate autonomously in the host without relying on integration. **(B) Correct:** A selectable marker (antibiotic resistance) allows identification and maintenance of transformed bacteria under selection pressure. **(C) Correct:** A multiple cloning site (MCS/polylinker) provides unique restriction enzyme sites for directional insertion of foreign DNA. **(D) WRONG:** Simple plasmid vectors do not require viral capsid genes; these are only needed for virus-like particle or phage packaging systems. Correct options: **(A), (B), (C)**.

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

Solution

(A) Correct: Eukaryotic genomes replicate from hundreds to thousands of origins of replication simultaneously (e.g., ARS elements in yeast), enabling the entire large genome to be copied within the S phase. **(B) WRONG:** Eukaryotic DNA replication uses a *DNA-dependent RNA polymerase* (primase) to synthesize short RNA primers, and then DNA polymerase δ/ε extends them. Reverse transcriptase (RNA-dependent DNA polymerase) is not used in standard nuclear replication. **(C) Correct:** On the lagging strand, DNA synthesis is discontinuous; primase repeatedly makes new RNA primers ahead of the fork, and Pol δ synthesizes short Okazaki fragments (100–200 nt in eukaryotes) that are later joined. **(D) Correct:** Telomerase (TERT + TERC) extends the 3′ telomeric overhang of linear chromosomes by copying its internal RNA template, preventing the loss of genetic information at chromosome ends due to the end-replication problem. Correct options: **(A), (C), (D)**.

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

Solution

(A) Correct: In *Saccharomyces cerevisiae* and other yeasts, pyruvate is decarboxylated to acetaldehyde by pyruvate decarboxylase (requiring TPP), and acetaldehyde is then reduced to ethanol by alcohol dehydrogenase using NADH, releasing CO_2. **(B) WRONG:** Oxidative phosphorylation requires O_2 (or another terminal electron acceptor) and the ETC. Anaerobic fermentation, by definition, occurs without O_2; ATP comes only from substrate-level phosphorylation in glycolysis. **(C) Correct:** The reduction of pyruvate (or acetaldehyde) regenerates NAD^+ from NADH, maintaining the cellular NAD^+/NADH ratio and allowing glycolysis to continue producing 2 net ATP per glucose. **(D) WRONG:** Fermentation is anaerobic and does not use O_2. Correct options: **(A), (C)**.

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

Solution

(A) Correct: mRNA is the product of transcription and serves as the template for ribosomal translation into protein. **(B) Correct:** tRNA molecules carry amino acids (as aminoacyl-tRNAs) and decode mRNA codons via anticodon–codon base pairing at the ribosome. **(C) WRONG:** Ribozymes are RNA molecules with catalytic activity, but they catalyse only a limited set of reactions (e.g., pre-mRNA splicing by the spliceosome, peptidyl transferase activity of 23S/28S rRNA). Protein enzymes perform the vast majority of cellular reactions. **(D) Correct:** rRNA is the structural scaffold and catalytic engine of the ribosome; the peptidyl transferase centre of the large subunit is composed of rRNA, making the ribosome a ribozyme. Correct options: **(A), (B), (D)**.

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

Solution

(A) Correct: Cas9 guided by an sgRNA makes a blunt double-strand break; NHEJ introduces insertions/deletions (indels) that typically disrupt the reading frame, knocking out gene function. **(B) Correct:** If a donor template with homology arms is co-delivered with Cas9/sgRNA, homology-directed repair (HDR) can introduce precise sequence changes (point mutation corrections, insertions). **(C) Correct:** Catalytically inactive dCas9 (D10A/H840A) retains sgRNA-guided DNA binding but cannot cut; fusion to VP64, p65, Rta, or other transcriptional activator domains enables CRISPR activation (CRISPRa) to upregulate target genes. **(D) WRONG:** CRISPR-Cas9 has been successfully used in bacteria, yeast, plants, insects, fish, rodents, primates, and human cells. It relies only on Watson–Crick base pairing and general cellular DNA repair machinery. Correct options: **(A), (B), (C)**.

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

Solution

(A) Correct: A competitive inhibitor occupies the active site, competing with substrate. This *decreases* the apparent affinity (increases apparent K_m^{app}): more substrate is needed to half-saturate the enzyme. **(B) WRONG:** $V_{\max}$ is *unchanged* in competitive inhibition. At sufficiently high [S] the inhibitor is outcompeted and the enzyme achieves full velocity. **(C) Correct:** Because the inhibitor and substrate compete for the *same* active site, excess substrate can displace the inhibitor, restoring $V_{\max}$. The Lineweaver–Burk plot for competitive inhibition shows lines intersecting on the $1/v$ axis (same y-intercept = same $V_{\max}$) with different slopes (different K_m^{app}). **(D) WRONG:** Competitive inhibition is typically reversible; the inhibitor dissociates from the active site. Irreversible inhibitors (e.g., DFPP) permanently modify the enzyme. Correct options: **(A), (C)**.

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

Solution

(A) Correct: Bt crops (e.g., Bt cotton, Bt corn) are engineered to express *cry* genes from *Bacillus thuringiensis*. Cry proteins form pores in the midgut epithelium of susceptible insects (Lepidoptera, Coleoptera). **(B) Correct:** Herbicide-tolerant crops such as Roundup Ready® soybean, corn, and cotton express a glyphosate-resistant EPSPS (5-enolpyruvylshikimate-3-phosphate synthase) from *Agrobacterium* strain CP4, allowing glyphosate application to kill weeds without harming the crop. **(C) WRONG:** Golden Rice was engineered to produce β-carotene (pro-vitamin A) in the endosperm to address vitamin A deficiency, *not* insulin. Insulin is produced in microbial or mammalian cell systems. **(D) Correct:** CRISPR-Cas9 disruption of plant susceptibility genes (e.g., *MLO* for powdery mildew resistance in wheat and barley, *eIF4E* for virus resistance) has been demonstrated in several crop species. Correct options: **(A), (B), (D)**.

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

Solution

(A) Correct: During the **lag phase**, bacteria are metabolically active but not dividing; they synthesise enzymes needed for the new environment, repair cellular damage, and build up metabolic intermediates. Cell number does not increase. **(B) Correct:** During the **exponential (log) phase**, nutrient levels are non-limiting and inhibitory products are absent. Each cell divides at the species-specific minimum doubling time, giving constant first-order (logarithmic) growth: $N = N_0 e^{\mu t}$ or $N = N_0 2^{t/t_d}$. **(C) Correct:** In the **stationary phase**, nutrient depletion, toxic

product accumulation, or crowding cause the growth rate to equal the death rate, so total viable count plateaus. **(D) WRONG:** The stationary phase does *not* have the highest growth rate — that occurs during the exponential phase. Correct options: **(A), (B), (C)**.

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

Solution

Chromosomal structural mutations rearrange the sequence or dosage of genetic material *within* chromosomes, while the total chromosome number remains diploid ($2n$). **(A) Deletion:** A chromosomal segment is lost, reducing gene dosage — examples include del(5p) causing Cri-du-chat syndrome. **(B) Duplication:** An extra copy of a segment is present — BRCA1 amplification in some tumours. **(C) Inversion:** A segment is excised and re-ligated in the reverse orientation (pericentric if the centromere is included, paracentric if not). **(D) WRONG: Aneuploidy** (e.g., trisomy 21, monosomy X) is a *numerical* chromosomal mutation (change in the total number of chromosomes), not a structural one. Correct options: **(A), (B), (C)**.

SECTION C — NAT

Q41. **Answer: (128)**

Solution

Number of doublings in 120 min with $t_d = 20$ min: $n = 120/20 = 6$.

$$N = N_0 \times 2^6 = 2 \times 10^3 \times 64 = 128 \times 10^3 \text{ CFU/mL}$$

Answer: **128** ($\times 10^3$ CFU/mL).

Q42. **Answer: (29)**

Solution

A polypeptide of n amino acid residues contains $n - 1$ peptide bonds (one bond formed per condensation, releasing water). For 30 residues: $30 - 1 = \mathbf{29}$ peptide bonds.

Q43. **Answer: (48)**

Solution

By Chargaff's rule in dsDNA: $[\text{A}] = [\text{T}]$ and $[\text{G}] = [\text{C}]$, and $(\text{A}+\text{T}) + (\text{G}+\text{C}) = 100\%$. Given A+T = 52%, therefore G+C = $100 - 52 = 48\%$.

Q44. **Answer: (6)**

Solution

Arginine codons in the standard genetic code: CGU, CGC, CGA, CGG (CG family, 4 codons) + AGA, AGG (AG family, 2 codons) = **6** codons total.

Q45. **Answer: (0.64)**

Solution

Under Hardy–Weinberg equilibrium, the frequency of AA = p^2. With $p = 0.8$: $p^2 = 0.8^2 = \mathbf{0.64}$.

Q46. **Answer: (720)**

Solution

A-T base pairs are held by 2 hydrogen bonds; G-C base pairs by 3 hydrogen bonds.

$$\text{H-bonds} = 180 \times 2 + 120 \times 3 = 360 + 360 = \mathbf{720}$$

Q47. **Answer: (2)**

Solution

Glycolysis from one molecule of glucose uses 2 ATP (hexokinase + PFK-1) and produces 4 ATP (two PGK + two pyruvate kinase steps) by substrate-level phosphorylation. Net ATP = $4 - 2 = \mathbf{2}$ ATP. (NADH produced in glycolysis yields ATP only via oxidative phosphorylation, which is not substrate-level.)

Q48. **Answer: (0.0625)**

Solution

56 days = $4 \times t_{1/2}$ (since $t_{1/2} = 14$ days). Fraction remaining after n half-lives $= (1/2)^n$:

$$(1/2)^4 = 1/16 = \mathbf{0.0625}$$

Q49. **Answer: (9.25)**

Solution

Henderson–Hasselbalch equation:

$$\text{pH} = pK_a + \log \frac{[\text{base}]}{[\text{acid}]} = 9.25 + \log \frac{0.1}{0.1} = 9.25 + \log(1) = 9.25 + 0 = \mathbf{9.25}$$

Q50. **Answer: (5)**

Solution

For a circular DNA molecule with restriction sites: the number of fragments equals the number of cuts. HindIII makes 3 cuts (3 fragments); EcoRI makes 2 cuts (2 fragments). With no overlapping sites, the combined digest makes $3 + 2 = \mathbf{5}$ cuts, giving **5** fragments.

Q51. **Answer: (60)**

Solution

Michaelis–Menten equation with $K_m = 5$ mM, $V_{\max} = 80$ μmol/min, [S] $= 15$ mM:

$$v = \frac{80 \times 15}{5 + 15} = \frac{1200}{20} = \mathbf{60}\ \mu\text{mol/min}$$

Q52. **Answer: (1024)**

Solution

In PCR, starting from 1 double-stranded template, after n cycles the number of double-stranded molecules is 2^n. After 10 cycles: $2^{10} = \mathbf{1024}$.

Q53. **Answer: (13)**

Solution

$f(x) = 3x^4 - 2x^2 + 5x - 1$. Differentiating term by term:

$$f'(x) = 12x^3 - 4x + 5$$

At $x = 1$: $f'(1) = 12(1)^3 - 4(1) + 5 = 12 - 4 + 5 = \mathbf{13}$.

Q54. **Answer: (7)**

Solution

Sorted dataset: $\{2, 4, 4, 6, 8, 8, 10, 12\}$ — 8 values ($n = 8$, even). The median is the mean of the 4th and 5th values: $\dfrac{6 + 8}{2} = \mathbf{7}$.

Q55. **Answer: (8)**

Solution

60 min with $t_d = 20$ min gives $n = 60/20 = 3$ doublings.

$$N = 10^4 \times 2^3 = 10^4 \times 8 = 8 \times 10^4$$

Answer: **8** ($\times 10^4$ cells).

Q56. **Answer: (12)**

Solution

$$\int_0^2 (3x^2 + 2)\, dx = \Big[x^3 + 2x\Big]_0^2 = \big(2^3 + 2 \times 2\big) - 0 = (8 + 4) - 0 = \mathbf{12}$$

Q57. **Answer: (0.42)**

Solution

Under Hardy–Weinberg equilibrium, heterozygote frequency $= 2pq$. With $p = 0.3$ and $q = 0.7$:

$$2pq = 2 \times 0.3 \times 0.7 = \mathbf{0.42}$$

Q58. **Answer: (20)**

Solution

$$\text{Specific activity} = \frac{\text{total activity (U)}}{\text{total protein (mg)}} = \frac{300}{15} = \mathbf{20}\ \text{U/mg}.$$

Q59. **Answer: (19800)**

Solution

Approximate molecular weight $= n_{\text{residues}} \times \overline{M}_{\text{residue}} = 180 \times 110 = \mathbf{19800}$ Da.

Q60. **Answer: (128)**

Solution

Let q^2 = frequency of albino$(aa) = 16/400 = 0.04$. Then $q = \sqrt{0.04} = 0.2$ and $p = 1 - 0.2 = 0.8$. Expected frequency of carriers $(Aa) = 2pq = 2 \times 0.8 \times 0.2 = 0.32$. Expected number of carriers $= 0.32 \times 400 = \mathbf{128}$.