INI CET Biochemistry

Sample Paper – 10

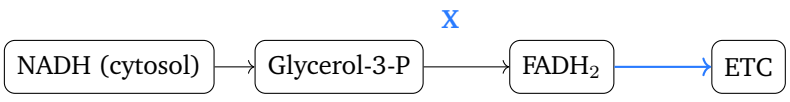
Duration: 14 Minutes **Maximum Marks: 15**

Instructions

- This paper contains **15** Multiple Choice Questions (Single Best Response), modelled on the Biochemistry content of **INI CET** (Institutes of National Importance Combined Entrance Test) conducted by AIIMS New Delhi.
- The **15-question** length matches the number of Biochemistry items you actually meet in the real 200-question paper.
- Each correct answer carries **+1 mark**. There is **negative marking of one-third (0.33) mark** for every incorrect answer; unattempted questions carry no penalty.
- Every question has **exactly one best answer**. Choose the single most appropriate option.
- Attempt this practice paper in one timed sitting of about **14 minutes**, the pace the real computer-based test demands.

Carbohydrate Metabolism

Q1. The pathway shown transfers reducing equivalents from cytosolic NADH into the mitochondrion, handing them to FAD (step **X**) and hence into the respiratory chain. This alternative NADH shuttle, prominent in skeletal muscle and brain, is the:



(A) Malate-aspartate shuttle

(B) Citrate-pyruvate shuttle

(C) Glycerol phosphate shuttle

(D) Carnitine shuttle

Q2. The biotin-dependent, anaplerotic enzyme that replenishes oxaloacetate for the citric acid cycle by carboxylating pyruvate is:

(A) Pyruvate dehydrogenase

(B) Citrate synthase

(C) Pyruvate carboxylase

(D) Phosphoenolpyruvate carboxykinase

Q3. The approximate net yield of ATP from the complete aerobic oxidation of one molecule of glucose to carbon dioxide and water is:

(A) About 30 to 32 ATP

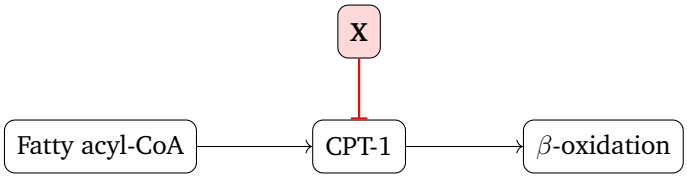
(B) About 2 ATP

(C) About 12 ATP

(D) About 100 ATP

Lipid Metabolism

Q4. In the scheme shown, the molecule marked **X** inhibits carnitine palmitoyltransferas 1 (CPT-1), thereby blocking fatty acid entry into mitochondria and coupling active fatty acid synthesis to switched-off oxidation. This molecule is:



(A) Malonyl-CoA

(B) Acetyl-CoA

(C) Citrate

(D) Free carnitine

Q5. The plasma enzyme that esterifies free cholesterol on the surface of HDL particles, allowing cholesterol to be packed into the lipoprotein core, is:

(A) Cholesteryl ester transfer protein (CETP)

(B) Lecithin-cholesterol acyltransferase (LCAT)

(C) Acyl-CoA cholesterol acyltransferase (ACAT)

(D) Lipoprotein lipase

Amino Acid and Protein Metabolism

Q6. The neurotransmitter serotonin (5-hydroxytryptamine) is synthesised in the body from which amino acid?

(A) Tyrosine

(B) Histidine

(C) Glutamate

(D) Tryptophan

Q7. The coupled process in which an amino group is first passed to alpha-ketoglutarate to form glutamate, which is then oxidatively deaminated by glutamate dehydrogenase to release free ammonia, is called:

(A) Transdeamination

(B) Direct (non-oxidative) deamination

(C) Transamination alone

(D) Reductive amination

Enzymes, Vitamins and Coenzymes

Q8. In terms of enzyme structure, the term **holoenzyme** refers to:

(A) The protein part alone, without its cofactor

(B) The complete, catalytically active enzyme (apoenzyme plus cofactor)

(C) A non-protein organic molecule that assists catalysis

(D) An inactive precursor that must be cleaved to become active

Q9. Which metal ion most commonly acts as the essential cofactor for kinases and other ATP-dependent enzymes, stabilising the ATP substrate?

(A) Zinc (Zn^{2+})

(B) Iron (Fe^{2+})

(C) Copper (Cu^{2+})

(D) Magnesium (Mg^{2+})

Q10. Vitamins are classified by solubility. Which group correctly lists the fat-soluble vitamins?

(A) Vitamin C and the B-complex vitamins

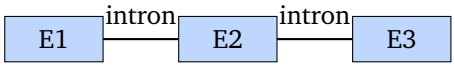
(B) Vitamin C only

(C) The B-complex vitamins only

(D) Vitamins A, D, E and K

Molecular Biology and Genetics

Q11. The eukaryotic gene shown has shaded segments and connecting introns. During splicing the introns are removed and the shaded segments are joined to form the mature mRNA. These shaded, retained coding segments are called:



(A) Introns

(B) Exons

(C) Promoters

(D) Codons

Q12. On the translating ribosome, which of the three tRNA-binding sites receives the incoming aminoacyl-tRNA carrying the next amino acid?

(A) The P (peptidyl) site

(B) The A (aminoacyl) site

(C) The E (exit) site

(D) The 5′ cap-binding site

Q13. A point mutation that changes a codon into another codon specifying the very same amino acid, so the protein sequence is unaltered, is termed a:

(A) Silent (synonymous) mutation

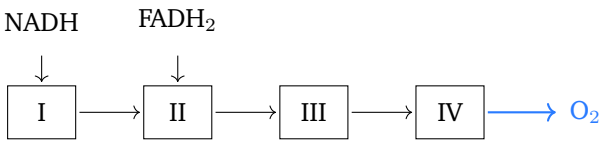
(B) Missense mutation

(C) Nonsense mutation

(D) Frameshift mutation

Bioenergetics, Nucleotides and Clinical Biochemistry

Q14. In the electron transport chain shown, NADH feeds electrons at complex I while $FADH_2$ feeds them at complex II. Using current (P/O) estimates, the approximate ATP yields per molecule through oxidative phosphorylation are:



(A) NADH about 1.5 and $FADH_2$ about 2.5 ATP

(B) Both yield about 3 ATP each

(C) NADH about 2.5 and $FADH_2$ about 1.5 ATP

(D) Both yield about 1 ATP each

Q15. Raised serum levels of which pair of aminotransferase enzymes are the classic biomarkers of hepatocellular (liver cell) injury?

(A) Amylase and lipase

(B) CK-MB and troponin

(C) AST and ALT

(D) Alkaline phosphatase and GGT

Detailed Solutions

Q1.

Solution

Concept – NADH shuttles across the mitochondrial membrane: Cytosolic NADH cannot cross the inner mitochondrial membrane, so its electrons are carried in by shuttle systems.

Step 1 – read the pathway: Cytosolic NADH reduces dihydroxyacetone phosphate to glycerol-3-phosphate, which is then re-oxidised by a membrane-bound dehydrogenase that hands the electrons to **FAD**, forming $FADH_2$.

Step 2 – name the shuttle: Because reducing equivalents are passed through glycerol-3-phosphate to FAD, this is the **glycerol phosphate shuttle**, which is prominent in skeletal muscle and brain.

Why the other options are wrong:

- A, malate-aspartate shuttle: hands electrons to NAD^+ (not FAD) and works mainly in liver, heart and kidney.
- B, citrate-pyruvate shuttle: exports acetyl units for fatty acid synthesis, not reducing equivalents for the chain.
- D, carnitine shuttle: carries long-chain fatty acids into mitochondria, unrelated to NADH transfer.

Final Answer: Glycerol phosphate shuttle $\Rightarrow$ $\boxed{C}$

Answer: (C) Go Back to Q1

Q2.

Solution

Concept – anaplerotic reactions: Anaplerotic ("filling up") reactions replenish citric acid cycle intermediates that are drained for biosynthesis.

Step 1 – identify the reaction: Carboxylation of pyruvate to oxaloacetate is the major anaplerotic step topping up the cycle.

Step 2 – name the enzyme: This step is catalysed by **pyruvate carboxylase**, a mitochondrial, biotin-dependent enzyme activated by acetyl-CoA.

Why the other options are wrong:

- A, pyruvate dehydrogenase: converts pyruvate to acetyl-CoA, it does not make oxaloacetate.

- B, citrate synthase: condenses oxaloacetate with acetyl-CoA, it consumes rather than makes oxaloacetate.
- D, PEP carboxykinase: converts oxaloacetate to phosphoenolpyruvate in gluconeogenesis, the opposite direction.

Final Answer: Pyruvate carboxylase $\Rightarrow$ C

Answer: (C) Go Back to Q2

Q3.

Solution

Concept – ATP accounting for full aerobic oxidation: Glycolysis, pyruvate dehydrogenase, the citric acid cycle and oxidative phosphorylation are all counted.

Step 1 – gather the yields: Using modern P/O ratios (NADH about 2.5 ATP, $FADH_2$ about 1.5 ATP), the reducing equivalents plus the substrate-level ATP and GTP are summed.

Step 2 – state the total: The complete aerobic oxidation of one glucose gives a net of **about 30 to 32 ATP**.

Why the other options are wrong:

- B, about 2 ATP: the net yield of anaerobic glycolysis only.
- C, about 12 ATP: far too low for full oxidation.
- D, about 100 ATP: grossly overstates the yield.

Final Answer: About 30 to 32 ATP $\Rightarrow$ A

Answer: (A) Go Back to Q3

Q4.

Solution

Concept – reciprocal control of fatty acid synthesis and oxidation: A single signal molecule prevents newly made fatty acids from being immediately broken down.

Step 1 – identify X: The inhibitor of CPT-1 shown is **malonyl-CoA**, the first committed intermediate of fatty acid synthesis.

Step 2 – the logic: When synthesis is active, malonyl-CoA is high; it blocks CPT-1 so fatty acyl groups cannot enter mitochondria for β-oxidation, avoiding a futile cycle.

Why the other options are wrong:

- B, acetyl-CoA: the precursor of malonyl-CoA, not the direct CPT-1 inhibitor.
- C, citrate: activates acetyl-CoA carboxylase but does not itself block CPT-1.
- D, free carnitine: is a substrate that promotes fatty acid entry, the opposite effect.

Final Answer: Malonyl-CoA $\Rightarrow$ A

Answer: (A) Go Back to Q4

Q5.

Solution

Concept – cholesterol esterification in HDL: Reverse cholesterol transport needs free cholesterol converted to cholesteryl ester.

Step 1 – name the enzyme: Lecithin-cholesterol acyltransferase (LCAT), activated by apo A-I, transfers a fatty acyl group from lecithin to cholesterol on HDL.

Step 2 – the result: The hydrophobic cholesteryl ester moves into the HDL core, maturing the particle and driving cholesterol pickup from tissues.

Why the other options are wrong:

- A, CETP: transfers cholesteryl esters between lipoproteins, it does not esterify cholesterol.
- C, ACAT: esterifies cholesterol inside cells, not on HDL in plasma.
- D, lipoprotein lipase: hydrolyses triglycerides in chylomicrons and VLDL.

Final Answer: Lecithin-cholesterol acyltransferase (LCAT) $\Rightarrow$ B

Answer: (B) Go Back to Q5

Q6.

Solution

Concept – amino acids as neurotransmitter precursors: Several monoamine transmitters are made by decarboxylating and hydroxylating specific amino acids.

Step 1 – name the precursor: Serotonin is synthesised from **tryptophan**, which is hydroxylated to 5-hydroxytryptophan and then decarboxylated.

Step 2 – confirm the route: Tryptophan $\rightarrow$ 5-hydroxytryptophan $\rightarrow$ serotonin (5-hydroxytryptamine).

Why the other options are wrong:

- A, tyrosine: the precursor of dopamine, noradrenaline and adrenaline.
- B, histidine: gives histamine on decarboxylation.
- C, glutamate: yields GABA, not serotonin.

Final Answer: Tryptophan $\Rightarrow$ D

Answer: (D) Go Back to Q6

Q7.

Solution

Concept – how amino groups become free ammonia: Most amino acids do not release ammonia directly; they funnel their nitrogen through glutamate.

Step 1 – describe the two coupled steps: First, transamination transfers the amino group to alpha-ketoglutarate, forming glutamate. Second, glutamate dehydrogenase oxidatively deaminates glutamate to release free ammonia.

Step 2 – name the combined process: This transamination-plus-oxidative-deamination sequence is called **transdeamination**.

Why the other options are wrong:

- B, direct deamination: applies to a few amino acids (for example serine, histidine), not the general route.
- C, transamination alone: only shuffles the amino group and releases no free ammonia.
- D, reductive amination: adds ammonia to a keto acid, the reverse direction.

Final Answer: Transdeamination $\Rightarrow$ A

Answer: (A) Go Back to Q7

Q8.

Solution

Concept – apoenzyme, cofactor and holoenzyme: Many enzymes are active only when a non-protein partner is bound.

Step 1 – define the parts: The apoenzyme is the protein part alone; the cofactor is the non-protein helper (metal ion or coenzyme).

Step 2 – define holoenzyme: The **holoenzyme** is the complete, catalytically

active enzyme, that is apoenzyme plus its cofactor.

Why the other options are wrong:

- A: the protein alone without cofactor is the apoenzyme, which is inactive.
- C: a non-protein organic helper is a coenzyme/cofactor, not the whole enzyme.
- D: an inactive precursor needing cleavage is a zymogen (proenzyme).

Final Answer: The complete active enzyme (apoenzyme plus cofactor) $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q8

Q9.

Solution

Concept – metal-ion cofactors: Kinases transfer a phosphate from ATP, and the true substrate is the metal-ATP complex.

Step 1 – identify the ion: Magnesium (Mg^{2+}) chelates the phosphates of ATP, shielding their negative charge and positioning them for transfer.

Step 2 – generalise: Hence Mg^{2+} is the routine cofactor for kinases, phosphatases and most ATP-dependent enzymes.

Why the other options are wrong:

- A, Zn^{2+}: a cofactor for carbonic anhydrase and carboxypeptidase, not the general ATP cofactor.
- B, Fe^{2+}: works in cytochromes and catalase.
- C, Cu^{2+}: found in cytochrome c oxidase and superoxide dismutase.

Final Answer: Magnesium (Mg^{2+}) $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q9

Q10.

Solution

Concept – classification of vitamins by solubility: Vitamins split into fat-soluble and water-soluble groups, which behave very differently.

Step 1 – list the fat-soluble group: The fat-soluble vitamins are **A, D, E and K**; they are stored in fat and can accumulate to toxic levels.

Step 2 – contrast: The water-soluble group is vitamin C and the B-complex vitamins, which are largely not stored and are excreted in urine.

Why the other options are wrong:

- A: vitamin C and B-complex are the water-soluble vitamins.
- B: vitamin C is water-soluble.
- C: the B-complex vitamins are water-soluble.

Final Answer: Vitamins A, D, E and K $\Rightarrow$ D

Answer: (D) Go Back to Q10

Q11.

Solution

Concept – gene structure and splicing: A eukaryotic gene alternates coding and non-coding segments.

Step 1 – read the figure: The shaded boxes (E1, E2, E3) are retained in the mature mRNA; the connecting lines between them are removed.

Step 2 – name the retained segments: The retained, expressed coding segments are the **exons**; the removed connecting segments are the introns.

Why the other options are wrong:

- A, introns: these are the removed segments, not the shaded retained ones.
- C, promoters: regulatory DNA upstream of the gene, not part of the transcript body.
- D, codons: three-nucleotide units within an exon, not the whole segment.

Final Answer: Exons $\Rightarrow$ B

Answer: (B) Go Back to Q11

Q12.

Solution

Concept – ribosomal tRNA sites: The ribosome has three tRNA sites, A, P and E, each with a defined role in elongation.

Step 1 – match the incoming tRNA: The incoming aminoacyl-tRNA, carrying the next amino acid, first binds the **A (aminoacyl) site**.

Step 2 – follow the cycle: After peptide bond formation the tRNA moves to the P (peptidyl) site, then leaves via the E (exit) site.

Why the other options are wrong:

- A, P site: holds the tRNA bearing the growing peptide chain.
- C, E site: holds the deacylated tRNA just before it exits.
- D, 5′ cap-binding site: part of translation initiation on mRNA, not a tRNA site.

Final Answer: The A (aminoacyl) site ⇒ B

Answer: (B) Go Back to Q12

Q13.

Solution

Concept – types of point mutation: The effect of a base substitution depends on how it changes the codon.

Step 1 – describe the change: A codon change that still codes for the same amino acid leaves the protein unchanged; this exploits the degeneracy of the genetic code.

Step 2 – name it: Such a mutation is a **silent (synonymous) mutation**.

Why the other options are wrong:

- B, missense: changes the codon to a different amino acid.
- C, nonsense: changes a codon to a stop codon, truncating the protein.
- D, frameshift: an insertion or deletion that shifts the reading frame.

Final Answer: Silent (synonymous) mutation ⇒ A

Answer: (A) Go Back to Q13

Q14.

Solution

Concept – ATP yield of NADH versus $FADH_2$: Where an electron carrier enters the chain sets how many protons it pumps and thus how much ATP it makes.

Step 1 – NADH entry: NADH donates at complex I, driving three proton-pumping complexes, giving **about 2.5 ATP**.

Step 2 – $FADH_2$ entry: $FADH_2$ donates at complex II, bypassing complex I, so it drives fewer pumps and gives **about 1.5 ATP**.

Why the other options are wrong:

- A: reverses the two values.
- B: the older whole-number estimate of 3 ATP for both is incorrect and not carrier-specific.
- D: about 1 ATP each is far too low for either carrier.

Final Answer: NADH about 2.5 and $FADH_2$ about 1.5 ATP $\Rightarrow$ C

Answer: (C) Go Back to Q14

Q15.

Solution

Concept – clinical enzymology of the liver: Damaged hepatocytes leak their cytoplasmic enzymes into the blood.

Step 1 – name the markers: Aspartate aminotransferase (AST) and alanine aminotransferase (ALT) rise with hepatocellular injury, ALT being more liver-specific.

Step 2 – interpret: A raised AST/ALT pattern points to liver-cell damage such as viral hepatitis or toxic injury.

Why the other options are wrong:

- A, amylase and lipase: markers of pancreatitis.
- B, CK-MB and troponin: markers of myocardial injury.
- D, alkaline phosphatase and GGT: rise mainly in cholestasis (biliary obstruction), not primarily hepatocellular injury.

Final Answer: AST and ALT $\Rightarrow$ C

Answer: (C) Go Back to Q15

Answer Key

Q	Ans	Q	Ans	Q	Ans	Q	Ans	Q	Ans
1	C	2	C	3	A	4	A	5	B
6	D	7	A	8	B	9	D	10	D
11	B	12	B	13	A	14	C	15	C