NEET PG Biochemistry Sample Paper-10

Duration: 15 Minutes **Maximum Marks: 64**

Instructions

- This paper contains **16** Multiple Choice Questions.
- Each correct answer carries **+4** mark. Incorrect answer: **−1** marks. Only **one** correct option.
- Unattempted questions carry **0** marks.
- Use of mobile phones, smartwatches, or any electronic gadgets is strictly prohibited.

Q1. A 3-month-old male infant presents with profound fasting hypoglycemia, severe lactic acidosis, hyperuricemia, and prominent hepatomegaly. A liver biopsy demonstrates marked glycogen accumulation with normal structure, alongside heavily elevated intracellular levels of Glucose-6-Phosphate. Biochemical analysis confirms a functional deficiency in the transport system responsible for translocating Glucose-6-Phosphate across the endoplasmic reticulum membrane (T1 transporter). Which of the following metabolic processes is directly and completely halted in this patient's hepatocytes?

(A) Glycogenolysis only

(B) Gluconeogenesis only

(C) Both Glycogenolysis and Gluconeogenesis

(D) Hexose Monophosphate Shunt and Glycolysis

Q2. A 45-year-old chronic alcoholic presents to the emergency department in a state of deep stupor. Laboratory analysis reveals a blood glucose level of 32 mg/dL and a significantly elevated serum NADH/NAD^+ ratio driven by hepatic ethanol oxidation via alcohol dehydrogenase. The profound suppression of gluconeogenesis in this patient is primarily mediated by the structural equilibrium shift of which critical substrate pair towards an unusable state?

(A) Oxaloacetate to Malate, and Pyruvate to Lactate

(B) Malate to Oxaloacetate, and Lactate to Pyruvate

(C) Phosphoenolpyruvate to 2-Phosphoglycerate

(D) Glyceraldehyde 3-phosphate to Dihydroxyacetone phosphate

Q3. A 22-year-old professional athlete undergoes an intensive muscle biopsy study during a maximal graded exercise test. At peak workload, the cytosolic rate of glycolysis accelerates over 100-fold. To sustain this continuous flux under anaerobic conditions without exhausting the finite cytosolic pool of oxidized NAD^+, the skeletal muscle relies crucially on the reduction of pyruvate. Which of the following describes the thermodynamic driving force and allosteric status of this adaptive mechanism?

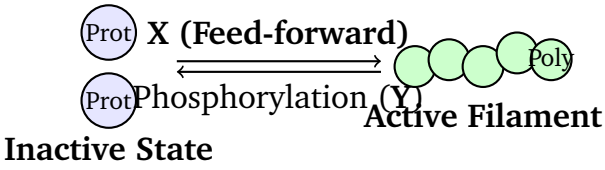
(A) Activation of pyruvate dehydrogenase by Acetyl-CoA

(B) Equilibrium shift of Lactate Dehydrogenase driven by high cytosolic NADH

(C) Allosteric activation of Phosphofructokinase-1 by Citrate

(D) Activation of the Malate-Aspartate shuttle to rapidly clear cytosolic NADH

Q4. An elegant kinetic analysis is performed on the rate-limiting enzyme of fatty acid synthesis, Acetyl-CoA Carboxylase (ACC), which converts Acetyl-CoA to Malonyl-CoA. The diagram below illustrates the regulatory transitions between its inactive monomeric state and active polymeric state. Identify the metabolic modulator labeled as **X** that allosterically drives polymer assembly, and the state labeled as **Y** induced by glucagon-mediated phosphorylation:



(A) **X**: Palmitoyl-CoA; **Y**: Depolymerized Protomer

(B) **X**: Citrate; **Y**: Depolymerized Protomer

(C) **X**: Citrate; **Y**: Highly Active Hyper-polymer

(D) **X**: Malonyl-CoA; **Y**: Inactive Cross-linked Lattice

Q5. A 6-month-old infant is evaluated for failure to thrive, persistent vomiting, and progressive hepatosplenomegaly following the introduction of fruit purees and juices into the diet. Urinalysis reveals highly positive reducing sugars, but a glucose oxidase dipstick test is completely negative. The molecular pathology of this condition involves the trapping of intracellular inorganic phosphate (P_i), directly halting which crucial process due to a lack of substrate for the glyceraldehyde 3-phosphate dehydrogenase reaction?

(A) Hepatic Glycogen Synthesis

(B) Hepatic ATP Synthesis via Oxidative Phosphorylation

(C) Renal Glucose Reabsorption

(D) Mitochondrial Beta-oxidation

Q6. A 34-year-old female experiences severe muscle cramping and dark burgundy-colored urine after participating in her first high-intensity cross-fit session. Laboratory values demonstrate an astronomical spike in serum creatine kinase (CK) and myoglobinuria. A ischemic forearm exercise test reveals flatline plasma lactate levels despite intense exertion. Muscle biopsy shows massive glycogen accumulation with a normal structural pattern. Which specific enzyme is defective, and what biochemical byproduct fails to accumulate?

(A) Debranching Enzyme (α-1,6-glucosidase); limit dextrins fail to accumulate

(B) Myophosphorylase; Glucose-1-Phosphate fails to accumulate

(C) Glucose-6-Phosphatase; free Glucose fails to accumulate

(D) Phosphofructokinase-1; Fructose-1,6-bisphosphate fails to accumulate

Q7. A molecular oncologist studies the mechanism of action of a novel antineoplastic compound designed to block eukaryotic DNA transcription. The drug binds directly to the C-terminal domain (CTD) heptapeptide repeat structure (Tyr-Ser-Pro-Thr-Ser-Pro-Ser) of a specific RNA polymerase, completely abolishing its ability to undergo mandatory phosphorylation events required for

promoter clearance and elongation. Which eukaryotic RNA polymerase is the exclusive target of this drug?

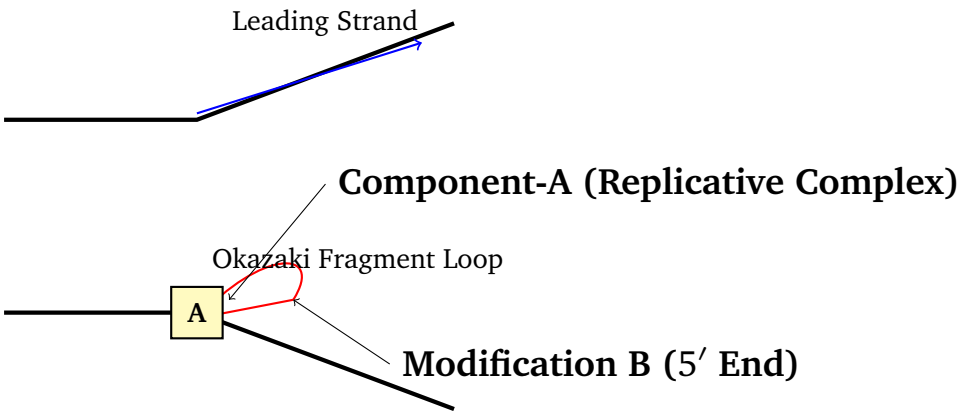
(A) RNA Polymerase I

(B) RNA Polymerase II

(C) RNA Polymerase III

(D) Mitochondrial RNA Polymerase

Q8. A diagnostic laboratory performs a high-resolution analysis of DNA replication mechanics in an *in vitro* eukaryotic cell system. The diagram below explicitly outlines the asymmetric macromolecular processing taking place at the replication fork. Analyze the topology and identify the specific enzyme/component labeled as **Component-A** that coordinates lagging strand synthesis loop dynamics, and the modification marked as **B** at the $5'$ end of Okazaki fragments:



(A) **Component-A**: DNA Polymerase δ complex; **Modification B**: Short RNA Primer sequence

(B) **Component-A**: DNA Polymerase ϵ monomer; **Modification B**: Poly-A tail component

(C) **Component-A**: DNA Topoisomerase I; **Modification B**: Single-stranded DNA Binding Protein

(D) **Component-A**: DNA Polymerase α; **Modification B**: Methylated Guanosine Cap

Q9. A 50-year-old male presents with multiple severe, ulcerated, and hyperpigmented cutaneous lesions exclusively on sun-exposed areas. History reveals extreme cutaneous photosensitivity since early childhood. Genetic testing confirms a mutation in an excision endonuclease responsible for scanning DNA and cleaving phosphodiester backbones on both sides of bulky pyrimidine dimers. Which DNA repair pathway is completely compromised in this patient, and during which phase of the cell cycle is it most vital?

(A) Base Excision Repair (BER); M Phase

(B) Nucleotide Excision Repair (NER); Throughout G1/S phases

(C) Mismatch Repair (MMR); Late G2 Phase only

(D) Non-Homologous End Joining (NHEJ); Mitotic Anaphase

Q10. A molecular biology research team synthesizes an artificial mRNA construct to study translational fidelity in a cell-free translation assay. The construct includes a specific mutation rendering the Shine-Dalgarno sequence completely non-functional in a prokaryotic test system, and separately eliminates the 5′-methylguanosine cap in an identical eukaryotic test system. Which specific phases of protein synthesis will fail to initiate in the prokaryotic and eukaryotic systems respectively?

(A) 16S rRNA assembly to mRNA in prokaryotes; eIF4F complex binding to mRNA in eukaryotes

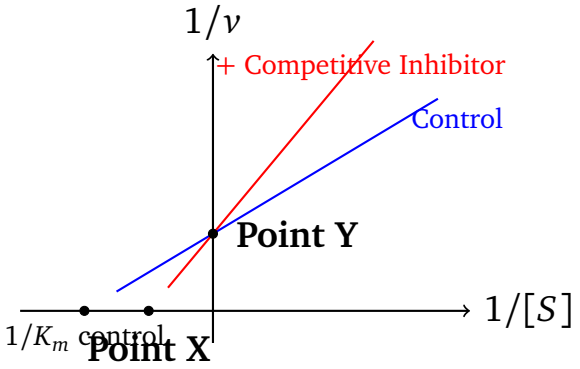
(B) 23S rRNA transpeptidation in prokaryotes; 60S subunit joining in eukaryotes

(C) tRNA charging by synthetases in prokaryotes; Kozak scanning initiation in eukaryotes

(D) EF-Tu mediated elongation in prokaryotes; Peptidyl transferase movement in eukaryotes

Q11. A biochemical research unit investigates the properties of a novel competitive inhibitor developed against a critical rate-limiting enzyme. The double-reciprocal Lineweaver-Burk plot below demonstrates the precise kinetic alterations observed during the assay. Based on the geometric intersection

points labeled along the axes, select the correct deduction regarding the changes to the apparent Michaelis constant (K_m) and maximum velocity (V_{max}):



(A) **Point X** represents $-1/K_m^{\text{apparent}}$ which increases in value (lower affinity); **Point Y** ($1/V_{max}$) remains completely unchanged.

(B) **Point X** represents $-1/K_m^{\text{apparent}}$ which decreases in value (higher affinity); **Point Y** ($1/V_{max}$) shifts upward.

(C) **Point X** shows that V_{max} is decreased; **Point Y** shows K_m is constant.

(D) **Point X** represents $1/V_{max}$ unaltered; **Point Y** represents a variable K_m tracking towards zero.

Q12. A 54-year-old poorly nourished male with severe alcohol dependence disorder presents with profound confusion, horizontal nystagmus, and a highly uncoordinated, wide-based gait (ataxia). The attending physician suspects Wernicke encephalopathy and requests an immediate assay of erythrocyte transketolase activity before and after adding a specific vitamin cofactor. Which multi-subunit mitochondrial enzyme complex shares an absolute requirement for this identical cofactor, and what biochemical reaction does it catalyze?

(A) Malate Dehydrogenase; reversible conversion of malate to oxaloacetate

(B) α-Ketoglutarate Dehydrogenase Complex; oxidative decarboxylation of α-ketoglutarate to succinyl-CoA

(C) Pyruvate Carboxylase; ATP-dependent carboxylation of pyruvate to oxaloacetate

(D) Succinate Dehydrogenase; FAD-dependent oxidation of succinate to fumarate

Q13. A pediatric clinical geneticist evaluates a 14-month-old child presenting with profound hypotonia, developmental delay, and severe megaloblastic anemia that has failed to respond to aggressive supplementation with both vitamin B12 (cobalamin) and folic acid. Urinalysis reveals massive crystallization of orotic acid. The primary metabolic block in this child resides in a bifunctional cytosolic enzyme complex. Which two distinct enzymatic activities are impaired, and what downstream nucleotide product must be supplemented to rescue the pathway?

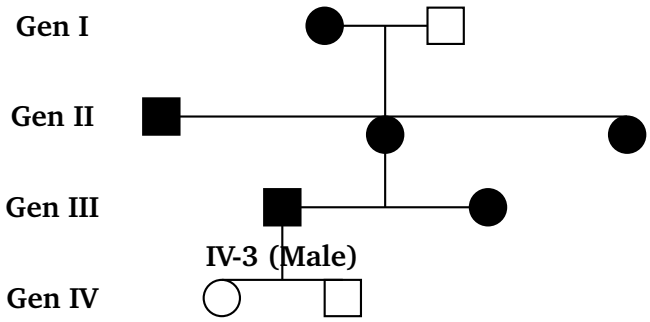
(A) Carbamoyl Phosphate Synthetase II and Aspartate Transcarbamoylase; supplement dAMP

(B) Orotate Phosphoribosyltransferase and Orotidine 5′-Monophosphate Decarboxylase; supplement Uridine

(C) Dihydroorotate Dehydrogenase and Thymidylate Synthase; supplement dTMP

(D) Ribonucleotide Reductase and Adenylosuccinate Synthetase; supplement Cytidine

Q14. A clinical geneticist evaluates an extensive four-generation family pedigree exhibiting a rare neuromuscular disorder characterized by progressive external ophthalmoplegia, proximal myopathy, and lactic acidosis. The pedigree below details the transmission dynamics within the kinship. Based on the pattern of inheritance shown, identify the specific genetic transmission model and determine the risk of disease expression for the offspring of male **Individual IV-3** when paired with an unaffected female:



(A) Autosomal Dominant Inheritance; 50% recurrence risk

(B) Mitochondrial (Maternal) Inheritance; 0% recurrence risk

(C) X-linked Recessive Inheritance; 100% of daughters will be carriers

(D) Autosomal Recessive with Pseudodominance; 25% recurrence risk

Q15. A 12-year-old boy presents with severe intellectual disability, coarse facial features, joint stiffness, and clear corneas. A battery of lysosomal enzyme assays demonstrates significantly elevated serum levels of beta-glucuronidase, hexosaminidase, and alpha-L-iduronidase, alongside a total absence of these enzymes within his intracellular lysosomal compartments. The molecular defect involves a missing phosphotransferase enzyme located in the cis-Golgi. Which targeting signal fails to form on these enzymes?

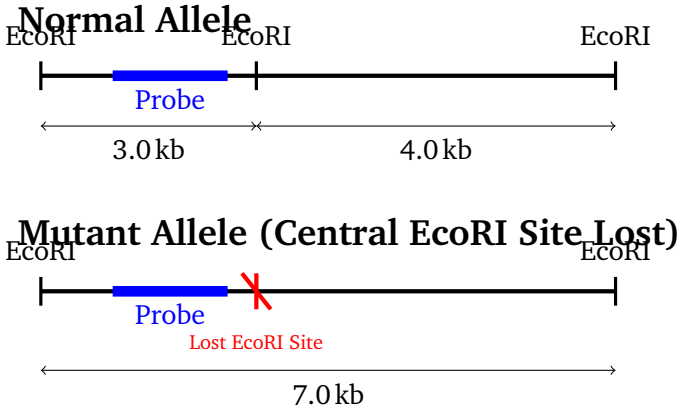
(A) Dolichol-phosphate-oligosaccharide core

(B) Mannose-6-Phosphate modification

(C) N-terminal amphipathic signal peptide sequence

(D) C-terminal KDEL retrieval sorting motif

Q16. A biomedical diagnostics laboratory uses restriction fragment length polymorphism (RFLP) analysis followed by Southern blotting to detect a disease-associated mutation. The normal allele contains three EcoRI restriction sites, whereas the mutant allele has lost the central EcoRI site because of a point mutation. A labeled probe hybridizes to the highlighted region shown below. If a patient's autoradiograph demonstrates a single intense hybridization band at exactly 7.0 kb, what is the most likely genotype?



(A) Homozygous for the Normal Allele

(B) Heterozygous Carrier of the Disease Mutation

(C) Homozygous for the Mutant Allele

(D) Hemizygous for a structural deletion fragment

Detailed Solutions

Q1.

Solution

Concept: Von Gierke disease Type Ib is caused by a structural defect in the glucose-6-phosphate translocase (T1) transporter. This microsomal transport system moves glucose-6-phosphate (G6P) from the cytosol across the endoplasmic reticulum (ER) membrane into the lumen, where the catalytic subunit of glucose-6-phosphatase resides.

Solution:

Let's trace the flow of carbohydrate intermediates through these metabolic checkpoints:

(a) Glycogenolysis converts storage glycogen into glucose-1-phosphate, which is rapidly mutated into glucose-6-phosphate by phosphoglucomutase in the cytosol.

(b) Gluconeogenesis processes non-carbohydrate substrates (such as lactate, glycerol, and alanine) up the pathway to synthesize cytosolic glucose-6-phosphate.

(c) Because both pathways converge on cytosolic G6P as their final shared intermediate, they both require the T1 translocation protein to deliver G6P into the ER lumen for dephosphorylation into exportable free glucose.

(d) When the T1 transporter is non-functional, glucose-6-phosphate is structurally trapped in the cytosol. Consequently, the terminal step releasing free glucose is blocked, which means **Both Glycogenolysis and Gluconeogenesis** are directly and completely halted.

Final Answer: Both Glycogenolysis and Gluconeogenesis

Answer: (C)

Go Back to Question 1

Q2.

Solution

Concept: Metabolizing high concentrations of ethanol via hepatic alcohol dehydrogenase and aldehyde dehydrogenase consumes localized NAD^+ pools and generates massive amounts of cytosolic NADH. This significantly elevates the cytosolic NADH/NAD^+ ratio.

Solution:

Let's analyze the thermodynamic equilibrium shifts of reversible dehydrogenase reactions driven by excess reducing equivalents (NADH):

(a) To drive gluconeogenesis, the liver must convert lactate into pyruvate using cytosolic lactate dehydrogenase, and malate into oxaloacetate (OAA) using cytosolic malate dehydrogenase. Both reactions require free NAD^+ as an electron acceptor.

(b) However, the high cytosolic NADH/NAD^+ ratio shifts the thermodynamic equilibrium of these reversible reactions in reverse:

$$\text{Pyruvate} + \text{NADH} + H^+ \rightarrow \text{Lactate} + NAD^+$$
$$\text{Oxaloacetate} + \text{NADH} + H^+ \rightarrow \text{Malate} + NAD^+$$

(c) This equilibrium shift effectively traps pyruvate as lactate (causing lactic acidosis) and depletes oxaloacetate by converting it into malate. Thus, gluconeogenesis is suppressed because **Oxaloacetate to Malate, and Pyruvate to Lactate** shifts these key entry substrates into an unusable state.

Final Answer: Oxaloacetate to Malate, and Pyruvate to Lactate

Answer: (A)

Go Back to Question 2

Q3.

Solution

Concept: Sustained high-intensity anaerobic glycolysis requires a constant supply of cytosolic NAD^+ to maintain the glyceraldehyde 3-phosphate dehydrogenase reaction. Under anaerobic conditions, mitochondrial shuttles cannot clear cytosolic NADH quickly enough to keep pace with rapid glycogen breakdown.

Solution:

Let's evaluate the metabolic and thermodynamic mechanism supporting anaerobic flux in skeletal muscle:

(a) As the rate of glycolysis spikes, cytosolic NADH levels rise rapidly. To prevent glycolysis from stalling due to a lack of oxidized cofactor, lactate dehydrogenase (LDH) reduces pyruvate into lactate in the cytosol.

(b) This reaction uses NADH and regenerates the free NAD^+ required to maintain high glycolytic throughput:

$$\text{Pyruvate} + \text{NADH} + H^+ \rightleftharpoons \text{Lactate} + NAD^+$$

(c) This rapid reduction is driven by the **Equilibrium shift of Lactate Dehydrogenase driven by high cytosolic NADH**. It functions as a mass-action thermodynamic response rather than an allosteric activation mechanism.

Final Answer: Equilibrium shift of Lactate Dehydrogenase driven by high cytosolic NADH

Answer: (B)

Go Back to Question 3

Q4.

Solution

Concept: Acetyl-CoA Carboxylase (ACC) regulates fatty acid biogenesis by converting acetyl-CoA into malonyl-CoA. Its activity is tightly controlled by both allosteric modulators and reversible covalent phosphorylation.

Solution:

Let's analyze the regulatory modifications illustrated in the pathway diagram:

(a) In its inactive state, ACC exists as separate protomer subunits. When signaling networks favor lipogenesis, **Citrate** acts as a forward allosteric activator (**X**), driving the assembly of these protomers into active, high-molecular-weight polymeric filaments.

(b) Conversely, counter-regulatory hormones like glucagon or epinephrine activate protein kinase A (PKA) or AMP-activated protein kinase (AMPK).

(c) These kinases phosphorylate specific serine residues on the enzyme, which disassembles the active filament back into its inactive, **Depolymerized Protomer** state (**Y**). This shuts down malonyl-CoA production during periods of fasting or energy stress.

Final Answer: **X**: Citrate; **Y**: Depolymerized Protomer

Answer: (B)

Go Back to Question 4

Q5.

Solution

Concept: Hereditary Fructose Intolerance (HFI) is an autosomal recessive disorder caused by a deficiency in Aldolase B. When fructose is ingested, it is rapidly phosphorylated into fructose-1-phosphate (F1P) by fructokinase, but cannot be cleaved further.

Solution:

Let's trace the downstream metabolic trap caused by an Aldolase B deficiency:

(a) The rapid accumulation of intracellular F1P traps organic phosphate, depleting the hepatocyte's pool of free inorganic phosphate (P_i).

(b) The depletion of cellular P_i directly stalls mitochondrial ATP synthase, which requires free ADP and P_i to generate energy. This disrupts **Hepatic ATP Synthesis via Oxidative Phosphorylation**.

(c) Additionally, a lack of free P_i inhibits glycogen phosphorylase (blocking glycogenolysis) and limits the glyceraldehyde 3-phosphate dehydrogenase reaction in glycolysis, causing ATP depletion and severe fasting hypoglycemia.

Final Answer: Hepatic ATP Synthesis via Oxidative Phosphorylation

Answer: (B)

Go Back to Question 5

Q6.

Solution

Concept: McArdle disease (Glycogen Storage Disease Type V) is an autosomal recessive disorder caused by a deficiency in the skeletal muscle isoform of glycogen phosphorylase (**myophosphorylase**). This enzyme cleaves α-1,4-glucosidic bonds from the non-reducing ends of glycogen chains during exertion.

Solution:

Let's evaluate the clinical presentation and metabolic test profile:

(a) The 34-year-old patient experiences severe cramping, rhabdomyolysis (marked by elevated creatine kinase and burgundy urine), and a flatline lactate response during ischemic exercise. This combination indicates a block in muscle glycogen breakdown.

(b) Under normal conditions, myophosphorylase breaks down glycogen to release **glucose-1-phosphate (G1P)**:

$$\text{Glycogen}_{(n)} + \text{P}_i \xrightarrow{\text{Myophosphorylase}} \text{Glycogen}_{(n-1)} + \text{Glucose-1-Phosphate}$$

(c) Because **myophosphorylase** is defective, glycogen cannot be converted into G1P. This deprives the muscle of its primary glycolytic substrate during intense exercise, preventing the accumulation of downstream intermediates and lactate.

Final Answer: Myophosphorylase; Glucose-1-Phosphate fails to accumulate

Answer: (B)

Go Back to Question 6

Q7.

Solution

Concept: Eukaryotic cells utilize three distinct classes of nuclear RNA polymerases to transcribe different genomic regions. High-efficiency synthesis of messenger RNA (mRNA) requires a specialized C-terminal domain (CTD) tail structure to coordinate transcription and processing factors.

Solution:

Let's pinpoint the structural target based on the heptapeptide repeat domain:

(a) **RNA Polymerase II** contains a unique C-terminal domain extended tail composed of multiple tandem consensus repeats of the sequence Tyr-Ser-Pro-Thr-Ser-Pro-Ser.

(b) During transcription initiation, specific cyclin-dependent kinases (such as CDK7 within TFIIH and CDK9 within p-TEFb) phosphorylate particular serine residues (Ser-5 and Ser-2) on this tail.

(c) This phosphorylation is required for the enzyme to achieve promoter clearance, transition into active elongation, and recruit RNA capping, splicing, and polyadenylation machineries. Thus, **RNA Polymerase II** is the exclusive target of this compound.

Final Answer: RNA Polymerase II

Answer: (B)

Go Back to Question 7

Q8.

Solution

Concept: Eukaryotic DNA replication is an asymmetric process. The leading strand is synthesized continuously by DNA Polymerase ϵ, while the lagging strand is synthesized discontinuously by DNA Polymerase δ as a series of short Okazaki fragments.

Solution:

Let's analyze the asymmetric components layout on the replication fork diagram:

(a) As the replication fork opens, the lagging strand template loops around to orient itself in the proper catalytic direction. The multiprotein **DNA Polymerase δ complex** (**Component-A**) coordinates synthesis along this loop, extending each Okazaki fragment in a $5' \rightarrow 3'$ direction.

(b) Before DNA polymerase can synthesize an Okazaki fragment, DNA polymerase α/primase must synthesize a **Short RNA Primer sequence** (**Modification B**) at the $5'$ end of each fragment to provide the required free $3'$-OH group for elongation.

Final Answer: **Component-A**: DNA Polymerase δ complex; **Modification B**: Short RNA primer sequence.

Answer: (A)

Go Back to Question 8

Q9.

Solution

Concept: Environmental ultraviolet (UV) radiation alters DNA topology by inducing covalent bonds between adjacent pyrimidines, creating bulky cyclobutane pyrimidine dimers that distort the double helix.

Solution:

Let's match the described excision endonuclease activity to its proper repair pathway and cell cycle phase:

(a) Bulky helical distortions are recognized and repaired by the **Nucleotide Excision Repair (NER)** pathway. This multi-subunit complex makes dual incisions on both sides of the dimer, removing an oligonucleotide fragment to allow patch resynthesis by DNA polymerase and ligase.

(b) Mutations in these excision repair proteins lead to Xeroderma Pigmentosum, which causes extreme photosensitivity and skin malignancies.

(c) Because UV radiation can damage resting or dividing cells at any time, the **Nucleotide Excision Repair (NER)** pathway must remain active **Throughout G1/S phases** (and across the entire interphase) to scan and protect the genome prior to and during replication.

Final Answer: Nucleotide Excision Repair (NER); Throughout G1/S phases

Answer: (B)

Go Back to Question 9

Q10.

Solution

Concept: Translation initiation requires the small ribosomal subunit to accurately recognize and dock onto mRNA templates before scanning or selecting the start codon.

Solution:

Let's analyze the distinct molecular docking mechanisms used by prokaryotic and eukaryotic translation systems:

(a) In prokaryotes, the 3′ end of the **16S rRNA** within the small 30S subunit binds directly to the purine-rich Shine-Dalgarno consensus sequence upstream of the start codon. Disruption of this sequence causes a **16S rRNA assembly to mRNA** failure.

(b) In eukaryotes, translation initiation factors (the **eIF4F complex**, including cap-binding eIF4E) must bind the 5′-methylguanosine cap to recruit the 43S pre-initiation complex.

(c) Eliminating the 5′ cap prevents **eIF4F complex binding to mRNA**, which halts translation initiation in eukaryotic systems.

Final Answer: 16S rRNA assembly to mRNA in prokaryotes; eIF4F complex binding to mRNA in eukaryotes.

Answer: (A)

Go Back to Question 10

Q11.

Solution

Concept: Competitive inhibitors bind reversibly to the free enzyme's active site, competing directly with the substrate. This competition alters the apparent affinity without changing the maximum potential velocity of the enzyme system.

Solution:

Let's evaluate the geometric intersection changes shown on the Lineweaver-Burk plot:

(a) Both the Control line (blue) and the Competitive Inhibitor line (red) intersect at the exact same point on the vertical axis, labeled as **Point Y**. This common intersection proves that $1/V_{max}$ is unchanged, meaning **V_{max} remains completely unchanged**.

(b) On the horizontal axis, the intercept shifts from $-1/K_m^{\text{control}}$ closer to the origin to reach **Point X**.

(c) This less-negative horizontal value at **Point X** represents $-1/K_m^{\text{apparent}}$. This indicates that the apparent Michaelis constant (K_m^{apparent}) has increased, which reflects a lower apparent affinity for the substrate in the presence of the competitive inhibitor.

Final Answer: **Point X** represents $-1/K_m^{\text{apparent}}$, which shifts toward zero (reflecting a lower apparent affinity); **Point Y** ($1/V_{\text{max}}$) remains unchanged.

Answer: (A)

Go Back to Question 11

Q12.

Solution

Concept: Wernicke encephalopathy is caused by a severe deficiency in thiamine (Vitamin B_1), a precursor for **thiamine pyrophosphate (TPP)**. TPP serves as an obligate organic coenzyme for multi-subunit alpha-keto acid dehydrogenase complexes that catalyze oxidative decarboxylation reactions.

Solution:

Let's find the multi-subunit enzyme that shares this cofactor requirement:

(a) Erythrocyte transketolase requires TPP to transfer two-carbon ketol groups in the pentose phosphate pathway, making it a reliable diagnostic marker for thiamine deficiency.

(b) Inside the mitochondria, the **α-Ketoglutarate Dehydrogenase Complex** (α-KGDH) within the Citric Acid Cycle utilizes an identical TPP cofactor on its E1 subunit.

(c) This complex catalyzes the **oxidative decarboxylation of α-ketoglutarate to succinyl-CoA**, a key energy-producing step:

$$\alpha\text{-Ketoglutarate} + NAD^+ + \text{CoA-SH} \xrightarrow{\alpha\text{-KGDH + TPP}} \text{Succinyl-CoA} + CO_2 + NADH + H^+$$

Pyruvate dehydrogenase shares this TPP requirement, but pyruvate carboxylase requires biotin, while succinate dehydrogenase uses FAD.

Final Answer: α-Ketoglutarate Dehydrogenase Complex; oxidative decarboxylation of α-ketoglutarate to succinyl-CoA.

Answer: (B)

Go Back to Question 12

Q13.

Solution

Concept: Hereditary Orotic Aciduria is an autosomal recessive disorder caused by a mutation in **UMP Synthase**, a bifunctional cytosolic protein that catalyzes the terminal steps of de novo pyrimidine synthesis.

Solution:

Let's analyze the metabolic block and therapeutic bypass strategy:

(a) The child exhibits developmental delay, megaloblastic anemia unresponsive to B_{12}/folate, and massive orotic acid crystalluria, indicating a complete block in UMP Synthase.

(b) UMP Synthase possesses two distinct catalytic domains: **Orotate Phosphoribosyltransferase** (which couples orotate to PRPP to form OMP) and **Orotidine 5′-Monophosphate Decarboxylase** (which decarboxylates OMP to form UMP).

(c) When these domains are defective, upstream orotic acid accumulates and spills into the urine. Pyrimidine nucleotide depletion impairs DNA synthesis, leading to megaloblastic anemia.

(d) To bypass this block, the pathway can be rescued by supplementing dietary **Uridine**. Nucleoside kinases salvage uridine directly into UMP, which restores pyrimidine pools and exerts feedback inhibition on the early steps of de novo synthesis to reduce orotic acid production.

Final Answer: Orotate Phosphoribosyltransferase and Orotidine 5'-Monophosphate Decarboxylase; supplement Uridine.

Answer: (B)

Go Back to Question 13

Q14.

Solution

Concept: Mitochondrial (maternal) inheritance describes traits encoded by genes within mitochondrial DNA (mtDNA). Because the zygote inherits its cytoplasm and organelles exclusively from the oocyte, mitochondrial mutations are transmitted down the maternal line.

Solution:

Let's evaluate the transmission dynamics across the four-generation pedigree:

(a) The affected mother in Generation I transmits the disorder to all of her children (both sons and daughters in Gen II).

(b) The affected daughter in Generation II (individual II-3) passes the trait to all of her children (Gen III).

(c) Conversely, the affected male in Generation III (**Individual IV-3**) has unaffected children in Generation IV. This absolute maternal transmission pattern confirms **Mitochondrial (Maternal) Inheritance**.

(d) Because sperm do not contribute functional mitochondria to the zygote, an affected male (**Individual IV-3**) cannot pass the mutation to his offspring, resulting in a **0% recurrence risk**.

Final Answer: Mitochondrial (Maternal) Inheritance; 0% recurrence risk

Answer: (B)

Go Back to Question 14

Q15.

Solution

Concept: I-cell disease (Mucolipidosis II) is an autosomal recessive lysosomal storage disorder caused by a deficiency in UDP-N-acetylglucosamine:lysosomal-enzyme N-acetylglucosaminyl-1-phosphotransferase. This enzyme is responsible for tagging newly synthesized acid hydrolases within the cis-Golgi network.

Solution:

Let's trace the molecular targeting pathway for these enzymes:

(a) The patient presents with intellectual disability, coarse facial features, and joint stiffness. Lysosomal enzymes are absent intracellularly but significantly elevated in the serum, which is characteristic of I-cell disease.

(b) Under normal conditions, the phosphotransferase enzyme adds a **Mannose-6-Phosphate (M6P)** tag onto specific terminal mannose residues on N-linked oligosaccharides within the cis-Golgi.

(c) This M6P modification is recognized by M6P receptors in the trans-Golgi network, which packages the hydrolases into clathrin-coated vesicles targeted for the lysosome.

(d) Without this **Mannose-6-Phosphate modification**, the sorting machinery fails, and the default pathway secretes these functional enzymes out of the cell into the extracellular space.

Final Answer: Mannose-6-Phosphate modification

Answer: (B)

Go Back to Question 15

Q16.

Solution

Concept: Restriction Fragment Length Polymorphism (RFLP) combined with Southern blotting detects variations in DNA sequence. Point mutations that create or destroy a restriction enzyme recognition site alter the size of the fragments produced upon digestion.

Solution:

Let's interpret the restriction fragment maps and the resulting blot data:

(a) The normal allele contains three EcoRI restriction sites. When digested, the flanking and middle EcoRI sites split the locus into two distinct fragments: a 3.0 kb fragment (which binds the hybridization probe) and an adjacent 4.0 kb fragment. A normal allele will therefore display a band at 3.0 kb.

(b) In the mutant allele, the central EcoRI site is lost due to a mutation. Digestion cleaves only at the outer boundary sites, leaving a single large fragment with a total length of **7.0 kb** (3.0 kb + 4.0 kb).

(c) Because the hybridization probe spans across this sequence region, it will bind to the 7.0 kb fragment from the mutant allele.

(d) Since the patient's autoradiograph displays a single, dense hybridization band exactly at the **7.0 kb** mark (with no band at 3.0 kb), both copies of the allele must lack the central restriction site, confirming they are **Homozygous for the Mutant Allele**.

Final Answer: Homozygous for the Mutant Allele

Answer: (C)

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Answer Key

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