# Answer product as it takes longer for

Answer 1Four spiral chains of keratin twist to form keratin. Spiralchains cross linked by hydrogen and disulfide bonds, changes of these linkagedetermine whether hair is curly or straight.

To change thearrangement disulfide bonds of Keratin chains is to be disrupted, reducingagents would oxidize keratin by disrupting the covalent bond between cysteinemolecules and favors formations of bonds between cysteine and hydrogen, whichis a weak covalent bond easily broken at this step hair can be rearranged. Inpresence of oxidizing agent, the hydrogen ions will be removed so that cysteineresidues forms disulfide bonds. Not all the brokendisulfide bonds do not reform again and form weak spots in keratin.

So, thebonds formed were weak and likely to break and allows protein to come back tooriginal state. Some type of hairs is curly as high number of disulfidebonds are formed along different sites of nearby chains when compared tostraight hair and cause keratin to fold, and follicle shape also a determiningfactor which helps in bringing hair to each other. Answer 2: Myo-inositolmonophosphates catalyzes the hydrolysis of inositol monophosphate is inhibitedby Lithium is an Uncompetitiveinhibition. Uncompetitive inhibition in which enzyme substrate complex isbinded with inhibitor (Lithium) to prevent formation of final product as it takes longer for the substrate or product toleave the activesite. At higher concentration of substrate, the inhibitor workswell.

Penicillinbinds to DD-transpeptidase and prevents it from binding and cross-linkingpeptidoglycans in the bacterial cell wall, which will cause the bacterial

cellto burst. This is an example of Irreversibleinhibitor . An irreversible inhibitor will bind to an enzyme so that noother enzyme-substrate complexes can form. It will bind to the enzymeusing a covalent bondat the active site which therefore makes the enzymedenatured. COX-2 catalyzes formation of prostaglandinswhich is competitively inhibited by NSAIDs. Competitive inhibition inwhich binding of an inhibitor prevents binding of substrate to enzyme.

This isdone by blocking binding to active site of substrate. Addition of substratedisplaces inhibitor from the active site of enzyme and increase binding ofsubstrate to enzyme, this alters only the Km, leaving the Vmax unchanged. Answer 3: ? G values which are negative valuesindicate forward reaction and positive values indicate reverse reactionstrongly favored.

In absence of inorganic phosphate which indicates thathexokinase (step 1) and phosphofructokinase (Step 3) favor forward reactions. ButAldolase (step 4) and phosphoglycerate mutase (step 8) never favor reactioneven in presence of inorganic phosphate as it has positive ? G but as a resultof indirect coupling these reactions are become favorable. Step 10 (PEP topyruvate) is favorable that low concentration of all intermediates prior tothis pushes reaction in forward direction to produce new substrate. Steps 6, 7, and 10 releases sufficient energy to drive theformation of NADH (step 6) or the formation of ATP (steps 7 and 10). Step 1 is formation of Glucose 6 phosphate (G6P)from glucose with use of ATP molecule which is irreversible reaction. It iscatalyzed by hexokinase which is feedback inhibited by G6P, so phosphorylationof glucose is controlled depending upon concentration of

formed G6P. ? G is negative as the ATP used as phosphatedonor. The glucose is locked up in cell and Italso enables the glucose to go on to step 2 of glycolysis.

Step 3 is conversion of fructose 6phosphate to fructose 1, 6 bisphosphate catalyzed by phospho fructokinase byutilizing ATP. Fructose? 2, 6? bisphosphate activates Phosphofructokinase, which is formed from fructose? 1? phosphate by phosphofructokinase II. This stepis activated under low energy when cell has high AMP and ADP and fructose 1, 6 bisphosphate. Step 1 and3 consumes ATP energy to take but prepares substrates for the production ofenergy in later steps. Step 7 Involves 1, 3-bisphosphoglycerate to3- phosphoglycerate catalyzes by phosphoglycerate Kinase. The first ATPforming step in glycolysis. ATP is formed by transfer of a phosphoryl groupfrom 1, 3-bisphosphoglycerate to ATP is called as substrate levelphosphorylation. Coupling of step 6 with step 7 produces one NADH per glucoseare to be reoxidized to regenerate NAD that is needed for the oxidation ofglyceraldehyde 3 phosphate.

Gibbs free energy If ? G < 0, this reaction will proceed in the forwarddirection, as written. If ? G > 0, however, the reaction will proceedin the reverse direction and B will be converted to A. This aids to bring the equilibrium point of the reaction, thus for every positive change there must be a preceding equalnegative change. For example Step 4 is formation of trioses G-3 P(glyceraldehyde 3 phosphate) and DHAP (Dihydroxy acetone phosphate) fromfructose 1, 6 bisphosphate catalyzed by Aldolase which has high positive gibbsfree energy. Aldolase reaction is a near equilibrium reaction in cells, which shows concentration of fructose 1, 6 bisphosphate is

highly relative totwo triose groups G-3 P and DHAP. The concentration of fructose 1, 6bisphosphate is very high in the cells which is formed due to high -ve(negative) gibbs free energy.

The concentration of these trioses is low incells when compared to fructose 1, 6 bisphosphate. Flux due to highconcentration of fructose 1, 6 bisphosphate which goes to next steps forpyruvate synthesis. Answer 4: In TCA cycle total of 20 ATP produced from 2 Acetyl COA molecules. For one it produces 10 ATPs. Conversion of Isocitrate to alfa Ketoglutarate produces one 1NADHEnzyme: isocitrate dehydrogenase. Conversion of Alphaketoglutarate to succinyl CoA produce 1 NADH Enzyme: alpha ketoglutarate dehydrogenase. Oxidation of Malate forms oxaloacetate, 1 NAD+ is reduced to NADH. Enzyme: malatedehydrogenase.

1 NADH = 2. 5 ATP: Total 3 NADHfor 1 Acetyl COA = 3*2. 5 = 7.

5 ATPOxidation of Succinate to fumarate.(FAD) is reduced and forms FADH2. Enzyme: succinate dehydrogenase. 1 FADH2 = 1. 5 ATP succinyl CoA converted to Succinate by removingthe COA using GTP and generate ATP in process Enzyme: succinyl-CoA synthetase. 1 ATP  Total ATP for 1Acetyl COA = 3 NADH + 1 FADH2 + 1 ATP = 7. 5+ 1.

5+ 1= 10 ATP. For2 Acetyl COA = 20 ATP. Answer 5: Glucose 1 phosphate conversion to lactate yields 3 ATPequivalents1 ATP from Phosphofructokinase reaction2 ATP form Phosphoglycerate Kinase reaction Converting two molecules oflactate to one molecule of glucose 1 phosphate needs 6 ATP. 2 ATP for Pyruvatecarboxylase reaction 2 ATP in the PEPcarbokinase reaction 2 ATP for PhosphoglycerateKinase reaction.

Answer6: rRNA are processed andassembled into their ribosomal subunits within nucleus and exported so it isresistant to nucleases. tRNA are processed from aprimary transcript and heavy modification in nucleoside was seen and have anextensive secondary structure which makes them resistant to ribonuclease degradation. Capping of mRNA was conducted duringthe transcription by an enzyme complex. Main reason for capping is protectionof mRNA from 5′ exonuclease enzymes. Removal of one nucleotide from mRNAsynthesizes an inefficient protein so that preservation of the mRNA translationis very important. Main functions of 5′ capping is regulating transport of mRNAfrom nucleus and protection from exonucleases and promotion of translation, 5'proximal intron excision. Answer 7: mRNA: It has codons for peptide synthesis.

It makes up to 3-5 % of total RNA. Showbase relationship to DNA. tRNA: It has anticodons that can base pair or link the exactrequired amino acid corresponding to mRNA codon. Also called as Adaptermolecules. It makes up to 15-20 % of total RNA. rRNA: It is a molecule in cell that form a part of ribosome andthen exported to cytoplasm and help in translation process.

Catalyzes the formation of the peptide bond. It makes up 80%of total RNA. I have no base relationship to DNA. Synthesis of mRNA, tRNA, rRNA: mRNA: It is formed by transcription process from DNA with the help of RNA polymerasewhich make a copy of gene from DNA form to mRNA. It is transferred from Nucleusto Cytoplasm. tRNA: It is also formed by transcription process from DNA with help if RNA polymerasethree enzyme in the nucleus.

It is formed by nuclear processing of precursormolecule. rRNA: It is formed by transcription from DNA using RNA polymerase one into large RNAmolecule. Later addition of sequences is added by many other polymerasessimultaneously to form giant RNA molecules. Structure and functionof mRNA, tRNA, rRNA: mRNA: It is linear shape molecule. IT carries genetic information from DNA to ribosomein Cytosol which serves as a template for proteins synthesis and unpaired basesare binded to mRNA and tRNA. 5'end terminal is capped by the 7 – methylguanosine triphosphate cap.

It helps in recognizing the mRNA by the translationmachinery. Capping prevents cleavage by 5′ exonucleases. 3′ end have a polymerof adenylate residues which protect from 3′ exonucleases.

tRNA: It has a primary and secondary structure. Primary structure the nucleotidesequence of all tRNA molecules allow intrastand complementary that forms asecondary structure. Each tRNA have extensive internal base pairing and forms aclover like structure. The hydrogen bonding stabilizes the structure. Cloverleaf structure have 5 arms1. Acceptor arm – It is 3′ end, the hydroxyl of Adenine bindswith carboxyl groups of Amino acid. 2.

Anticodon arm- Opposite ends of Acceptor arms, it bindsspecifically with mRNA by hydrogen bonding. 3. DHU arm – Serves as site to recognize enzymes that helpsto add amino acid to acceptor arm. 4. T, C arm- Involves binding of tRNA to ribosomes. 5. Extra arm – Only 75% of tRNA has extra arm.

The tertiary structure is also formed by internal bonding ofhydrogen in clover leaf between T and D arms. rRNA: large, small rRNA combine along ribosomal proteins to form large, small subunit ofribosome. These complex structures, which physically move along an mRNAmolecule. Also help in binding tRNAs and accessory molecules that are requiredfor synthesis of proteins.

Answer 8: After DNA strands areseparated two strands were formed one is Leading and other is called as laggingstrands. Leading strands always lead from 5′ to 3′ and lagging strand readsfrom 3′ to 5′. As DNA strands are antiparallel only one continuous strand cansynthesis at 3′ end of the leading strand because of DNA polymerase property tostart synthesis from 5′ to 3′. DNA polymerase is highly specific for 3′- OHterminal of new strand. DNA polymerase attacks by nucleophilic by the 3′-OH of thenucleotide at the 3′ end of the strand on the 5′-?-phosphorus of the deoxynucleoside 5′-triphosphate.

A primer(segment of new strand) is needed opposite to leading strand to whichnucleotide are attached. The primer should be in place before DNA polymerasestart to act. The polymerase can only add nucleotides to a preexisting strand. So, the lagging end is unavailable for the DNA polymerase tointeract. Lagging strand forms a short section of DNA a result ofdiscontinuation replication. Many RNA primers are made by primase and bind tomany sites of lagging strand and forms chunks of DNA called as Okazakifragments and then added to lagging strand in 5′ to 3′. Answer9: Step 2: Isomerization of glucose-6-phosphateto fructose 6- phosphate.

Enzyme: Phosphoglucomutase; ? G=+2. 8 KJ. Phosphoglucomutase belongs to Isomerases. Isomerase catalyzes the shifting of afunctional group from one carbon to other within a molecule. Step 4: Fructose-1, 6-bisphosphate isbreak down to: dihydroxyacetonephosphate (DHAP) and glyceraldehyde 3-phosphate. Enzyme: Aldolase; ? G= +24.

6 KJ. Aldolasebelongs to class Lyases. Aldolase catalyze an aldol cleavage reaction. Step 5: DHAP and GAP areisomers of are readily inter-converted.

GAP is a substrate for the next step in glycolysis so all of the DHAP iseventually depleted. Enzyme: Triose phosphate Isomerase; ? G= +7. 6 KJ. Triosephosphate Isomerase belongs to Isomerasesclass. Interconverting of aldolases and ketoses are Involved.

Step6: GAP is dehydrogenated toform 1, 3-bisphosphoglycerate. Enzyme: Glyceraldehyde 3-phosphate dehydrogenase (GAPDH); ? G= +2. 6 KJ. Glyceraldehyde3-phosphate dehydrogenase belongs to classOxidoreductases. Step 8: Conversionof 3-phosphoglycerate to 2-phosphoglycerate. The phosphate shifts fromC3 to C2 to form 2-phosphoglycerate. Enzyme: Phosphoglycerate mutase; ? G= +6.

4 KJ. Phosphoglyceratemutase belongs to class Isomerases. Answer 10: Synonymous codons thatinstruct ribosome complex to add arginine are: CGU, CGC, CGA, CGG, AGA, AGGSynonymous codons forMethionine: AUGSynonymous codons fortermination of proteins synthesis: UAA, UGA, UAG Synonymous codons thatsignal the initiation of synthesis: AUG. Bonus Question: Tumorcells grow under limited oxygen supply initial stages as they devoid ofcapillary supply.

So, the cells depend on glycolysis by converting glucose topyruvate and lactate for ATP production but the ATP produced is only 2 ATP perglucose, to compensate that tumor cells absorb more glucose than normal cells. More lactic acid is formed there will be change in pH to acidic.

Increase in glycolysis is achieved by increased synthesis of glycolytic enzymesand plasma membrane transporters. With high rate of glycolysis, the tumor cellscan survive anaerobic conditions. High rate of glucose uptake used in pinpoint location oftumors.

In positron emission tomography isotope labelled glucose analog istaken up and not metabolized by tissue. The decay of isotope yields positronsthat will be detected by a detector and help in pinpointing the location oftumor precisely. The intensity of the positrons emitted is detected in the petscan is translated from green to red.