

AP[®] BIOLOGY
2006 SCORING GUIDELINES (Form B)

Question 2

The relationship of structure to function is one of the major themes in biology. For **three** of the following structure/function pairs, describe the structure and then explain how the function is related to the structure.

(a) Enzyme structure/catalysis (**4 points maximum**)

Description (2 points)

- 3-D shape that results from folding of polypeptide chains
- Folding produces a pocket in which substrate may bind
- Levels of protein structure (primary, secondary, tertiary)

Explanation (2 points)

- Complementary 3-D shape of enzyme and substrate are required for proper interaction and catalysis in active site—reduction of activation energy; induced fit
- Allosteric modulation, effect of pH, temperature (or other environmental factors) on enzyme shape
- Elaboration points: competitive/non-competitive inhibition—effect on enzyme action; amino acid side groups in active site interact with substrate to stress bonds in substrate and reduce activation energy of reaction

(b) mRNA structure/protein synthesis (**4 points maximum**)

Description (2 points)

- Linear sequence of RNA nucleotides
- Details: 5' cap; poly-A tail; introns
- Description of origin and/or fate of mRNA (transcription, processing and translation)
- Fine details of RNA nucleotide structure

Explanation (2 points)

- The linear sequence of RNA nucleotides, read as codons (three at a time; contiguous; nonoverlapping)
- specify the sequence of amino acids incorporated in a new protein being constructed at a ribosome
- start codon and/or stop codon roles

(c) Cell membrane structure/signal transduction (**4 points maximum**)

Description (2 points)

- A phospholipid bilayer that incorporates malleable (and, often, mobile) integral or membrane associated proteins
- Membrane-embedded receptor molecules with transmembrane domains

Explanation (2 points)

- Receptor proteins undergo shape changes when proper stimulus is present—signal is communicated through membrane by allosteric shape change
- The altered proteins may then influence other cellular events or states: activation of G-proteins and/or tyrosine-kinase receptor protein auto- and heterophosphorylations leading to cellular response

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Question 2 (continued)

(d) Membrane protein structure/active transport or facilitated diffusion **(4 points maximum)**

Description (2 points)

- Phospholipid bilayer (credited unless already described in c)
- Integral protein in membrane
- Protein's 3-D shape allows it to act as a channel, bind solutes, and/or bind ATP, as necessary

Explanation (2 points)

- Some solutes, like ions and larger hydrophobic molecules cannot cross phospholipid membranes unassisted.
- Integral proteins allow such substances to pass: hydrophilic channel; binding of solute leads to shape change in protein.
- Hydrolysis of ATP causes shape change in protein leading to shuttle of material from one side of membrane to the other.

2. The relationship of structure to function is one of the major themes in biology. For three of the following structure/function pairs, describe the structure and then explain how the function is related to the structure.
- (a) Enzyme structure/catalysis
 - (b) mRNA structure/protein synthesis
 - (c) Cell membrane structure/signal transduction
 - (d) Membrane protein structure/active transport or facilitated diffusion

a) An enzyme is a protein that lowers the energy of activation required by ~~the reaction~~ a chemical reaction without being consumed by the reaction itself. An enzyme does this by temporarily binding to a particular substrate and holding it in such a position that it is easier for the reaction to take place. An enzyme's 3-d shape ~~is~~ is critical to its function: the shape of its active site (the site where the enzyme binds to the substrate) is specific to a single substrate only. An enzyme therefore catalyzes specific reactions only. If an allosteric inhibitor binds to the enzyme and changes its shape, the shape of the active site is changed also and the enzyme cannot catalyze a reaction. This is one way that reactions are controlled. An enzyme's shape is determined by the sequence of amino acids in the polypeptide chain or chains that make it up, and the interactions that these amino acids have either with each other (hydrogen bonds, disulfide bridges) or with the environment (some are ~~hydrophobic~~ hydrophobic and so move to the center of the enzyme).

b) mRNA is essentially an RNA transcription of a certain

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DNA sequence that codes for a certain polypeptide. The difference between an mRNA sequence for a polypeptide and a DNA sequence aside from the fact that one is RNA and the other is DNA is that the mRNA contains no 'introns' or 'inactive genetic information', only exons — genetic information that is actually expressed. The nucleotide sequence in mRNA ~~forms~~ forms a template or base onto which tRNA attaches. The nucleotide sequence in mRNA is read in sets of three nucleotides. A set of three is called a 'codon' and each one of these 64 possible codons ($4 \times 4 \times 4$ possible nucleotides) codes for either a specific amino acid in a protein, or for a 'start' or 'stop' signal for the ~~ribosome~~ ribosome manufacturing a polypeptide using mRNA as a template. Polypeptides are what make up proteins. If mRNA sequence is disrupted or damaged in any way, the protein built from it will not work.

d) membrane proteins responsible for active transport or facilitated diffusion must ~~form~~ form a passage that goes through the whole membrane — they must be transmembrane proteins. Proteins that allow facilitated diffusion are analogous to drainage pipes — they simply provide passage for a material to diffuse ~~without~~ down a concentration gradient. They don't need to actively pump the material. Active transport proteins are analogous to pipes with pumps attached — they pump material (like K^+ , for example) against

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2A3

ADDITIONAL PAGE FOR ANSWERING QUESTION 2

a concentration gradient. Active transport membrane proteins are specific to certain materials and require ~~ATP~~ ~~energy~~ ~~to~~ ~~provide~~ ~~the~~ ~~energy~~ to 'pump' materials.

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2B₁

a) ~~Enzymes~~ Enzymes are proteins consisting of a unique amino acid chain bonded by polypeptide bonds. The amino acid chain undergoes a variety of bonding such as ionic, covalent, and hydrogen bonds as well as disulfide bridges which ~~form~~ form based on the molecules that exist on each type of amino acid. The unique sequence folds into a tertiary protein. Enzymes have a bonding site in which ~~substrates bond~~ specific substrates bond to, as enzymes are substrate-specific. Enzymes ~~operate~~ catalyze reactions by lowering the activation energy required to start a reaction. The bonding site on the enzyme is unique to one substrate because of the unique amino acid sequence and how it was folded. This aids in catalysis in which enzymes are reused to allow substrates to bond in the site, providing a conformational change in the enzyme. This change in shape stresses the bonds in the substrate, forcing a change in the substrate, ~~the~~ changing it into a product where it then leaves the enzyme to allow another substrate to go in. Some enzymes have allosteric sites where cofactors or coenzymes such as vitamins and Ca^{2+} may be required to help the enzyme bond to the substrate. Inhibitors can block the ~~the~~ bonding site or allosteric site that disallow any substrates to be ~~the~~ catalyzed. Enzymes operate at an optimum temperature and pH and if placed in extreme conditions, the bonds holding the protein *

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b) mRNA is a single strand of RNA nucleotides formed from a DNA template in a process called transcription. After RNA nucleotides are assembled, in eukaryotes the strand is modified by adding a methyl-guanosine cap and a polyadenine tail. Both increase the shelf life of the mRNA, and the methyl-guanosine cap allows the mRNA to thread onto a ~~ribosome~~ ribosome much easier. A group of 3 RNA nucleotides ~~starting from the start~~ forms a codon, which complements to a specific amino acid. All mRNA strands begin with AUG, the start codon which codes for methionine and ends with either UAA, UAG, or UGA, stop codons. mRNA is used for protein synthesis, a process in which a tRNA carrying an amino acid binds to the P site of a ribosome to line up with the start codon of the mRNA strand already threaded into the ribosome. As each codon codes for specific amino acids, tRNA that correspond bring that amino acid and adds to the chain of amino acids ~~is~~ forming. After the tRNA is used it leaves the ribosome at the E site. When the stop codon is reached and the last amino acid is added, the chain breaks away and becomes a protein to be used in bodily functions and the mRNA can be reused to synthesize more proteins. This process is called translation.

c) A cell membrane of eukaryotes consists of a phospholipid bilayer ~~and~~ containing cholesterol to provide stability and fluidity. ~~are~~ Integral proteins are embedded in the phospholipids and are used for transport, cell recognition, and cell communication. This is the site for signal transduction pathways, a form of communication in the cell.

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~~It~~ in a STP, a signal molecule ^{can} activates a G-protein, and GDP is displaced by a GTP. The G protein is embedded in the cell membrane. It ~~is~~ ~~is~~ now mobile and can activate the next protein, possibly inside the cell, and a cascade effect of ~~activations~~ activating inactive kinases occurs. The last protein elicits some sort of desired response. These proteins are activated by phosphorylation. The signal molecule remains outside the cell ~~is~~ in the first G-protein, but it is that membrane protein that begins the cascade effect inside the cell.


(*) together break. The ~~primary structure~~ peptide bonds can withstand extreme temperatures and pHs so all that is left is a strand of amino acids. Usually damage is permanent and enzymes can no longer catalyze reactions.

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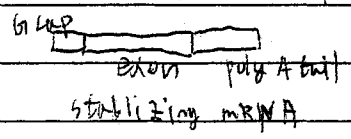
2C1

a) Enzyme is composed of protein. And it has active site. The shape of active site determine the act of Enzyme. Enzyme can act as a catalyst. When substrate bind to active site of Enzyme, enzyme lowered the activation energy and speed up the reaction. Sometimes the form of active site change due to ~~allosteric~~ allosteric protein, inhibiting catalysis. Other coenzyme ~~attached~~ bind to active site and help catalyzing of enzyme.



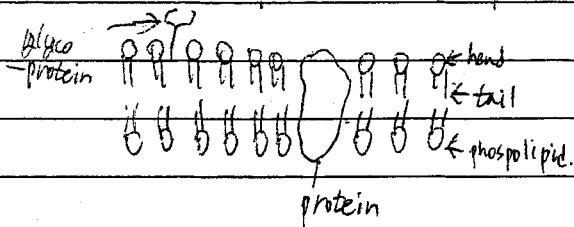
active site

b) mRNA is composed of nucleotid. nucleotid is composed of ribose 5' and ~~nucleic acid~~ nitrogen base and phosphate group. mRNA has AGCU. If mRNA undergoes maturing, it has cap on 5' and poly A tail on 3'. The sequence of nitrogen base is ~~complement~~ complement with template DNA. mRNA act as a blueprint in protein synthesis. It gives information to tRNA which amino acid to bring. When ribosome (large and small subunit) bind to AUG, the start codon, tRNA bring right amino acid and make prolonged protein, primary structure. When the codon is UGA or UAG, something indicate termination, ribosome detached from mRNA and result in protein.



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c) Cell membrane is composed of phospholipid bilayer. Characteristic of phospholipid that has hydrophobic in tail and hydrophilic in head, it can be barrier with outer condition and inner cell, Not only phospholipid but protein, glycoprotein are also composer of cell membrane. Some glycoprotein attached to the cell membrane and protein is on the cell membrane. Cell use protein as a channel to use it ~~for~~ signaling. For example when cell infected by virus and secreting cytokinine, they eject it by help of channel protein.



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2006 SCORING COMMENTARY (Form B)

Question 2

Sample: 2A

Score: 9

In part (a) the maximum of 4 points was earned. A description point was earned for the enzyme holding the substrate in a position that facilitates the reaction, and an explanation point was earned for the 3-D shape of the enzyme being critical to the active site's function. An explanation point was earned for the effect of allosteric inhibitors on the shape of the active site, and a description point for the levels of protein structure. In part (b) the maximum of 4 points was earned. One description point was earned for the mRNA being a transcript of a segment of DNA, and another description point for the mRNA lacking introns. One explanation point was earned for the codons being nucleotides read three at a time, and another explanation point for the start and stop codons. In part (d) the response earned a description point for transmembrane proteins allowing facilitated diffusion.

Sample: 2B

Score: 8

In part (a) the response earned 3 points. A description point was earned for the enzyme folding to form a specific bonding site for the substrate, and an explanation point for induced fit. Another explanation point was earned for the effect of pH and temperature. In part (b) the maximum of 4 points was earned. One description point was earned for the mRNA being a transcript of a segment of DNA, and another description point for the cap and poly-A tail. One explanation point was earned for the codons being nucleotides read three at a time, and another explanation point for the start and stop codons. In part (c) the response earned a point for the activation of the g-protein.

Sample: 2C

Score: 6

In part (a) the response earned a description point for a substrate binding to an active site with a certain shape, and an explanation point for the effect of allosteric inhibitors. In part (b) the response earned 1 point for the description of mRNA as a sequence of nucleotides, another point for the description of the cap and poly-A tail, and a third point for the explanation of the role of the start codon. In part (c) the response earned a point for the description of the composition of the cell membrane. No points were earned for the mixture of facilitated diffusion and cell signaling.