PROTEIN MODELING - DIVISION C CONDENSED KEY

Orlando Science School Invitational 2019

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AUTHOR’S NOTE: USE THIS KEY FOR GRADING PURPOSES.

Instructions and Clarifications:
- You have 50 minutes to finish this exam and the computer exploration of protein structure. The exam and computer exploration are worth 60% of the overall grade.
- Each participant may bring one 8.5” x 11” sheet of paper that contains information about this event without any annotations or labels affixed along with writing utensils for each participant.
- You may split the exam but you are responsible for placing them in the correct order afterwards. The page numbers are located in the lower right corner for your convenience.
- There are five tiebreakers in this exam. They are labeled as TB#.
- Write your team number on every page of the answer sheet.
- Anything written on the exam will not be graded. Only the answer sheet will be graded.
- If you have any questions or comments about this exam, feel free to email me at velasco.scienceolympiad@gmail.com. Happy testing!
I. General Biochemistry of Macromolecules

Multiple Choice: Each letter is worth one point.

1. A
2. C
3. D
4. D
5. E
6. A
7. B
8. C
9. C
10. B

Short Answer: Each letter is worth one point.

1. Gibbs free energy $\Delta G$ between the folded and unfolded states.
2. $G = H - TS$
3. Kinetically stable protein
4. There are so many of them.
5. Conformational entropy
6. Kinetic stability
7. 3’5’ phosphodiester bridges (give 0.5 point phosphodiester bridges)
8. Adenine, guanine, cytosine, and uracil. (Do not accept A, G, C and U)
9. Magnesium
10. Pentose sugar (2-deoxyribose), a phosphate group (H3PO4), and a nitrogen-containing base

Illustration

- 1 point for amine group
- 1 point for carboxyl group
- 1 point for hydrogen bonded to alpha carbon
- 1 point for the correct R group/side chain of histidine
Diagram-based questions

1.

A. (1) Electrostatic interactions
B. (1) Hydrogen bonding
C. (1) Salt bridge
D. (1) Noncovalent
E. (1) Glutamic acid and lysine (0.5 points per amino acid)

2.

A. (1) alpha helix
B. (1) carbonyl
C. (1) N-H group
D. (2) 100
E. (2) 3.6

3.

A. (1) a protein’s three dimensional shape
B. (2) primary, secondary, tertiary (give one point if incomplete)
C. (1) hydrophobic/nonpolar
D. (1) hydrogen bonds

4.

A. (1) deoxyribonucleic acid (do not accept DNA)
B. (2) covalent bonds
C. (3) alternating (1) sugar(1)-phosphate(1) backbone
D. (4) cytosine, guanine, adenine, thymine (one point for each, do not accept C, G, A, T)
E. (1) Hydrogen bonds
II. CRISPR-Cas9 and Cytidine Deaminase

Multiple Choice (each letter is worth one point)

1. A
2. A
3. C
4. C
5. B

Diagram-based Questions

A. (1) Cas9
B. (1) Alpha-helical lobe
C. (1) nuclease lobe
D. (2) single bridge helix
E. (1) cyan/light blue/sky blue/mint blue (anything BUT dark blue; give 0.5 points for blue)
F. (1) Gray
G. (2) protospacer adjacent motif (accept PAM)
H. (2) HNH domain (accept HNH)
I. (2) sgRNA
J. (2) C-terminal end (accept C)
K. (2) between the alpha-helical lobe (dark blue) and the nuclease lobe (cyan, orange, and grey).

Short Answer: Each question is worth one point.

1. Highly conserved enzymes from bacteria that mutate cytidine into other nucleotides.
2. Uracil
3. It does not.
4. Give one point for any of the following: If uncontrolled, it can cause misfolded peptides, dominant-negative proteins, mutations in tumor suppressor genes, contribution to tumor formation.
5. Activation-induced cytidine deaminase
6. Activation of zinc-bound water in the active center of the enzyme
7. Clustered Regularly Interspaced Short Palindromic Repeats
8. Acquisition, crRNA biogenesis, targeting
9. Type II
10. cas1 and cas2
Diagram-based Questions: Each letter is worth one point.

A. Guide RNA  
B. Target specific crRNA sequence  
C. Active sites  
D. Cas9  
E. Target DNA sequence  
F. Deactivated Cas9 (accept Cas9)  
G. Repressor  
H. Target gene  
I. Activator  
J. mRNA

Free-Response Questions

1.  
   a. (2) Type II  
   b. (2) Type II  
   c. (2) Type II

2.  
   a. (1) RuvC  
   b. (1) HNH  
   c. (2) 3  
   d. (3) C-terminal domain  
   e. (2) II

3.  
   a. (2) nonhomologous end-joining  
   b. (1) False  
   c. (1) False  
   d. (4) The system does not use CRISPR-Cas9 components (1) in a form of DNA vectors (1). Each component is either RNA (1) or protein (1).
III. Computer Exploration of a Protein Structure

Point values are addressed in the parentheses.

1.  
   a. (2) 321  
   b. (2) 321  
   c. (2) 24

2.  
   a. (1) Accept one of the following: Lysine, Lys, K  
   b. (1) basic  
   c. (1) aliphatic  
   d. (1) True  
       Do not award partial credit for this question. The 4 main parts of an amino acid must be shown.

   ![Amino Acid Diagram]

   e.

3.  
   a. (1) Accept one of the following: Methionine, Met, M  
   b. (3) S-methyl (1) thioether (1) side chain  
   c. (1) nonpolar  
   d. (1) aliphatic  
   e. (2) Cysteine
4. 
   a. (1) Accept one of the following: Histidine, His, H 
   b. (2) imidazole (1) side chain that is partially protonated (1) 
   c. (2) 6 
   d. (2) 2 
   e. (2) it has the ability to switch between protonated and unprotonated states 

5. 
   a. (1) Accept one of the following: Leucine, Leu, L 
   b. (1) protonated 
   c. (1) deprotonated 
   d. (3) the side chain is an isobutyl group; overall nature is non-polar (1) and aliphatic 
      (1) amino acid 
   e. (1) True 

6. 
   a. (1) Accept one of the following: Proline, Pro, P 
   b. (1) True 
   c. (1) both 
   d. Do not award partial credit for this question. The 4 main parts of an amino acid must be shown. 
   e. (2) pyrrolidine