Protein Modeling - Division C Condensed Key

University of Texas-Austin Invitational

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Instructions and Clarifications:

- You have **50** minutes to finish the written exam and the computer exploration of protein structure. **Part I** of this exam refers to the written exam portion. **Part II** refers to the computer exploration of protein structure. This section is worth **60%** of the overall grade.
- Each **participant** may bring **one** 8.5" x 11" sheet of paper that may be in a sheet protector or laminated that contain information without any annotations or labels affixed along with writing utensils for each participant.
- You **may** not write on this exam. Only the **answer sheet** will be graded.
- Write your team number on every page of the answer sheet.
- Tiebreakers are labeled as **TB#**. There are **five** tiebreakers in this exam.
- If you have any questions or comments about this exam, feel free to email me at velasco.scienceolympiad@gmail.com. **Happy testing!**

Part I: Written Exam - *I. General Biochemistry of Macromolecules*

Multiple Choice: Each answer is worth **one** point

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

Short Answer: Point values are addressed in the parenthesis.

1. Increased entropy in the surrounding aqueous solution resulting from burial of hydrophobic surfaces. (2)
2. There is a resonance structure or partial sharing of two pairs of electrons (1) between the carbonyl oxygen and amide nitrogen (1).
3. Partial double-bond character (1)
4. Oxygen; Nitrogen
5. The negatively charged groups (1) of adjacent Glu residues repel each other (1), prohibiting the formation of the alpha helix (1)
6. The nitrogen atom of proline is part of a rigid ring structure (1), so the rotation about the N-alpha Carbon bond is impossible (1). The N atom of Proline (1) also does not have hydrogen available to participate in H bonds with other residues (1).
7. Oxidation (1) of sulfhydryl groups (1)
8. The phi-angle (ϕ) (1) - around the N-Cα bond (1). The psi-angle (ψ) (1)- around the Cα-C bond (1). The omega-angle (ω) (1)- around the peptide bond between the C and N (1).
9. 0.133 nm (1), 0.149 nm (1), 0.127 nm (1) **TB#1**
10. The trans isomer is more stable (1) because there is less physical contact between the side chains of the two amino acids involved in the formation of the peptide bond (1). Also, trans isomers are mores table than cis isomers for acylic systems. (1) There is an increased unfavorable steric interaction of the substituents in the cis isomer. (1) Trans isomers have a higher thermochemical stability due to less exothermic heat of combustion. (1)

Diagram-based Questions: Point values are addressed in the parenthesis.

1. **TB#2**

    A. Glycine (1)
    B. It is the only achiral amino acid. (2)
    C. False
    D. 2.4
    E. 9.6
    F. Flexible

2.

    A. Between the main chain C=O and N-H groups. (1)
    B. They point in opposite directions. (1)
    C. 3.5 Angstroms.
    D. Parallel beta-sheets run in one direction (1); antiparallel sheets run in opposite directions (1).
    E. Hydrogen bonds (1)
    F. Globular proteins (1)
    G. Twisted (2)

II. CRISPR-Cas Systems and Cytidine Deaminase

Multiple Choice: Each answer is worth **one** point.

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

Labeling: Each letter is worth **one** point. **TB#3**

A. Pre-cRNA
B. mat-cRNA
C. Cas3
D. PAM
E. Cas9
F. pre-crRNA
G. RNase
H. tracrRNA
I. int-crRNA
J. mat-crRNA
K. PAM
L. RuvC
M. HNH
N. Cas6
O. pre-crRNA
P. cmr/cas10 csm/cas10
Q. int-crRNA
R. mat-crRNA
S. csm/Cas10
T. cmr/Cas10
U. III-A (DNA Target)
V. III-B (RNA Target)
W. Type I
X. Type II
Y. Type II

Diagram-Based Questions

1.
   a. Cas9 (2)
   b. sgRNA (2)
   c. nonhomologous end joining (NHEJ) (2)
   d. homologous recombination (HR) (2)
   e. Indels (2) that introduce knock-out frameshift mutations (2)
2.
   a. dCas9
   b. RNA polymerase (RNAP)
3.
   a. Give credit for any of the two examples. Each example would be worth two (2) points: Transcription repression, transcription activation, chromatin remodeling, fluorescent reporter, histone modification, recombinase, methylase **TB#4**

Short Answers

1.
    a. *CDA* gene (1)
    b. cytidine (1), deoxycytidine (1), uridine (1)
2.
    a. The cutting is guided by an RNA strand rather than a protein. (2)
    b. nonhomologous end-joining (1)
    c. False (1)
    d. Downstream (1)
3.
    a. I and III (2) (only give one point for one type)
    b. III (2)
    c. III (2)
    d. I and III (give one point for one system)
    e. III-A (2)

4. **TB#5**
    a. Cas9 (3)
    b. *trans*-activating crRNA or tracrRNA (3)
    c.
        i. I and II (2 points for one of these types)
        ii. III (4)
5.
    a. adaptation → crRNA biogenesis → targeting (do not give any partial credit for an incorrect order) (2)
    b. New spacers are taken from exogenous nucleic acid into the CRISPR locus. (2)
    c. There is a transcribing of CRISPR arrays that are eventually processed into small interfering CRISPR RNAs (crRNAs). (2)
    d. crRNAs guide Cas nucleases for cleavage of homologous sequences. (2)

Part II: Computer Exploration of Protein Structure

Author's Note: Everything is worth **one** point unless otherwise stated.

1. 0
2.
    a. Proline
    b. Nonpolar
    c. (2) Interior, would be located in the hydrophobic core since proline is hydrophobic
3.
    a. Valine
    b. True
    c. True
4.
    a. Glycine
    b. True
    c. False
5.
    a. Tyrosine
    b. False
    c. Phosphotyrosine (2)
6. 6 (2)
7. 0 (2)
8. 80
9. 890
10. 361