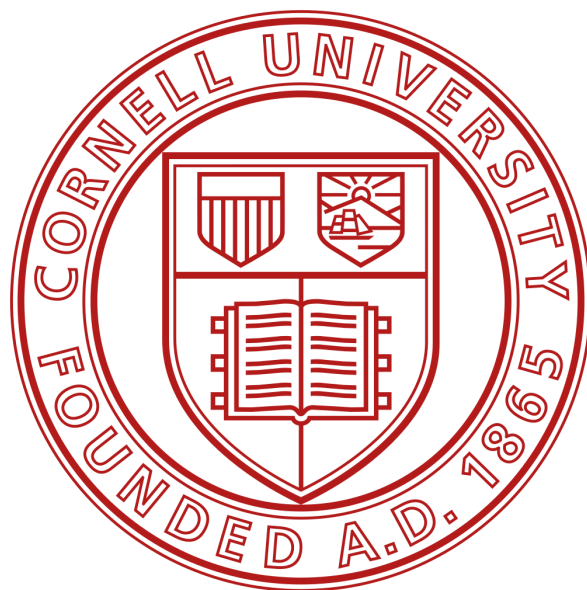


Protein Modeling Division C - Condensed Key

Cornell University Science Olympiad Invitational

November 23, 2019



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AUTHOR'S NOTE: USE THIS KEY TO EXPEDITE THE GRADING PROCESS.

Instructions and Clarifications:

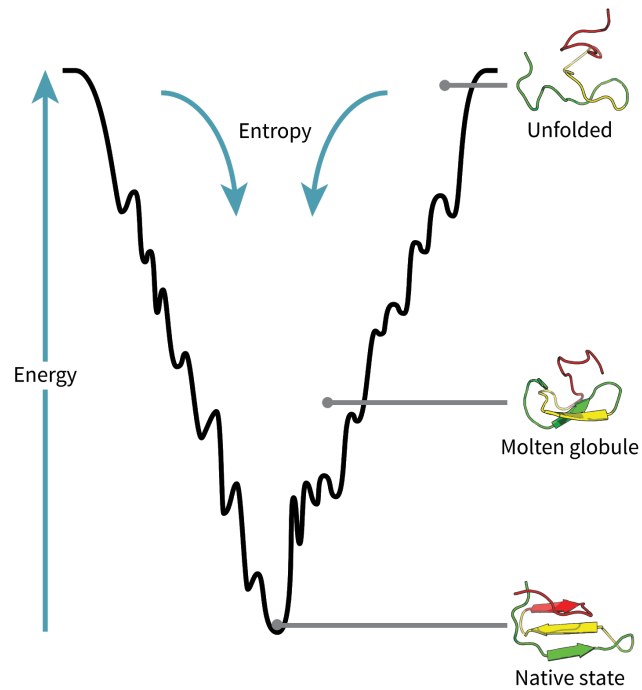
- You have **50** minutes to finish this exam and the computer exploration of protein structure. The **Exam** portion is composed of Section **I** and **II** and is worth 30% of the overall score. The **Computer Exploration** portion is composed of Section **III** and is worth 30% of the overall score.
- 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.
- Write your team number in **every** page of the answer sheet.
- There are **5** tiebreakers in this exam. They are marked **TB#**.
- 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!**

Section I: General Biochemistry

Directions: Answer the following questions about biochemistry in the most concise way possible. The point values for each question are addressed in the parentheses.

1. Hydrophobic chains of a protein collapse into the core of the protein. (1) As a result, the hydrophilic chains of a protein is located in the protein's exterior. (1)
2.
 - a. (1) Negative change/less entropy in the system/decreases entropy in the system/less disorder in the system/more order in the system.
 - b. (1) They fold inwards and form the interior of the protein.
 - c. (1) The hydrophobic collapse (hydrophobic groups folding inward) causes the breaking of the ordered watered cages. This frees the water molecules.
3.
 - a. False (1)
 - b. (2) Proteins fold through a series of metastable intermediate states.
4. Natural evolved proteins optimize their folding energy landscapes. (2) Nature has chosen amino acid sequences so that the folded state of the protein is stable. (2) The process of acquiring the folded state is relatively fast. (2)
5. (2) The conformation that must be assumed by every molecule of the protein if the protein wants to assume its native structure.

6.



Answer:

- (1) - drawing the energy arrow pointing up
- (1) - drawing entropy pointing downwards
- (1) - addressing unfolded protein in the top of the drawing
- (1) - addressing molten globule in the middle of the drawing
- (1) - addressing the native state in the bottom of the drawing
- (1) - drawing the squiggly downwards cone representing energy

7.

- a. $n+4$ (four residues earlier) (2)
- b. $n+3$ (three residues earlier) (2)
- c. $n+5$ (five residues earlier) (2)

8. Each answer is worth **one** point.

- a. Middle
- b. Edge
- c. Middle
- d. Middle
- e. Middle
- f. Middle
- g. Middle

9. Each answer is worth **two** points.

- a. Beta meander
- b. Beta-hairpin
- c. Greek key
- d. Psi-loop

10.

- a. 4 and 5 (2)
- b. Beta-strand 4 is hydrogen bonded to beta-strand 1. (2) Beta-strand 1 is hydrogen bonded to beta-strand 2. (2) Beta-strand 2 is hydrogen bonded to beta-strand 3. (2) Beta-strand 3 is hydrogen bonded to beta-strand 5. (2)

11.

- a. One (1)
- b. Two (1)
- c. i (2), $i+2$ (2), $i+3$ (2)
- d. Type I (1)
- e. Type II (1)

12. Each question is worth **one** point.

- a. Proline
- b. False
- c. First residue of an alpha helix
- d. Edge strands
- e. True
- f. Inflexible

13.

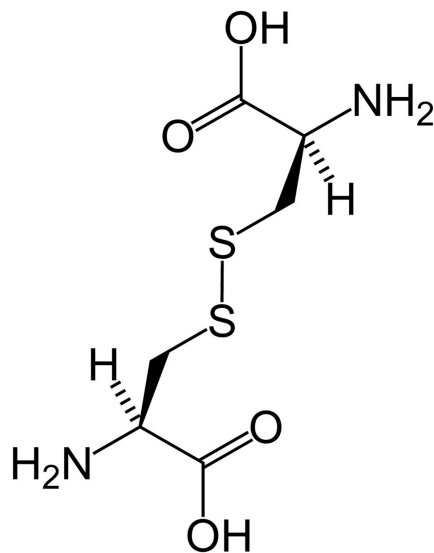
- a. Glycine (1)
- b. (5 points total) Glycine has a hydrogen atom for its side chain. (1) It also has a smaller van der Waals radius than the CH_3 , CH_2 , or CH group that is usually characteristic of all other amino acids. (1) As a result, glycine is the least restricted of all amino acids. (1) Because of this characteristic, the Ramachandran plot has a lot of allowable area, as shown in this plot. (1)

14.

- a. $\Psi (1)$
- b. $\Phi (1)$
- c. $\Omega (1)$

15.

- a. Oxidation (1)
- b. (3) $RS-SR + R'SH \rightleftharpoons R'S-SR + RSH$
- c. False (1)
- d. (1) - give one point for drawing the sulfide bond (S-S)
(2) - give two points for correctly drawing two cysteines



Section II: DNA/RNA Structure, CRISPR-Cas 9 and Cytidine Deaminase

Directions: Answer the following questions about DNA/RNA, CRISPR-Cas 9 and Cytidine Deaminase in the most concise way possible. The point values for each question are addressed in the parentheses.

1.
 - a. 1' nitrogen (1) of pyrimidine base (1) and 9' nitrogen (1) of purines base are bonded to 1' carbon (1) of the pentose sugar (1). (Award two points if locations were not specified).
 - a. (1) glycosidic bond
 - b. (2) 1' to 5' (one point for each number)
 - c. (1) 2'

2.
 - a. (1) True
 - b. (2) ribose sugar connected to a base through the 1'C
 - c. (1) hairpin loop
 - d. (3) hydrogen bond donors/acceptors (1) that are not in Watson and Crick base pairs (AU and GC) (1) interact and hydrogen bond (1)
 - e. (2) the extra hydroxyl group attached to 2' C (anomeric C)

3.
 - a. (1) True
 - b. (1) True
 - c. (2) phosphate group
 - d. (2) they both have N (nitrogen atoms) (1) in the C (carbon) based ring (1)
 - e. (3) nitrogen atom (1) to 1' carbon (1) of deoxyribose sugar in a nucleotide (1)

4.
 - a. (1) hydrogen bond
 - b. (1) 2
 - c. (1) 3
 - d. (2) Chargaff's rule
 - e. (1) False

5.
 - a. (2) base pairing of molecules between two DNA strands of a single DNA molecule
 - b. (2) three-dimensional shape of a DNA molecule
 - c. (1) right
 - d. (1) the bonded bases are parallel in relation
 - e. (1) the bases runs perpendicular to the sugar phosphate backbone

- 6.
- (1) weak
 - (1) False
 - The nitrogen atom (1) has a tendency to attract the electrons in the N-H bond (1), leaving the hydrogen short of electrons (1).
 - (2) Makes the charge slightly negative
 - (2) There are a lot of hydrogen bonds.
- 7.
- (1) hydrogen bonds
 - (1) False
 - (2) RNA is more unstable than DNA.
- 8.
- (2) Cas9 nuclease and sgRNA (single artificial chimeric guide RNA)
 - II (1)
 - Three (1)
 - Heterogenous (1)
 - REC domain (2)
- 9.
- 3' (1)
 - Cas9-crRNA-tracrRNA (2)
 - (2) 5'NGG
- 10.
- (2) pre-crRNA
 - (1) III
 - (1) II
 - (1) I
 - (2) Cas3 nuclease (accept Cas3)
- 11.
- (1) SpCas9
 - catalytically inactivating (1) the RuvC (1) or HNH nuclease domains (1) via point mutations (1)
 - (2) base excision repair
 - It can be used to increase the overall bases (2) that are specifically recognized in the target DNA (2).
 - (1) HR

12.

- a.
 - i. It doubles (2) (give 1 point for “gets longer”)
 - ii. (1) No, it would not.
- b. U6 (1) RNA (1) polymerase (1) III (1) promoter
- c. Cas9 can be coupled to fluorescent receptors (2) that can be used for live imaging of DNA loci (2).

13.

- a. (2) adaptation
- b. (2) targeting
- c. (1) 12
- d. sequence in exogenous nucleic acid element (1) that corresponds to a CRISPR spacer (1)
- e. (2) Type II systems

14.

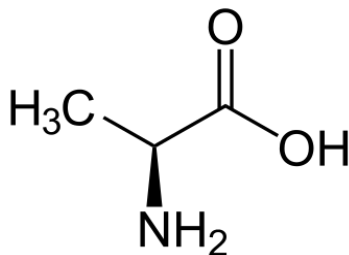
- a. (2) Type III-B (1 point for Type III, 1 point for -B)
- b. (2) Type II
- c. (2) double-stranded substrate
- d. (2) RNase III
- e. (1) Cas9

15.

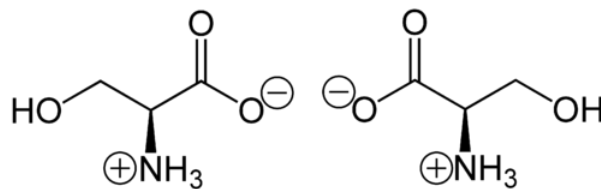
- a. (1) Zinc
- b. Uridine (1) or deoxyuridine (1)
- c. (2) Glutamic acid
- d. Lysine residue (2) at position 27 (2) and glutamate residue (2) at position 24 (2)

Section III: Computer Exploration

1.
 - a. (1) Arginine
 - b. (1) deprotonated
 - c. (1) protonated
 - d. (1) aliphatic
 - e. 2) Since tyrosine is nonpolar, the protein chain would move from the exterior and move more towards the interior (hydrophobic core).
2.
 - a. (1) Phenylalanine
 - b. (2) inert and hydrophobic nature (1) of the benzyl side chain (1)
 - c. (1) L-isomer
 - d. (2) tyrosine
 - e. (2) $C_9H_{11}NO_2$
3.
 - a. (1) Alanine
 - b. (1) True
 - c. (1) False
 - d. (1) True



- e. (3)
4.
 - a. (1) Serine
 - b. (1) Polar
 - c. (6) S-version is the one on the left. R version is the one on the right. 3 points per version. No partial credit granted.



5.

a. (1) 970

b. (1) 0

c. (1) 508

d. (1) 440

e. (1) 145

6. (2) 0

7. (2) 59

8. (2) 22

9. (2) 39

10. (2) 0