

Protein Modeling - Division C Condensed Key

University of Texas-Austin Regional Competition

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USE THIS KEY FOR GRADING.

Instructions and Clarifications:

- You have **50** minutes to finish this exam and the computer exploration of protein structure. This packet contains **60%** of the overall score.
 - The **Exam** is comprised of Section **I and II**. The exam accounts for **30%** of the overall score.
 - The **Computer Exploration** is comprised of Section **III**. The computer exploration accounts for **30%** of the overall score.
- 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.
- Anything written on the exam packet will **not** be graded. 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!**

I. Protein Biochemistry

Multiple Choice: No partial credit will be given for multiple select questions. Each question is worth **two** points. **(30)**

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

Diagram-based Questions: Answer the questions below referring to the diagram or ideas behind the diagram. Complete sentences are **not** required for this section. **(70)**

- 16.
- a. (1) Antiparallel
 - b. (3) Yes, it is more stable. (1) The hydrogen bonds has the ideal 180 degree angle compared to the slanted hydrogen bonds in parallel beta sheets. (2)
 - c. (2) -140 degrees
 - d. (2) 135 degrees
 - e. (3) **TB#2** Tyrosine, phenylalanine, tryptophan, threonine, valine, isoleucine. (Give 3 points for any one of the amino acids listed)
- 17.
- a. (1) José Onuchic
 - b. (2) Large number of pathways and intermediates
 - c. (2) Top
 - d. (2) Saddle point
 - e. (1) True
- 18.
- a. (1) Histidine
 - b. (1) Positively charged
 - c. (2) CAU and CAC (give two points for any of the two listed)
 - d. (4) Imidazole
 - e. (2) 6.0

19.

- a. (3) Cystine (1 point for cysteine)
- b. (2) 60
- c. (2) Longer
- d. (2) Oxidizing
- e. (2) Unstable

20. Each question is worth **two** points.

A. 3.6

F. 5.8

K. 4.8

B. 3_{10} helix

G. 6

L. 1.5

C. 2.2

H. 5.2

M. 2.0

D. Pi (π) helix

I. 2.3

N. 2.72

E. 5.4

J. 1.9

O. 1.1

II. DNA/RNA Structure and CRISPR-Cas Systems

Multiple Choice: Choose the most appropriate response for each question. Each question is worth two points. **(30)**

- | | | |
|-------|-------------------|-------|
| 21. A | 26. A | 31. D |
| 22. D | 27. B | 32. A |
| 23. D | 28. B | 33. B |
| 24. E | 29. B TB#3 | 34. A |
| 25. B | 30. E | 35. E |

Short Answer: The point values are indicated by the number in the parentheses. Complete sentences are **not** required for this section. **(62)**

- 36.
- a. (1) RNA
 - b. (1) DNA
 - c. (2) 2
 - d. (2) B-DNA structure
 - e. (4) steric restrictions (2) imposed by 2' hydroxyl (-OH) residue on ribose (2)
37. **TB#4**
- a. (2) 3
 - b. (2) 2
 - c. (2) 2
 - d. (4) hydrogen bonding (2) and base stacking (2)
 - e. (2) False
- 38.
- a. (10) APOBEC1 deaminase enzyme (5) and Uracyl Glycosylase (UGI) protein (5);
(provide 2 points partial credit for APOBEC; do **not** accept cytidine deaminase)
 - b. (5) transfer RNA adenosine deaminase
 - c. (5) Activation-induced adenosine deaminase (AID)

39.

- a. (1) yes
- b. (3) RNA polymerase III promoter
- c. (6) promoter (3) and polyadenylation sequence (3)
- d. (8) use a pair of “nickase” (4) CRISPR-Cas9 complexes with binding sites on opposite strands flanking the target site (4)
- e. (2) True

Diagram-based Questions: Answer the questions referring to **Figure 2.1** or ideas behind **Figure 2.1**. Complete sentences are **not** required for this section. **(18)**

40.

- A. DNA bubble
- B. Z-DNA
- C. Slipped loop
- D. Cruciform
- E. H-DNA
- F. G-quadruplex/*i-motif* in double stranded DNA

III. Computer Exploration - Jmol

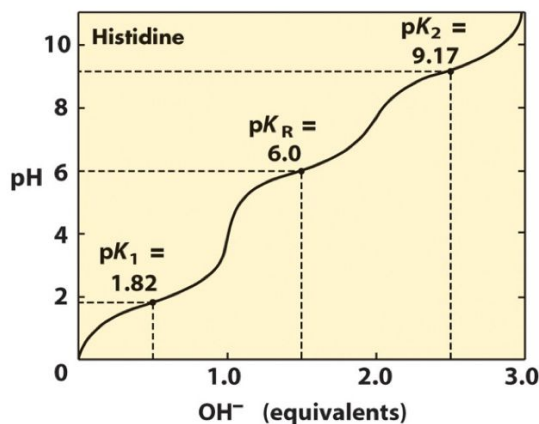
Directions: Answer these questions in the most concise and specific way possible. The point values for each question are addressed in the parentheses. **(123) TB#5**

41.

- (1) Proline
- (3) -2.815, 27.041, -27.552
- (3) pyrrolidine
- (2) True
- (2) True

42.

- (2) H
- (2) protonated
- (8) it can **switch** (2) between **protonated** (3) and **unprotonated** (3) states
- d.



Point breakdown:

- 2 points for curve having three hills
- 2 points per pK label (pK₁, pK_r, and pK₂) for a total of 6 points
- 2 points for having the axes labeled (1 point for pH, 1 point for OH⁻ or equivalents like NaOH)
- 2 points each for correct values of pK (1.82, 6.0, and 9.17 for a total of 6 points)
- 2 points each for correct general area of pH values (~2, 6, and ~9 for a total of 6 points)

- 43.
- a. (1) phenylalanine, Phe, F
 - b. (2) (*S*)-2-Amino-3-phenylpropanoic acid
 - c. (2) tyrosine
 - d. (2) $C_9H_{11}NO_2$
 - e. (2) nonpolar
- 44.
- a. (1) Valine, Val, V
 - b. (4) nonpolar (2) aliphatic (2) amino acid
 - c. (10) glutamic acid is hydrophilic (5) whereas valine/residue 78 is hydrophobic (5)
 - d. (2) protonated
 - e. (2) deprotonated
- 45.
- a. (2) Ile
 - b. (8) hydrocarbon (2) side chain with a branch (2) (central carbon atom [2] bound to three other carbon atoms [2])
 - c. (2) $C_6H_{13}NO_2$
 - d. (2) nonpolar
 - e. (2) uncharged
- 46.
- a. (2) 306
 - b. (2) 48
 - c. (2) 16
 - d. (2) 58
 - e. (2) 0
- 47.
- a. (2) 89
 - b. (2) 0
 - c. (2) 5
 - d. (2) 2
 - e. (2) 4

48. (2) 1457

49. (2) 838

50.

a. (2) 0

b. (2) 2119

c. (2) 1047

d. (2) 403

e. (2) 362