

Protein Modeling Division C - Condensed Key

Northview Science Olympiad Invitational

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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. 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 as **TB#**.
- Anything written on the exam will **not** be graded. Only the **answer sheet** will be graded.
- If you have any comments or questions about this exam, feel free to contact us at the emails below. **Happy testing!**

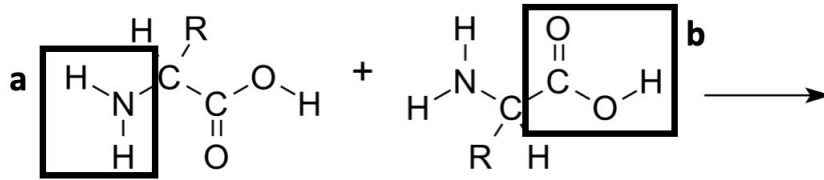
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I. General Biochemistry and CRISPR-Cas Systems¹

Multiple Choice: Each question is worth **two** points.

1. A
 2. E
 3. C
 4. C
 5. E
 6. A
 7. E
 8. D
 9. E
- 10.
- a. Amine (primary) (1)
 - b. Carboxylic acid (1)



One point per box (2 points total)

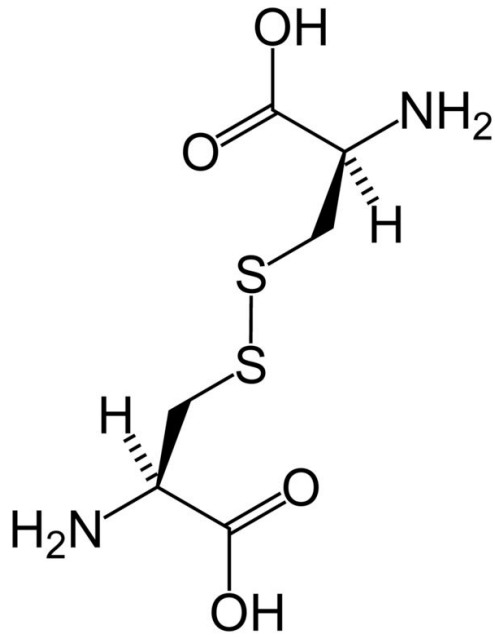
One point for a correct combination of amino acids with a correct peptide bond.

Overall Question: 5 points total

Each question is worth **one** point.

11. cysteine
12. false
13. true
14. false
15. false
16. thiol

17.



- One point per correct drawn cysteine amino acids (2 points total)
- Two points for correctly drawn disulfide bond (2 points)
- 4 points total

18. (TB#1; Extra Credit - do not count this towards the final score). Allows them to make wool. (3)

II. DNA, RNA, and CRISPR-Cas Systems²

Multiple Choice: Each question is worth **two** points.

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

Identification: Each letter is worth **two** points. **TB#3 (30)**

- | | |
|--------------------|-------------------|
| A. Adenine | I. Deoxythymidine |
| B. Adenosine | J. Uracil |
| C. Deoxyadenosine | K. Uridine |
| D. Guanine | L. Deoxyuridine |
| E. Guanosine | M. Cytosine |
| F. Deoxyguanosine | N. Cytidine |
| G. Thymine | O. Deoxycytidine |
| H. 5-Methyluridine | |

Short Answer: Point values are addressed in each answer.

1.

- a. (1) II
- b. (1) II
- c. (1) Type III-B (do not accept Type III)
- d. (1) III
- e. (2) I and III

2.

- a. (1) RNA-guided
- b. (3) crRNA-Cas ribonucleoprotein complex (no partial credit for this question)
- c. (2) tracrRNA
- d. (2) RNaseIII (provide 1 point for RNase only; do **not** provide credit for RNase I or RNase II)
- e. (3) sgRNA (single-guide RNA)

3. TB#4

- a.
 - i. (2) NGG
 - ii. (6) 20 bp in length (2) upstream of the PAM (2) to its 5' end (2)
- b.
 - i. (4) for inserting guide sequences (2) into backbone vectors (2)
 - ii. (2) pX330
 - iii. (4) including the “NGG” PAM sequence (2) in the guide sequence (2)
- c.
 - i. (2) 3
 - ii. (4) the actual cleavage efficiency could be affected guide-specific or cell-type-specific factors (2), including but not limited to the following: guide sequence, accessibility of local chromatin, activity of endogenous DNA repair pathways (provide 2 points for one of these factors or another answer similar to it that supports the competitor's answers)
 - iii. (1) True
- d.
 - i. Indel percentage (%) = $(1 - \sqrt{1 - x}) \times 100$, where $x = (a + b)/(a + b + c)$
5 points per correct equation. There is no partial credit for this question.
- e.
 - i. (2) HDR pathway
 - ii. (8) the cleavage site (2) of the guide (2) should be as close as possible (2) to the junction of the homology arm (2)
 - iii. (3) double nickase design

- f.
 - i. (2) single-stranded DNA (ssDNA) oligos
 - ii. (2) plasmid DNA vector
 - iii. (4) possible answers: mutate the PAM “NGG” (2) within the HR template (2) to “NGT” or “NGC” OR mutations in the PAM and in the spacer itself (4)
- g. X (Provide 3 points extra credit if the competitors wrote a big X below 2fiii)

Diagram-based Questions: Point values are addressed in each question. Question **9** is **TB#5**.

1. (2) RNA
2. (2) secondary structure
3. (2) 11
4. (4) adenosine (2) base-zipper motif (2)
5. (2) Hydrogen bonds
6. (2) stacking interactions
7. (6) conversion of the free tetraloop receptor (3) to the bound form (3)
8. (4) adenosine (2) zipper motif (2)
9. (4) hydroxyl (OH) radicals
10. (4) magnesium

III. Computer Exploration²

1.
 - a. (1) glycine (accept Gly)
 - b. (2) alpha helices
 - c. (1) True
 - d. (1) both
 - e. (3) The side chain is only one hydrogen atom.
2.
 - a. (1) alanine (accept Ala, A)
 - b. (2) 2-aminopropanoic acid
 - c. (1) nonpolar
 - d. (2) interior/inside of the protein
 - e. (2) L-isomer
3.
 - a. (1) Threonine (Thr, T)
 - b. (2) glycine
 - c. (1) False
 - d. (3) accept one of the following and award 3 points: ST turns, ST motifs, ST staples
 - e. (3) *O*-linked glycosylation
4.
 - a. (1) Tryptophan
 - b. (1) W
 - c. (3) 283.83, -5.566, 1252.864 (award one point for each coordinate; the order is X, Y, Z, respectively)
 - d. (2) B
 - e. (2) CA

5.

- a. (2) 7.967
- b. (2) 1.167
- c. (2) 28.81
- d. (2) 36.84
- e. (2) 1940.0

6. (2) 654

7. (2) 28

8. (2) 159

9. (2) 0/none

10.

- a. (2) 3856
- b. (2) 65
- c. (2) 1728
- d. (2) 2466
- e. (2) 4059

11. If the competitors display the carbons or hydrogens, they immediately do **not** get any credit. There is no partial credit for these questions. Each question/compound drawing is worth **four** points. **(20)**

