MSOE Center for BioMolecular Modeling

SCIENCE OLYMPIAD
Exploring the World of Science

3-D Molecular Designs
...where molecules become real™

Protein Modeling Event

School Name: ______________________________

School Number: ______________________________

Team Member 1: ______________________________

Team Member 2: ______________________________

For Judges Use Only:

Pre-Build Score:	
On-Site Build Score:	
Test Score:	
Tie Breaker:	
Total:	
Final Rank:	

Part I: Pre-Build (40% of total score)

Your Pre-Build Model should have been impounded the morning of the competition. You may pick up your Pre-Build model at the end of the competition after all models have been scored. Unclaimed models will be thrown away.

Part 2: On-Site-Build (30% of total score)

The workstation should have the On-Site Model Competition Environment open on the computer. Using the 314 cm Mini-Toober provided, construct a model of amino acids 1-157 of chain A of 1g73.pdb. The scale should be 2 cm per amino acid. A meter stick/ruler has been provided for you. Your Mini-Toober model of amino acids 1-157 of chain A of 1g73.pdb should include the following:

A: Two amino acids: Ala1 and Glu150 (use metal clips to connect amino acids to your Mini-Toober)

B: Blue end cap indicating the amino terminus (N-terminal end) of this region (amino acids 1-157)

C: Red end cap indicating the carboxylic acid terminus (C-terminal end) of this region (amino acids 1-157)

Part 3: On-Site Exam (30% of total score)

The On-Site Exam consists of both multiple choice and short answer questions. You may use any materials provided at your work station as well as the five sheets you brought with you to answer these questions. You may NOT use the Internet to answer these questions.

There are ten multiple choice questions in the On-Site Exam (each worth 1 point for a total of 10 points). Clearly print the letter of the one BEST answer to each question in the blank provided for that question. Illegible answers will be incorrect.

There are also short answer questions in the On-Site Exam. The point value for each question is given in parentheses at the end of the question (20 pts total). The points for the tie-breaker questions (identified with ★ **Tie Breaker**) will be included in the final score but may be used to determine team placement in case of a tie.

On-Site-Exam

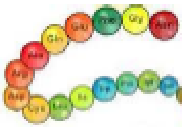
Multiple Choice Questions:

__________ 1. Which of the following amino acids is hydrophilic?

A. Valine
B. Leucine
C. Arginine
D. Proline

__________ 2. Which level of protein structure does the image below represent?

A. Primary
B. Secondary
C. Tertiary
D. Quaternary



__________ 3. How many carbon atoms are found in the backbone of each amino acid?

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

__________ 4. Which class of amino acids will most likely be located on the surface of a protein that is embedded within the phospholipid cell membrane?

A. Hydrophobic amino acids
B. Hydrophilic amino acids
C. Basic amino acids
D. Acidic amino acids

__________ 5. Where is the protein, Diablo, stored when a cell is not undergoing apoptosis?

A. In the nucleus
B. In the cytoplasm
C. In the endoplasmic reticulum
D. In the mitochondria

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Score for this page: ☐

__________ 6. Which of the following combinations of amino acids would form a salt bridge, or ionic interaction?

A. Aspartic acid and Leucine
B. Glutamic Acid and Aspartic Acid
C. Lysine and Glutamine
D. Arginine and Glutamic Acid

__________ 7. The major force stabilizing protein secondary structure is:

A. Hydrophobic interactions
B. Hydrogen bonds
C. Electrostatic interactions
D. Disulfide bonds

__________ 8. What role does Diablo play in regulating the apoptotic pathway?

A. Diablo eliminates the inhibitory effect of inhibitor of apoptosis proteins (such as XIAP) by binding to the inhibitor protein, preventing interaction with caspases.
B. Diablo cleaves the zymogen form of caspase, thus activating the protein for the apoptotic pathway.
C. Diablo binds to caspases, enabling the activation of the protein for the apoptotic pathway.
D. Diablo cleaves the inhibitory proteins (such as XIAP) in order to activate the apoptotic pathway.

__________ 9. Alpha helices represent which level of protein structure?

A. Primary
B. Secondary
C. Tertiary
D. Quarternary

__________ 10. When was the first draft sequence of the human genome published?

A. 1968
B. 1975
C. 2001
D. 2011

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Score for this page: ☐

Short Answer Questions:

1. What is the name of the chemical reaction that occurs when a peptide bond is formed? (1 pt)

What molecule is released when this reaction takes place? (1 pt)

A peptide bond occurs between which two atoms? (2 pts)

2. What is the difference between the 3_{10} helix versus a traditional alpha helix? (4 pts) ★ **Tie Breaker**

3. What is a zymogen? (1 pt)

What is the advantage of having a zymogen form of caspases? (3 pts)

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Score for this page:

4. On your onsite build of Diablo you positioned Ala1. What is the significance of this amino acid with respect to the function of Diablo? (4 pts) ★ **Tie Breaker**

5. What does the name "Caspase" tell you about the function of this protein? (3 pts)

Caspases cleave in a very specific location. A short peptide sequence is listed below (using the one letter codes for the amino acids). Please circle the bond that would be cleaved by a caspase. (1 pt)

A—F—G—H—D—Q—R—T—P—K

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Score for this page:

On-Site-Exam

Multiple Choice Questions:

____C____ 1. Which of the following amino acids is hydrophilic?

A. Valine
B. Leucine
C. Arginine
D. Proline

____A____ 2. Which level of protein structure does the image below represent?

A. Primary
B. Secondary
C. Tertiary
D. Quaternary

____B____ 3. How many carbon atoms are found in the backbone of each amino acid?

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

____A____ 4. Which class of amino acids will most likely be located on the surface of a protein that is embedded within the phospholipid cell membrane?

A. Hydrophobic amino acids
B. Hydrophilic amino acids
C. Basic amino acids
D. Acidic amino acids

____D____ 5. Where is the protein, Diablo, stored when a cell is not undergoing apoptosis?

A. In the nucleus
B. In the cytoplasm
C. In the endoplasmic reticulum
D. In the mitochondria

For Judges Use Only

Score for this page:

Short Answer Questions:

1. What is the name of the chemical reaction that occurs when a peptide bond is formed? (1 pt)

   Dehydration Synthesis
   or
   Condensation

   What molecule is released when this reaction takes place? (1 pt)

   Water

   A peptide bond occurs between which two atoms? (2 pts)

   Nitrogen and carbon

2. What is the difference between the 3_{10} helix versus a traditional alpha helix? (4 pts) ★ **Tie Breaker**

   In a traditional alpha helix, every backbone N-H group of the amino acid within the helix donates a hydrogen bond to the backbone C=O group of the amino acid FOUR residues earlier. There are 3.6 amino acid residues per turn. (2 pts)

   In a 3_{10} helix, every backbone N-H group of the amino acid within the helix donates a hydrogen bond to the backbone C=O group of the amino acid THREE residues earlier. There are 3 amino acid residues per turn. (2 pts)

3. What is a zymogen? (1 pt)

   A zymogen is an inactive precursor form of the active protein.

   What is the advantage of having a zymogen form of caspases? (3 pts)

   Since the zymogen form of the caspase is inactive, the zymogen could be present within the cytoplasm of the cell, without signaling apoptosis (1pt). If a signal is received for the cell to undergo apoptosis, the zymogen would need to undergo a cleavage event to activate it (1 pt), but this is a much faster response than requiring the cell to transcribe and translate the protein. If protein is currently present in the cytoplasm, as the inactive precursor form, a response will be faster than having to create the protein de novo. (2 pts)

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Score for this page:

____D____ 6. Which of the following combinations of amino acids would form a salt bridge, or ionic interaction?

A. Aspartic acid and Leucine
B. Glutamic Acid and Aspartic Acid
C. Lysine and Glutamine
D. Arginine and Glutamic Acid

____B____ 7. The major force stabilizing protein secondary structure is:

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____A____ 8. What role does Diablo play in regulating the apoptotic pathway?

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____B____ 9. Alpha helices represent which level of protein structure?

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____C____ 10. When was the first draft sequence of the human genome published?
A. 1968
B. 1975
C. 2001
D. 2011

For Judges Use Only
Score for this page:

4. On your onsite build of Diablo you positioned Ala1. What is the significance of this amino acid with respect to the function of Diablo? (4 pts) **★ Tie Breaker**

   Alanine 1 is part of a tetrapeptide at the beginning of the protein that is essential for the binding of Diablo to XIAP. (2 pts)

   Mutation of Ala1 to another amino acid eliminates the binding of Diablo to XIAP, thus preventing Diablo from alleviating the inhibition of XIAP on the caspase protein. (2 pts)

5. What does the name "Caspase" tell you about the function of this protein? (3 pts)

   Proteins use Cysteine in the active site (1 pt)

   Caspases cleave target proteins in specific site – after an aspartic acid residue (1 pt)

   Caspases are proteases (1 pt)

Caspases cleave in a very specific location. A short peptide sequence is listed below (using the one letter codes for the amino acids). Please circle the bond that would be cleaved by a caspase. (1 pt)

A—F—G—H—D—Q—R—T—P—K

For Judges Use Only

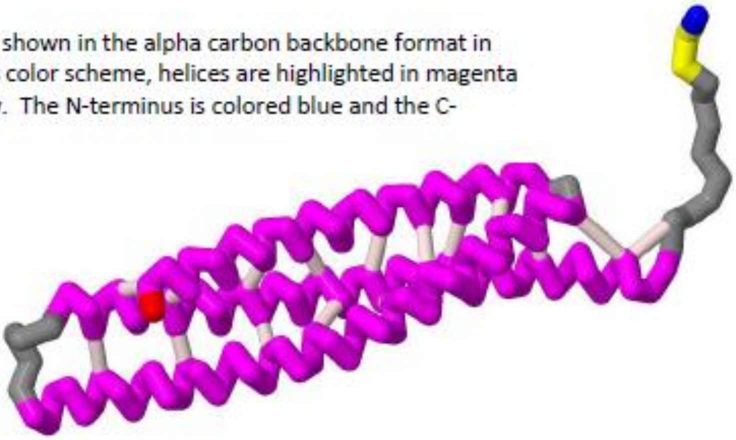
Score for this page:

Guide to Using the Rubric to Score the Diablo ON-SITE Build Model for Science Olympiad 2011-2012 Invitational Competitions

These instructions are to help the event supervisor and scoring judges use the rubric developed by the MSOE Center for BioMolecular Modeling when scoring the 2011-2012 Science Olympiad **Invitational On-Site Build** Mini-Toober models of Diablo, based on **1g73.pdb**. Each category on the rubric is addressed within these instructions and is accompanied by a short description and picture, if appropriate.

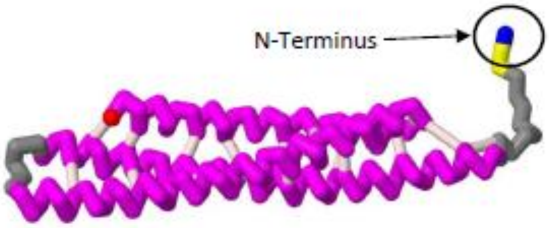
Overview of the Molecule:

Diablo, based on 1g73.pdb, is shown in the alpha carbon backbone format in the image to the right. In this color scheme, helices are highlighted in magenta and sheets are colored yellow. The N-terminus is colored blue and the C-terminus is colored red.



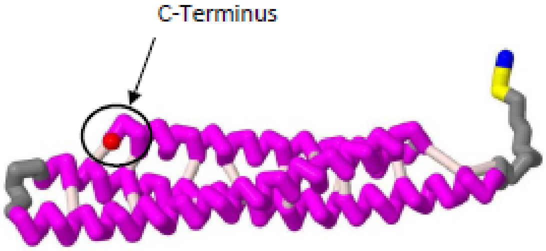
1. Blue Cap on N-terminal Amino Acid (Ala1) (2 pts)

- To receive credit, the blue cap needs to be located at the N-terminus of the protein, which is located at the beginning of the only beta-strand within the protein. Please see the figure to the right for the correct positioning of the blue end cap.



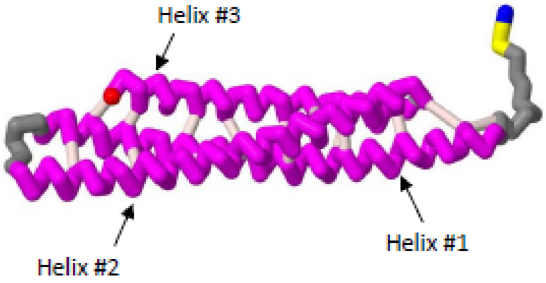
- If the blue end cap is located at the end of a long helix (the end of the protein (the C-terminus)), then the model does not receive credit for this feature.

2. Red Cap on C-terminal Amino Acid (Gln157) (2 pts)



- To receive credit, the red cap needs to be located at the C-terminus of the protein, which is located at the end of the third helix. Please see the figure to the right for the correct positioning of the red end cap.
- If the red end cap is positioned near the beta-strand (the beginning of the protein (the N-terminus)), then the model does not receive credit for this feature.

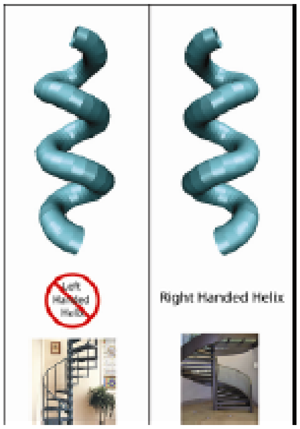
3. Model has 3 alpha helices according to Jmol selection criteria (1 pt per helix for a total of 3 pts)



- To receive these points, there should be 3 helices within the model. Please see figure to the right for the correct location of these helices. (Helices are colored magenta on the model and on the figure to the right.)
- Deduct 1 point for each extra helix. For example, if a model has 4 helices, then the model would receive 2 pts rather than the full 3 pts.

4. Alpha helices are right-handed (1 pt each; total of 3 pts)

- Alpha helices are right-handed. Check each alpha helix in the model to confirm that the helix is right-handed. For each right-handed helix, the model should receive 1 point, for a total of 3 points if all three helices are correct.
- To determine if the helix is right-handed, find one of the ends of the helix and imagine that the helix is a spiral staircase. Pretend that you are climbing that staircase and you need to have a hand-rail and the helix is the hand-rail, which is always on the outside edge of the staircase. If you would put your right hand on the toober as you go up the staircase, you have a right-handed helix. If you would put your left hand on the toober, you have a left-handed helix and the modeled helix would not receive the points.
- Be sure to check each helix as it is not uncommon for a model to have a single left-handed helix.

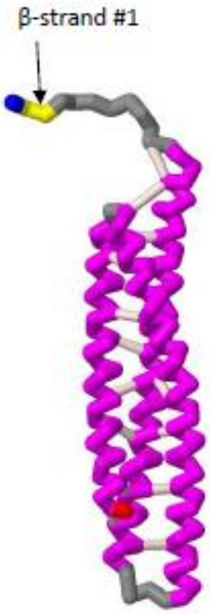


Left-handed vs right-handed helices

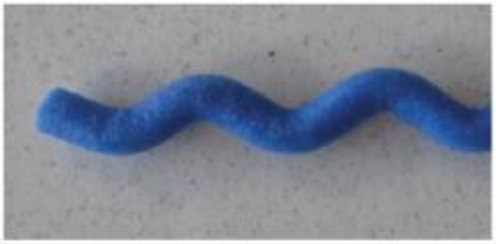
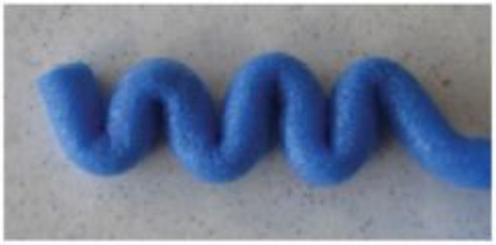
5. Alpha helices are of the correct length. (1 pt each; total of 3 pts)

- Helix #1 is the longest with 53 amino acids. This helix should have approximately 14-16 turns.
- Helix #2 is the next longest helix with 49 amino acids. This helix should have approximately 13-15 turns.
- Helix #3 is the shortest helix with 37 amino acids. The helix should have approximately 9-11 turns.
- Each helix that is of the correct length should receive 1 pt, for a total of 3 pts.

6. Model has a single β-strand according to Jmol selection criteria (1 pt)

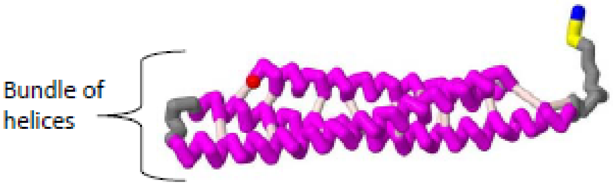


- To receive this point, there should be a single, short (2 amino acids) β-strand within the model. This short β-strand should be followed by an extended region (9 amino acids in length) leading into the first helix. As this β-strand is so short, the points awarded here will reflect both the presence of the short strand and the non-sheet/non-helix region between the β-strand and the first helix. Please see figure to the right for the correct location of this beta strand. (The β-strand is colored yellow on the model and on the figure to the right.)
- β-strands need to be clearly distinguishable from loops; there may be some slight 'zig-zag' folding of the toober to indicate the up-and-down positioning of the amino acids. Alternately, teams might color-code their beta strands to distinguish them from loops or write on the toober indicating the location of the β-strands. The event supervisor should not have to guess what a beta-strand is within the model.
- If there is more than 1 β-strand in this model, deduct 0.5 pts. For example, if there are two β-strands in the model, only 0.5 pts should be awarded, rather than the full 1 pt.

	
This is a good example of a beta strand, slightly folded. It would also be acceptable to color code or in some other way mark the backbone to indicate β strands.	Although this model shows a beta strand, it is actually too kinked, such that the length of the beta strand is disproportionate to the width. If ALL of the β strands are hyper-kinked, deduct 1 pt.

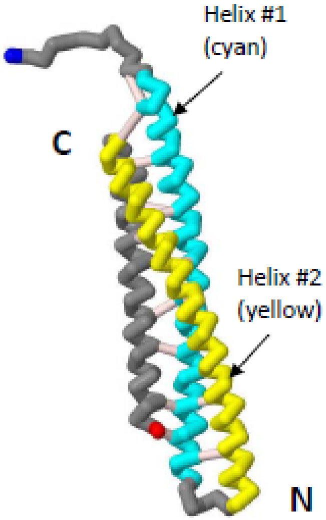
7. Helices form a bundle (2 pts)

- The three helices in this model should be positioned near each other to form a long bundle.
- To receive credit for this feature, the helices should lie close to one another, and not extended or at angles to one another.



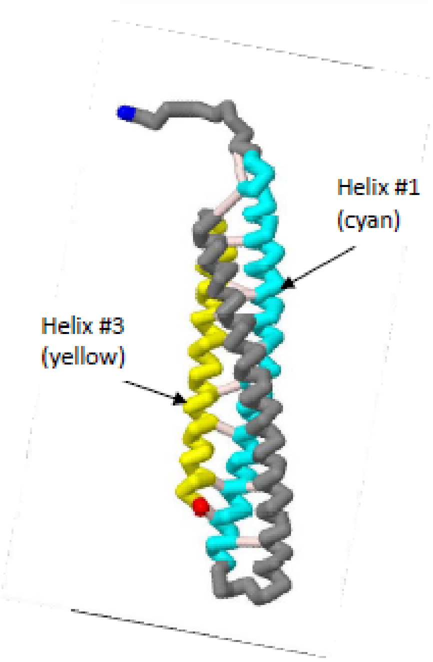
Feature #8-#10 Refer to the Arrangement of Helices in Bundle

8. Helix #2 crosses over helix #1 (2 pts)



- Position the model so that helix #1 (the longest helix and the one closest to the N-terminus) is centered, with the N-terminus at the top of the model and pointing to the left. See the image to the right for the correct positioning. Helix #1 is colored cyan in this image.
- Helix #2 (colored yellow in image to the right) should cross over helix #1. The N-terminal end of the helix should be positioned at the bottom right of the model (indicated on the image to the right with an "N"). The C-terminal end of the helix should be positioned at the top left of the model (indicated on the image to the right with a "C"). (1 pt)
    - If Helix #2 crosses over the other way (with the N-terminus on the bottom left and crossing over the top right), then no points should be awarded.
- Helix #2 should cross over Helix #1 at around the midpoint of Helix #1. (1 pt)
    - If Helix #2 crosses over at the C-terminal or N-terminal portion of Helix #1, no points should be awarded.

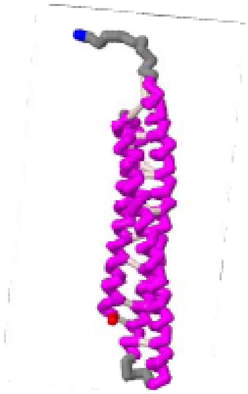
9. Helix #1 and helix #3 lie parallel to one another (2 pts)



- Position the model so that helix #1 (the longest helix and the one closest to the N-terminus) is centered, with the N-terminus at the top of the model and pointing to the left. See the image to the right for the correct positioning. Helix #1 is colored cyan in this image.
- Helix #1 and Helix #3 (yellow in image to the right) should lay parallel to one another. (1 pt)

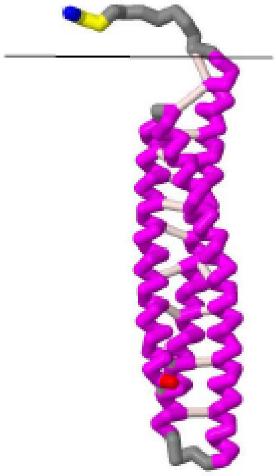
- Helix #1 and Helix #3 should be positioned close together, without a large space between the two helices. The two helices should be ~2-3cm away from one another. (1 pt)
    - If Helix #1 and Helix #3 are positioned further apart, with a noticeably large gap between the helices (more than 4 cm away from each other), no points should be awarded.

10. The helix bundle has a slight left-handed twist (2 pts)



- Position the model so that helix #1 (the longest helix and the one closest to the N-terminus) is centered, with the N-terminus at the top of the model and pointing to the left. See the image to the right for the correct positioning.
- The helix bundle should have a slight twist to the left.

11. N-terminal region is extended away from the helix bundle (2 pts)

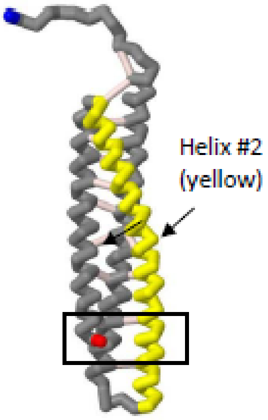


- Position the model so that helix #1 (the longest helix and the one closest to the N-terminus) is centered, with the N-terminus at the top of the model and pointing to the left. See the image to the right for the correct positioning.

- The N-terminal region (including β-strand #1 and the non-sheet/non-helix region preceding Helix #1) should be positioned out away from the helix bundle. The helices in the bundle are positioned very close together compared to the space between the N-terminal region and the helix bundle. (1 pt)

- The N-terminus should be positioned higher than the start of helix #1 (above the line in the figure to the right). (1 pt)
    - The N-terminus should not extend out directly from Helix #1, but be elevated above the start of the Helix #1. If the N-terminus lines up with the start of Helix #1, no points should be awarded for this feature.

12. C-terminus positioned near Helix #2 (2 pts)



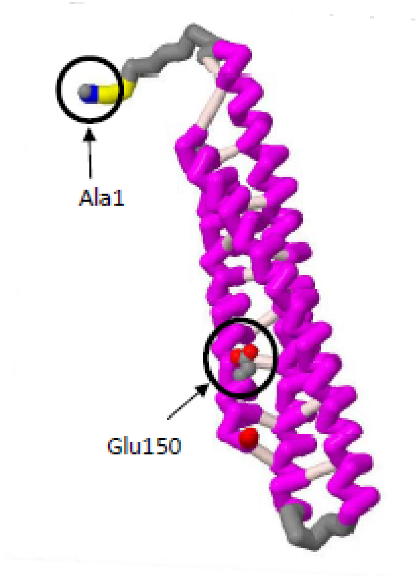
- Position the model so that helix #1 (the longest helix and the one closest to the N-terminus) is centered, with the N-terminus at the top of the model and pointing to the left. See the image to the right for the correct positioning. Helix #2 is colored yellow in this image.

- The C-terminus (colored red in figure to the right) should be positioned at approximately the ¾ mark of Helix #2. (1 pt)
    - If the C-terminus (red end cap) is positioned at or above the midpoint of Helix #2, or, near the "bottom" of the model (if the model is positioned in the figure to the right), no points should be awarded.

- The C-terminus should be pointing toward the helix bundle. (1 pt)
    - The C-terminus should not be pointing out away from the helix bundle. If it is, no points should be awarded for this feature.

13. Correct positioning of the two amino acids Ala1 and Glu150 (4 pts)

- The provided amino acids should be positioned correctly within the sequence of the protein (Ala1 at position 1, Glu150 at position 150). (1 pt for each sidechain correctly positioned at the right location in the protein.)
    - Ala1 is located at the beginning of the protein and should be placed on or near the blue end cap, which indicates the N-terminus, or first amino acid in the protein, which in this case, is Ala1.
    - Glu150 is located toward the end of Helix #3. The red cap demarcates the C-terminus of the protein and this is position 157 in the protein. Glu150 should be positioned 7 amino acids away from the C-terminus.



- The amino acids should also be oriented correctly within 3-dimensional space. (1 pt for each sidechain correctly oriented)
    - Ala1 should be pointing toward the Helix #2 side of the helix bundle.
    - Glu150 should be pointing toward the space between Helix #3 and Helix #2 and it should be pointing "up" toward the "top" of the model (if oriented in the same position as figure to the right).
    - Please see figure to the right and the physical model for proper location and positioning.