

## Scoring for the 2006 Science Olympiad

### TATA-binding Protein Model (Regional & State)

What we were looking for	Possible Points
Model has symmetry with two lobes	1
Model has “three layers”: alpha helices cradled on top of a curved beta sheet, with two “stirrups” at the ends of the beta sheet	3
4 alpha-helices	2
Alpha-helices are “right-handed”	2
10 beta-strands with correct topology	5
Indicated N-term and C-term end	2
The N-term and C-term are on same end and same surface of protein	1
Two alpha-helices are on same surface	1
Two short alpha-helices on the ends of the lobes and “perpendicular” and beneath the longer helices	2
Correct scale of model (2 cm per amino acid)	1
Display amino acids that contact DNA: <ul style="list-style-type: none"> <li>○ Lys, Arg binding the phosphate groups of DNA (2pts)</li> <li>○ 4 Phe in DNA minor groove (2pts)</li> <li>○ 2 Asn in center (2 pts)</li> </ul>	6
Original features (such as DNA or associated transcription factors)	4

### Written Description (Regional & State)

What we were looking for	Possible Points
Turned in a written description	1
Style: Well written and concise	1
Function:	1
<ul style="list-style-type: none"> <li>• Binds DNA sequence in promoter to initiate gene transcription</li> </ul>	2
• 0.5 pts for each of the following with 2 pts max.	
<i>binds TATA(a/t)A(a/t)</i>	
<i>bends DNA</i>	
<i>component of TF11D</i>	
<i>recruits additional Transcription factors</i>	
<i>TF may be positive activators or inhibitors</i>	
Structure: Binds DNA with 2 types of interactions	1
Non-specific (ie: lys, arg bind DNA phosphates)	0.5
Specific: (ie: 4 phe bind minor groove, 2 asn hydrogen bind DNA)	0.5
<ul style="list-style-type: none"> <li>• Two symmetrical halves</li> </ul>	1
Features of Mini-Toober model Are all model features described? May include: Red/blue caps, Specific amino acids, Additional factors: DNA, Transcription factors	2

### 1PSV Protein Folding Map (Regional)

What we were looking for	Possible Points
N-terminal amino acid: Lys1	1
C-terminal amino acid: Arg 28	1
Alpha-helix: Glu 15-Glu 23	2
Beta strand 1: Tyr 3 -Thr 4	1
Beta strand 2: Thr 11- Phe 12	1
Asp 20	1
Arg 10	1
Ile 7	1
Phe 21	1

### 1PSV Model (Regional)

Blue cap on N-terminal amino acid: Lys1	2
Red cap on C-terminal amino acid: Arg 28	2
Alpha-helix: Glu 15-Glu 23	2
Alpha-helix is right-handed	2
Beta strand 1: Tyr 3 -Thr 4	2
Beta strand 2: Thr 11- Phe 12	2
Two beta strands form a beta sheet	2
Beta sheet is correctly positioned in relationship to the alpha helix	2
Hydrophobic amino acids are in the "interior" and correctly positioned Ile 7, Phe 12	2
Charged amino acids are on the "surface" and correctly positioned: Asp 20, Arg 10	2

## Written Questions about 1psv/de novo proteins (Regional)

### Directions:

There are 6 questions in this section, each worth 5 points. Clearly print the letter of the one BEST answer to each question in the blank provided for that question. Illegibly answers will be incorrect.

- B**\_\_\_\_\_1. When was the pdb file 1PSV released to the public?  
A. Oct. 29, 1997  
B. Jan. 28, 1998  
C. Aug. 7, 1997  
D. Nov. 15, 1997
- C**\_\_\_\_\_2. Which display feature in RasMol most closely resembles the Mini-Toobers you use to model proteins?  
A. hydrophobic sidechains  
B. hydrogen bonds  
C. alpha carbon backbone  
D. spacefill alpha helices and beta sheets
- B**\_\_\_\_\_3. Who is the author of the "Molecule of the Month" on the Protein Data Bank website?  
A. Tim Herman  
B. David Goodsell  
C. Helen Berman
- C**\_\_\_\_\_4. Which level of protein structure does the protein folding map contain?  
A. Primary structure  
B. Secondary structure  
C. Primary and secondary structure  
D. Tertiary structure
- A**\_\_\_\_\_5. Which amino acids are likely to be found on the inside regions of folded protein structures?  
A. carbon-rich amino acids  
B. charged amino acids  
C. hydrogen-bonding amino acids
- A**\_\_\_\_\_6. What is the experimental method used to define the structure of 1PSV?  
A. Nuclear Magnetic Resonance  
B. X-Ray Diffraction  
C. Circular Dichroism

### 1XTC Protein Folding Map (State)

What we were looking for	Possible Points
N-terminal amino acid: Thr 1	0.25
C-terminal amino acid: Asn 103	0.25
<b>3 Alpha-helices, 0.5 points each:</b> <ul style="list-style-type: none"> <li>• Ile 5-Glu 11</li> <li>• Asp 59- Lys 62</li> <li>• Ala 64-Tyr 76</li> </ul>	1.5
<b>6 Beta strands, 0.5 points each:</b> <ul style="list-style-type: none"> <li>• Thr 15-Thr 19</li> <li>• Ser 26-Ser 30</li> <li>• Ala 38-Thr 41</li> <li>• Phe 48-Val 50</li> <li>• Lys 84-Trp 88</li> <li>• Ile 96-Ile 99</li> </ul>	3
Asp 70	1
Arg 73	1
Ile 74	1
Leu 77	1
Trp 88	1

### 1XTC Protein Model (State)

<b>N- and C-terminus on same surface</b>	1
<b>2 (3) alpha helices</b> (helices 2 and 3 appear to be 1 long helix in model)	2
<b>Helices on the same surface</b>	1
<b>Helices are right-handed</b>	1
<b>6 beta strands, 0.5 pt each</b>	3
<b>Beta strands arranged in 2 beta sheets with 3 strands each</b>	2
<b>Trp 88</b> on 2nd strand of 1st sheet	1
<b>Asp 70</b> , helix 2(3) pointing out from helix	1
<b>Arg 73</b> , helix 2(3) pointing out from helix	1
<b>Ile 74</b> , helix 2(3) pointing out from helix	1
<b>Leu 77</b> , helix 2(3) pointing out from helix	1
<b>Correct topology, 0.5 pt each</b> <ul style="list-style-type: none"> <li>• Nterm-alpha helix</li> <li>• Strand 1 in 1st sheet</li> <li>• Strand 2 in 2nd sheet</li> <li>• Strand 3 AP in middle of 2nd sheet</li> <li>• Strand 4, AP in 2nd sheet</li> <li>• Helix 2(3)</li> <li>• Strand 5, AP middle of 1st sheet</li> <li>• Strand 6, AP 1st sheet to C-terminus</li> </ul>	4
<b>Globular shape with “3 layers”</b> “bottom” with the 2nd sheet “middle” with 1st sheet & long helix 2(3) top with helix 1	1

## Written Questions about 1xtc/cholera toxin (state)

### Directions:

There are 10 questions in this section, each worth 3 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.

- C**\_\_\_\_\_1. When was the pdb file 1XTC released to the public?  
A. Jan. 8, 1996  
B. Jan. 10, 1996  
C. Aug. 1, 1996  
D. Oct. 1, 1996
- B**\_\_\_\_\_2. Who is the author of the "Molecule of the Month" on the Protein Data Bank website?  
A. Tim Herman  
B. David Goodsell  
C. Helen Berman  
D. Gary Graper
- C**\_\_\_\_\_3. Which display format in RasMol most closely resembles the format of the foam amino acid sidechains you use to model proteins?  
A. spacefill  
B. wireframe  
C. ball and stick  
D. backbone
- C**\_\_\_\_\_4. Which level of protein structure does the protein-folding map contain?  
A. Primary structure  
B. Secondary structure  
C. Primary and secondary structure  
D. Tertiary structure
- A**\_\_\_\_\_5. Which amino acids are **NOT** likely to be found on the outside regions of folded protein structures?  
A. hydrophobic amino acids  
B. acidic amino acids  
C. basic amino acids  
D. polar amino acids
- B**\_\_\_\_\_6. What is the experimental method used to define the structure of 1XTC?  
A. Nuclear Magnetic Resonance  
B. X-Ray Diffraction  
C. Circular Dichroism
- D**\_\_\_\_\_7. Who is the principal investigator of the research lab that reported the 1XTC cholera structure?  
A. R.G. Zhang  
B. D. L. Scott  
C. M. L. Westbrook  
D. E. M. Westbrook

- B**\_\_\_\_\_8. What is the resolution of the structure of 1XTC?
- A. 0.185 Angstroms
  - B. 2.40 Angstroms
  - C. 73 Angstroms
  - D. 90 Angstroms
- A**\_\_\_\_\_9. How many molecules of the cholera toxin are necessary to kill a cell?
- A. one
  - B. ten
  - C. one hundred
  - D. one thousand
- C**\_\_\_\_\_10. Which chains form the cell binding subunit of the cholera toxin?
- A. A, C, D, E, F, G, H
  - B. A, C
  - C. D, E, F, G, H
  - D. D