

1. **DESCRIPTION:** Students will use computer visualization and online resources to construct physical models of the **CRISPR Cas9 protein**, that is being engineered to edit plant and animal cell genomes, and answer a series of questions about the chemistry of protein folding and the interaction of structure and function for model proteins.

A TEAM OF UP TO: 3

IMPOUND: Yes

APPROXIMATE TIME: 50 minutes

2. **EVENT PARAMETERS:**

- a. Each participant must bring a pencil or pen for the exam, a marker for marking the toobers, a metric ruler with cm marks, and one 8.5" x 11" sheet of paper that may contain information on both sides in any form and from any source. This sheet may be contained in a sheet protector or laminated.
- b. Each team must impound a pre-built model of a portion of the CRISPR Cas9 protein along with a 4" x 6" note card describing functionally relevant features (see 3.Part I.b.-f.).
- c. Supervisors will provide all other materials for on-site model construction and test.

3. **THE COMPETITION:**

Part I: The Pre-Built Model

- a. Participants will use the program Jmol/JSmol to visualize a model of residues 1-85 of the CRISPR Cas9 protein, based on the coordinate data found in the 4un3.pdb file. The 4un3.pdb file can be accessed for free from the RCSB Protein Data Bank (www.rcsb.org). Jmol/JSmol can be accessed at <http://cbm.msos.edu/scienceOlympiad/designEnvironment/prebuild.html> for free.
- b. Using this visualization, participants should build a model based on the alpha carbon backbone of the protein with a scale of 2 cm per amino acid using Mini-Toobers[®] or another comparable bendable material (e.g., Kwik Twists, 12-gauge dimensional house wire, etc.).
- c. Participants will use materials of their own choosing to add functionally relevant features to their model (e.g. selected amino acid sidechains, DNA or associated molecules). Additions to the model should highlight the significance of structure to function of the protein.
- d. Participants must explain their functionally relevant features using clear and concise descriptions on a 4" x 6" notecard, in the form of a table with 3 columns, headed:
 - i. What is displayed
 - ii. How it is displayed
 - iii. Why it is important
- e. Three Dimensional (3D) printed materials may NOT be used to build the protein backbone but may be used for functionally relevant features.
- f. All models, including all functionally relevant features, must fit within a 61.0 cm x 61.0 cm x 61.0 cm space.
- g. The model must be sufficiently sturdy that judges can pick it up and rotate it for judging. Teams may pick up all pre-build models after the competition.

Part II: The On-Site Model Build

- a. On-site, participants will build a physical model of a selected region of a specific protein using materials provided by the event supervisor. Resources listed below will provide background information about the molecules that may be built at all levels of competition.
- b. Each team will use a computer provided by the event supervisor to access the Jmol/JSmol application and use the appropriate coordinate files on it to guide their model construction.
- c. The event supervisor will provide identical computers to all teams along with all construction materials for the model (Kwik Twists, 12-gauge dimensional house wire, Mini-Toobers[®], amino acid sidechains, crosslinkers, plastic red & blue end caps, etc.)
- d. Any model not handed to the judges by the end of the team's scheduled event session will not be accepted for scoring.

Part III: The On-Site Written Exam

- a. Teams will complete a written exam consisting of multiple choice and short answer questions.
- b. Topics addressed include:
 - i. the principles of chemistry that drive protein folding
 - ii. the structural and functional relationships of the modeled proteins; both pre-built and on-site.



PROTEIN MODELING (CONT.)

See General Rules, Eye Protection & other Policies on www.soinc.org as they apply to every event.

4. **SCORING:**

- a. High Score wins. Final score will be derived from all three parts of the competition:
 - i. The pre-built model (Part I) will count for 40% of the final score and be scored based on the accuracy and scale of the secondary structures, as well as the relevant functional features added to the model (e.g., sidechains, DNA, or associated molecules). As the competition level increases, the scoring rubrics for the pre-built model will reflect higher expectations for model accuracy, detail, and addition of relevant functional features. Features that are not relevant or do not explain the structure/function relationship of the protein will not receive credit.
 - ii. The on-site built model (Part II) will count for 30% of the final score. The on-site built protein model will be scored based on accuracy of folding the model and positioning specific amino acid sidechains.
 - iii. The written exam (Part III) will count for 30% of the final score. The exam will be scored for accuracy.
- b. Ties will be broken using identified questions from the written exam.

Recommended Resources: The Science Olympiad store (store.soinc.org) carries the Chem/Phy Sci CD (CPCD); other resources are on the event page at soinc.org.

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