

Measuring and Mapping Out Your Model

Once a protein has been designed in the online visualization webpage it can be transformed into the actual physical model of the structure.

All of the models for the Science Olympiad Protein Modeling Event will use a scale of 2cm for every 1 amino acid. It is often a good idea to start by mapping this scale directly onto the toober. To do this, straighten the toober out to its full length, lay it above a ruler and, using a pen or a marker, mark each amino acid with a light line. Once the amino acids are marked, it is often useful to go back and write a number every 10 lines so that a specific amino acid can be found quickly in the future.

Every protein chain has both a beginning known as the amino terminus or N-terminus and an end known as the carboxylic acid terminus or C-terminus. These should be represented by the blue and red end caps. The blue cap represents the amino terminus and the red cap represents the carboxylic acid terminus

This is often a good time to annotate or mark any other features of the protein that will need to be recognized later in the model construction. For example by using the **color structure** command in the online visualization environment it can be seen that the zinc finger protein model of amino acids 4-31 has a two stranded beta sheet. The first strand in this sheet is from amino acid 5 to amino acid 7 and the second strand is from amino acid 14 to amino acid 16. The beginning and end of the beta strands should be marked - perhaps with a thicker line or a different colored marker. The zinc finger protein also contains an alpha helix from amino acid 19 to amino acid 30. Again, the beginning and end of this should be marked for later reference.

Some proteins have very specific amino acids that may be important to the protein's structure or function. These sidechains can be represented in the protein model. The first step in doing this will be marking their location on the toober. In this sample zinc finger model, four sidechains - cysteine 7, cysteine 12, histidine 25, and histidine 29 are necessary to hold a zinc atom in place. By marking the location of these with the amino acid's three letter abbreviation and, for the on-site model, the small metal clips, we will later be able to tell what sidechain belongs at each of the marked locations.

