# Going Beyond Just a Backbone Model

To help teams create a better understanding of how models will be judged, it may be useful to compare two different sample models of the same protein. The model on the right is a well designed model while the model on the left is a poorly designed model. The online visualization environment is also shown and should be used as a key for how the final model will look.

The more accurately you can create your model based on the online visualization environment, the better the score it willbe awarded.
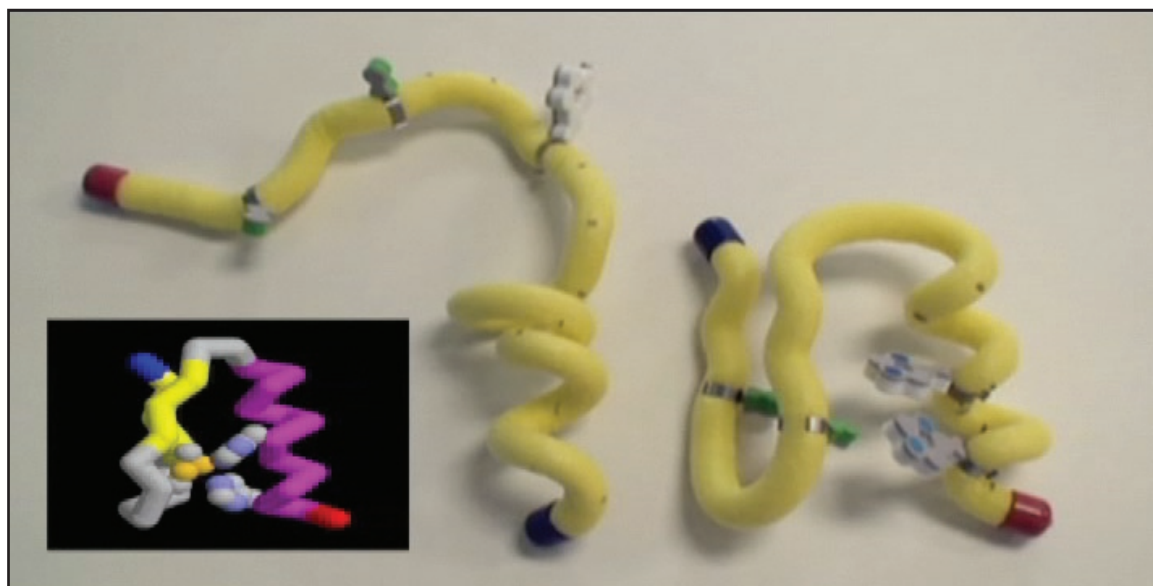
Poor model on the left	Well designed model on the right
Blue and red end caps incorrectly switched	Blue and red end caps on correct ends
Does not have a smooth alpha helix and the alpha helix is incorrectly left handed	Has a smooth and even alpha helix that is correctly right handed
Only one beta strand instead of two beta strands making up a beta pleated sheet	The model contains the correct pair of beta strands that make up the beta pleated sheet
Incorrect overall shape with the beta sheet area too far away from the alpha helix area	Correct overall shape with the beta sheet area close to the alpha helix area
Only three of the four sidechains shown and at least one of them is in the incorrect position	All four sidechains are shown in their correct locations