

Folding Secondary Structures

Once the toober has been annotated, its 3-dimensional structure can be folded. It is often easiest to start by folding the secondary structures of a protein first - the alpha helices and the beta strands that make up the beta pleated sheets.

A beta strand can be made by crimping the toober every amino acid to create an extended zig-zag structure. In our zinc finger sample protein, there are just two short beta strand sections. Note that the length and location of these secondary structures can vary from protein to protein. Some have much longer beta pleated sheets while others may have none at all.

An alpha helix can be folded by wrapping the toober around a finger. In the zinc finger sample protein, there is an alpha helix from amino acid 19 to amino acid 30. This entire area should be folded into an alpha helix.

It is important to make extra sure that your alpha helices are always right handed. One simple way to check this is to imagine the alpha helix as a spiral staircase. When walking up the staircase, your right hand should be on the outside railing of the staircase. If this is not the case, the helix is left handed and will have to be re-made. The final step is to extend the helix slightly so that the toober is not squished on to itself.

