



Section III: Using Mini-Toobers to Construct a Physical Model of a Protein.

- Toobers are used to construct an **alpha carbon backbone model** of a protein. (The scale:.....1 amino acid per 2 cm of toober)
- An alpha helix is a coiled structure.
This is a “right-handed” helix
3.6 amino acids per turn of helix
- Beta sheets consist of extended zig-zag shaped backbones --- in either a parallel or anti-parallel orientation.
- Sections of alpha helix and/or beta sheet can be mapped onto the linear toober before it is folded.
- To precisely position important amino acid sidechains on the backbone, these positions should be mapped onto the linear toober, before it is folded.
- In general, polar or charged amino acid sidechains will be oriented on the outside of a folded protein, and hydrophobic amino acid sidechains will be oriented on the inside of a folded protein.