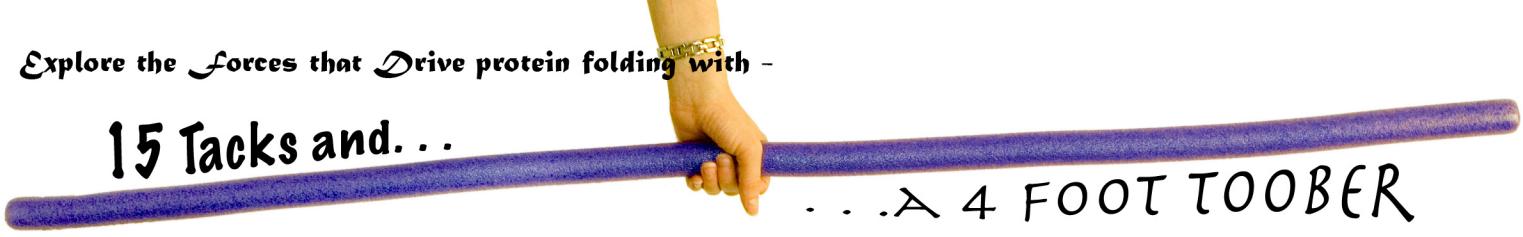
Explore the Forces that Drive protein folding with –

15 Tacks and. . .



6 Yellow Tacks = Hydrophobic (nonpolar) Sidechains

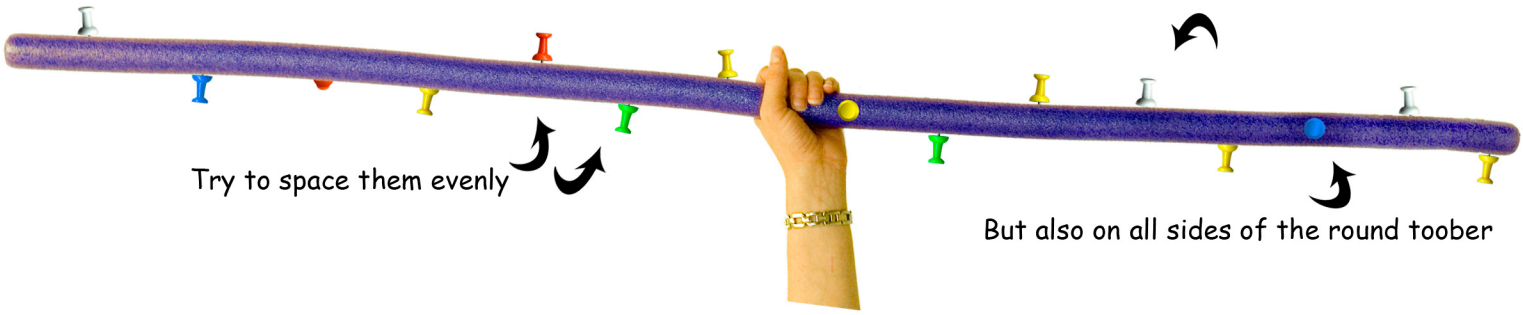
3 White Tacks = Hydrophilic (polar) Sidechains

2 Red Tacks = Acidic (- charged) Sidechains

2 Blue Tacks = Basic (+ charged) Sidechains

2 Green Tacks = The amino acid Cysteine

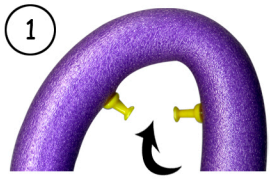
Step One: Place 15 tacks randomly around the toober



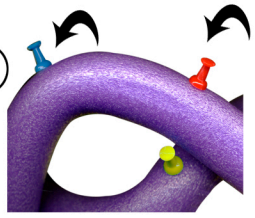
Try to space them evenly

But also on all sides of the round toober

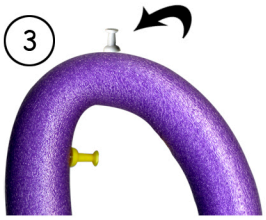
Step Two: Fold your protein, following these laws of chemistry:



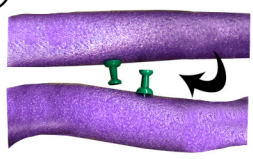
1. Hydrophobic sidechains are nonpolar and "hate" water, which is polar. They will be buried on the inside of the globular protein.



2. Charged sidechains will be on the outer surface of proteins, where they often neutralize each other and form salt bridges.

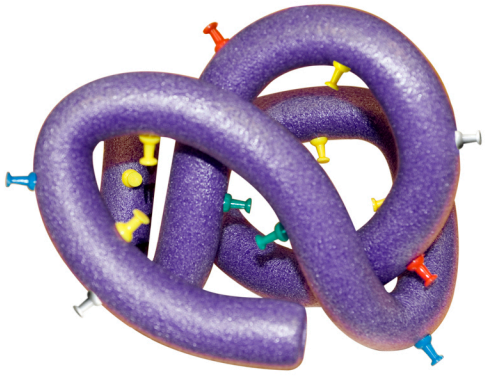


3. Hydrophilic sidechains, which are polar, "love" water, which is also polar, and so will be on the surface of the protein where they can hydrogen-bond with water.



4. Cysteine's sidechain contains a sulfur molecule. These often interact with each other to form covalent disulfide bonds that stabilize the protein's structure.

Step Three: Compare your protein to your classmates' proteins



Does each protein have the same three-dimensional shape? Why or why not?

How easy was it to fold your protein? Why was it difficult/easy?

If you "mutated" your protein by substituting a hydrophilic sidechain for a hydrophobic one, what happens to the 3-D shape of the protein? How would this mutation effect the protein's function?

Adapted from the MSOE Center for Biomolecular Modeling.