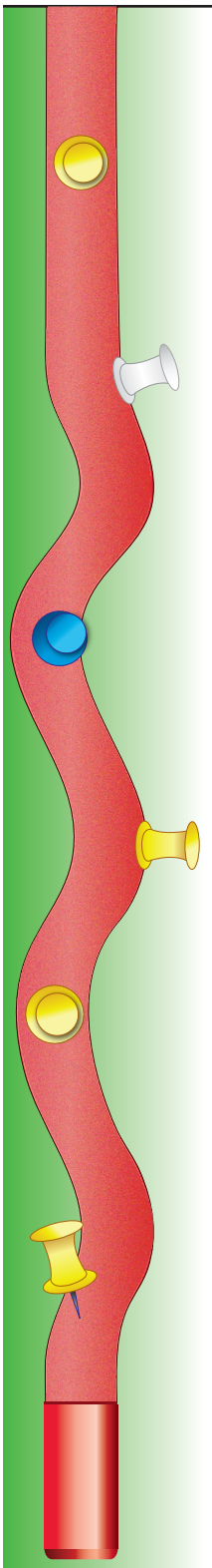

Teacher Notes

Teaching Tips

Students should have no trouble folding their toober so that all of the yellow, hydrophobic tacks cluster together in the central core of the folded structure. However, it may be difficult for them to maintain this structure while simultaneously:

- Pairing blue and red tacks (positive and negative charges that neutralize each other)
- Pairing green tacks to form disulfide bonds, and
- Keeping all of the polar white tacks on the surface of the protein

After students have folded their toobers, you can point out:

- Every toober had a different random sequence of tacks (amino acids) and therefore each toober (protein) folded into a different structure.
- Some sequences of tacks were more easily folded into a reasonable structure than others. In fact, the 30,000 proteins encoded by the human genome have been selected from an enormous number of possible amino acid sequences based on their ability to spontaneously fold into a stable structure that simultaneously satisfies these basic laws of chemistry.

TOOBER VARIATIONS

There are many variations to the basic mini toober folding exercise activites titled, ***15 Tacks and a 1-Meter Mini Toober***. Each one can be used to emphasize a different point related to molecular structure. Examples of variations are described below.

Reversible Denaturation

Many proteins undergo reversible denaturation, by re-folding into their original shape (native structure) following their complete unfolding (denaturation) by heating.

1. Have each student document the “native “shape of their folded protein with a digital photo.
2. Ask the students to unfold their protein and then re-fold it.
3. Check the refolded protein against the photo of the native structure.

Reverse Engineering

Some students will randomly generate a sequence of tacks that is very difficult to fold into a shape that simultaneously satisfies principles of chemistry that drive protein folding. This is a good “teaching moment” that you can use to emphasize that such “proteins” would not be selected from the enormous pool of possible protein sequences.

How can students arrive at a perfectly optimized sequence of tacks that have been selected over evolutionary time to always fold into the same globular shape?
ANSWER: By reverse engineering the sequence.

1. Have each group of students fold their toober into a compact globular shape without any tacks.
2. Have each group of students then add the tacks to the pre-folded toober, positioning them such that all of the “laws of chemistry” are satisfied in the folded structure.
3. Unfold the toober and document the sequence of tacks.
4. Have the students then re-fold the sequence into the original shape (see reversible denaturation).

The Effect of Mutations

Some mutations inactivate a protein by destabilizing its native shape.

1. Starting with the “reverse engineered” sequence of tacks as described above, mutate one of the hydrophobic amino acids (yellow tack) to a positively charged amino acid (blue tack).
2. Can the students fold this mutated sequence back into its native shape?

Additional Uses for Mini Toobers

You can also use your mini toobers to form DNA or mRNA, or show light or sound waves. If you discover other uses, please let us know.

Preserving Your Mini Toober

You can extend the life of your mini toobers by removing the tacks and end caps from the mini toobers and loosely coiling them at the end of class. Leaving in the tacks and/or tightly creasing the mini toober compresses the foam. Tightly twisting while using the mini toober could also permanently compress the foam.