* Why must proteins fold into a specific structure? What happens when they don’t?
* Observations from simulation of protein folding
* Entropy/Binomial distribution
	+ If you shake up a cup of coins that start all heads up, why don’t they end up all heads? What is *entropy?*
	+ What is a *random walk?* How does it relate to the possible structures of an unfolded protein? To coin flipping?
	+ If you flip N coins, how likely are you to get NH heads?
* Energy/Boltzmann distribution
	+ What is potential energy? If a system moves in the direction of a force (ex. opposite charges brought together, ball rolls down hill), does its potential energy increase or decrease?
	+ Does a protein have more potential energy when it is folded or unfolded? Where do proteins get “jolts” of energy that allow them to unfold, even if forces (ex. charge attraction) tends to make a protein fold?
	+ Suppose a protein has E energy “units”. In how many ways can the remaining
	NE-E energy units in the cell be distributed among N molecules?

* Protein folding/denaturation
	+ According to our model for protein folding, what is the probability pF that a protein is folded as a function of temperature, the energy of folding E, and the number of monomers N (and the Boltzmann constant *kB*)?
	+ Explain how protein folding is a competition between energy and entropy. Under what conditions do we expect a protein to be folded? How about unfolded? How does protein *denaturation* (unfolding) relate to disease?