

# Homework 3B

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11. According to the thermodynamic hypothesis in protein folding, primary structure drives tertiary structure without requiring external template. That is to say, "proteins will fold spontaneously into their functional shapes without external agents" (p. 191 *Molecules of Life*). With that in mind, soluble human proteins expressed in *E. coli* or *in vitro* systems will eventually spontaneously fold into their nascent state with some probability, assuming that that it is a "standalone" protein or all of its partners in a protein complex are present.
16. Certain sequences within a family of proteins must remain conserved in order to conserve the function of these proteins. In our particular case, the catalytic arginine is conserved in all members of this family because it is an essential active site for function. While sequence similarity is an important factor in determining the function, structure, and homology of a class of proteins, it is not the only determining factor. Of note, identical amino acid sequences can take on different conformational folds depending on the environment around it. In particular, sequences in related members of protein families can vary widely so as long as certain folds and domains are conserved. In addition, some amino acid substitutions have less penalty than others, meaning that insignificant mutations relative to the structure and function of a protein can occur and cause even greater sequence divergence relative to its family.
17. The globins from two mammals share a more recent common ancestor than that of plant globin and any mammal globins (well, at least, that is statistically true). As a result, the mammal globins diverged from a more related sequence and, therefore, are more likely to have sequence similarity to each other than to a plant globin.
18. Variation would be more constrained as substitutions of smaller hydrophobic amino acids to bulkier hydrophobic would be excluded in order to conserve packing.
19. In chapter 4, Kuriyan *et al* defines protein domains as "parts of or whole polypeptide chains chains that form an independent structural unit". Characteristics that can classify particular domains into families are subjective but generally are bound by strong sequence identity, similar structure, function, folds, or some combination of those.
21. The number of protein folds that exist are limited because of evolutionary selection pressure. Many mutational deviations from a functional protein often cause the protein to be nonfunctional; though over billions of years of evolution, the state space of protein folds can be explored, many of these mutational steps will lead to nonfunctional proteins and, as a result, nonviable organisms. The folds that exist are on the order of thousands.