

October 21, 2002

ID number _____

Grade: _____

Biochemistry Cumulative Exam

This exam has to do with a fundamental area of biochemistry: protein structure.

Please answer each question as completely as possible.

1. What are the basic elements of protein secondary structure? How are they held together? Describe them as completely as possible, and make a sketch of how they appear, with labels and hydrogen-bonding arrangements.

2. Anfinsen performed the classic experiment in which ribonuclease was denatured with urea and then allowed to renature after dilution of the urea. A certain portion of the enzyme was active after this treatment, but only about 1%. However, this enzyme has 4 disulfide bonds. If they included a trace amount of β -mercaptoethanol ($\text{HO-CH}_2\text{-CH}_2\text{-SH}$) after removing the urea, they eventually got a much higher amount of active ribonuclease. Explain this effect and how it was interpreted.

Of course, this is really a minor point; the major point was that *any* ribonuclease activity was found. Explain why I say this -- what *was* the major point? And what does the implication of Anfinsen's experiment have to say about the flow of information in the central dogma of molecular biology? (Note: this is the central question of this exam – everything else depends upon it, so you would be advised to give it some thought.)

3. Explain what the driving forces are that determine a protein's structure. Be as specific as you can (examples would be good).

4. Explain briefly how protein structures are obtained experimentally. What are the two main techniques? What is the basis of each technique? (You do *not* have to get technical here – I just want the *basics*.)

5. A *lot* of information about gene sequences is becoming available at a very rapid rate due to the various genome sequencing efforts. Now there is a new effort underway to determine protein structures. They cannot determine the structure of every protein, for fairly obvious reasons. However, there is a plan to determine the structure of one member of each protein family. A “family” in this case refers to a group of proteins that share similar sequences (primary structures). Explain why they need to determine the structure of only one family member. (You should be able to relate this to your answer to question 2.) Explain briefly how one could use this information to predict structures of the other family members.

6. A long-term goal (and perhaps one of the “holy grails” of molecular biology) is to be able to predict a protein’s structure based solely on its sequence. Explain why this would be so desirable. Then explain briefly how this is being attempted now (again, just the *basics*) and/or how it *could* be attempted.