**Possible CHEM524 Final Exam Questions**

1. We discussed a peptidyl-prolyl isomerase in lecture. Discuss how this enzyme works.
2. DNA ligases consist of several distinct domains. What are these domains and how do they work together to help the enzyme function?
3. The following questions are about serine proteases.
4. What are the three catalytically important residues in this family of enzymes?
5. What determines substrate specificity in these enzymes?
6. What stabilizes the tetrahedral intermediate in the reaction?
7. You have found a new serine protease that hydrolyzes the peptide bond between adjacent glycine residues. Go ahead and draw the mechanism for your new enzyme.
8. Aspartyl proteases are very similar to the inverting glycosyl hydrolases. Both use general acid/base catalysis and both use a catalytic water molecule in the first step. Aspartyl proteases use two catalytic aspartate (one acidic and one basic) residues and a water molecule to catalyze the hydrolysis of a peptide bond.
9. Draw a possible reaction mechanism for an aspartyl protease.
10. Given the similarity of the mechanisms between the two different enzyme classes, would it surprise you to find that members of the two families share a common three-dimensional structure? This is an extreme example of what type of evolution?
11. Describe 3 types of posttranslational modifications found on proteins. You must mention the exact chemical type of modification and the role of each modification in the function of the protein.
12. Based upon what you know about x-ray crystallography, give some potential problems that you may encounter if you were to perform an experiment to determine the structure of a protein using the technique.
13. Protein evolution can happen through a variety of mechanisms, but we focused on two specific mechanisms. What were these and how do they work to increase the diversity of protein function?
14. What are the three basic mechanisms used within the cell to control/regulate protein function? Briefly describe each.
15. The following questions deal with protein active sites and binding sites.
	1. Briefly describe the features of an active site and contrast it to a binding site.
	2. What are the differences between binding affinity and binding specificity? Be certain to include the chemical factors that define each.
	3. We looked at several examples of the importance of microenvironments in protein active sites. What is meant by this term? Give a specific example of a protein altering a microenvironment and state the chemical basis by which the microenvironment may be altered. Your example may be completely made up as long as it serves to answer the question.
16. The parallel beta-helix is a perfect example of the relationship between protein structure and function as well as the relationship between biology and chemistry. Talk about this novel tertiary structure with respect to the following: biology, active site topology, protein structure and the interplay of substrate and enzyme (especially in terms of what the enzyme does to promote successful binding).
17. You knew this one was coming, so don’t act surprised.
18. Describe the four intermolecular forces that play a role in protein structure and function. State the Coulombic potential energy relationships for each force.
19. Go ahead and rank the interactions from highest occurrence to lowest occurrence in protein structures. In order to help you answer this question, go ahead and give a specific example of each force and use your examples to guide your ranking.
20. Which force(s) drive(s) protein folding?
21. Which forces are normally dominant in the active site of a protein?
22. What force(s) is (are) found in a zinc finger domain?
23. What force(s) is (are) found in a leucine zipper?
24. What force(s) is (are) found in a Type II beta turn?