**CHEM523 Bioinformatics Assignment Name\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

Answer the following questions to the best of your ability. If you are stumped, try to discern the rationale for each question and try again, or take the smarter approach and just ask me!

When complete, upload the assignment into the CHEM523 Dropbox folder as a Microsoft Word document with the format of: **FirstName\_LastName\_BioinformaticsAssignment.doc.** Failure to save your file in the correct format will result in no points.

1. Perform an Entrez search for your protein. a) Paste the amino acid sequence of the protein below. Surround the sequence with a text box and give it a caption in Microsoft Word b) How many amino acids are in the protein? c) Paste two citations for your protein in the space below. One of these citations can include the paper in which the structure is published.
2. Paste the results of a Conserved Domain search for both of your assigned proteins below. What information about your proteins can you glean from the conserved domains they have?
3. For both of your assigned proteins, perform a BLAST search of: a) the non-redundant database and b) the PDB. For each search, what the 3 proteins with the highest sequence identity (excluding your protein), and show the sequence alignment of the protein with the highest identity (that isn’t your actual protein).
4. Based upon your results from the BLAST search of the PDB with your assigned proteins, perform a structural alignment of a single chain of your protein with single chains from the top 3 homologous proteins from the PDB. Color each protein chain differently.
5. Where are the largest differences between the aligned proteins from question 4? Zoom in on a region that is not aligned well in the structural alignment. Evaluate the sequence alignments from the BLAST search of the PDB in this region with the structural alignment. What do you see?