1. (10 pts) Please resubmit your solution for the protein purification lab from problem set 7. It is likely that the software that you were working with was cached and your solution may not have been uploaded to the server.

2. (10 pts, 20 min) Two experiments were performed to determine the quaternary structure of HIV reverse transcriptase as well as the molecular size of each subunit. In these experiments, HIV reverse transcriptase was mixed with equal masses of two proteins with known molecular weights of 10 KDa and 80 KDa (i.e. molecular weight standards). Both of the standard proteins consisted of a single polypeptide chain. This mixture was then separated by size exclusion (right diagram) or by SDS-PAGE electrophoresis (also to the right).

   **Size Exclusion Column:** The absorption as a function of the elution volume is shown to the right. The 1st peak is the HIV reverse transcriptase.

   **SDS-PAGE:** The SDS gel is shown on the right (turned sideways). The bands indicate regions of the gel that are stained with a stain for protein. The thicker the band, the more protein. The arrow marks the top of the gel (where the mixture of proteins would be applied to the gel before the electric field would be turned on). The lower scale gives the distance from the starting point. The lane marked S contains the standards.

   **i)** Use the SDS-PAGE gel to determine the molecular weight(s) of the polypeptide chains that are present in this enzyme. Be sure to show your work (5 pts).

   **ii)** Determine the quaternary structure of HIV reverse transcriptase by combining the information from the gel filtration data with that from SDS-PAGE. Indicate the presence of any disulfide bonds. Please show your work (5 pts). (Note: Molecular weights determined by either technique are generally accurate to within 10-15%).

3. (5 pts, 10 min) An electron density map can be viewed on a Jmol page by selecting the link to jmol_xray on the Jmol link page. The buttons on this page will trace the main-chain through this electron density as well as give you some choices regarding the sidechain of the residue. Determine the amino acid sequence that best fits the experimental electron density. Briefly justify your answer.

4. (5 pts, 5 min) We recently determined the structure of a protein in our lab and the Ramachandran plot for the final fitted structure is shown on the right. Is our model of the structure likely correct, or not? Briefly justify your answer.

5. (5 pts, 5 min) Name the disaccharide shown to the right. Are the two linear forms of the monosaccharides epimers of each other? (Note: the anomeric carbon is not considered when evaluating whether two sugars are epimers).

6. (5 pts, 5 min) Draw $\beta$-fructofuranosyl (2-2) $\alpha$-glucopyranose using the reduced Haworth representation.

7. (5 pts, 5 min) When glucose is dissolved in water an equilibrium mixture that contains linear glucose, $\alpha$-glucopyranose, and $\beta$-glucopyranose is formed. There is slightly more $\beta$-glucopyranose than $\alpha$-glucopyranose, why?

8. (5 pts, 10 min) Draw the reduced Haworth representation for both the D and L forms of the sugar shown on the right. You can assume the configuration of the anomeric carbon is $\alpha$.

9. (5 pts, 10 min) Navigate to the Jmol page labeled “Mystery polysaccharide”. What is this polysaccharide? Briefly justify your answer.