The excel spreadsheet shows $\Delta\Delta G_{water \to octanol}$ for blocked Ala-X-Ala peptides at 25 $^{\circ}C$, where X is an amino acid. The $\Delta\Delta$ arises because these energies are determined relative to the energy to transfer the amino acid glycine from water to octanol (note that this is 0 $kJ \cdot mol^{-1}$).

1. Which amino acids are *most* favorable to transfer? Does this make sense?

2. Which amino acids are *least* favorable to transfer? Does this make sense?

Now we're going to try to understand where these transfer energies come from, and practice *PyMOL* on the way. Download pdb.zip (or pdb.tar.gz) from canvas and uncompress it. It contains has a directory of model structures of blocked Ala-X-Ala peptides.

1. How might you predict/calculate amino acid transfer free energies from these structures?

2. Go to it.

1. Open one of the pdb files. For each structure, run the following commands and record the output numbers. What are you calculating?

   (a) get_area (name N*,O*)

   (b) get_area (name C*,S*)

2. Ignoring the charged amino acids (at the bottom of the spreadsheet), plot:

   (a) $\Delta\Delta G$ vs the N/O areas. Fit a line to the data. What do you observe?

   (b) $\Delta\Delta G$ vs the C/S areas. Fit a line to the data. What do you observe?

3. Justify these graphs in molecular/atomic terms.

4. Now add the charged amino acids as a different series to the C/S graph. Fit a line to the data.

   (a) What do you observe?

   (b) Can you justify the new "charged" curve relative to the other curve?

5. How do you think these results relate back to protein (and other macromolecule) folding?