

PDB

We will start with discussing protein structure – amino acids, backbone, side chains (use wikipedia and google as necessary). Proteins are very diverse (20 choices at each position, can be 20-400 positions long!) and this diversity gives rise to a whole array of functions.

Look at the PDB (<http://www.rcsb.org/pdb/home/home.do>). Make sure to check out the **Education Corner** and the Molecule of the Month.

Here are some links to visualization software:

VMD: <http://www.ks.uiuc.edu/Research/vmd/>

Chimera: <http://www.cgl.ucsf.edu/chimera/>

Here are some lists of other free visualization programs:

http://www.edinformatics.com/mathmol/mm_software.htm

<http://www.umass.edu/microbio/rasmol/othersof.htm>

Look at some online software that will access and analyze pdb files:

MolProbity: <http://molprobity.biochem.duke.edu/>

Sequence alignment – BLAST: <http://www.ebi.ac.uk/Tools/>

Protein-DNA contact determination - PDBsum: <http://www.ebi.ac.uk/pdbsum/>