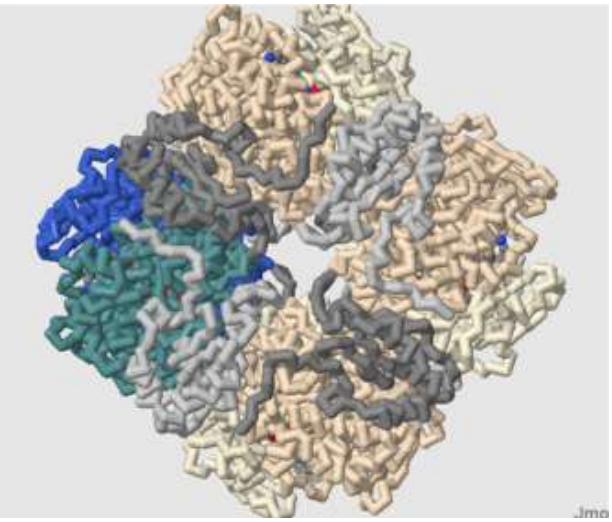
Model Summary Sheet

1UPM Hexadecamer Model



Teachers: Brenda Bott, Pat Delwiche, Joe Kinscher, JoAnn Miller

Contact person (if not ST Teacher, please provide email address):

Primary: JoAnn Miller

PDB File: **1upm**

Jpg filename: 1UPM_hexadecamer model.jpg

Model Abstract:

Across all organisms, rubisco enzymes consist of more than one subunit. There are two structural forms of rubisco based on number of subunits. The simplest rubisco (form II) is found in some photosynthetic bacteria, and is a dimer of two large subunits (L), each of which is composed of approximately 475 residues. Form I as demonstrated by this model, is the more common type of rubisco. It is composed of two different sized subunits, small (S) and large (L). Large subunits of form I are also approximately 475 residues and small subunits are approximately 120 residues in length. Form I rubisco is a hexadecamer, made of eight L and eight S subunits (8L8S). All 8L subunits are identical to each other and are arranged in the hexadecamer complex as four dimers around a central axis. This octameric core is roughly spherical; a cluster of four S subunits forms a cap on both ends of the sphere. The L subunit is roughly pear-shaped in all forms of rubisco, The narrower, amino-terminal end of the L subunit is composed of the first 150 residues. The larger, carboxy-terminal end is built of residues 151 to 475, and consists of a / barrel structure made of eight -strands and eight helices.

What do the colors in your model indicate?

royal blue = I chain

cadetblue = b chain

cornsilk = k, r, e chains

bisque = o, v, h chains

light grey = s, m, c, p chains

cpk = ligand = RuBP analogue

magenta = ligand = RuBP analogue

lime = ligand= Ca

cpk = sidechains; lys334, lys201, asp203, glu204, thr65, glu60, lys128

Which amino acids are displayed and WHY did you display them (what is the function of these amino acids)?

lys334, **lys201**, asp203, glu204, thr65, glu60, lys128

These residues form the catalytic site of rubisco. The active site of rubisco must be activated prior to the introduction of the substrate RuBP. Activation requires two processes: 1) the carbamylation of a lysine residue (LYS 201) within the pocket; and 2) the addition of an Mg^{2+} ion to the active site. The carbamylated lysine is located on the C-terminal end of one of the b-strands of the b/a barrel structure. Carbamylation stabilizes a Mg2+ ion that is crucial to the activation of the site. Once the active site has been activated, the introduction of RuBP into the active site occurs.