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**Understanding Color Vision in Mammals: X-ray Crystal Structures of Some Cellular Retinoic Acid Binding Protein II Mutants as a Mimic of Rhodopsin.** S. Vaezeslami, E. Mathes, C. Vasileiou, R.M. Crist, J.H. Geiger, B. Borhan, Dept. of Chemistry, Michigan State Univ., East Lansing, MI 48824-1322, USA.

We are studying the interactions that result in tuning of the visual pigments. While rhodopsin is a transmembrane protein and not soluble in water, CRABPII is cytosolic and crystalizes much easier than rhodopsin. In order to make a mimic of rhodopsin CRABPII has been re-engineered from a non-covalent retinoic acid binding protein to a protein that binds to retinal by forming a protonated Schiff base necessary for wavelength regulation. We are interested in crystallizing those proteins that are of interest in mutagenesis studies of CRABPII. We have determined the structures of both wild type and several mutant forms of CRABPII, unbound and bound to retinoic acid, which diffract significantly better than the currently available structures. These structures provide insights into the interactions in the binding pocket of the mutants, which could enable more systematic mutants to be engineered. Further, the best diffracting crystals, 1.5 Å, were soaked in retinal and diffraction data was obtained. More work is being done on these data to probe the effect of bulky and charged residues on the chromophore.