

## HOMOLOGY MODELING, DOCKING, AND BIOLOGICAL ASSAY DEVELOPMENT FOR LYCOPENE CYCLASE ENZYMES IN FRUIT

**Tyler Nguyen** and Tat Lee (Ryan Denton), Department of Chemistry and Chemical Biology, Purdue School of Science Indiana University–Purdue University Indianapolis, Indianapolis, Indiana 46202

Plants, as well as many bacteria and fungi, catalyze a ring-forming reaction to transform lycopene into a variety of carotenoids by utilizing  $\beta$ -lycopene cyclase among several related enzymes. Though this highly homologous enzyme class has been studied in a variety of organisms, structural and functional characteristics of the enzymes still remain unsolved and no crystal structure is currently known. Introductory computational analysis on lycopene  $\beta$ -cyclase from *Capsicum annuum* (bell pepper) was performed due to the significant amount of available biological activity data. Computational work included regression analysis on molecular descriptors of several known inhibitors using JMP® Statistical Discovery Software, preliminary homology modeling on the above enzyme using SWISS-MODEL and Chimera Molecular Modeling and Drug Docking software, and preliminary docking experiments utilizing a small test set of known and synthesized inhibitors using ArgusLab software. In addition to the computational study, a whole fruit assay for lycopene cyclases was developed on lemons. Analysis of known inhibitors led our group to synthesize a series of substituted chalcone inhibitors which were assayed along with known negative and positive control molecules. The extracted carotenoids were analyzed by Liquid Chromatography Mass Spectrometry (LCMS) to monitor the accumulation of lycopene upon inhibition.

Funding provided by the Indiana University-Purdue University Indianapolis Undergraduate Research Opportunities Program (UROP).