Genome sequences are being determined and analyzed for several photosynthetic bacteria. Finished genome sequences of these organisms will fill large gaps in the available genomic data for photosynthetic prokaryotes and will help to understand the origin and early evolution of photosynthesis. Each organism that has been selected has unique individual characteristics such as agricultural applications and environmental aspects such as understanding global photosynthetic productivity.

The genomes of several of these organisms have now been sequenced to single-contig status. An annotation workshop for two or three genomes will be held at Washington University beginning on June 3, 2012 and continuing until August 10. The genomes will be subjected to automated annotation prior to the annotation workshop. Students who are interested in participating in this workshop should contact the Project Director Robert Blankenship (Blankenship@wustl.edu). The workshop will include an introduction to genomics and genome annotation methods, as well as extensive hands-on work annotating the bacterial genomes and metabolic pathway analysis. It is anticipated that students who participate in the entire workshop will be co-authors on scientific publications reporting the genomes. Students should have completed Biochemistry (Chem 4810/4820 or Bio 451) or Research Explorations in Genomics (Bio 4342) or obtain permission of the instructor to be considered for the project team. Stipend support for the student members of the team will be available.

Photosynthesis is the conversion of light energy to chemical energy as mediated by living organisms. This central biological process provides energy that sustains almost all life on Earth and is also the basis of all agriculture. Understanding how this complex process works at a molecular, cellular and ecosystem level, as well as how it originated and evolved are fundamental problems that are essential to obtaining the deep understanding required to lead to practical results to improve agriculture and complex environmental interactions.