

Brookhaven National Laboratory  
Biosciences Seminar

*“Omic-Methods to Divine  
Gene Function”*

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Monday, March 17, 2014

11:00 a.m.

Biosciences John Dunn Seminar Room  
Bldg. 463, Room 157



Host: David Schlyer

Served 10:45

**Abstract:** Determination of gene function remains the primary biological goal in the post-genomic era. *Chlamydomonas reinhardtii*, a JGI flagship organism, is a premier reference for studies in fundamental processes, such as photosynthesis, cilia biogenesis, micronutrient homeostasis and value-added commodities. Yet only ~10% of predicted genes are associated with an experimentally validated functional annotation. Fortunately, significant advances in the depth, throughput and reduced cost of sequencing technologies are opening new avenues for probing gene function and assigning annotations. Recently, we have employed timecourse RNA-Seq approaches to investigate the molecular basis enabling a nitrogen-deprived starch-null mutant to accumulate more triacylglycerol (TAG) than starch-plus strains. Our transcriptomes were supported with selected *in vitro* biochemical assays, targeted metabolite studies and whole genome sequencing, and have provided novel insights to TAG production. More recent investigations have included: i) employment of gene co-expression analyses to predict protein localizations in a day/night cycling culture analyzed by high temporal-resolution transcriptomes, and ii) development of systems required for high-throughput, automated, phenotyping in conjunction with genome sequencing in a genome wide mutant collection we have constructed.