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## **Baseline Proteome Analysis of the Anoxygenic Phototrophic Bacterium *Rhodospseudomonas palustris* under all Major Metabolic States**

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Rapidly advancing LC-MS/MS technologies have now allowed for the reproducible and rapid analysis of protein complexes and proteomes from simple microbial species. These technologies can now be directly tied to genomic tools to allow for a detailed analysis of a microbial species at the systems level. *Rhodospseudomonas palustris* is a purple nonsulfur anoxygenic phototrophic bacterium that is ubiquitous in soil and water samples. While many bacteria are metabolically versatile, *R. palustris* is unique in its ability to catalyze more cellular processes than any other known bacterium. Our goal is to use multi-level proteomics technologies to obtain a greater understanding of the diverse metabolic states of this microbe and the proteins important to the individual growth states. For the initial foundation of this global project, we have analyzed the baseline proteome of *R. palustris* wild-type strain grown under numerous conditions including photoheterotrophic, chemoheterotrophic, nitrogen fixation, photoautotrophic, stationary phase, as well as benzoate as an alternate carbon source. The basic methodology for baseline proteome analysis involves fractionating each growth state by centrifugation techniques, followed by digestion with trypsin and analysis by fully automated 1D and 2D LC-MS/MS techniques. The resultant MS/MS spectra from each growth state are searched with SEQUEST against all predicted ORFs from *R. palustris*. Specifically, we are studying the expression of redundant genes, identifying changes unique to each growth state, and developing tandem affinity purification targets for large-scale analysis of protein machines from this microbe. We have currently completed in replicate the analysis of WT strain under the conditions listed above. This analysis resulted in the overall identification of 1,646 proteins with conservative filtering constraints. Qualitative analyses of these growth conditions have revealed over 300 proteins exhibiting large-scale differences between conditions, many of these being hypothetical or conserved hypothetical proteins showing strong correlations with different metabolic modes.

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