

Proteomic profiles of *Rhodopseudomonas palustris*

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We recently described (VerBerkmoes, et al., *J. Proteome Research* 1:239-252, 2002,) a comprehensive method for proteome analysis that integrates both intact protein measurement ("top-down") and proteolytic fragment characterization ("bottom-up") mass spectrometric approaches, capitalizing on the unique capabilities of each method. This approach is being applied to proteomic profiling of the anoxygenic photobacterium *Rhodopseudomonas palustris*. Multiple physiological states, i.e., aerobic heterotrophic growth, anaerobic heterotrophic growth, anaerobic photoheterotrophic growth, and anaerobic phototrophic growth, are being profiled. In addition, profiles of mutants defective in major assembly and regulatory processes are being profiled. The proteomic profiles are also being used to enhance the annotation of the genome: a significant number of "genes of unknown function" have been authenticated, and their cellular localization and physiological response are now known. Over 25% of the proteins profiled represent the "unknown" class.

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