YZGD from *P. thiaminolyticus* and NAGD from *E. coli*, Novel Enzymes of a Unique Phosphatase Family of the Haloacid Dehalogenase (HAD) Superfamily

Isaac Tirrell, Chris Daley, Lyndsay McFarland, and Suzanne O'Handley
Department of Chemistry, Rochester Institute of Technology, 85 Lomb Memorial Drive, Rochester, NY 14623

We have identified YZGD from *P. thiaminolyticus* and NAGD from *E. coli* as members of a unique phosphatase family of the haloacid dehalogenase (HAD) superfamily. We have determined YZGD to be a pyridoxal phosphatase (PLPase) and NAGD to be a UMPase. Though there are over 100 identified open reading frames with sequence homology, the only other known enzymes of the family are a human PLPase and 2 yeast nitrophenyl phosphatases. In addition to YZGD being a member of the HAD superfamily, it also contains a Nudix signature sequence. We are carrying out site-directed mutagenesis on conserved amino acids to show which amino acids are responsible for catalysis. NAGD may be involved in cell surface lipopolysaccharide (LPS) and cell wall biosynthesis through hydrolysis of UMP, an intermediate of both pathways. Development of antibiotics toward NAGD may be prove fruitful, particularly if sequence homologues from pathogens are determined to be functional homologues as well. This research has been supported by the Jeffress Memorial Trust, a Cottrell College Science Award from the Research Corporation, and an NIH AREA grant.