Structure and Activity Analyses of *E. coli* K-12 NagD Provide Insight Into the Evolution of Biochemical Function in the HAD Enzyme Superfamily [†,‡]

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SUPPORTING INFORMATION

1 Figure of sequence alignment of NagD homologues from various bacterial species. 2 pages total.

Figure S1. The sequence alignment of NagD homologues from various bacterial species. In red-highlight and boxed in blue are shown the stringently conserved residues. In red text and boxed in blue are conserved residues. Accession codes for sequences or PDB: *E. coli* K-12: P15302; *Salomnella enterica*: NC_004631.1; *Yursinia pseudotuberculosis*: NC_006155.1; *Shweanella oneidensis:* NC_004347.1; *Streptomyces*: CAB65573; *Nocardia farcinica*: YP_121565; *Leifsonia xyli*: NC_006087.1; *Arthrobacter*: AAHG1000001.1; *Enterococcus faecalis* NP_814917; *Streptococcus mutans*: AAN59079; *Staphylococcus aureus*: YP_040313; *Thermatoga maritima*: NP_229540.