

**NMR-based Structural proteomics of hyperthermophile
Methanobacterium Thermoautotrophicus and *Helicobacter pylori*
proteins**

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Recently, structural proteomics approach has been considered as a major initiative project within the biological research community. The large number of protein structures determined by NMR spectroscopy and X-ray crystallography have provided valuable information for protein folding as well as their biological functions. We initiated structural genomics project targeting functionally unknown protein MTH1880 from *Methanobacterium Thermoautotrophicus* and *Helicobacter pylori* proteins. Solution structure of MTH1880 determined by NMR spectroscopy showed an alpha-beta sandwich fold. Divalent cation titration experiments indicated that only Ca²⁺ ions bind to MTH1880 protein, suggesting that MTH1880 is a novel Ca²⁺ binding fold. For *Helicobacter pylori*, eight proteins including HP1067 and HP1043 have been selected for NMR structure determination. To determine the biochemical properties of these proteins, biophysical techniques, such as NMR, CD and sedimentation equilibration experiments have been performed. In this presentation, current progress of structural proteomics project for two pilot projects will be discussed.