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# NMR Studies on putative response regulator protein, *Helicobactor pylori* 1043 derived from Korean Strain 51

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Recently, we have initiated NMR-based structural genomics project targeting *Helicobacter pylori* proteins from Korean strain 51. HP1043 which is a putative two component transcriptional regulator based on sequence database contains unknown biological function. From sequence homology data, this protein is consisted of two functional domains, an N-terminal phosphorylation domain (14kDa) and C-terminal DNA-binding/transactivation domain (11kDa). To determine structure-function relationship of HP1043, heteronuclear NMR methods including TROSY and RDC techniques have been applied. Most of NMR data used for backbone resonance assignment were acquired at 303K on Bruker DRX 500 and DMX 600 and the following three-dimensional TROSY based spectra were acquired: HNCACB, HN(CO)CACB, HN(CA)CB, HN(COCA)CB, HNCA, HN(CO)CA, HNCO. The weak alignment of protein molecules in solution induced by liquid crystalline media which provide information on the orientation of two functional domains. And the residual dipolar couplings data were measured by the difference between anisotropic and isotropic phases. The solution structure of HP1043 will promise us the information about putative regulating role in *H. pylori* as well as the clue to infer its molecular function. We now report the backbone resonance assignment and secondary structures based on NMR data.