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# Letter to the Editor

## Resonance assignments for the hypothetical protein TA0938 from *Termoplasma acidophilum*

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One common approach for investigating the molecular function of a protein is to determine its three-dimensional conformation, and then to compare the solved structure against known structures. As a consequence, completion of sequencing efforts of many genome projects has shifted attention towards rapid structure and function determination for all the proteins encoded by newly discovered genes. These structures, and the corresponding protein production vectors and resonance assignments, will provide a valuable resource for structural and functional studies of the hundreds of proteins and their homologues that are targeted by the international structural proteomics efforts (Yee et al., 2003). We report here the resonance assignments of TA0938 as part of a structural proteomics project on the feasibility of the high-throughput generation of samples and NMR analysis from *Thermoplasma acidophilum*. The U−$^{15}$N and U−$^{13}$C, $^{15}$N labeled protein contained the complete sequence of TA0938 plus additional N-terminal histidine tag (MGSSHHHHHHSSGLVPRGSH). Samples were prepared in 20 mM Tris (pH = 6.7), 100 mM NaCl, 1 mM DTT, 0.01% NaN3, 1 mM benzamidine, 95% $H_20$/5% $D_2O$. The concentration of the purified protein ranged between 0.8 and 1.5 mM. The combined use of automated and manual analysis of triple resonance 3D data (Monleon et al., 2004, and references therein) provided assignments for ~99% of assignable backbone atoms (i.e., 108/109 $^{15}$N−$^{1}$H$^{N}$ sites) and ~96% of total $^{1}$H atoms in TA0938. These $^{1}$H, $^{13}$C and $^{15}$N chemical shift data have been deposited in BioMagResBank database (accession number 6812). Overall, based on these chemical shifts and some $H_N$–$H_\alpha$ NOE connectivities, secondary structure for this protein contains six segments of β-strand and one α-helix.

References: Yee et al. (2003) *Acc. Chem. Res.*, **36**, 183–189; Monleon et al. (2004) *J. Biol. NMR*, **28**, 81–84.

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