magnetic resonance (NMR) spectroscopy. We suggest that this kind of combination of structural information could be useful for clever inspection of structure by structural genomics.

Infection of the gastric pathogen, *H. pylori*, induces severe gastric disorders including peptic ulcer and stomach cancer. HP0902, identified as one of secretory proteins from *H. pylori*, is predicted to interact with VacA, a representative virulence factor secreted from the bacterium. In addition, HP0902 is over-expressed in a mutant strain lacking the *VacA* gene, which regulates the resistance of *H. pylori* to an antibiotic. It would be reasonable to consider the secreted proteins from *H. pylori* as candidates for virulence factor of the bacterium, as they can contribute to gastric inflammation. One such protein is HP0902, of which function is unknown. In this respect, crystal structure of HP0902 was approached, in terms of structural genomics.

We first succeeded in solving the crystal structure HP0902 using a construct with an N-terminal His-tag, at 1.4Å resolution. Although the His-tag was not seen in the electron density map, the N-terminal residues were located at dimeric interface and contributed significantly to dimer contact. Thus, we additionally solved the structure using a different construct with a C-terminal His-tag, to ensure the N-terminal conformation in the absence of His-tag attached. Unfortunately, the protein without tagging was not crystallized. Thus, structural inspection for untagged HP0902 was further complemented by NMR spectroscopy in solution, via backbone NMR assignments and chemical shift analysis.

The determined structure of HP0902 showed an all-ß topology forming a symmetric homodimer. The monomer was formed primarily by two entirely antiparallel ß-sheets that form a jelly roll ß-sandwich. The homodimer is formed by a domain swapping between adjacent edge strands ß1 and ß8 from two different subunits in the dimer. The larger ß-sheet has a six-stranded 2310581' topology, while the smaller ß-sheet has a four-stranded 4967 topology, respectively. All those are conserved features in cupin superfAMILY proteins. Cupins are ubiquitous proteins sharing a highly conserved topology of ß-barrel, but are classified into 35 protein families, with greatly diversified functions and sequences. In addition, most proteins with the highest score of structural homology to HP0902 are functionally uncharacterized. Thus, unfortunately, a structural fold and homolog search could not be successful in suggesting function of HP0902. However, HP0902 is folded without bound metal ion and possesses additionally extended stretch between ß1 and ß2 strands. Its dimeric interface is formed by frequent hydrogen bonding, instead of hydrophobic clustering. Those structural properties distinct from other cupin family proteins might provide functional specificity to HP0902. Thus, the present results constitute fundamental, critical data for progressing studies to identify function and/or virulence and to elucidate its structural mechanism.

**Keywords:** Helicobacter pylori, HP0902, structural genomics

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**MS57.P03**


**MS57.P04**


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**Strategies for analysis expression and protein solubility**


To get soluble protein is one of the major bottlenecks that precede crystallographic studies. During the last years several techniques and strategies have been developed to address this problem. However, many of them imply an economical cost and technologies that are not always available.

We will describe a general plan for protein solubility analysis by using a combination of four different but complementary strategies. In this plan, different constructs of a protein of interest are designed and