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Crystal Structure of HP0242, a Hypothetical Protein from *Helicobacter pylori* with a Novel Fold. Jia-Yin Tsai, Bo-Tsang Chen, Hui-Chun Cheng, Hsin-Yi Chen, Nai-Wan Hsaio, Ping-Chiang Lyu, and Yuh-Ju Sun, Inst. of Bioinformatics and Structural Biology, National Tsing Hua Univ., Hsinchu 300, Taiwan, Republic of China.

HP0242 is a hypothetical protein from a human gastric pathogen, *Helicobacter pylori*. Here, we report the first crystal structure of HP0242 determined at 2.27 Å resolution by multiwavelength anomalous dispersion (MAD) phasing. The overall structure of HP0242 folds like a musical instrument-triangle with four helices. Two monomers tightly interlock each other by Helix2 to form a dimer with extremely strong interactions. Helix2 is essential in the formation of HP0242 dimer. We suggest that dimer might represent the functional state for HP0242. A structure-based homology analysis with the DALI algorithm indicates that HP0242 has a novel fold. To date, none of the HP0242 and its homologues has been assigned a cellular function. Our results may shed a light on further functional studies based on the unique protein folding.