Structural Analysis of the Peptidyl Prolyl *cis*,*trans*-Isomerase HP0175 from *Helicobacter pylori*

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Infections caused by the gram-negative bacterium *Helicobacter pylori* are associated with several pathways that include epidermal growth factor receptor (EGFR) and production of vascular endothelial growth factor receptor (VEGF). Of the several proteins secreted by *H. pylori*, HP0175 a peptidyl prolyl *cis*-, *trans*-isomerase (PPIase) has been linked to bind to toll-like receptors (TLR) allowing for the trans-activation of EGFR and VEGF. TLRs are major players in innate immunity through their ability to recognize pathogens such as bacteria, fungi or viruses. HP0175 also causes cell damage, apoptosis and inflammatory responses. The following protein was initially crystallized as a homodimer (PDB ID:5EZ1), complexed with its inhibitor indole-2-carboxylic acid (I2CA) at 2.4 Å resolution. Here, we examine apo-HP0175 as a monomer with structure resolution of 2.34 Å. Apo-HP0175 crystallizes in space group $p3_121$, with unit cell dimensions a=b=91.5 Å, c=67.7 Å with one molecule in the asymmetric unit.