The Crystal Structures of HcpB and –C: Two Proteins with Sel1-like Repeat Architectures Involved in the Modulation of Innate Immune Response

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Many epsilon-proteobacteria, such as *Helicobacter pylori*, *Campylobacter jejuni* and *Wollinella succinogenes*, settle in the stomachs of higher organisms, requiring proteins to resist the harsh conditions of this ecological niche. The family of Helicobacter cysteine-rich proteins (Hcp) was identified using the method of comparative genome analysis and seems to be specific for this class of microorganisms. So far this family of secreted proteins was lacking a functional and structural description. Using recombinant HcpA, -B, -C and –E we identified high anti-Hcp antibody titers in the sera of *H. pylori* positive patients, confirming that these proteins are expressed *in* vivo [1]. The crystal structures of HcpB and –C were refined at 2 Å resolution and serve as the prototype structures for the large family of Sel1-like repeat proteins [2, 3]. The structure of HcpC reveals a peptide-binding mode that is strikingly similar to TPR proteins suggesting that Hcp proteins might be involved in protein-protein interactions. This hypothesis is corroborated by the secretion of high IFN-gamma and IL12 levels from naïve mouse splenocytes upon addition of recombinant HcpA [4], indicating an implication in the modulation of innate immune response and survival of *H. pylori* in the human stomach.

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Keywords: innate immune response, structural genomics, protein-protein interactions