E value	Estimated Precision	Fold/PDB Descriptor	Superfamily	Family
3.4e-10	100%	PDB Header: hydrolase	PDB Molecule: lipase	PDB Title: crystal structure of the extracellular lipase from Pseudomonas 2 sp. mis38
1.9e-09	100%	PDB Header: hydrolase	PDB Molecule: extracellular lipase	PDB Title: crystal structure of extracellular lipase lipa from serratia 2 marcescens
1.6e-07	100%	Single-stranded right-handed beta-helix	Pectin lyase-like	Virulence factor P.69 pertactin
1.2e-06	100%	PDB Header: hydrolase	PDB Molecule: serralysin	PDB Title: Psychrophilic protease from pseudolateromonas 'tac ii 18'
2e-06	100%	PDB header: hydrolase	PDB Molecule: protease c	PDB Title: the metzincins's methionine: prtc m226l mutant
3.7e-0.6	95%	PDB Header: structural protein	PDB Molecule: invasin	PDB Title: crystal structure of invasin: a bacterial integrin binding protein

Supplemental Figure 1. Results from PHYRE1 analysis using the first 1200 amino acids of the ImaA protein sequence from *H. pylori* G27. Search run on January 25, 2012, using the original Phyre program as described in Kelley and Sternberg (**Kelley LA, Sternberg MJ.** 2009. Protein structure prediction on the Web: a case study using the Phyre server. Nat Protoc **4:**363-371).