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Supporting information for article:

Crystal structure of the HINT protein from *Helicobacter pylori*

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Table S1 Structural superposition and percentage sequence identities of HpHINT with homologous HINT structures

The organisms from which these proteins were obtained are listed in Figure 7.

PDB ID of the protein	Number of alpha carbons aligned	RMSD (Å)	% sequence identity
3N1S	101	1.6	36
1XQU	101	1.2	46
4EGU	101	1.3	38
2EO4	99	1.4	31
3LB5	100	1.5	29
3O0M	99	1.6	34
1Y23	99	1.5	38
3IMI	99	1.4	40
3KSV	100	1.6	37
3TW2	100	1.3	39
3O1Z	100	1.3	38
3OJ7	98	1.4	40
3L7X	100	1.5	34
3R6F	95	1.7	32

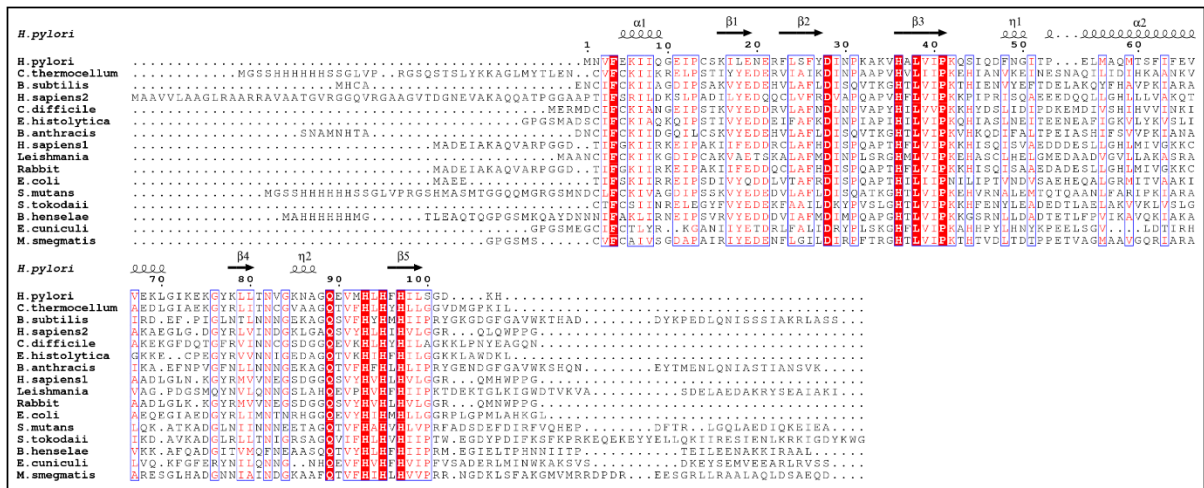


Figure S1 Multiple sequence alignment. Multiple sequence alignment of HpHINT with other members of the HINT family taken from the PDB. The alignment was generated by ESPrpt (Gouet *et al.*, 2003) with clustalW (McWilliam *et al.*, 2013). Secondary structural elements of HpHINT as determined by the “Defined Secondary Structure Prediction” (DSSP) are shown above the sequences (α -helices, β -strands, η -3₁₀ helices and TT- β turn). All members of this family share a similar core structure and conserved residues essential for substrate binding and hydrolysis, in particular H-X-H-X-H just following beta strand 4. (red: totally conserved and pink: partially conserved). The PDB IDs for these structures and the organisms to which they belong are listed in Figure 6.