

**Supplementary Table S1.** Structural comparison of ClpP homologues

<i>Organism</i>	<i>PDB code</i>	<i>Resolution (Å)</i>	<i>Reference</i>	<i>Seq. id. (%)</i> <sup>1</sup>	<i>Rmsd (Å), # Cα</i> <sup>1</sup>
<i>Escherichia coli</i>	1YG6	1.90	(Bewley et al, 2006)	100	
<i>Escherichia coli</i> <sup>2</sup>	3MT6	1.90	(Li et al, 2010)	100	0.5, 180
<i>Bacillus subtilis</i>	3KTG	2.40	(Lee et al, 2010)	68.3	0.7, 183
<i>Homo sapiens</i>	1TG6	2.10	(Kang et al, 2004)	55.2	0.8, 183
<i>Streptococcus pneumoniae</i>	1Y70	2.51	(Gribun et al, 2005)	52.1	0.9, 169
<i>Mycobacterium tuberculosis</i>	2CE3	2.60	(Ingvarsson et al, 2007)	54.9	1.5, 164
<i>Plasmodium falciparum</i>	2F6I	2.45	(El Bakkouri et al, 2010)	40.8	1.1, 157
<i>Plasmodium falciparum</i> <sup>3</sup>	4GM2	2.80	(El Bakkouri et al, 2013)	37.6	1.4, 162
<i>Helicobacter pylori</i>	2ZL0	2.60	(Kim & Kim, 2008)	70.5	0.6, 173
<i>Staphylococcus aureus</i>	3STA	2.28	(Zhang et al, 2011)	63.4	0.8, 183
<i>Francisella tularensis</i>	3P2L	2.29	-	64.6	0.7, 181
<i>Coxiella burnetii</i>	3Q7H	2.50	-	64.8	0.9, 179

<sup>1</sup>Compared with *Escherichia coli* ClpP monomer and calculated using SSM (Krissinel & Henrick, 2004) within COOT (Emsley et al, 2010).

<sup>2</sup>*Escherichia coli* ClpP+ ADEP1

<sup>3</sup>*Plasmodium falciparum* ClpR

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