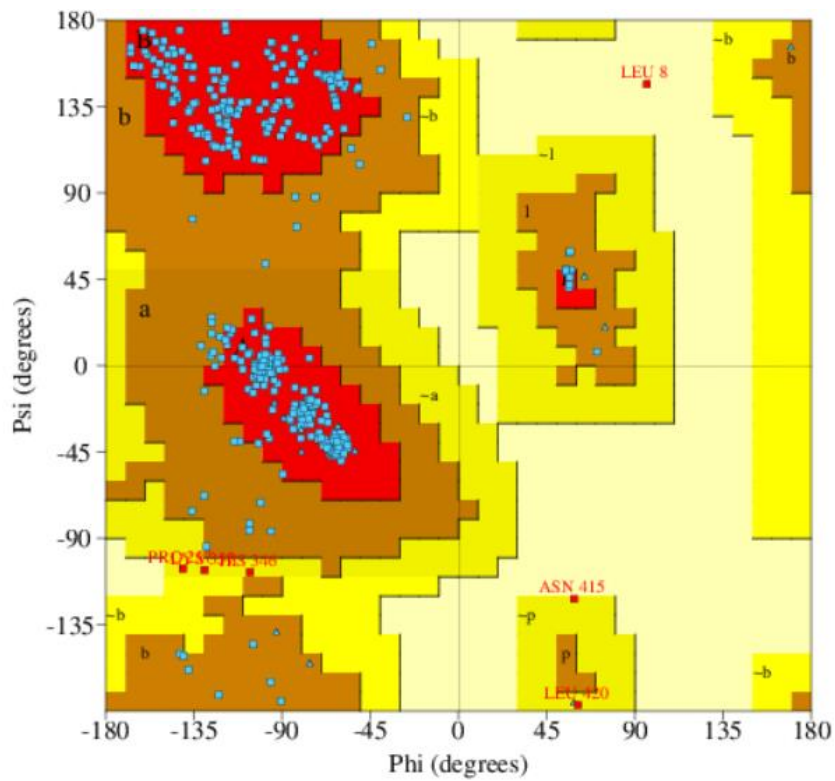


Supplementary Figure S1. Ramachandran plot of the homology modelled G6PD from *Helicobacter pylori*.



PROCHECK statistics

1. Ramachandran Plot statistics

	No. of residues	%-tage
Most favoured regions [A,B,L]	350	88.8%
Additional allowed regions [a,b,l,p]	39	9.9%
Generously allowed regions [~a,~b,~l,~p]	4	1.0%
Disallowed regions [XX]	1	0.3%*
Non-glycine and non-proline residues	394	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	14	
Number of proline residues	15	
Total number of residues	425	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20.0 a good quality model would be expected to have over 90% in the most favoured regions [A,B,L].