

Supplementary Materials:

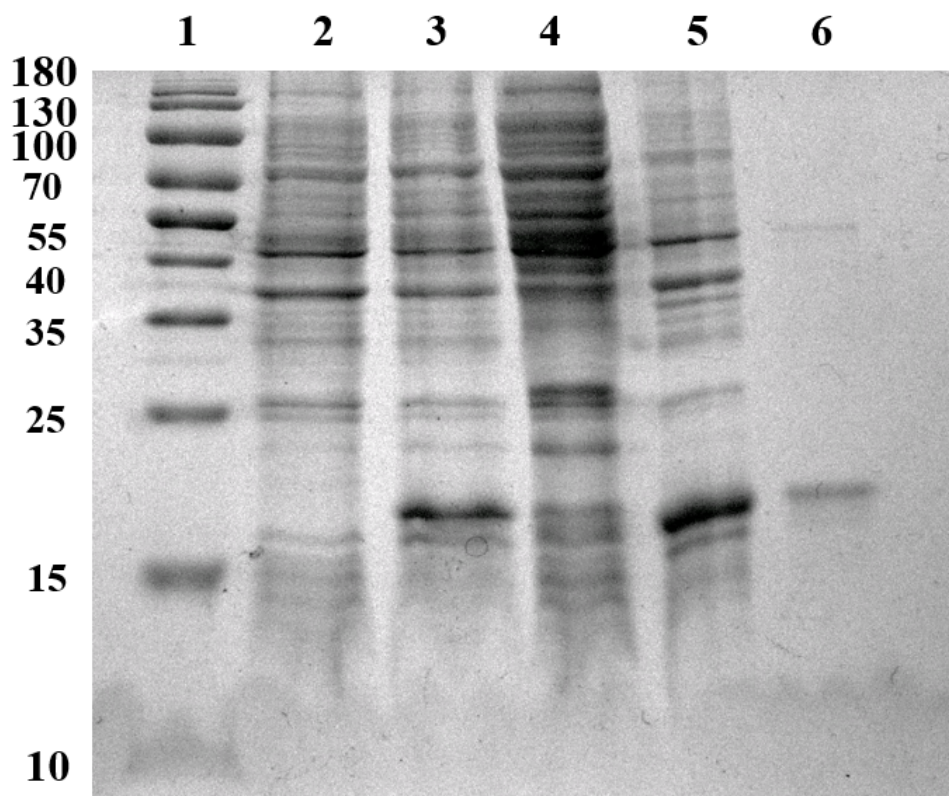
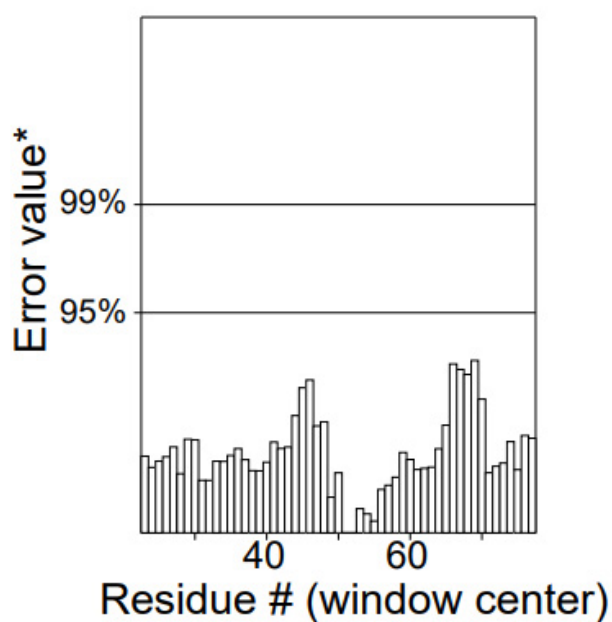


Figure S1. SDS-PAGE analysis for the expression and purification of CrufCSP1. M, protein marker; lane 1, non-induced PET30a/CrufCSP1 before IPTG induction; lane 2, IPTG-induced PET30a/CrufCSP1; lane 3, supernatant of induced PET30a/CrufCSP1; lane 4, sediment of induced PET30a/CrufCSP1; lane 5, purified CrufCSP1 with His-tag.

Program: ERRAT2
File: csp456.pdb
Chain#:A
Overall quality factor**: 100.000



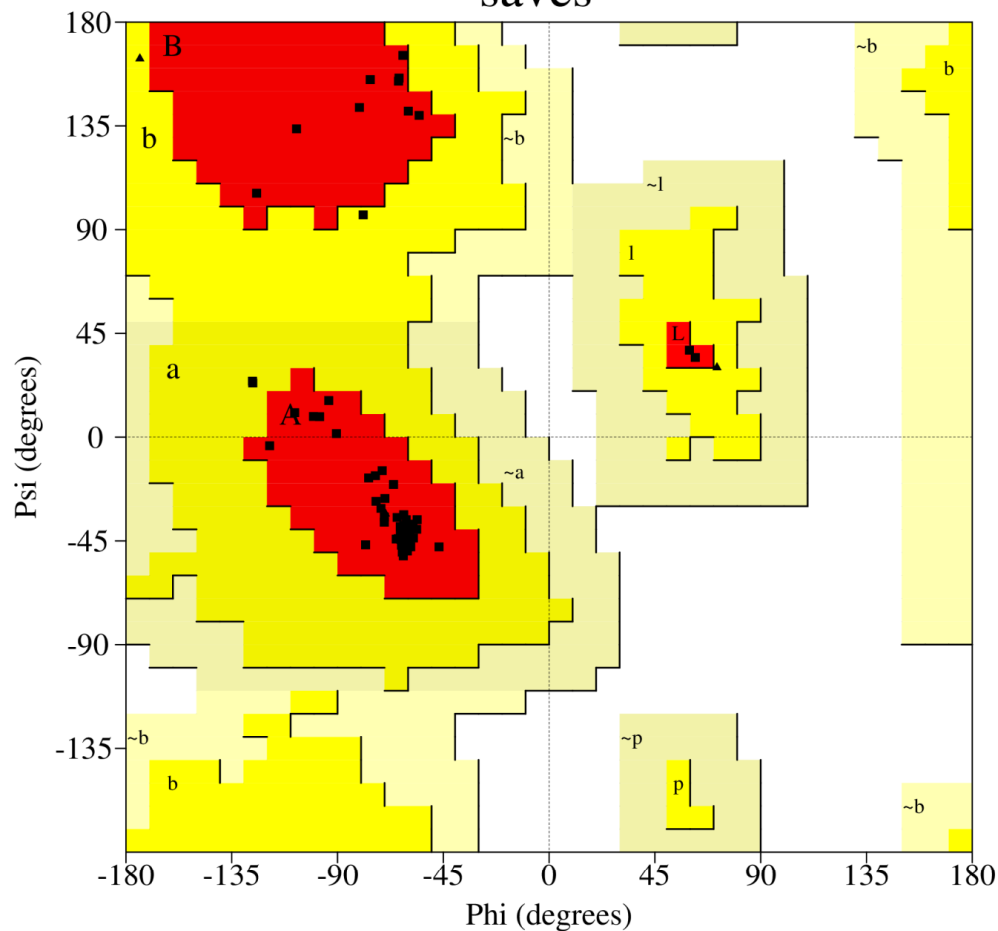
*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

**Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3Å) the average overall quality factor is around 91%.

Figure S2. ERRAT results of the constructed 3D model of CrufCSP1.

Ramachandran Plot

saves



Plot statistics

Residues in most favoured regions [A,B,L]	52	94.5%
Residues in additional allowed regions [a,b,l,p]	3	5.5%
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%

Number of non-glycine and non-proline residues	55	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	4	
Number of proline residues	2	

Total number of residues	63	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.

Figure S3. Ramachandran plot of the constructed 3D model of CrufCSP1.