Crystallographic structure of CP190-BTB/POZ

Supplementary Table 1. Data collection and refinement statistics of the CP190-BTB/POZ crystal structure.

Data collection		
Space group	$P3_221$	
Cell dimensions		
a,b,c (Å)	84.98, 84.98, 40.87	
α, β, γ (°)	90, 90, 120	
Resolution, (Å)	42.49 – 2.03 (2.14 – 2.03)*	
R_{merge} %	5.4 (51.6)	
Mean(*I*)/σ*I*	16.6 (3.1)	
Completeness %	100. (100.)	
Redundancy	6.9 (7.1)	
Refinement		
Resolution (Å)	2.03	
No of reflections	77479	
No unique reflections	11252	
R/R_{free}	19.1/24.1	
$B_{factors}$ (Å^2)		
protein	60.6	
waters	63.8	
solvent	63.9	
Rmsd bond lengths (Å)	0.007	
Rmsd bond angles °	1.037	
Ramachandran plot (%)	98.3/1.7/0.0	
(favoured/allowed/disallowed)		

* the values in parenthesis are for the highest-resolution shell.