Table S1. Data collection and refinement statistics

	PDB code: 5WZZ
Data collection	
Space group	P 21
Cell dimensions	
a, b, c (Å)	41.5, 86.4, 117.4
α, β, γ (°)	90.00, 98.43, 90.00
Resolution (Å)	20–2.1 (2.14-2.20) *
Rsym or Rmerge	8.1 (58.9) *
I / σI	30.0 (1.8) *
$CC_{1/2}$	0.955 (0.869) *
Completeness (%)	99.6 (98.7) *
Redundancy	6.3 (5.2) *
Refinement	
Resolution (Å)	38 - 2.1
No. reflections	47,337
Rwork / Rfree	18.27, 20.75
No. atoms	
Protein	6235
Ion	8
Water	244
B-factors	
Protein	53.4
Ion	48.6
Water	50.4
R.m.s. deviations	
Bond lengths (Å)	0.010
Bond angles (°)	1.384

*Values in parentheses are for highest-resolution shell.