Table S1. Data collection and refinement statistics

Data collection	
Space group	$P222_1$
Cell dimensions *a*, *b*, *c* (Å)	70.39, 83.68, 190.15
Resolution (Å)	28.88 – 2.38 (2.40 – 2.38)
R_{merge} (%)	6.5 (76.1)
I/s*I*	27.3 (2.2)
Unique reflections	45,283 (1,094)
Completeness (%)	98.8 (100.0)
Redundancy	6.0 (6.0)
Wilson B-factor (Å^2)	59.4
Refinement	
Resolution (Å)	28.88 – 2.38 (2.44 – 2.38)
No. of reflections (work/free)	43,755/1,528 (3,186/105)
Cut-off (s)	0
R_{work} / R_{free}	22.8/26.5 (28.0/30.0)
No. of atoms	
Protein	5,094
Peptide	549
GDP	56
Ions	15
Water	97
B-factors (Å^2)	
Protein	60.7
Peptide	79.7
GDP	45.5
Ions	102.2
Water	51.4
R.m.s. deviations	
Bond lengths (Å)	0.009
Bond angles (°)	1.086
Ramachandran	
Favored (%)	98.0
Generally Allowed (%)	2.0
Disallowed (%)	0.0
Missing residues	A: 27-31, 348-354 B: 27-31, 349-354 C: 496 D: 530-531

Values in parentheses denote highest resolution shell