Table EV1: Crystallography data collection and refinement statistics

Data Collection	
Space group	P 2_1 2_1 2_1
Cell dimensions	
a, b, c (Å)	40.52 67.82 75.49
α, β, γ (°)	90 90 90
Resolution range (Å)	40.52 - 1.26
I / σ (I)	26.12 (1.62)
Completeness (%)	99.2 (95.6)
Refinement	
Refinement program	phenix.refine 1.19.2_4158
Resolution (Å)	31.59 - 1.26 (1.31 - 1.26)
R_{work} / R_{free}	0.19/0.225
Reflections used in refinement	56848 (5585)
Reflections used for R-free	2846 (280)
No. of molecules in ASU	1
Total no. of atoms	2072
Protein	1789
Peptide	65
Ligand	1
Water	217
Wilson B-factor (Å^2)	18.7
RMSD bond length (Å)	0.006
RMDS bond angle (°)	0.98
Ramachandran favored (%)	97.22
Ramachandran allowed (%)	2.78
Ramachandran outliers (%)	0.00

Values for the highest-resolution shell are given in parentheses.