Table S1. **Crystallographic statistics**

Data collection	
Space group	1,222
Cell dimensions *a*, *b*, *c* (Å)	51.17, 69.64, 120.65
Wavelength (Å)	1.5418
Resolution range (Å)	50.00 − 2.03 (2.10 − 2.03)
R_{merge}	0.044 (0.204)
I/σI	31.2 (5.61)
Completeness (%)	98.4 (96.1)
Redundancy	3.2 (3.1)
Refinement	
Resolution (Å)	60.3 − 2.03 (2.09 − 2.03)
No. reflections R_{work}	13,365 (965)
No. reflections R_{free}	710 (49)
R_{work}	0.19 (0.21)
R_{free}	0.24 (0.27)
No. atoms	
Protein	1,163
Peptide	193
Water/ions	136
Rms deviations	
Bond lengths (Å)	0.015
Bond angles (°)	1.181
Chiral	0.084

Numbers in parentheses represent statistics for highest resolution shell.