Supplementary Table 1 Data collection and refinement statistics (molecular replacement)

	Synchrotron		XFEL	
Data collection				
Space group	C 1 2 1		C 1 2 1	
Cell dimensions				
a, *b*, *c* (Å)	160.55, 86.12, 94.68		156.2, 89.3, 96.4	
α, β, γ (°)	90.0, 92.2, 90.0		90.0, 92.3, 90.0	
Resolution (Å)	40.0-3.30 (3.51-3.30)*		33.5-2.70 (2.80-2.70) *	
R_{merge} or R_{split}	0.173 (0.875) R_{merge}		0.118 (0.879) R_{split}	
$I / \sigma I$	11.7 (1.9)		6.0 (1.3)	
Completeness (%)	96.3 (97.3)		100 (100)	
Redundancy	4.3 (4.4)		560 (209)	
Refinement				
Resolution (Å)	37.97-3.28		33.45-2.70	
No. reflections	17,904		34,653	
R_{work} / R_{free}	0.239 / 0.273		0.212 / 0.230	
No. atoms	A	B	A	B
Protein	2,921	2,901	3,039	3,044
DIPP-NH_2	49	49	49	49
Na^+	0	0	1	1
Lipids and other	14	0	80	79
B-factors				
Protein	93.1	96.1	66.3	66.5
DIPP-NH_2	93.8	101.5	62.7	56.8
Na^+	N/A	N/A	66.2	66.1
Lipids and other	92.5	N/A	74.3	77.8
r.m.s. deviations				
Bond lengths (Å)	0.007		0.005	
Bond angles (°)	1.1		0.9	

Number of crystals used for Synchrotron structure – 21, for XFEL structure – 36,083.
*Values in parentheses are for highest-resolution shell.