

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		
<i>a</i> , <i>b</i> , <i>c</i> (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) *
<i>R</i> _{merge} or <i>R</i> _{split}	0.173 (0.875) <i>R</i> _{merge}	0.118 (0.879) <i>R</i> _{split}
<i>I</i> / σI	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
<i>R</i> _{work} / <i>R</i> _{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
<i>B</i> -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.