Supplementary information, Table S1 Data collection and refinement statistics.

	FabZ-ACP	apo-ACP	holo-ACP
Data collection			
Space group	P23	$P3_1$	$P3_1$
Cell dimensions			
a, b, c(Å)	127.705, 127.705, 127.705	49.596, 49.596, 72.949	50.3438, 50.3438, 73.2997
α, β, γ (°)	90.00,90.00,90.00	90.00, 90.00, 120.00	90.00, 90.00, 120.00
Wavelength (Å)	1	1	1.5418
Resolution (Å)*	31.9-2.55(2.64-2.55)	15-2.60(2.69-2.60)	43.6-2.50(2.59-2.50)
R_{merge} (%)	4.8(38.1)	11.5(61.3)	8.7 (27)
$I/\sigma I$	49.5(5.2)	8.5(1.4)	6.6 (2.3)
Completeness (%)	99.7(99.5)	99.4(98.3)	98.5(97.8)
Redundancy	10.0(8.9)	2.4(2.2)	3.0(2.0)
Refinement			
Resolution (Å)	15-2.55	15-2.6	15- 2.5
No.reflections	22941	6091	6736
R_{work}/R_{free}	0.194/0.231	0.241/0.286	0.218/0.252
No.atoms			
Protein	3070	1239	1782
Water	72	41	20
Ligand/ion	13	N/A	N/A
B-factors			
Protein	65.341	37.135	35.409
Water	53.596	27.707	30.601
Ligand/ion	80.625	N/A	N/A
R.m.s deviations			
Bond lengths (Å)	0.012	0.012	0.013
Bond angles (°)	1.4	1.3	1.4

*Highest-resolution shell is shown in parentheses.