Table S1. Data collection and structure refinement statistics

	PLDα1-PA	PLDα1-Apo	Se-Met
Resolution (Å)	34.7-2.30 (2.37-2.30)	37.7-1.80 (1.87-1.80)	38.7-2.00 (2.07-2.00)
Space group	P 2_1 2_1 2_1	C 1 2 1	P 2_1 2_1 2_1
Until cell			
a, *b*, *c*, (Å)	99.04,123.03 138.90	118.89 127.44 55.36	99.23 123.57 140.22
α, β, γ, (°)	90, 90, 90	90 95.472 90	90, 90, 90
Unique reflections	74,502 (6,209)†	75,085 (7,370)	117,128 (11,282)
Multiplicity	12.6	13.4	13.2
I/σ(I)	13.1 (2.3)	27.6 (1.4)	21.6 (1.4)
R_{merge}	0.219 (1.145)	0.096 (0.798)	0.125 (0.872)
Completeness (%)	99.8 (98.3)	99.5 (99.9)	100 (100)
R_{work}/R_{free}‡ (%)	19.70/24.99	16.64/19.23	
Number of atoms	6,298[A]/6,298[B]	6,199	
Ligand			
di8:0PA	28/28		
Ca^{2+}	2	1	
Water	500	595	
Protein residues	1572	771	
r.m.s. deviations			
bonds (Å)	0.010	0.007	
Angles (°)	1.12	0.89	
Average B factor	15.9	21.6	
Protein	15.9	20.8	
Ligand	15.8	13.5	
Water	15.1	30.3	
Ramachandran			
Favored (%)	93.3	95.9	
Allowed (%)	6.7	4.1	

† Numbers in parentheses represent the highest-resolution shell.

‡ $R = \Sigma hkl||Fo|-|Fc||/\Sigma hkl|Fo|$.

[A] Chain A; [B] Chain B.