Table S1 Data collection, phasing and refinement statistics.

	*Sc*Cdc13$_{OB1}$	*Sc*Cdc13$_{OB1}$	*Sc*Cdc13$_{OB1}$ - Pol1$_{CBM}$
Data collection	*Hg peak*	*Native*	*Native*
Space group	$P2_12_12$	$P2_12_12$	$P2_12_12_1$
Cell dimensions			
a, *b*, *c* (Å)	62.441, 69.024, 52.064	62.515, 68.641, 52.815	60.393, 85.090, 60.376
α, β, γ (º)	90, 90, 90	90, 90, 90	90, 90, 90
Wavelength (Å)	1.12721	0.97856	0.97872
Resolution (Å)	50-3.3	50-2.5	100-2.4
R_{merge}	0.085(0.263)*	0.063(0.313)*	0.074(0.393)*
$I/\sigma I$	27.3(6.0)*	41.8(3.6)*	42.7(2.9)*
Completeness (%)	93.2(72.0)*	96.4(76.8)*	97.3(83.1)*
Redundancy	8.7(7.1)*	6.6(4.7)*	6.9(3.9)*
Phasing			
Figure of Merit (anomalous)	0.24893(acen) 0.08433(cent)		
Phasing power (anomalous)	0.750		
Refinement			
Resolution (Å)		50-2.5	50-2.4
No. reflections		7498	9706
R_{work}/ R_{free}		0.211/0.267	0.224/0.264
No. atoms			
Protein		1608	1741
Water		35	34
Wilson B-factors (Å^2)		61.9	55.5
B-factors (Å^2)			
Protein		66.293	37.844
Water		61.067	43.306
R.m.s deviations			
Bond lengths (Å)		0.006074	0.004976
Bond angles (º)		1.23652	1.15154
B-factors (Å^2)		5.782	5.821

*The numbers in parentheses represent the highest resolution shell numbers.