Table S1. Statistics for crystallographic analyses – Related to Figure 2.

	Rtt109	Rtt109-Asf1-H3-H4	Rtt109-Asf1-H3-H4-CoA
Data collection			
Wavelength (Å)	0.9786	0.9788	0.9785
Space group	$P2_12_12_1$	$P6_522$	$P6_522$
Cell dimensions			
a, b, c (Å)	81.18, 92.02, 98.37	112.25, 112.25, 333.05	111.90, 111.90, 332.71
α, β, γ (º)	90, 90, 90	90, 90, 120	90, 90, 120
Resolution (Å)	50.00-2.50 (2.59-2.50)	50.00-3.60 (3.73-3.60)	50.00-3.50 (3.63-3.50)
R_{merge}	0.140 (0.726)	0.249 (0.831)	0.177 (0.527)
R_{pim}	0.057 (0.290)	0.058 (0.195)	0.080 (0.240)
I / σI	13.6 (2.7)	14.6 (4.7)	8.8 (2.5)
$CC_{1/2}$ for the highest resolution shell	0.800	0.938	0.777
Completeness (%)	100.0 (100.0)	99.9 (99.9)	99.5 (99.7)
Redundancy	6.9 (7.1)	18.9 (19.1)	5.2 (5.4)
Total/Unique reflections	179906/26067	289958/15314	84699/16416
Refinement			
Resolution (Å)	50.00-2.50 (2.60-2.50)	50.00-3.60 (3.83-3.60)	50.00-3.50 (3.72-3.50)
No. reflections	25943 (2744)	15148 (2440)	16286 (2634)
R_{work} / R_{free} (%)	16.6(23.3)/20.9(28.8)	21.4(29.3)/26.4(30.9)	24.3(30.4)/29.5(33.9)
No. atoms			
Protein	3178	5468	5449
Ligand/Ion	6	36	85
Waters	195		
B-factors ($Å^2$)			
Protein	41.0	56.6	65.8
Ligand/Ion	28.3	60.0	68.7
Waters	40.4		
R.m.s deviations			
Bond lengths (Å)	0.005	0.003	0.003
Bond angles (°)	0.846	0.612	0.496
Ramachandran plot			
Favored	97.2%	96.7%	96.3%
Allowed	2.8%	3.3%	3.7%
Outliers	0	0	0

* Numbers in parentheses indicate values in the highest resolution shell.