Supplementary Table S1. Summary of diffraction and refinement statistics of AbaSI crystals

PDB	4PAR	4PBA	4PBB	-	-
AbaSI	C3S	C3S	C3S	C3S/SeMet	C3S/SeMet
DNA	14 bp + 4 nt	32 bp	-	32 bp	32 bp
Data collection					
Space group	$P2_1$	$P2_1$	$P2_12_12_1$	$P2_1$	$P2_1$
Cell dimensions	$\alpha=\gamma=90°$,	$\alpha=\gamma=90°$, $\beta=94°$	$\beta=94.6°\alpha=\beta=\gamma=90°$	$\alpha=\gamma=90°$, $\beta=94°$	$\alpha=\gamma=90°$, $\beta=94°$
a, b, c (Å)=	54.8, 144.7, 105.0	55, 147, 104	67, 92, 181	55, 146, 103	55, 146, 104
Beamline (SERCAT)	APS 22-ID	APS 22-ID	APS 22-ID	APS 22-ID	APS 22-ID
Wavelength (Å)	1.00000	0.97919	1.00000	0.97945	0.97945
Resolution (Å)*	34.90-2.89 (2.99-2.89)	35.09-3.29 (3.41-3.29)	32.21-3.45 (3.61-3.45)	39.30-3.59 (3.72-3.59)	35.02-4.27 (4.44-4.27)
[a] R_{merge}*	0.089 (0.789)	0.211 (0.777)	0.116 (0.820)	0.254 (0.950)	0.211(0.624)
[b] $\langle I/\sigma I\rangle$ *	13.4 (1.4)	6.4 (2.0)	9.8 (2.0)	12.7 (3.3)	21.8 (7.7)
Completeness (%)*	98.6 (89.3)	99.9 (99.8)	99.9 (100.0)	99.8 (99.6)	100.0 (100.0)
Redundancy*	3.7 (3.2)	4.7 (4.0)	4.8 (5.0)	17.1 (16.3)	39.6 (38.8)
Observed reflections	134,083	113,556	73,539	317,558	450,551
Unique reflections*	35,953 (3209)	24,388 (2450)	15,301 (1495)	18,543 (1828) (17,741 have both I^+ and I^-)	11,381(1113) (10,774 have both I^+ and I^-)
Mean FOM (SAD):				0.34	0.45
Density Modification, R-factor				0.278	0.328
Refinement					
Resolution (Å)	2.89	3.29	3.45		
No. reflections	35,850	24,348	15,029		
[c] R_{work} / [d] R_{free}	0.194/0.251	0.249/0.288	0.254/0.297		
No. Atoms	11,694	10,742	5,214		
Protein	10,386	9,478	5,194		
DNA	1,304	1,264	-		
B Factors (Å^2)					
Protein	95.6	93	111		
DNA	104.2	129	-		
R.m.s. deviations					
Bond lengths (Å)	0.003	0.003	0.003		
Bond angles (°)	0.64	0.77	0.97		

* Values in parenthesis correspond to highest resolution shell.

[a] $R_{merge} = \Sigma \mid I - \langle I\rangle \mid / \Sigma I$, where I is the observed intensity and $\langle I\rangle$ is the averaged intensity from multiple observations.

[b] $\langle I/\sigma I\rangle$ = averaged ratio of the intensity (I) to the error of the intensity (σI).

[c] $R_{work} = \Sigma \mid F_{obs} - F_{cal} \mid / \Sigma \mid F_{obs} \mid$, where F_{obs} and F_{cal} are the observed and calculated structure factors, respectively.

[d] R_{free} was calculated using a randomly chosen subset (5%) of the reflections not used in refinement.