Supplementary Table 1. Structure refinement statistics

Structure	**5z2t** (original)	**6dfy** (remodeled)
Resolution range (Å)	83.3 - 2.62	83.3 - 2.62
Space group	$P4_12_12$	$P4_12_12$
Unit cell dimension (Å)		
a	51.6	51.6
b	51.6	51.6
c	166.6	166.6
R-factor (%)	27.6	24.6
R-factor (high resolution shell)[b]	43.7	42.6
R_{free} (%)[c]	29.9	27.9
R_{free} (high resolution shell)[b]	52.3	47.0
Total number of non-hydrogen atoms	1412	1420
Protein atoms	868	857
DNA atoms	533	551
Water molecules	11	12
R.m.s.d. from ideal geometry		
Bond length (Å)	0.006	0.006
Bond angle (º)	0.99	0.97
Wilson *B*-factor (Å^2)	72.9	72.9
Average *B*-factor macromolecule atoms (Å^2)	77.2	93.3
Ramachandran statistics (%)		
Most favored region	95.2	99.0
Allowed regions	4.8	1.0
Outlier regions	0	0

[b] Highest resolution shell: 2.717 - 2.622 Å

[c] Calculated for the test-set reflections as defined in the original work[1]