

**Table S1. Summary of Diffraction Data and Structure Refinement Statistics Related to Figure 1-6**

<b>Crystals</b>	<b>Binary</b>	<b>Ternary DNA1<sup>a</sup></b>	<b>Ternary DNA2<sup>b</sup></b>	<b>Ternary DNA3<sup>c</sup></b>
Beam line	APS-ID24E	APS-ID24E	APS-ID24C	APS-ID24C
Wavelength (Å)	0.9794	0.9792	0.9792	0.9792
Space group	P2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub>	I222	I222	I222
Cell parameters				
<i>a</i> (Å)	83.47	117.25	116.75	113.51
<i>b</i> (Å)	128.20	182.15	184.81	179.29
<i>c</i> (Å)	155.79	216.79	214.29	217.35
Resolution (Å)	50.0-3.25 (3.48-3.25) <sup>d</sup>	50.0-2.89 (2.98-2.89)	50.0-2.92 (3.02-2.92)	50.0-3.75 (4.05-3.75)
R <sub>pim</sub>	0.063 (0.823)	0.074 (0.711)	0.062 (0.859)	0.136 (1.633)
Average I/σ(I)	10.2 (1.0)	11.7 (1.2)	10.1 (0.8)	5.2 (0.6)
Completeness (%)	99.2 (95.6)	100.0 (100.0)	99.8 (100.0)	99.8 (99.7)
CC(1/2)	0.990 (0.318)	0.996 (0.480)	0.998 (0.368)	0.995 (0.399)
Average redundancy	5.9 (5.7)	14.3 (11.8)	5.5 (5.6)	5.9 (5.7)
No. of unique reflections	26,144	52,222	50,264	22,006
<b>Refinement and structure model</b>				
R <sub>work</sub> /R <sub>free</sub> (%)	26.1/32.4	19.4/24.2	19.9/24.4	24.2/28.4
No. of non-H atoms	9340	11854	11846	11817
Average B factor (Å <sup>2</sup> )				
Protein	104	55	85	159
DNA	-	63	68	166
RNA	156	73	106	188
RMS deviations				
Bond lengths (Å)	0.689	0.614	0.666	0.723
Bond angles (°)	0.004	0.002	0.003	0.004
<b>Ramachandran plot (%)</b>				
Favored	90.6	94.4	92.7	92.5
Allowed	9.4	5.6	7.3	7.5
Outliers	0	0	0	0

<sup>a</sup> Aac2c1 in complex with 8-mer excess ssDNA.

<sup>b</sup> Aac2c1 in complex with extended target DNA strand.

<sup>c</sup> Aac2c1 in complex with extended non-target DNA strand.

<sup>d</sup> Highest resolution shell (in Å) shown in parentheses.