Supplementary Table 1. Data collection and refinement statistics

	Mre11-DNA1[1]	Mre11-DNA2[1]
Data collection		
Wavelength (Å)	0.9795	0.9795
Space group	$P2_1$	$P2_1$
Cell dimensions a,b,c (Å)	91.5 185.6 106.2	90.5 184.0 106.6
α, β, γ (°)	90 99.9 90	90 99.5 90
Resolution[2] (Å)	50-3.55 (3.6-3.55)	50-3.52 (3.58-3.52)
Measured reflections	318,323	194,226
Unique reflections	41,919	42,468
Completeness (%)	100 (100)	98.8 (98.8)
Average (I/σ)	13.3 (2.3)	13 (2.5)
R_{sym}[3]	0.166 (0.971)	0.200 (0.950)
Resolution (Å) ($R_{sym} < 0.5$)[4]	3.82	3.83
Refinement		
Resolution range (Å)	42.42-3.55	47.29-3.59
No. reflections	39,539	39,755
$R_{working}$ (%)/R_{free} (%)[5]	18.4/23.6	19.4/25.3
No. atoms (B-factors (Å^2))		
Total	16104 (144.4)	16013 (181.9)
Protein	15480 (143)	15480 (179.5)
DNA/Mg^{2+}	592/ 12 (189.3/ 70.8)	533/ - (256.9/ -)
water	20 (66.8)	-
R.m.s. bond lengths (Å)	0.009	0.005
R.m.s. bond angles (°)	1.2	1.1
Ramachandran plot[6]		
Favored (%)	94.9	93.2
Allowed (%)	4.5	6.3
Disallowed (%)	0.6	0.5

[1] Mg^{2+} ions are added in the crystallization buffer for the Mre11-DNA1 and –DNA2 complexes. However, we observed the clear Mg^{2+} ion density only in the Mre11-DNA1 structure.

[2] Values in parentheses are for the highest shell.

[3] $R_{sym}=\Sigma_h\Sigma_i|I_{h,i}-I_h|/\Sigma_h\Sigma_i I_{h,i}$, where I_h is the mean intensity of the i observations of symmetry related reflections of h. [4]

[4] Resolution where the R_{sym} values are lower than 0.5

[5] $R=\Box|F_{obs}-F_{calc}|/\Box F_{obs}$, where $F_{obs} = F_{pi}$ and F_{calc} is the calculated protein structure factor from the atomic model (R_{free} was calculated with 5% of the reflections). R.m.s. deviation in bond lengths and angles are the deviations from ideal values.

[6] Ramachandran plot is calculated by Molprobity (Chen et al, 2010).