Supplementary Table S1 Data collection and refinement statistics (**Molecular replacement**)

	$tmRad50^{NBD}$-$Mre11^{HLH}$
Data collection	
Space group	P1
Cell dimensions	
a, *b*, *c* (Å)	50.2, 107.6, 97.1
α, β, γ (°)	90.6, 98.3, 89.4
Resolution (Å)	50.2-2.7
R_{sym} or R_{merge}	13.5 (68.6)*
$I/\sigma I$	9.3(1.9)
Completeness (%)	93.8(80.5)
Redundancy	3.4(3.1)
Refinement	
Resolution (Å)	47.7-2.7
No. reflections	51439
$R_{work/}$ R_{free}	21.5/27.0
No. atoms	14169
Protein	12556
DNA/AMPPNP/Mg^{2+}	1218/124/4
Water	267
B-factors	**43.4 (overall)**
Protein	35.1
DNA/AMPPNP/Mg^{2+}	146.1/19.3/14.9
Water	30.8
R.m.s deviations	
Bond lengths (Å)	0.010
Bond angles (°)	1.3

*Highest resolution shells (2.8- 2.7 Å) are shown in parenthesis.

Ramachandran statistics
outliers (%): 0.5
allowed (%): 5.0
favoured (%): 94.5