SUPPLEMENTARY DATA

Table S1. **Data collection and refinement statistics**

	PNK-FHA	PNK-FHA / XRCC1
PDB accession code	2BRF	2W3O
Data collection		
Space group	$P2_1$	P3
Cell dimensions		
a, *b*, *c* (Å)	31.81, 40.05, 37.51	56.90, 56.90, 62.77
α, β, γ (°)	90, 90.96, 90	90, 90, 120
Resolution (Å)	37.50- 1.40 (1.44-1.40)*	38.75-1.85 (1.95-1.85)
R_{merge}	0.050 (0.16)	0.069 (0.299)
Mn $I/\sigma I$	18.4 (6.3)	13.3 (2.3)
Completeness (%)	97.2 (88.0)	99.0 (95.3)
Redundancy	3.4 (2.4)	3.4 (2.1)
Refinement		
Resolution (Å)	37.5 – 1.40	37.85-1.85
No. unique reflections	15643	19211
R_{work}/ $_{Rfree}$	0.15 / 0.18	0.18 / 0.24
No. atoms		
Protein	775	1508
Peptide		148
Ion	10	6
Water	144	286
B-factors		
Protein	9.5	25.7
Peptide	n/a	29.7
Ion	19.4	54.7
Water	9.5	36.9
R.m.s deviations		
Bond lengths (Å)	0.009	0.018
Bond angles (°)	1.320	1.715

* Highest resolution shell is shown in parenthesis