

PARP1 condensates differentially partition DNA repair proteins and enhance DNA ligation

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Appendix Table S1. Phase separation predictions for proteins investigated in this study using PScore, CatGRANULE, and PLAAC prediction algorithms. PScore (Vernon *et al*, 2018) uses pi-pi interactions, PLAAC (Lancaster *et al*, 2014) uses prion-like domain features, and catGRANULE (Bolognesi *et al*, 2016) uses similarities to sequence features found in RNA granule components. Values reflect percentiles of scores within the human proteome, with 100 percent indicating the highest likelihood for phase separation (Vernon & Forman-Kay, 2019).

Name	UniProt ID	PScore	CatGRANULE	PLAAC
PARP1	P09874_HUMAN	62.36	96.31	54.59
XRCC1	P18887_HUMAN	65.47	86.39	73.13
LigIII	P49916_HUMAN	66.35	86.10	58.98
Polβ	P06746_HUMAN	18.36	82.30	9.743

Appendix Table S2. Sequences of oligonucleotides used in this study.

Nicked dumbbell DNA	5'-P-GCTGGCTTCGTAAGAAGCCAGCTCGCGGTCAGC TTGCTGACCGCG-3'	
Cy5-triplex	5'-GCTTAGCTTGGAATCGTATCATGTACACTCGTGT GCCGTGTAGACCGTGCC-3' 5'-P-TGTACATGATACGATTCCAAGCTAAGC-3' 5'-Cy5-GGCACGGTCTACACGGCACACGAG-3'	
20 nt DNA	5'-ATCTTGCTGATGGTCTAGGC-3'	
40 nt DNA	5'-ACCGCCAAGTCGGTTTCGACTCATACCGCAGCC CTCTATA-3'	
60 nt DNA	5'-GATGGTGGGGTCCGTTGATGTCAAGCATAGTCG AAAAAGGGTGCGGGACGACAACCCATG-3'	
20 nt DNA RC	5'-GCCTAGACCATCAGCAAGAT-3'	
40 nt DNA RC	5'-TATAGAGGGCTGCGGTATGAGTCGAAACCGACT TGGCGGT-3'	
60 nt DNA RC	5'-CATGGGTTGTTCGTCCCGCACCCCTTTTTCGACTAT GCTTGACATCAACGGACCCCACCATC-3'	
Lab07	5'-P-AGGTCCCGCCC-BioTEG-3'	
Lab06	5'-Phos/GGGCGGCGACCT-BioTEG-3'	
Oligo1	5'-ACGAAGTCTTATGGCAAAACCGATGGACTATGT TTCGGGTAGCACCAGAAGTCTATAACA-3'	
Oligo2	5'-TGTTATAGACTTCTGGTGCTACCCGAAACATAGT CCATCGGTTTTGCCATAAGACTTCGT-ATTO647N-3'	