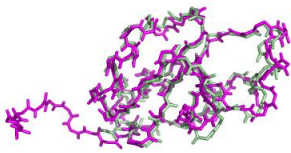


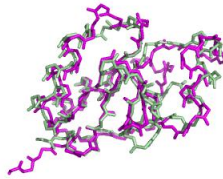
Figure S1. Comparison of the yeast Rev1 BRCT domain to other BRCT domains. The structure of the yeast Rev1 BRCT domain (green) is shown aligned with twelve other single-copy BRCT domains (purple). These other BRCT domains include the human Rev1 BRCT domain (unpublished structure), the topoisomerase II β binding protein 1 (TopBP1) BRCT domain (1), the human X-ray repair cross-complementing protein 1 (XRCC1) BRCT domain (unpublished structure), the human microcephalin (MCPH1) BRCT domain (2), the poly [ADP-ribose] polymerase 1 (PARP-1) BRCT domain (3), the human DNA ligase IV BRCT domain (unpublished structure), the replication factor C subunit 1 (RFC1) BRCT domain (unpublished structure), the yeast Dbf4 BRCT domain (unpublished structure), the human DNA polymerase μ (Pol μ) BRCT domain (4), human DNA polymerase λ (Pol λ) BRCT domain (unpublished structure), the human terminal deoxynucleotidyltransferase (TdT) BRCT domain (unpublished structure), and the yeast Rap1 BRCT domain (5). The PDB ID codes, the percent sequence identity, the RMSD, and the number of C α atoms used in the RMSD calculation are provided for each structural alignment.

References

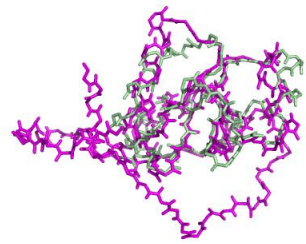
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2. Richards MW, Leung JWC, Roe SM, Li K, Chen J, Bayliss R. A Pocket on the Surface of the N-Terminal BRCT Domain of Mchp1 Is Required to Prevent Abnormal Chromosome Condensation. *Journal of Molecular Biology*. 2010;395(5):908-15.
3. Loeffler PA, Cuneo MJ, Mueller GA, DeRose EF, Gabel SA, London RE. Structural studies of the PARP-1 BRCT domain. *Bmc Structural Biology*. 2011;11.
4. DeRose EF, Clarkson MW, Gilmore SA, Galban CJ, Tripathy A, Havener JM, et al. Solution structure of polymerase mu's BRCT domain reveals an element essential for its role in nonhomologous end joining. *Biochemistry*. 2007;46(43):12100-10.
5. Zhang W, Zhang J, Zhang X, Xu C, Tu X. Solution structure of Rap1 BRCT domain from *Saccharomyces cerevisiae* reveals a novel fold. *Biochemical and Biophysical Research Communications*. 2011;404(4):1055-9.



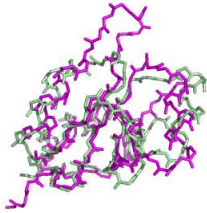
Human Rev1 BRCT domain
 PDB ID: 2EBW
 Sequence identity: 44 %
 RMSD: 1.0 Å
 C α atoms aligned: 86



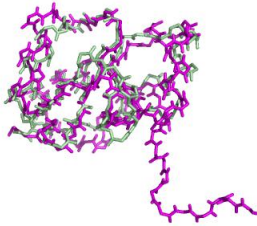
TopBP1 BRCT domain
 PDB ID: 3JVE
 Sequence identity: 21 %
 RMSD: 1.6 Å
 C α atoms aligned: 82



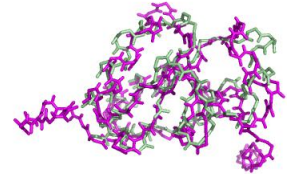
XRCC1 BRCT domain
 PDB ID: 2D8M
 Sequence identity: 23 %
 RMSD: 1.7 Å
 C α atoms aligned: 82



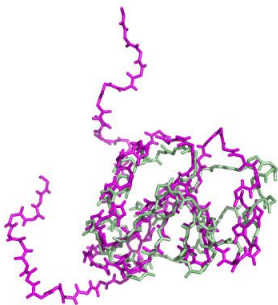
MCPH1 BRCT domain
 PDB ID: 2WT8
 Sequence identity: 17 %
 RMSD: 1.9 Å
 C α atoms aligned: 81



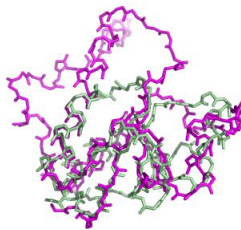
PARP-1 BRCT domain
 PDB ID: 2LEO
 Sequence identity: 25 %
 RMSD: 2.1 Å
 C α atoms aligned: 84



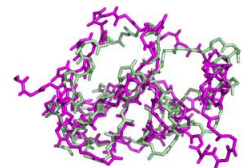
DNA Ligase IV BRCT domain
 PDB ID: 2E2W
 Sequence identity: 19 %
 RMSD: 2.2 Å
 C α atoms aligned: 84



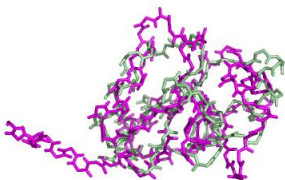
RFC1 BRCT domain
 PDB ID: 2EBU
 Sequence identity: 17 %
 RMSD: 2.6 Å
 C α atoms aligned: 75



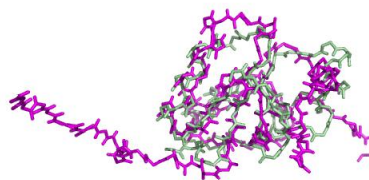
DBF4 BRCT domain
 PDB ID: 3OQ4
 Sequence identity: 16 %
 RMSD: 2.7 Å
 C α atoms aligned: 73



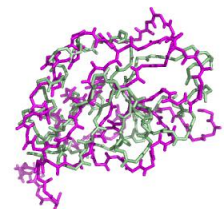
Pol μ BRCT domain
 PDB ID: 2HTF
 Sequence identity: 18 %
 RMSD: 2.7 Å
 C α atoms aligned: 82



Pol λ BRCT domain
 PDB ID: 2JW5
 Sequence identity: 22 %
 RMSD: 2.8 Å
 C α atoms aligned: 82



Td BRCT domain
 PDB ID: 2COE
 Sequence identity: 21 %
 RMSD: 2.9 Å
 C α atoms aligned: 84



Rap1 BRCT domain
 PDB ID: 2L42
 Sequence identity: 24 %
 RMSD: 3.0 Å
 C α atoms aligned: 59

Table S1. UV survival of yeast strains ^a

UV Dose (J/M ²)	0	50	100	150	200
Wild-type	100	91 ± 6	66 ± 9	44 ± 3	25 ± 1
Vector	100	56 ± 5	37 ± 3	15 ± 1	8 ± 1
N174A	100	88 ± 8	58 ± 7	43 ± 4	17 ± 3
R181A	100	78 ± 1	46 ± 2	35 ± 6	18 ± 2
K217A	100	84 ± 8	50 ± 5	37 ± 6	9 ± 1
R181A,K217A	100	87 ± 12	56 ± 17	34 ± 9	22 ± 6
L182A	100	79 ± 9	50 ± 10	30 ± 6	12 ± 4
E186A	100	77 ± 7	45 ± 14	27 ± 4	14 ± 4
L190A	100	73 ± 2	52 ± 8	23 ± 4	17 ± 2
K194A	100	83 ± 8	45 ± 7	23 ± 4	11 ± 4
F195A	100	85 ± 5	47 ± 5	32 ± 6	14 ± 7
G193V	100	42 ± 1	33 ± 7	20 ± 1	4 ± 2
G193D	100	43 ± 2	26 ± 3	15 ± 3	4 ± 1
G193R	100	51 ± 6	36 ± 9	22 ± 5	10 ± 4
W231A	100	49 ± 8	91 ± 5	27 ± 1	17 ± 4

^a Data are the average of at least 4 independent data sets, standard deviations are reported.

Table S2. UV mutagenesis of yeast strains ^a

UV Dose (J/M ²)	0	50	100	150	200
Wild-type	-	1000 ± 400	2200 ± 1000	2600 ± 800	4100 ± 700
Vector	-	26 ± 20	78 ± 8	150 ± 100	320 ± 100
N174A	-	1100 ± 600	1900 ± 800	2200 ± 1000	4400 ± 2000
R181A	-	1200 ± 500	2400 ± 1000	3800 ± 1500	2900 ± 1800
K217A	-	1000 ± 600	2000 ± 700	3100 ± 1500	2900 ± 1800
R181A,K217A	-	1200 ± 700	2000 ± 600	2500 ± 500	4100 ± 200
L182A	-	1200 ± 400	3000 ± 800	3900 ± 400	3700 ± 500
E186A	-	1300 ± 400	3000 ± 800	3500 ± 100	2800 ± 1000
L190A	-	1200 ± 600	2100 ± 1000	3200 ± 1700	4500 ± 1500
K194A	-	1100 ± 200	2900 ± 700	3800 ± 100	4500 ± 1000
F195A	-	1200 ± 700	1900 ± 800	2600 ± 700	2800 ± 1500
G193V	-	200 ± 120	300 ± 120	520 ± 230	950 ± 800
G193D	-	140 ± 110	190 ± 90	320 ± 210	720 ± 500
G193R	-	160 ± 70	280 ± 80	590 ± 220	940 ± 270
W231A	-	180 ± 40	360 ± 90	520 ± 170	1200 ± 700

^a Data are the average of at least 4 independent data sets, standard deviations are reported.