Table S1. Putative taperin interaction partners. List of the top hits in the nuclear ECFP-taperin quantitative interactome screen, including the specific peptides identified for each and their respective heavy: light amino acid ratios. These ratios indicate the degree of enrichment above the background contamination due to non-specific binding of proteins to the affinity matrix (observed as a peptide ratio of 1:1 due to equal binding in the control and taperin IP). The asterisks (*) indicate where specific PP1 isoform peptides were identified (the remaining PP1 peptides are common to all 3 mammalian isoforms).

IPI number	Gene Name	Description	H:L Ratio	log H:L ratio	Peptide
IPI00479897.1	C9orf75; TPRN	Taperin	285.44	8.16	ATFVSSVRPESSR
IPI00479897.1	C9orf75; TPRN	Taperin	92.19	6.53	QSVELPK
IPI00479897.1	C9orf75; TPRN	Taperin	52.38	5.71	HSVAFSK
IPI00479897.1	C9orf75; TPRN	Taperin	18.58	4.22	ASGAPPPEGR
IPI00479897.1	C9orf75; TPRN	Taperin	18.15	4.18	WQEQALEQAPR
IPI00479897.1	C9orf75; TPRN	Taperin	16.08	4.01	ALASLR
IPI00479897.1	C9orf75; TPRN	Taperin	14.61	3.87	SPLEVEAQWAVEEGACPR
IPI00479897.1	C9orf75; TPRN	Taperin	12.66	3.66	TATALADR
IPI00479897.1	C9orf75; TPRN	Taperin	10.97	3.46	EAEPPPVEAMLTPASQNDLSDFR
IPI00413611.1	TOP1	DNA topoisomerase I	2.82	1.50	VEHINLHPELDGQEYVVEFDFLGK
IPI00413611.1	TOP1	DNA topoisomerase I	2.28	1.19	SGDHLHNDSQIEADFR
IPI00413611.1	TOP1	DNA topoisomerase I	2.22	1.15	AVALYFIDK
IPI00413611.1	TOP1	DNA topoisomerase I	1.82	0.86	AEEVATFFAK
IPI00178667.3	TOP2A	DNA topoisomerase II alpha	1.52	0.60	YDTVLDILR
IPI00178667.3	TOP2A	DNA topoisomerase II alpha	1.30	0.38	TLAVSGLGVVGR
IPI00449049.4	PARP1	Poly [ADP-ribose] polymerase 1	1.76	0.81	HPDVEVDGFSELR
IPI00449049.4	PARP1	Poly [ADP-ribose] polymerase 1	1.47	0.56	TTNFAGILSQGLR
IPI00449049.4	PARP1	Poly [ADP-ribose] polymerase 1	1.44	0.53	VFSATLGLVDIVK
IPI00449049.4	PARP1	Poly [ADP-ribose] polymerase 1	1.39	0.48	AEPVEVVAPR
IPI00449049.4	PARP1	Poly [ADP-ribose] polymerase 1	1.37	0.45	SLQELFLAHILSPWGAEVK
IPI00449049.4	PARP1	Poly [ADP-ribose] polymerase 1	1.37	0.45	TLGDFAAEYAK
IPI00449049.4	PARP1	Poly [ADP-ribose] polymerase 1	1.32	0.40	NTHATTHNAYDLEVIDIFK
IPI00449049.4	PARP1	Poly [ADP-ribose] polymerase 1	1.31	0.39	LQLLEDDKENR
IPI00449049.4	PARP1	Poly [ADP-ribose] polymerase 1	1.20	0.26	VVSEDFLQDVSASTK
IPI00449049.4	PARP1	Poly [ADP-ribose] polymerase 1	1.14	0.19	VGTVIGSNK
IPI00449049.4	PARP1	Poly [ADP-ribose] polymerase 1	1.01	0.01	VGTVIGSNK
IPI00220834.7	XRCC5	Ku80; ATP-dependent DNA helicase II 80 kDa subunit	1.59	0.67	LTIGSNLSIR
IPI00220834.7	XRCC5	Ku80; ATP-dependent DNA helicase II 80 kDa subunit	1.44	0.53	VITMFVQR
IPI00220834.7	XRCC5	Ku80; ATP-dependent DNA helicase II 80 kDa subunit	1.39	0.48	EDIIQGFR
IPI00220834.7	XRCC5	Ku80; ATP-dependent DNA helicase II 80 kDa subunit	1.37	0.45	DDEAAAVALSSLIHALDDLDMVAIVR
IPI00220834.7	XRCC5	Ku80; ATP-dependent DNA helicase II 80 kDa subunit	1.19	0.25	QLNHFWEIVVQDGITLITK
IPI00220834.7	XRCC5	Ku80; ATP-dependent DNA helicase II 80 kDa subunit	1.15	0.20	TDTLEDLFPTTK
IPI00220834.7	XRCC5	Ku80; ATP-dependent DNA helicase II 80 kDa subunit	1.10	0.14	YAPTEAQLNAVDALIDSMSLAK

Table S1. (*Continued*)

IPI number	Gene Name	Description	H:L Ratio	log H:L ratio	Peptide
IPI00220834.7	XRCC5	Ku80; ATP-dependent DNA helicase II 80 kDa subunit	1.03	0.04	FNNFLK
IPI00465430.4	XRCC6	Ku70; ATP-dependent DNA helicase II 70 kDa subunit	1.44	0.53	EVAALCR
IPI00465430.4	XRCC6	Ku70; ATP-dependent DNA helicase II 70 kDa subunit	1.40	0.49	LGSLVDEFK
IPI00465430.4	XRCC6	Ku70; ATP-dependent DNA helicase II 70 kDa subunit	1.37	0.45	LEDLLR
IPI00465430.4	XRCC6	Ku70; ATP-dependent DNA helicase II 70 kDa subunit	1.32	0.40	DLLAVVFYGTEK
IPI00465430.4	XRCC6	Ku70; ATP-dependent DNA helicase II 70 kDa subunit	1.31	0.39	DSLIFLVDASK
IPI00465430.4	XRCC6	Ku70; ATP-dependent DNA helicase II 70 kDa subunit	1.17	0.23	TFNTSTGGLLLPSDTKR
IPI00465430.4	XRCC6	Ku70; ATP-dependent DNA helicase II 70 kDa subunit	1.05	0.07	NIYVLQELDNPGAK
IPI00465430.4	XRCC6	Ku70; ATP-dependent DNA helicase II 70 kDa subunit	1.05	0.07	ILELDQFK
IPI00465430.4	XRCC6	Ku70; ATP-dependent DNA helicase II 70 kDa subunit	1.01	0.01	FDDPGLMLMGFKPLVLLK
IPI00005705.1	PPP1CC*	Protein phosphatase 1C catalytic subunit, gamma isoform	1.21	0.28	NVQLQENEIR
IPI00550451.1	PPP1C	Protein phosphatase 1C catalytic subunit	1.16	0.21	IFCCHGGLSPDLQSMEQIR
IPI00550451.1	PPP1CC*	Protein phosphatase 1C catalytic subunit, gamma isoform	1.12	0.16	NVQLTENEIR
IPI00550451.1	PPP1C	Protein phosphatase 1C catalytic subunit	1.05	0.07	AHQVVEDGYEFFAK
IPI00550451.1	PPP1CA*	Protein phosphatase 1C catalytic subunit, alpha isoform	1.02	0.03	LNLDSIIGR
IPI00550451.1	PPP1C	Protein phosphatase 1C catalytic subunit	1.02	0.03	ICGDIHGQYYDLLR