

Supplementary Table S1

LOG ₂ (ratio) ¹⁷⁷ Lu-PP-F11N /CON	P-VALUE	SYMBOL; NAME UniProt	SEQUENCE WINDOW POSITION (PROBABILITY>0.5)
7.85	0.02107	HNRPU; Heterogeneous nuclear ribonucleoprotein U Q00839	SSS(1)PVNVK
7.17	9.71E-05	SRRM2; Serine/arginine repetitive matrix protein 2 Q9UQ35	RVPS(0.95)PTPAPK
6.77	3.79E-06	RSL1D1; Ribosomal L1 domain-containing protein 1 O76021	EKS(1)PSLGKK
6.28	0.00043	DPM1; Dolichol-phosphate mannosyltransferase subunit 1 O60762	ASLEVS(0.74)RSPPR
4.88	0.00062	DNTTIP2; Deoxynucleotidyltransferase terminal-interacting protein 2 Q5QJE6	WNNNKS(1)PIK
4.21	0.00037	TGS1; Trimethylguanosine synthase Q96RS0	DRPHASGT(0.98)DGDES(0.99)EEDPPEHKPSK
4.16	0.00127	SH2D5; SH2 domain-containing protein 5 Q6ZV89	LGNPYCS(0.94)PTLVRK
4.11	0.00054	RPP30; Ribonuclease P protein subunit p30 P78346	KPRP5(1)EGDEDCLPASK
4.04	0.00174	RAB11FIP1; Rab11 family-interacting protein 1 Q6WKZ4	TAS(0.99)TDLCK
3.83	0.00111	TGS1; Trimethylguanosine synthase Q96RS0	DRPHASGT(0.91)DGDES(1)EEDPPEHKPSK
3.72	0.00041	WDR33; pre-mRNA 3' end processing protein WDR33 Q9C0J8	DTPRPDHPHDGHS(0.98)PASR
3.70	0.00024	EIF4ENIF1; Eukaryotic translation initiation factor 4E transporter B1AKL4	SS(0.82)PVESLKK
3.66	0.00411	ARHGEF1; Rho guanine nucleotide exchange factor 1 Q92888	QLLFPAEEDNGAGPPRDGDGVPGGGLS(1)PAR
3.42	0.00036	DENND4C; t DENN domain-containing protein 4C R4GN35	RSS(0.77)LPDGHSPAQENPESEK
3.41	0.01414	FIP1L1; Pre-mRNA 3'-end-processing factor FIP1 Q6UN15	ERDHS(0.99)PTSPVFN5(0.98)DEERYR
3.40	9.73E-05	TJP2; Tight junction protein ZO-2 Q9UDY2	SFS(1)PEER
3.40	0.00142	TRA2A; Transformer-2 protein homolog alpha Q13595	S(1)RS(1)HS(1)PMSNR
3.37	0.00098	TRA2A; Transformer-2 protein homolog alpha Q13595	S(1)RS(1)HS(0.99)PMSNR
3.21	0.00832	WARS; Tryptophan-tRNA ligase, cytoplasmic P23381	KLS(1)FDFQ
3.20	0.00146	TRA2A; Transformer-2 protein homolog alpha Q13595	S(1)RS(1)HS(0.99)PMSNR
3.12	0.00101	USP10; Ubiquitin carboxyl-terminal hydrolase 10 Q14694	LLS(0.99)PSNEK
3.11	5.25E-05	TP53; Cellular tumor antigen p53sp P04637	LMFKTEGPD5(1)D
3.10	0.00066	ITGB4; Integrin beta-4 P16144	DYNS(0.59)LT(0.59)RS(0.59)EHSHTTLPR
2.98	0.00540	RPL19; Ribosomal protein L19 J3QR09	TLS(1)KEEETKK
2.95	0.00106	FAM83B; Protein FAM83B Q5T0W9	S(1)FPLFDNSK
2.91	0.00423	ANLN; Actin-binding protein anillin Q9NQW6	TQS(1)LPVTEK
2.68	9.87E-05	ZFP36; Tristetraprolin P26651	STS(0.99)LVEGR
2.37	0.01377	FOS; Proto-oncogene c-Fos P01100	GKVEQLS(1)PEEEEK
2.37	0.00047	PAK2; Serine/threonine-protein kinase PAK 2 Q13177	YLS(1)FT(1)PPEK
2.27	0.01769	ARHGEF2; Rho guanine nucleotide exchange factor Q92974	SES(1)LESPRGER
2.22	0.00539	EGFR; Epidermal growth factor receptor P00533	MHLPS(1)PTDSNFYR
2.09	0.00689	SLC20A2; Sodium-dependent phosphate transporter 2 Q08357	VQEAES(1)PVFK
2.09	0.00354	CCNL2; Cyclin-L2 Q96594	GSKP5(0.99)PLSVK
2.06	0.00080	CCDC82; Coiled-coil domain-containing protein 82 F5H777	HLS(1)QEDNDLNK
2.01	0.00049	CTTNBP2NL; CTTNBP2 N-terminal-like protein Q9P2B4	VSSPLSPLS(1)PGIK
1.96	0.00209	SH3BP4; SH3 domain-binding protein 4 Q9P0V3	DNPFRRS(1)K
1.88	0.01072	ZYX; Zyxin Q15942	S(1)PGAGPLTLK
1.86	0.00209	IRF6; Interferon regulatory factor 6 O14896	LQIS(0.83)TPDIKDNIQAQLK
1.77	0.01594	EGFR; Epidermal growth factor receptor P00533	MHLPS(0.96)PTDS(0.99)NFYR
1.66	0.01298	AHCTF1; Protein ELYS Q8WYP5	STPLASPS5(0.81)PGRS(0.91)PQR
1.66	0.00650	PFKP; ATP-dependent 6-phosphofructokinase, platelet type Q01813	S(1)FAGNLNTYK
1.52	0.00050	SH2D4A; SH2 domain-containing protein 4A Q9H788	TLS(0.99)SSAQEDIIR
1.51	0.00818	PPP1R12A; Protein phosphatase 1 regulatory subunit 12A O14974	TGS(0.99)YGALAEITASK
1.44	0.00740	UBAP1; Ubiquitin-associated protein 1 Q9NZ09	VLS(1)PPHK
1.43	0.00091	EGFR; Epidermal growth factor receptor P00533	MHLPS(1)PTDSNFYR
1.43	0.00024	PPP1R12A; Protein phosphatase 1 regulatory subunit 12A O14974	RLAS(0.99)TSDIEEK

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1.42	0.00855	NCKAP5L; Nck-associated protein 5-like H7C1V4	VDLEPV ^S (1)PR
1.36	0.00348	ABL2; Abelson tyrosine-protein kinase 2 P42684	VPVLIS(0.86)PTLK
1.26	7.47E-07	AKAP11; A-kinase anchor protein 11 Q9UKA4	S(0.99)FSEDFVQSVK
1.25	0.01012	PAC3IN3; Protein kinase C and casein kinase substrate in neurons protein 3 A0A0C4DGG1	GGRS(0.99)PDEVTLTSIVPTR
1.20	0.00206	JUN; Transcription factor AP-1 P05412	LAS(1)PELER
1.11	0.00845	TNS4; Tensin-4 Q8IZW8	ASSPHGLGSPLVAS(1)PR
1.11	0.00079	ITGB4; Integrin beta-4 P16144	VLS(0.99)TSSTLTR
1.09	4.57E-05	CD97; CD97 antigen P48960	ALRAS(0.99)ESGI
1.04	0.00424	LARP1; La-related protein 1 Q6PKG0	S(0.99)LPPTVPES(1)PNYR
1.04	0.00424	LARP1; La-related protein 1 Q6PKG0	S(0.99)LPPTVPES(1)PNYR
1.02	0.00620	BCL9L; B-cell CLL/lymphoma 9-like protein Q86UU0	SVS(1)VDSGEQR
1.01	0.00817	RPS27; 40S ribosomal protein S27 P42677	DLLHPS(1)PEEEK
0.99	0.00668	MAPK1; Mitogen-activated protein kinase 1 P28482	VADPDHDTGFLT(0.98)EY(0.99)VATR
0.98	0.00579	CENPF; Centromere protein F P49454	SVPVNNLPER ^S (0.87)PTDS(0.96)PREGLR
0.97	0.00165	MARCKS; Myristoylated alanine-rich C-kinase substrate (A0A087WZH7) P29966	GEPAAAAPEAGAS(1)PVEK
0.92	0.00610	FCHO2; F-BAR domain only protein 2 Q0JRZ9	VSIGNITL ^S (0.98)PAISR
0.89	0.00603	UBA1; Ubiquitin-like modifier-activating enzyme 1 P22314	ATLPS(0.99)PDKLPGFK
0.88	0.00540	DCAF5; DDB1- and CUL4-associated factor 5 Q96JK2	AEEPPS(1)PPVPK
0.87	0.00701	RBM34; RNA-binding protein 34 A2A2V2	S(1)VQEGENPDDGVR
0.86	0.00583	EIF4G1; Eukaryotic translation initiation factor 4 gamma 1 Q04637	EALPPV ^S (1)PLK
0.82	0.00404	TJAP1; Tight junction-associated protein 1 Q5JTD0	AFVDR ^T (1)PPPAVAQR
0.80	0.00079	PKP3; Plakophilin-3 Q9Y446	ADYDTLS(0.99)LR
0.79	0.00014	NSUN2; tRNA (cytosine(34)-C(5))-methyltransferase Q08J23	AGEPNS(1)PDAEEANS(0.99)PDVTAGCDPAGVHPPR
0.78	0.00218	LIMA1; LIM domain and actin-binding protein 1 Q9UHB6	LRS(1)PPEALVQGR
0.75	0.00138	RGPD5; RANBP2-like and GRIP domain-containing protein 5/6 Q99666	YVASVLGLTPS(0.96)PR
0.74	0.00184	STMN1; Stathmin P16949	SKEVPEFPLS(1)PPK
0.64	0.00018	CCDC88A; Girdin H0Y7K3	FYDPS(1)PPR

Supplementary Table S1. Significantly increased phosphopeptide relative abundance in A431/CCKBR cells treated with [¹⁷⁷Lu]Lu-PP-F11N. MS2-based quantification shown as log₂ ratio, $P < 0.05$.

Supplementary Table S2

LOG ₂ (ratio) ¹⁷⁷ Lu-PP-F11N /CON	P-value	LEADING PROTEIN ACCESSION No.	SEQUENCE WINDOW POSITION (PROBABILITY>0.5)
-9.06	0.00323	HNRPU; Heterogeneous nuclear ribonucleoprotein U Q00839	SS(0.75)SPVNVK
-8.51	3.38E-05	EGFR; Epidermal growth factor receptor P00533	ELVEPLT(1)PS(1)GEAPNQALLR
-8.09	9.02E-05	SRRM1; Serine/arginine repetitive matrix protein 1 Q81YB3	T(1)PS(1)PPPR
-7.94	4.33E-05	SRRM1; Serine/arginine repetitive matrix protein 1 Q81YB3	T(1)PS(1)PPPR
-6.40	1.9E-05	TCOF; Treacle Ribosome Biogenesis Factor Q13428	SLGNLQAKPTS(0.64)SPAK
-6.11	7.02E-05	H31; Histone H3.1 P68431	KS(1)APATGGVK
-5.87	8.81E-05	SRRM2; Serine/arginine repetitive matrix protein 2 Q9UQ35	S(1)RT(1)PPSAPSQSR
-5.37	0.00043	MARK2; Serine/threonine-protein kinase MARK2 Q7KZ17	SVS(1)ANPK
-5.29	9.59E-06	SRC8; Src substrate cortactin Q14247	TQT(0.84)PPVSPAPQPTTEERLPS(0.86)SPVYEDAASF
-5.09	0.01798	SRRM2; Serine/arginine repetitive matrix protein 2 Q9UQ35	ELS(0.92)NSPLRENSFGS(0.99)PLEFR
-4.95	0.00011	MDC1; Mediator of DNA damage checkpoint protein 1 Q14676	SQPPGEDS(0.99)DT(0.99)DVDDSDRRPPRPAEVHLER
-4.91	9.42E-06	TAF12; Transcription initiation factor TFIIID subunit 12 Q16514	IPGTPGAGGRLS(0.99)PENNQVLTKK
-4.58	0.00109	DKC1; H/ACA ribonucleoprotein complex subunit 4 O60832	S(1)LPEDVAEIQAHEEFLIKPESK
-4.55	0.00017	TR150; Thyroid hormone receptor-associated protein 3 Q9Y2W1	GSFS(1)DTGLGDGK
-4.47	0.00060	SRRM2; Serine/arginine repetitive matrix protein 2 Q9UQ35	S(1)RT(1)PPSAPSQSR
-4.45	0.00066	NIBL1; Niban-like protein 1 Q96TA1	QVVSVVQDEEVLPLFEASPE(0.97)PPASPDPGVTEIR
-4.35	0.00076	F2Z2H1; RNA helicase Mov10l1 F2Z2H1	MLS(1)LAAKLVAFWR
-4.31	0.00025	PGRMC2; Membrane-associated progesterone receptor component 2 U3KQM0	LLKPGEEPSEY(0.99)DEEDTK
-4.28	0.00489	EGFR; Epidermal growth factor receptor P00533	YSSDPTGALTEDSIDTFLPVPEY(0.97)INQSVPK
-3.99	0.00248	A0A087WZ13; Ribonucleoprotein PTB-binding 1 A0A087WZ13	AADVSVTHRPPLS(1)PK
-3.91	0.00024	NELFE; Negative elongation factor E P18615	SGAHS(0.67)ASPPR
-3.81	0.00028	FOXO3; Forkhead box protein O3 O43524	AEAPAS(0.99)PAPLSPLEVELDPEFEPQSRPR
-3.73	0.00227	SOS1; Son of sevenless homolog 1 G5E9C8; G5E9C8	RRPESAPAES(0.81)PSK
-3.70	0.00322	POLR2A; DNA-directed RNA polymerase subunit A0A0C4DGZ0	YSPTS(0.99)PTYSPSPK
-3.64	0.00226	SART3; Squamous cell carcinoma antigen recognized by T-cells 3 Q15020	ATAAETS(0.99)ASEPEAESK
-3.62	4.07E-05	SF3B2; Splicing factor 3B subunit 2 Q13435	SSLGQS(1)AS(1)ETEEDTVSVSKK
-3.61	0.00041	NOTCH4; Neurogenic locus notch homolog protein 4 Q99466	LEDPCPS(1)FCS(1)K
-3.53	0.00011	NOTCH4; Neurogenic locus notch homolog protein 4 Q99466	LEDPCPS(1)FCS(1)K
-3.50	0.00038	ZN800; Zinc finger protein 800 Q2TB10	VKQDSESPKTS(0.71)PSAAGGQKQK
-3.49	0.00188	RPA1; Replication protein A 70 kDa DNA-binding subunit P27694	GARVS(1)DFGGR
-3.46	0.00357	CHAP1; Chromosome alignment-maintaining phosphoprotein 1 Q96JM3	KPGPPLS(1)PEIRS(1)PAGS(1)PELR
-3.43	0.00308	CHAP1; Chromosome alignment-maintaining phosphoprotein 1 Q96JM3	KPGPPLS(1)PEIRS(1)PAGS(1)PELR
-3.38	8.86E-05	CCDC6; Coiled-coil domain-containing protein 6 Q16204	SGGIVIS(0.99)FRLEELTNR
-3.33	0.00137	RAVER1; Ribonucleoprotein PTB-binding 1 A0A087WZ13	AADVSVTHRPPLS(0.99)PKS(1)GAEEVAGDAAER
-3.31	0.00087	LAD1; Ladinin-1 O00515	RATASEQPLAQEPPASGGS(0.74)PATTK
-3.30	0.00036	YAP1; Transcriptional coactivator YAP1 P46937	NINPSTANS(0.99)PK
-3.22	0.02100	RRP1B; Ribosomal RNA processing protein 1 homolog B Q14684	VAFDPEQKPLHGLVTKT(0.99)PTSSPASSPLVAK
-3.19	0.00138	HDAC7; Histone deacetylase 7 Q8WUI4	TVS(1)EPNLK
-3.16	0.00042	MECP2; Methyl-CpG-binding protein 2 P51608	AETSESGSAPAVEASAS(0.92)PK
-3.12	0.00317	SLK; STE20-like serine/threonine-protein kinase Q9H2G2	SNS(0.99)EDKLNK
-3.11	0.00408	CHAP1; Chromosome alignment-maintaining phosphoprotein 1 Q96JM3	KPGPPLS(1)PEIRS(1)PAGS(1)PELR
-3.03	0.00148	ARHG5; Rho guanine nucleotide exchange factor 5 Q12774	TTPQQGASGPGRS(0.94)PVGQAR
-3.02	0.00075	RAD18; E3 ubiquitin-protein ligase RAD18 Q9N591	NHLLQFALES(1)PAKS(0.98)PASSSSK
-3.00	0.00021	RPA34; DNA-directed RNA polymerase I subunit RPA34 O15446	ILEGQQQLSGS(0.78)PLQPIPAS(1)PPPQIPPLRPR
-2.96	0.00131	NUCKS; Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 Q9H1E3	S(0.99)GKNSQEDSESDKDVK
-2.95	0.00126	CCKBR; Gastrin/cholecystokinin type B receptor E9PIC8	CRPETGAVGEDSDGCY(1)VQLPR

Supplementary Table S2

-2.91	0.00112	ZMYND8; Protein kinase C-binding protein 1 H7C4X9	TPPSTTVGSHS(0.92)PPETPVLTR
-2.90	0.00023	DCP1A; mRNA-decapping enzyme 1A Q9NPI6	HAPTYTIPLS(0.84)PVL(0.94)PTLPAAEPTAQVPPSLPR
-2.85	0.00733	CENPC; Centromere protein C Q03188	ILATDVSSKNT(0.96)PDSK
-2.85	0.00059	KMT2A; Histone-lysine N-methyltransferase 2A Q03164	ALSSAVQASPTS(0.81)PGGSPSS(0.55)PSSGQR
-2.85	0.00429	RPA34; DNA-directed RNA polymerase I subunit RPA34 O15446	ILEGPQQSLSGS(0.96)PLQPIPASPPPQIPGLRPR
-2.83	8.03E-06	CGN; Cingulin A6PVU7	SHS(0.98)QASLAGPGVDPNSNR
-2.79	0.00578	NUP50; Nuclear pore complex protein Nup50 Q9UKX7	KVDSSVGLSLSVPLTGFFS(0.98)PGNSSLFGK
-2.79	0.00074	NUP153; Nuclear pore complex protein Nup153 P49790	CIACQAAKLS(1)PR
-2.76	0.00543	PAXB1; PAX3- and PAX7-binding protein 1 Q9Y5B6	LVREENDAS(1)DDEDDEK
-2.72	0.00290	RAD18; E3 ubiquitin-protein ligase RAD18 Q9NS91	NHLLQFALES(1)PAK
-2.72	0.00130	RFC1; Replication factor C subunit 1 P35251	NKPLS(1)PIKLT(0.99)PTSVLDYFGTGSVQR
-2.72	0.00243	ABCD3; ATP-binding cassette sub-family D member 3 P28288	S(1)GKPLQNNK
-2.65	0.00052	CNTROB; Centrobilin I3L465	AQLYLPST(0.63)PPHEGLDGFQELSR
-2.61	0.00012	SSB; Lupus La protein P05455	S(0.92)PSKPLPEVTDEYKNDVK
-2.58	0.00199	PPP1R13L; RelA-associated inhibitor Q8WUF5	HGGPGPGGPEPELS(0.99)PITEGSEAR
-2.57	0.00038	RFC1; Replication factor C subunit 1 P35251	SSPAKESVS(0.97)PEDSEK
-2.57	0.00658	DCP1A; mRNA-decapping enzyme 1A Q9NPI6	HAPTYTIPLS(0.88)PVL(0.87)PTLPAAEPTAQVPPSLPR
-2.56	0.00054	DNMT1; DNA (cytosine-5)-methyltransferase 1 P26358	SDGEAKPEPS(1)PS(1)PR
-2.56	0.00053	RFC1; Replication factor C subunit 1 P35251	NKPLS(1)PIK
-2.52	0.00992	MINK1; Misshapen-like kinase 1 Q8N4C8	NRVGVSSKPDSS(0.95)PVLSPGNK
-2.51	0.00185	BCLF1; Bcl-2-associated transcription factor 1 Q9NYF8	SGSS(0.86)PKWTHDK
-2.45	0.01394	CNOT4; CCR4-NOT transcription complex subunit 4 O95628	ELSVQDQPSLS(0.92)PTSLQNSSHTTTAK
-2.45	0.00210	KMT2A; Histone-lysine N-methyltransferase 2A Q03164	ALSSAVQASPTS(0.63)PGGSPSS(0.65)PSSGQR
-2.44	0.00233	RHAGAP29; Rho GTPase-activating protein 29 Q52LW3	SLDSEIS(0.99)PGDFHR
-2.44	0.00620	RS6; 40S ribosomal protein S6 P62753	RLS(1)S(1)LRAS(0.96)TSK
-2.43	0.00442	PKP3; Plakophilin-3 Q9Y446	LSS(0.99)GFDIDLPSAVK
-2.41	0.00600	CIC; Protein capicua homolog I3L2J0	ACTGLSGPGSGSKS(0.64)PPATR
-2.34	0.00334	DYNC1L12; Cytoplasmic dynein 1 light intermediate chain 2 O43237	KTGS(0.94)PGS(0.99)PGAGGVQSTAKK
-2.29	0.00174	KIF1B; Kinesin-like protein KIF1B A0A087WWA3	AS(0.5)S(0.5)PCPEFEQFQIVPAVETPYLAR
-2.27	0.00068	CCDC9; Coiled-coil domain-containing protein 9 Q9Y3X0	EGAASPAPETPQPTS(0.69)PETS PK
-2.25	0.00275	DTL; Denticleless protein F5GZ90	TPSSS(0.80)PPIT(0.99)PPASETK
-2.25	0.01660	RL1D1; Ribosomal L1 domain-containing protein 1 O76021	KS(1)PAKS(0.99)PNPSTPR
-2.22	0.00771	KIF1B; Kinesin-like protein KIF1B A0A087WWA3	AS(0.5)S(0.5)PCPEFEQFQIVPAVETPYLAR
-2.19	0.00429	CDR2; Cerebellar degeneration-related protein 2 Q01850	SSS(0.85)ETILSLAGSDIVK
-2.17	0.00033	RHPN2; Rhophilin-2 Q8IUC4	SAS(0.95)TLCLPSVGAARPQVK
-2.07	0.01372	RBM34; RNA-binding protein A2A2V2	SVQEGENPDDGVRGS(0.99)PPEDYR
-2.05	0.00085	MAGI3; Membrane-associated guanylate kinase Q5TCQ9	IFYGEKQPEDDSSQAFISTQNGS(0.99)PR
-2.043	9.9E-05	SRCAP; Helicase SRCAP A0A0A0MS59	GAASTLVPGVSETSAS(0.59)PGSPSVR
-1.93	0.01488	CLDN4; Claudin-4 O14493	SAAASNY(1)V
-1.91	0.00112	ATP13A1; Manganese-transporting ATPase 13A1 Q9HD20	DS(0.98)PTLSNSGIR
-1.87	0.01166	ZC3HC1; Nuclear-interacting partner of ALK C9J0I9	SWDSSS(0.75)PVDRPEPEAS(0.71)PTTR
-1.86	0.0146	PDLIM2; PDZ and LIM domain protein 2 Q96JY6	AGS(1)PFS(0.99)PPSSSLTGEEAISR
-1.84	0.00059	SETD2; Histone-lysine N-methyltransferase SETD2 H7BZ93	LNDS(0.99)PTLK
-1.82	0.01259	ZN318; Zinc finger protein 318 Q5VUA4	RSS(0.8)PPPPPGSSSRTPAR
-1.79	0.01615	TJP1; Tight junction protein ZO-1 Q07157	LEEPTPAPSTYS(0.98)PQADSLR
-1.73	0.00989	DNMT1; DNA (cytosine-5)-methyltransferase 1 P26358	SDGEAKPEPS(1)PS(1)PR
-1.72	0.00104	RPS6; 40S ribosomal protein S6 P62753	RLS(1)S(1)LRASTSK

Supplementary Table S2

-1.72	0.01616	MCM2; DNA replication licensing factor MCM2 P49736	AIPELD ^Y EAEGLALDDEDVEEL ^T (0.55)ASQREAAER
-1.69	0.01214	RPS6; 40S ribosomal protein S6 P62753	LSSLRA ST SK ^S (0.96)ES ^S (0.69)QK
-1.67	0.01230	LRWD1; Leucine-rich repeat and WD repeat-containing protein 1 Q9UFC0	ACAS ^S (0.9)PSAQVEG ^S (1)PVAGSDG ^S QPAVK
-1.65	0.01201	RPL3; 60S ribosomal protein L3 P39023	^S (1)LLVQTK
-1.61	0.00736	RSL1D1; Ribosomal L1 domain-containing protein 1 O76021	^K S(1)PAK ^S (0.99)PNPSTPR
-1.59	0.00030	UBE2O; (E3-independent) E2 ubiquitin-conjugating enzyme Q9C0C9	IMSC ^S (0.97)PDTQCSR
-1.56	0.01326	AFF4; AF4/FMR2 family member 4 Q9UHB7	ELLSPL ^S (0.99)EPDDRPLIVK
-1.51	0.00699	PAX; Paxillin P49023	DGGR ^S (0.79)SPGGQDEGGFMAQ ^G K
-1.47	0.01439	BAG3; BAG family molecular chaperone regulator 3 O95817	SST(0.94)PLHS(^{PS} (0.93)PIR
-1.42	0.0092	NPM1; Nucleophosmin P06748	^S (1)APGGGSKVPQK
-1.33	0.01066	HNRNP1; Heterogeneous nuclear ribonucleoprotein H P31943	EGRPSGEAFVELE ^S (1)EDEVK
-1.30	0.00048	DDX39A; ATP-dependent RNA helicase DDX39A O00148	NRS(0.99)FSLK
-1.14	0.00396	H14; Histone H1.4 P10412 , H15; Histone H1.5 P16401 , H13; Histone H1.3 P16402 , H12; Histone H1.2 P16403 , H11; Histone H1.1 Q02539	GTGAS(0.8)GSFK
-1.11	0.00914	FANCI; Fanconi anemia group I protein Q9NV11	TIETS(0.95)PSLSR
-1.11	0.00589	CALM1; Calmodulin P62158	VFDKDGNGY(1)ISAAELR
-1.10	0.00953	FGD1; FYVE, RhoGEF and PH domain-containing protein 1 P98174	RGS(0.7)GSALGGPLDPQFVGPSTSLGAAPGHR
-1.06	0.00434	H15; Histone H1.5 P16401	SETAPAETAT(1)PAPVEK ^S (1)PAKK
-1.06	0.00434	H15; Histone H1.5 P16401	SETAPAETAT(1)PAPVEK ^S (1)PAKK
-0.97	0.00071	MYBBP1A; Myb-binding protein 1A Q9BQG0	SPS(1)LLQSGAK
-0.89	0.00044	SKA3; Spindle and kinetochore-associated protein 3 Q8IX90	NSVHEQEAIN ^S (1)DPELNCENCFQK
-0.76	0.00137	NUP93; Nuclear pore complex protein Nup93 Q8N1F7	GTS(0.98)PSSSRPQR
-0.74	0.002855	ACOX1; Peroxisomal acyl-coenzyme A oxidase 1 Q15067	DSASFPELLTHILDG ^S (1)PEK
-0.64	0.002831	RANBP2; E3 SUMO-protein ligase RanBP2 P49792	NADSEIKH ST (0.97)PS(0.94)PTR

Supplementary Table S2. Significantly decreased phosphopeptide relative abundance in A431/CCKBR cells treated with [¹⁷⁷Lu]Lu-PP-F11N. MS2-based quantification shown as log₂ ratio, $P < 0.05$.

Supplementary Table S3

LOG ₂ (ratio) EBRT / CONTROL	P-VALUE	SYMBOL; NAME UniProt	SEQUENCE WINDOW POSITION (PROBABILITY>0.5)
8.69	0.00010	NUCKS1; Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 Q9H1E3	IRS(0.5)S(0.5)PREAK
6.74	0.00033	EIF4G1; Eukaryotic translation initiation factor 4 gamma 1 E7EX73	SSLS(0.99)RERGEK
6.19	0.00053	EIF4G1; Eukaryotic translation initiation factor 4 gamma 1 E7EX73	RVVQR(0.69)SLSR
6.15	0.00013	RIF1; Telomere-associated protein RIF1 Q5UIP0	RSEVVSTTES(1)QDK
6.07	0.00043	SRRM2; Serine/arginine repetitive matrix protein 2 Q9UQ35	S(1)KT(0.95)PSRQSHS(0.95)S(0.64)SP
5.88	7.13E-05	SRRM2; Serine/arginine repetitive matrix protein 2 Q9UQ35	S(0.99)KT(0.99)PSRQSHSSSSPHPK
5.77	4.83E-05	ZNF638; Zinc finger protein 638 Q14966	AVIVS(0.81)SPK
5.74	0.00073	RPL29; 60S ribosomal protein L29 P47914	RTQAPTKAS(1)E
5.68	0.00039	SRRM2; Serine/arginine repetitive matrix protein 2 Q9UQ35	PES(1)PKPAPAPGSHREIS(0.98)S(0.68)S
5.68	1.51E-05	ZNF318; Zinc finger protein 318 Q5VUA4	RAS(1)PS(1)PPRGR
5.61	0.00021	IWS1; Protein IWS1 homolog Q96ST2	KFHS(1)S(1)DS(1)EEEEHKK
5.60	0.00046	ZNF318; Zinc finger protein 318 Q5VUA4	RAS(1)PS(1)PPRGR
5.60	0.00051	CRKL; Crk-like protein P46109	LVRSS(0.73)PHGK
5.41	0.00058	SNIP1; Smad nuclear-interacting protein 1 Q8TAD8	RTS(0.96)NERPGSGGQQGR
5.40	0.00054	CRKL; Crk-like protein P46109	LVR(0.5)S(0.5)PHGK
4.65	0.01448	MDC1; Mediator of DNA damage checkpoint protein 1 Q14676	DTQRGEPGGS(1)QDQK
4.64	0.00868	DUT; Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial HOYNJ9	PCS(1)EETPAIS(1)PSK
4.55	0.00190	MAP4; Microtubule-associated protein E7EVA0	RAS(0.99)PSKASAPASR
4.51	0.00010	RIF1; Telomere-associated protein RIF1 Q5UIP0	NVS(1)QESLETK
4.51	0.00023	POLE; DNA polymerase epsilon catalytic subunit A FSH1D6	IHCGLQDS(1)QK
4.43	0.00235	ZZZ3; ZZ-type zinc finger-containing protein 3 Q81VH5	RAAPTRGS(0.99)PTK
4.35	7.60E-06	ADAR; Double-stranded RNA-specific adenosine deaminase P55265	TMLLS(0.87)RSPAQPK
4.34	0.00026	OXSR1; Serine/threonine-protein kinase OSR1 O95747	TAQALSSGSGS(0.88)QETK
4.28	0.00601	MCM4; DNA replication licensing factor MCM4 P33991	S(0.5)S(0.5)PAST(0.73)PSRRGSR
4.28	0.00270	PRPF38B; Pre-mRNA-splicing factor 38B Q5VTL8	RRS(1)QS(1)IEQES(1)QEK
4.13	0.00139	SP100; Nuclear autoantigen Sp-100 P23497	DTTSKDDSLGS(1)QQTNEQCAQK
4.13	0.00013	RB1; Retinoblastoma-associated protein P06400	LQNNHTAADMY(0.72)LSPVRS(0.96)PK
4.06	0.00192	SSRM1; Serine/arginine repetitive matrix protein 1 A9Z1X7	QRS(0.7)PVTK
4.04	0.00032	DSG2; Desmoglein-2 Q14126	AAS(1)YTEEDENHTAK
3.89	0.00023	POLR2A; DNA-directed RNA polymerase II subunit RPB1 A0A0C4DGZ0 P24928	LLVDS(1)NNPKIK
3.85	0.01577	SRRM2; Serine/arginine repetitive matrix protein 2 Q9UQ35	YSHSGS(0.88)SPDTK
3.83	0.00087	CHEK1; Non-specific serine/threonine protein kinase J3KN87	VTS(1)GGVSESPGFSK
3.82	0.00011	ENSA; Alpha-endosulfine O43768	S(1)QKQEEENPAEETGEEK
3.79	0.00487	RIF1; Telomere-associated protein RIF1 Q5UIP0	NVS(0.99)QES(0.93)LETKEEKPEETPK
3.72	0.00384	NFIC; Nuclear factor 1 C-type P08651	KTEMDS(1)PFNSPSPQD5PR
3.64	0.00235	RNF181; E3 ubiquitin-protein ligase RNF181 C9J1C6	TVIRGS(0.99)QAEK
3.59	0.00075	USP1; Ubiquitin carboxyl-terminal hydrolase 1 O94782	RALDFTDS(1)QENEEK
3.54	0.00098	TP53; Cellular tumor antigen p53 P04637	MEEPQSDPSVEPPLS(0.98)QETFSDLWK
3.53	0.00055	RNF168; E3 ubiquitin-protein ligase RNF168 Q81YW5	VAAERRAS(1)EEEEENK
3.52	0.00228	CHAF1A; Chromatin assembly factor 1 subunit A Q13111	GLLSNHTGS(0.98)PR
3.49	0.00671	PATJ; InaD-like protein Q8NI35	VPDS(1)PENELK
3.45	0.00288	DYNC1L2; Cytoplasmic dynein 1 light intermediate chain 2 O43237	ASESPARGPS(0.6)GSPR
3.40	0.00082	UTP14A; U3 small nucleolar RNA-associated protein 14 homolog A Q9BVJ6	DSGS(1)QEVLSLR
3.39	0.00285	CEP152; Centrosomal protein of 152 kDa O94986	NVS(1)PEFVPCGEGGGFLHK
3.35	0.01188	RAD50; DNA repair protein RAD50 Q92878	LFDVCGS(1)QDFESDLRLKEEIEK
3.31	0.00058	DDX47; Probable ATP-dependent RNA helicase DDX47 Q9H0S4	AAPEEHSPTAS(1)QPIVEEETK
3.23	0.00036	SLC4A1AP; Kanadaplin A0A087X0M4	ETQTHENMS(1)QLS(1)EEEQNK
3.21	0.00076	NTHL1; Endonuclease III-like protein 1 P78549	SRS(0.99)LGGGAGPR
3.20	0.00101	KHSRP; Far upstream element-binding protein 2 Q92945	VQS(1)PDSGGLPER
3.17	0.00101	TWISTNB; DNA-directed RNA polymerase I subunit RPA43 Q3B726	KKDPETYEVD(0.83)GTTK
3.08	0.00075	UIMC1; BRCA1-A complex subunit RAP80 Q96RL1	MSEQAREVNS(1)QEEEEELLRK
3.03	0.00187	SIPA1L1; Signal-induced proliferation-associated 1-like protein O43166	HSA(1)PVPVFTSAR
3.03	0.00623	PHLDB1; Pleckstrin homology-like domain family B member 1 Q86UU1	SES(0.99)PRLSRK
3.01	0.00442	NCOR2; Nuclear receptor corepressor 2 C9J777	SRS(0.99)PAPPADK
2.93	0.00016	HMG1; High mobility group protein HMG-I/HMG-Y P17096	KLEEEEEGIS(1)QES(1)S(1)EEEEQ

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2.92	0.00019	THRAP3; Thyroid hormone receptor-associated protein 3 Q9Y2W1	SSS(0.98)KDS(0.76)RPSQAAGDNQGD E
2.89	0.00044	GIN52; DNA replication complex GINS protein PSF2 Q9Y248	LRTNLQPLESTQS(1)QDF
2.85	0.01394	THRAP3; Thyroid hormone receptor-associated protein 3 Q9Y2W1	SSS(0.98)KDS(0.76)RPSQAAGDNQGD E
2.83	9.40E-05	MAP2K2; Dual specificity mitogen-activated protein kinase kinase 2 P36507	ELEAIFGRPVVDGEEGEPHS(0.8)PR
2.76	0.00082	ARID1A; AT-rich interactive domain-containing protein 1A O14497	SNS(1)VGIQDAFNGSDSTFQK
2.71	0.00647	ZSWIM8; Zinc finger SWIM domain-containing protein 8 H0YCW2	GWGS(1)JGRPK
2.67	0.00671	HNRNPM; Heterogeneous nuclear ribonucleoprotein M P52272	MGS(1)GIER
2.63	0.00074	RCHY1; RING finger and CHY zinc finger domain-containing protein 1 Q96PM5	RIS(1)LDQK
2.61	0.00658	RADS1AP1; RAD51-associated protein 1 F5H1Y0	ELPTVTTNVQNS(1)QDK
2.57	0.00702	TRIM28; Transcription intermediary factor 1-beta Q13263	S(1)GEGEVSLMR
2.57	0.00963	FAM83G; Protein FAM83G A6ND36	LLPDPGS(1)PR
2.55	0.00124	TCOF1; Treacle protein Q13428	GSLGS(1)QGAKEPEEELQK
2.54	0.01405	MCM6; DNA replication licensing factor MCM6 Q14566	EIESEID(1)EELINKK
2.53	0.01208	PPP2R5A; Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform Q15172	RSQGS(0.91)S(0.92)QFRSQGSQAEHLPL
2.50	0.00047	C2CD5; C2 domain-containing protein 5 Q86Y57	SLQRAST(0.54)DNEELLQFPLELCSDSLPS
2.48	0.01367	CAST; Calpastatin A0A0C4DGB5	SESELIDELS(0.99)EDFDRSECK
2.47	0.00940	PHAX; Phosphorylated adapter RNA export protein Q9H814	ETFASDTNEALASLDES(0.99)QEGHAEAK
2.47	0.00555	RREB1; Ras-responsive element-binding protein 1 Q92766	VTENGSPQGIKS(0.77)PSKPPGPNR
2.42	0.00076	YBX1; Nuclease-sensitive element-binding protein 1 P67809	NYQNYQNSE(0.97)GEK
2.41	0.00179	SNW1; SNW domain-containing protein 1 Q13573	ALTSFLPAPTQLS(1)QDQLEAEK
2.38	0.00867	CCP110; Centriolar coiled-coil protein of 110 kDa Q43303	LPSPEPMS(0.96)PK
2.35	0.01272	NDRG1; Protein NDRG1 Q92597	SRS(0.59)HT(0.54)SEGALDITPNSGAA
2.34	0.00305	YAP1; Transcriptional coactivator YAP1 P46937	AHS(0.91)SPASLQLGAVSPGLTPTGVVS
2.33	0.00089	RALGPS2; Ras-specific guanine nucleotide-releasing factor RalGPS2 Q86X27	SVAAGALLPQT(0.91)PPSPR
2.32	0.00432	CHEK2; Serine/threonine-protein kinase Chk2 O96017	FAIGS(1)AREADPALNVETEILK
2.32	0.00082	CHD4; Chromodomain-helicase-DNA-binding protein 4 F5GWX5	IEENS(1)LKEEESIEGK
2.25	0.00847	TP53BP1; Tumor suppressor p53-binding protein 1 Q12888	LVPETEAS(1)EESLQFNLEK
2.23	0.00668	MAPK14; Mitogen-activated protein kinase 14 Q16539	S(1)QERPTFYR
2.17	0.00801	SYNCRIP; Heterogeneous nuclear ribonucleoprotein Q O60506	YGGPPPSVYSGQQPS(0.93)VGTEIFVG
1.98	0.01174	CDC26; Anaphase-promoting complex subunit CDC26 Q8NHZ8	QKEDVEVVGGS(1)DGEGAIGLSSDPK
1.94	0.00812	MYPN; Myopalladin A0A087WX60	TPVDES(1)DDEIQHDEIPTGK
1.83	0.00705	PABPN1; Polyadenylate-binding protein 2 Q86U42	APGPGPGSGAPGS(1)QEEEEEPGLVEGD
1.82	0.00629	CBX3; Chromobox protein homolog 3 Q13185	LTWH(0.99)CPEDEAQ
1.76	0.01134	HMG1; High mobility group protein HMG-I/HMG-Y P17096	KQPPVSPGTALVGS(1)QJK
1.74	0.01094	TRIO; Triple functional domain protein E7EPJ7	GGSFWSIPAS(0.90)PASRPGSFTFPGDS
1.68	0.00295	UTP14A; U3 small nucleolar RNA-associated protein 14 homolog A Q9BVJ6	RSELSQDAEPAGS(1)QETK
1.53	0.00778	LRBA; Lipopolysaccharide-responsive and beige-like anchor protein E9PEM5	ANLPTQLQDNL(0.93)PAASEAGEK
1.28	0.00377	MCM2; DNA replication licensing factor MCM2 P49736	EGLALDDEVEELTAS(0.99)QREAAER
0.97	0.00416	BCLAF1; Bcl-2-associated transcription factor 1 Q9NYF8	S(1)QEEPKDTEFHDPSEIDFNK
0.71	0.00061	UPF1; Regulator of nonsense transcripts 1 Q92900	SQIDVALS(0.99)QDSTYQGER

Supplementary Table S3. Significantly increased phosphopeptide relative abundance in A431/CCKBR cells after EBRT. MS2-based quantification shown as log₂ ratio, $P < 0.05$.

Supplementary Table S4

LOG ₂ (ratio) EBRT / CONTROL	P-VALUE	SYMBOL; NAME UniProt	SEQUENCE WINDOW POSITION (PROBABILITY>0.5)
-7.62	1.43E-05	ARHGEF16; Rho guanine nucleotide exchange factor 16 Q5VV41	AQRHSDS(0.96)SLEEK
-7.60	1.8E-06	HIST3H3; Histone H3.1t Q16695	VARKS(1)JAPATGGVK
-6.77	0.00037	NOLC1; Nucleolar and coiled-body phosphoprotein 1 Q14978	VAGGAAPSKPAS(1)AKK
-6.53	0.01849	NPM1; Nucleophosmin P06748	T(1)PKGSSVEDIK
-6.14	4.61E-05	SRRM2; Serine/arginine repetitive matrix protein 2 Q9UQ35	SST(0.98)PPGESYFGVSSLLQK
-6.01	1.46E-05	NPM1; Nucleophosmin P06748	T(1)PKT(1)PKGSSVEDIK
-5.98	4.31E-05	EPRS; Bifunctional glutamate/proline--tRNA ligase P07814	EYIPGQPPLSQSSDS(0.84)SPTRNSEPAG
-5.73	0.00030	UBAP2L; Ubiquitin-associated protein 2-like Q14157	NPSDSAVHS(0.98)PFTK
-5.41	0.00027	RSL1D1; Ribosomal L1 domain-containing protein 1 O76021	AAESET(1)PGKS(1)PEK
-5.32	0.01799	NCL; Nucleolin P19338	ALVAT(1)PGKK
-5.30	0.00032	JUN; Transcription factor AP-1 P05412	LAS(1)PELER
-5.28	0.00050	HIST1H1B; Histone H1.5 P16401	SETAPATAT(1)PAPVEKS(1)PAK
-5.19	6.3E-05	RPRD2; Regulation of nuclear pre-mRNA domain-containing protein 2 Q5VT52	NTGVSPASRSPGPTGS(0.81)PSNLTSGL
-5.14	1.03E-05	MKI67; Proliferation marker protein Ki-67 P46013	RES(1)VNVLGK
-5.06	0.01149	RSRC2; Arginine/serine-rich coiled-coil protein 2 Q7L4I2	AAS(0.99)DTERDGLAPEK
-5.05	0.00012	DIS3L2; DIS3-like exonuclease 2 Q8IYB7	GVSAVAGPHDIGAS(1)PGDKK
-5.00	1.49E-05	MKI67; Proliferation marker protein Ki-67 P46013	GRDVESVQT(0.99)PSK
-4.96	0.00020	PRCC; Proline-rich protein PRCC Q92733	KPSDGS(0.99)PDTKPSR
-4.82	0.00404	MTA2; Metastasis-associated protein MTA2 O94776	GHLSRPEAQSL(0.99)PYTTSANR
-4.74	0.00054	ESF1; ESF1 homolog Q9H501	ALAEAS(1)EEELPS(1)DVDLNDPYFAEEV
-4.72	2.4E-05	CTPS1; CTP synthase 1 P17812	DTYSDRSGS(0.88)SS(0.80)PDSEITELK
-4.70	0.00012	DTNB; Dystrobrevin E7EVB6	LRLHEQASQPT(1)PEK
-4.57	0.00079	LASP1; LIM and SH3 domain protein 1 Q14847	GFVVADT(1)PELQR
-4.53	0.00048	SPAG1; Sperm-associated antigen 1 Q07617	GQTPEAGADKRS(1)PR
-4.53	0.00032	A0A087WUU9; A0A087WUU9	RHSAS(0.59)NLHALAHPAPSPGSCSPK
-4.49	0.00555	TRA2B; Transformer-2 protein homolog beta P62995	S(1)RS(0.99)YSRDYR
-4.48	2.74E-05	MINT; Msx2-interacting protein Q96T58	DLEPGEVPS(1)DS(1)DEDEGEHK
-4.47	0.00072	PSIP1; PC4 and SFRS1-interacting protein O75475	S(1)LAEQRQHEEANK
-4.45	4.53E-05	NOLC1; Nucleolar and coiled-body phosphoprotein 1 Q14978	S(1)PAVKPAAAPK
-4.41	0.00040	MKI67; Proliferation marker protein Ki-67 P46013	LDQPGNLPGS(1)NRR
-4.32	0.00064	CBX5; Chromobox protein homolog 5 P45973	S(1)NFSNSADDIK
-4.30	0.00140	KPNA2; Importin subunit alpha-1 P52292	STNENANT(1)PAAR
-4.29	0.00082	TRA2A; Transformer-2 protein homolog alpha Q13595	S(1)RS(1)HS(1)PMSNR
-4.27	0.00045	GOLGA2; Golgin subfamily A member 2 A0A0C4DG55	LREYQQRNS(0.99)PGVPTGAK
-4.25	8.83E-05	MINT; Msx2-interacting protein Q96T58	DLEPGEVPS(1)DS(1)DEDEGEHK
-4.22	0.00946	NCL; Nucleolin P19338	VAVAT(1)PAKK
-4.18	0.00144	MKI67; Proliferation marker protein Ki-67 P46013	RRS(0.97)GASEANLIVAK
-4.13	0.00015	RPA1; Replication protein A 70 kDa DNA-binding subunit P27694	GARVS(1)DFGGR
-4.11	0.01401	TOR1AIP1; Torsin-1A-interacting protein 1 A0A0A0MSK5	RGLRDS(1)HS(1)S(1)EEDEASSQDLSQTI
-4.10	0.00029	SMTN; Smoothelin P53814	VNS(1)PGTLAR
-4.07	0.00325	RFX7; DNA-binding protein RFX7 H0YLX2	HHDTHFGLT(0.99)PV(1)PVQHQGAT
-4.04	1.98E-05	PPP1R14B; Protein phosphatase 1 regulatory subunit 14B Q96C90	VYFQS(1)PPGAAGEGGGADDEGPVRR
-4.04	0.00123	DIDO1; Death-inducer obliterator 1 Q9BTC0	SILAKPS(0.70)SSPDR
-3.99	0.01379	ATXN2L; Ataxin-2-like protein Q8WWM7	TLSS(0.88)PSNRPSGETSVPPPAVGR
-3.99	0.00070	TRA2A; Transformer-2 protein homolog alpha Q13595	S(1)RS(1)HS(1)PMSNR
-3.98	0.00013	VAPB; Vesicle-associated membrane protein-associated protein B/C O95292	IISTTASKE(0.98)PIVSK
-3.95	3.97E-05	LAD1; Ladinin-1 O00515	RATASEQLAQEPPASGGS(0.98)PATTK
-3.94	0.00039	CLCC1; Chloride channel CLIC-like protein 1 Q96S66	FQTGNKS(1)PEVLR
-3.94	4.79E-05	MAZ; Myc-associated zinc finger protein I3L2Z5	QVHS(0.86)TERPFK
-3.91	0.00326	TRA2A; Transformer-2 protein homolog alpha Q13595	S(1)RS(1)HS(1)PMSNR
-3.89	0.0002	MDC1; Mediator of DNA damage checkpoint protein 1 Q14676	NRS(0.81)SGKT(1)PETLVPTAPK
-3.88	0.00193	UTP18; U3 small nucleolar RNA-associated protein 18 homolog Q9Y5J1	VQEHEDS(1)GDS(1)EVENEAK
-3.88	0.00240	METAP2; Methionine aminopeptidase 2 P50579	QLERS(1)ALEDK
-3.87	0.00494	AATF; Protein AATF Q9NY61	YLVDTGKPNAGS(0.99)EIS(1)S(1)EDDE
-3.86	0.00021	PTPN1; Tyrosine-protein phosphatase non-receptor type 1 P18031	VVGSRLGAQAAS(1)PAK

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-3.86	0.00113	GPATCH2; G patch domain-containing protein 2 Q9NW75	KDHS(1)DS(1)DDQMLVAK
-3.86	0.00069	NEDD1; Protein NEDD1 Q8NHV4	LVTSGAESGLNLT(0.99)PSSNQTR
-3.85	0.00205	NUP98; Nuclear pore complex protein Nup98-Nup96 P52948	ALTT(0.95)PTHYKLT(0.87)PRPATR
-3.85	0.00107	TMPO; Lamina-associated polypeptide 2, isoforms beta/gamma P42167	HAS(1)PILPTEFSDIPIR
-3.85	0.00632	MCM4; DNA replication licensing factor MCM4 P33991	QRPDLGS(1)JAQK
-3.77	0.00216	MKI67; Proliferation marker protein Ki-67 P46013	TFKES(1)PK
-3.76	0.00014	DDX20; Probable ATP-dependent RNA helicase DDX20 Q9UHI6	S(0.99)YLEGSSDNQLK
-3.76	8.15E-05	NUMA1; Nuclear mitotic apparatus protein 1 Q14980	LGS(1)PDYGNALLSLPGYRPTTR
-3.71	0.00193	GTSE1; G2 and S phase-expressed protein 1 Q9NYZ3	LLASS(0.92)PALPSSGAQAR
-3.66	0.00015	MAP7D1; MAP7 domain-containing protein 1 Q3KQU3	WSWAGALHHS(0.61)SPGHK
-3.64	2.58E-05	PDLIM1; PDZ and LIM domain protein 1 Q00151	SAMPFTAS(0.99)PASSTTAR
-3.61	0.00055	NCKAP5L; Nck-associated protein 5-like H7C1V4	VPTSAPSLGKPNKS(0.93)PHS(0.66)SPTK
-3.60	0.01068	MTDH; Protein LYRIC Q86UE4	WNSVS(0.99)PASAGK
-3.59	0.00123	AATF; Protein AATF Q9NY61	DGTPNAGS(0.99)EES(1)S(1)EDDELVE
-3.59	0.00125	KLC3; Kinesin light chain 3 Q6P597	TLASTQDLS(1)PH
-3.58	0.00812	MYO9B; Unconventional myosin-Ixb M0R300	KKPGDASSLPDAGLS(0.97)PGSQVDSK
-3.58	0.00378	DDX39A; ATP-dependent RNA helicase DDX39A O00148	DLLDYDEEEEPQAPQES(0.59)TPAPPKK
-3.54	1.66E-05	MKI67; Proliferation marker protein Ki-67 P46013	ELFQT(1)PVCTDKPTTTEK
-3.53	0.00221	NUP98; Nuclear pore complex protein Nup98-Nup96 P52948	ALTT(0.89)PTHYKLT(0.98)PRPATR
-3.51	0.01230	MYBBP1A; Myb-binding protein 1A Q9BQG0	SPAPGAPTRS(0.87)PSTPAK
-3.50	0.00016	OSBPL11; Oxysterol-binding protein-related protein 11 Q9XB4	VSESEKLEGQATAVT(1)PNK
-3.49	0.00079	DDX39A; ATP-dependent RNA helicase DDX39A O00148	DLLDYDEEEEPQAPQEST(0.74)PAPPKK
-3.49	0.00057	RFX7; DNA-binding protein RFX7 H0YLX2	HHDTFGRLT(0.99)PVS(1)PVQHQGAT
-3.45	0.01152	EP58; Epidermal growth factor receptor kinase substrate 8 Q12929	QNS(0.93)SSSDSGGSIVR
-3.34	0.00435	NONO; Non-POU domain-containing octamer-binding protein Q15233	FGQAATMEGIGAIGT(1)PPAFNR
-3.32	0.00024	AHNAK; Neuroblast differentiation-associated protein AHNAK Q09666	LSGPS(1)LK
-3.28	0.00035	NCAPD2; Condensin complex subunit 1 Q15021	YQPLASTASDNDFVT(1)PEPR
-3.25	0.00279	ACIN1; Apoptotic chromatin condensation inducer in the nucleus E7EQT4	S(1)KS(1)PS(0.98)PPRLTEDR
-3.24	0.00155	CLASP1; CLIP-associating protein Q7Z460	NSSNTSVGS(0.94)PSNTIGTRPSR
-3.22	0.00225	RTN4; Reticulon-4 Q9NQ63	RRGS(0.73)SGS(0.78)VDETLFALPAASEP
-3.22	0.00400	PPP1R10; Serine/threonine-protein phosphatase 1 regulatory subunit 10 Q96QC0	RQSNVAAPGDA(1)PPAEK
-3.20	0.00017	TJP2; Tight junction protein ZO-2 Q9UDY2	LISDFEDTDGEGGAYT(1)DNELDEPAEPL
-3.16	0.00132	GPATCH2; G patch domain-containing protein 2 Q9NW75	KDHS(1)DS(1)DDQMLVAK
-3.15	0.01275	EXOSC10; Exosome component 10 Q01780	VSSQDFPNKQT(0.80)PSGKK
-3.15	7.68E-06	NCKAP5L; Nck-associated protein 5-like H7C1V4	VPTSAPSLGKPNKS(0.93)PHS(0.66)SPTK
-3.12	0.00130	CHMP4B; Charged multivesicular body protein 4b Q9H444	NLLEIS(0.99)GPETVPLPNVSPALPSKPA
-3.10	0.00416	DYNC1L1; Cytoplasmic dynein 1 light intermediate chain 1 Q9Y6G9	SVSSNVASVS(0.96)PIPAGSK
-3.10	0.00016	DLGAP5; Disks large-associated protein 5 Q15398	NTASQNS(1)JLEEGETK
-3.08	0.00122	HMG1; High mobility group protein HMG-1/HMG-Y P17096	KQPPVS(1)PGTALVGSQK
-3.07	0.00234	MKI67; Proliferation marker protein Ki-67 P46013	DINTFLGT(1)PVQK
-3.06	0.00382	MYBBP1A; Myb-binding protein 1A Q9BQG0	PGAPTRSPS(0.54)T(0.54)PAKS(0.99)PK
-3.04	0.00088	MAP7D1; MAP7 domain-containing protein 1 Q3KQU3	EAKES(0.99)PSAAGPEDK
-3.02	0.00057	PPP1R10; Serine/threonine-protein phosphatase 1 regulatory subunit 10 Q96QC0	INVQEILTSIMGS(0.97)PNSHPSEELLK
-2.99	0.01269	TPX2; Targeting protein for Xklp2 Q9ULW0	S(1)PAFALK
-2.95	0.00360	SLC4A7; Anion exchange protein C9JRP1	KHS(1)DPHLLER
-2.93	0.00251	ADRM1; Proteasomal ubiquitin receptor ADRM1 Q16186	SQSAAVT(0.99)PSSTTSSTR
-2.91	0.00057	MYBBP1A; Myb-binding protein 1A Q9BQG0	S(1)PLSALAR
-2.88	0.00028	PCM1; Pericentriolar material 1 protein Q15154	LRDQLNNS(0.96)SSSPQRSVDQR
-2.86	0.01086	DDX21; Nucleolar RNA helicase 2 Q9NR30	DCNPSEASEENS(0.67)EIEQEIPVEQK
-2.84	0.00298	LMNB2; Lamin-B2 Q03252	AGGPAT(1)PLS(0.63)PTRLR
-2.84	0.00579	ANKRD2; Ankyrin repeat domain-containing protein 2 Q9GZV1	AEHNGLEGPNDS(0.91)GRETPQVPAQ
-2.81	0.00492	RAB8A; Ras-related protein Rab-8A P61006	KLEGN5(1)PGGS(1)NQGVK
-2.79	0.00950	NIFK; MKI67 FHA domain-interacting nucleolar phosphoprotein Q9BYG3	EIEIQTQT(0.99)PTHSR
-2.78	0.00281	C8orf33; UPF0488 protein C8orf33 Q9H7E9	AALGHLAGAAAAAPGGT(0.98)PCASR
-2.78	0.00243	TP53BP1; TP53-binding protein 1 Q12888	IDEDGENTQIEDTEPMS(0.99)PVLNSK
-2.77	0.00011	MCM4; DNA replication licensing factor MCM4 P33991	GLQVDLQ(1)DGAAAEDIVASEQLGQK
-2.77	0.01547	SYVN1; E3 ubiquitin-protein ligase synoviolin Q86TM6	LES(1)PVAH
-2.76	3.6E-08	MKI67; Proliferation marker protein Ki-67 P46013	KPVGEVHSQFSTGHANS(0.98)PCTIIGK

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-2.76	0.00028	SRRM2; Serine/arginine repetitive matrix protein 2 Q9UQ35	DVNPGGKEET(0.93)PGQRPAVTETHQL
-2.75	0.00171	CHEK1; Serine/threonine-protein kinase Chk1 J3KN87	VTSGGVSE5(0.93)PSGFSK
-2.74	0.00062	NACC1; Nucleus accumbens-associated protein 1 Q96RE7	RLWDS(1)GQK
-2.73	0.00342	SIPA1; Signal-induced proliferation-associated protein 1 F6RY50	SVPSADSETPLTQDRPGS(0.84)PSGSEDK
-2.73	0.01251	ZNF644; Zinc finger protein 644 Q9H582	HVVS(1)PEQIATSDK
-2.70	0.00770	NOLC1; Nucleolar and coiled-body phosphoprotein 1 Q14978	LQT(1)PNT(1)FPK
-2.68	0.00051	PALB2; Partner and localizer of BRCA2 Q86YC2	QFDSSGS(0.92)PAKPHTLQVSGR
-2.66	0.00112	ADAT1; tRNA-specific adenosine deaminase 1 Q9BUB4	IAPGS(1)AK
-2.60	0.00381	ELAVL1; ELAV-like protein 1 Q15717	NVALLSQLYHS(1)PAR
-2.60	0.00599	PML; Protein PML P29590	AVS(1)PPHLDGPPS(1)PRS(1)PVIGSEVFL
-2.58	0.00749	KAT7; Histone acetyltransferase KAT7 O95251	NTADHDES(0.83)PPRT(0.89)PTGNAPSS
-2.56	0.00658	HNRNPA1; Heterogeneous nuclear ribonucleoprotein A1 P09651	GGNFGGRSS(0.91)GPYGGGGYFAK
-2.53	0.00076	CCD86; Coiled-coil domain-containing protein 86 Q9H6F5	RALVEFESNPEET(0.58)REPGSPSPVQR
-2.52	3.28E-05	JPT1; Jupiter microtubule associated homolog 1 Q9UK76	MASNIFG(1)PEENQASWAK
-2.51	0.00098	STAU2; Double-stranded RNA-binding protein Staufien homolog 2 A0A0A0MTD1	GSSPT(0.98)PPCS(1)PVQPSK
-2.46	0.00083	ARHGEF7; Rho guanine nucleotide exchange factor 7 B1ALK7	SGTLKS(1)PPK
-2.45	0.00225	MKI67; Proliferation marker protein Ki-67 P46013	LDLLGNLPGS(1)K
-2.43	0.00950	JPT2; Jupiter microtubule associated homolog 2 Q9H910	AMKPPGGESNLFGS(0.99)PEEATPSSRP
-2.42	0.00078	DEK; Protein DEK P35659	S(1)LIVEGKREK
-2.41	0.00914	TJAP1; Tight junction-associated protein 1 Q5JTD0	HLHSGQEAS(0.97)PGPAPSLAPGAVVP
-2.39	0.00252	NOLC1; Nucleolar and coiled-body phosphoprotein 1 Q14978	LQT(1)PNT(1)FPK
-2.39	0.00871	TCOF; Treacle protein Q13428	VGDVT(1)PQVK
-2.38	0.00698	PPP1R2; Protein phosphatase inhibitor 2 P41236	GDDEDACS(0.94)DTEATEAMAPDILARK
-2.38	0.00860	CDC42EP1; Cdc42 effector protein 1 Q00587	ASWES(1)LDEEWRAQAGSR
-2.37	0.00476	NUP153; Nuclear pore complex protein Nup153 P49790	FSS(1)PIVK
-2.36	0.00116	MK67; MKI67 FHA domain-interacting nucleolar phosphoprotein Q9BYG3	TVDS(0.99)QGPT(1)PVCT(0.97)PTFLER
-2.34	0.00951	LMNB2; Lamin-B2 Q03252	AGGPATPLS(0.98)PTRLR
-2.33	0.00715	SFPQ; Splicing factor, proline- and glutamine-rich P23246	GMGPGT(1)PAGYGR
-2.33	0.01197	RPRD2; Regulation of nuclear pre-mRNA domain-containing protein 2 Q5VT52	QYPDS(0.99)PHVPVHR
-2.32	0.00039	NAP1L4; Nucleosome assembly protein 1-like 4 Q99733	LDNVPHT(0.93)PSSYIETLPK
-2.29	9.88E-05	MEPCE; 75K snRNA methylphosphate capping enzyme Q7L2J0	GGGPQAQSHGEARLS(1)DPPGR
-2.28	0.00214	KAT7; Histone acetyltransferase KAT7 O95251	NTADHDES(0.80)PPRT(0.97)PTGNAPSS
-2.27	0.00503	HMMR; Hyaluronan mediated motility receptor O75330	RFNDPSGCAPS(0.99)PGAYDVK
-2.26	0.00034	HMG1; High mobility group protein HMG-1/HMG-Y P17096	EPSEVPT(1)PK
-2.25	0.00180	CBX8; Chromobox protein homolog 8 Q9HC52	RQDSDLVQCQVTS(0.76)PSSAEATGK
-2.24	0.00384	TOR1AIP1; Torsin-1A-interacting protein 1 A0A0A0MSK5	VNFSEEGT(1)EEDDQDSSHSVTTVK
-2.23	0.01114	HUWE1; E3 ubiquitin-protein ligase HUWE1 Q72627	AGSST(0.82)PGDAPPAAVEVQGR
-2.22	0.00550	TNS3; Tensin-3 Q68C22	LRKLS(1)LGQYNDAGGQLPFSK
-2.21	0.01007	EAPP; E2F-associated phosphoprotein G3V2W9	VATAPTRYDDIYFDS(1)DS(1)EDEDRAV
-2.19	0.00763	MAP4; Microtubule-associated protein E7EVA0	DGVLTLANNVT(1)PAK
-2.15	0.00402	WNK2; Serine/threonine-protein kinase WNK2 F8W9F9	RPEQQDVSS(0.94)PAK
-2.15	0.00165	NAP1L4; Nucleosome assembly protein 1-like 4 Q99733	ADHS(1)FS(1)DGVPSDSVEAAK
-2.15	0.00197	TMPO; Lamina-associated polypeptide 2, isoform alpha P42166	SHISDQS(1)PLSSK
-2.14	0.00128	APC; Adenomatous polyposis coli protein P25054	SGRS(0.82)PTGNTPPVIDSVSEK
-2.10	0.00299	CDCA3; Cell division cycle-associated protein 3 Q99618	LGRS(0.99)PLTLQDDNS(0.99)PGTLTLR
-2.10	0.00096	PARG; Poly(ADP-ribose) glycohydrolase Q86W56	WGAATS(0.95)PAASDAR
-2.07	0.00245	CDCA3; Cell division cycle-associated protein 3 Q99618	LGRS(0.99)PLTLQDDNS(0.99)PGTLTLR
-2.07	0.00604	MKI67; Proliferation marker protein Ki-67 P46013	ELFQT(1)PDHTEESTDDK
-2.07	0.00895	PPP1R18; Phostensin A0A0G2JHC2	DWRQS(1)PGEVGDR
-2.06	0.01277	MDC1; Mediator of DNA damage checkpoint protein 1 Q14676	TVPIAPELPPSTTEQPV(0.71)PEPTSR
-2.05	0.00319	MRTFB; Myocardin-related transcription factor B Q9ULH7	SGEISLPIKEEPS(1)PISK
-2.04	0.00844	A0A087WUL7; A0A087WUL7	DAAALQTSKPSAEDAEGQS(1)PLSQK
-2.04	0.00069	ANLN; Anillin Q9NQW6	SCEGQNPPELLPKT(1)PIS(1)PLK
-2.01	0.00014	RRM2; Ribonucleoside-diphosphate reductase subunit M2 P31350	ENT(1)PPALSGTR
-2.01	0.01083	DIDO1; Death-inducer obliterator 1 Q9BTC0	STT(0.71)PPGS(0.99)PPPPPLPEPPVLK
-2.01	0.00952	MKI67; Proliferation marker protein Ki-67 P46013	ELFQT(1)PGHTEELVAAGK
-2.00	0.00044	PHF14; PHD finger protein 14 O94880	SNEDS(1)LILEK
-1.99	0.00416	PDLIM5; PDZ and LIM domain protein 5 Q96HC4	EVVKVPVITS(0.99)PAVSK

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-1.95	0.00180	RBM15B; Putative RNA-binding protein 15B Q8NDT2	TTHS(0.99)PYEER
-1.95	0.00103	RACGAP1; Rac GTPase-activating protein 1 Q9H0H5	VSLGPPVTT(0.80)PEHQLLK
-1.95	0.00469	PBK; Lymphokine-activated killer T-cell-originated protein kinase Q96K85	GLSHS(1)PWAVK
-1.95	9.87E-06	RICTROR; Rapamycin-insensitive companion of mTOR Q6R327	HIEDTGS(0.90)TPS(0.98)IGENDLK
-1.94	0.00252	MDC1; Mediator of DNA damage checkpoint protein 1 Q14676	DLEPFTPTDQSVT(0.93)PEAIAQGGQSK
-1.92	0.00451	NECAP2; Adaptin ear-binding coat-associated protein 2 Q9NVZ3	VRPAS(0.74)TGGLSLPPPPGGK
-1.90	0.00869	NUP107; Nuclear pore complex protein Nup107 P57740	RVLLQASQDENFGNTT(0.78)PRNQVIPR
-1.90	0.00025	TNKS1BP1; 182 kDa tankyrase-1-binding protein Q9C0C2	VNLFPGLS(0.87)PSALK
-1.88	0.00762	PDLIM1; PDZ and LIM domain protein 1 O00151	VWS(1)PLVTEEGK
-1.87	0.00786	TP53BP1; TP53-binding protein 1 Q12888	TGTRETAVPPLGIEDIS(1)PNLS(1)PDDK
-1.87	0.00968	KI67; Proliferation marker protein Ki-67 P46013	ELFQT(0.99)PGTDKPTTDEK
-1.87	0.00798	CASC3; Protein CASC3 O15234	LEQTSVRDPS(0.97)PEADAPVLGS(1)PEK
-1.86	0.00088	ANKHD1; Ankyrin repeat and KH domain-containing protein 1 Q8IWZ3	TVSLPLS(0.99)PNIK
-1.84	0.00685	ANKZF1; Ankyrin repeat and zinc finger domain-containing protein 1 Q9H8Y5	LAALQAGPTS(0.92)PIPDASIVNTRR
-1.83	0.00040	LAMTOR1; Ragulator complex protein LAMTOR1 Q6IAA8	LLDPS(0.97)PPTK
-1.83	0.00195	RBMXL1; RNA binding motif protein, X-linked-like-1 Q96E39	GLPPS(1)VER
-1.82	0.00145	PCBP1; Poly(rC)-binding protein 1 Q15365	DLEGPLDAYSIQGQHTIS(0.88)PLDLAK
-1.82	0.00394	CTTN; Src substrate cortactin Q14247	DY(1)SSGFGGK
-1.81	0.00255	MARK2; Serine/threonine-protein kinase MARK2 Q7KZ17	EGDTITLKRPSADLNTSSAPS(0.89)PSHK
-1.80	0.00057	ATF7IP; Activating transcription factor 7-interacting protein 1 Q6VMQ6	EAFVLS(1)DEEDISGEK
-1.78	0.00835	KPNA3; Importin subunit alpha-4 O00505	KRNVPQES(1)LEDS(1)DVDADFK
-1.76	0.00554	NCBP3; Nuclear cap-binding protein subunit 3 Q53F19	MIST(0.98)PS(0.99)PKK
-1.76	0.00683	HDLBP; High density lipoprotein binding protein (Vigilin), isoform CRA_a A0A024R4E5	DCDPS(1)PRRCDIHSGR
-1.72	0.00529	ZYX; Zyxin Q15942	FTPVASKFS(1)PGAPGSGSQPNQK
-1.71	0.00092	MYBBP1A; Myb-binding protein 1A Q9BQG0	LSLVIRS(0.81)PSLLQSGAK
-1.70	0.00136	CIC; Protein capicua homolog I3L2J0	SRQPS(0.77)PLLLPPAAGLTSDPGPSVR
-1.70	0.00039	CASP8AP2; CASP8-associated protein 2 A0A087WTW5	VLRNES(1)PPQVPVYNNSHK
-1.69	0.00945	RRBP1; Ribosome-binding protein 1 A0A0A0MRV0	NTDVAQS(1)PEAPKQEAPAKK
-1.68	0.00238	TOP2A; DNA topoisomerase 2-alpha P11388	MEVS(1)PLQPVNENMQVNK
-1.66	0.00950	RRP1B; Ribosomal RNA processing protein 1 homolog B Q14684	PLHGVLT(0.88)PT(0.81)SSPASSPLVAK
-1.61	0.00066	SHC1; SHC-transforming protein 1 P29353	ELFDDPSY(0.74)VNVQNLDK
-1.61	0.01055	MAP7; Ensconsin Q14244	LFVT(0.99)PPEGSSR
-1.59	0.00645	FAM83H; Protein FAM83H Q6ZRV2	GS(0.99)PTSAYPERK
-1.58	0.00768	BCLFA1; Bcl-2-associated transcription factor 1 Q9NYF8	DTFEHPSES(1)IDEFNK
-1.58	0.00069	RGPD3; RanBP2-like and GRIP domain-containing protein 3 A6NKT7 . RGPD1; RanBP2-like and GRIP domain-containing protein POJDJO . RANBP2; E3 SUMO-protein ligase RanBP2 P49792 . RGPD4; RanBP2-like and GRIP domain-containing protein 4 Q723J3 . RGPDS; RanBP2-like and GRIP domain-containing protein 4 Q99666	ITPHVS(0.63)RS(0.71)S(0.71)T(0.69)PR
-1.57	0.00024	CAVIN1; Caveolae-associated protein 1 Q6NZ12	SFT(1)PDHVYYAR
-1.56	0.00373	CDC42EP1; Cdc42 effector protein 1 Q00587	QARAS(1)WES(0.99)LDEEWRAQAGSR
-1.56	0.00010	ARFGAP1; ADP-ribosylation factor GTPase-activating protein 1 Q8N6T3	LAEGREWSLESSPAQNW(0.98)PPQPR
-1.51	0.00591	DCP2; m7GpppN-mRNA hydrolase H0Y9T5	FRHSQQLFPDGS(1)PGDQWVK
-1.50	0.00530	SCRIB; Protein scribble homolog A0A0G2JNZ2	ALS(1)PAELR
-1.46	0.00639	PGAM1; Phosphoglycerate mutase 1 P18669	S(0.99)YDVPPPEPDPHPFYSNISK
-1.42	0.00864	TMCC3; Transmembrane and coiled-coil domain protein 3 Q9ULS5	RGGS(0.68)DTNLNFDVDPDGLDFHK
-1.41	0.00430	UCHL3; Ubiquitin carboxyl-terminal hydrolase isozyme L3 P15374	FLEESVMS(0.99)PEERAR
-1.37	0.00749	MAPK1IP1L; MAPK-interacting and spindle-stabilizing protein-like Q8NDCO	SDEFSLADALPEHS(1)PAK
-1.36	0.00279	NUCKS1; Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 Q9H1E3	ATVT(1)PS(1)PVK
-1.36	0.00791	TOP2A; DNA topoisomerase 2-alpha P11388	TQMAEVLPS(1)PR
-1.36	0.00422	JPT2; Jupiter microtubule associated homolog 2 Q9H910	TSDFGS(1)PVTATSR
-1.33	0.00152	ZC3HAV1; Zinc finger CCCH-type antiviral protein 1 C9J6P4	GESTAPAQVSTLP(0.91)PAALSSSNR
-1.27	0.00634	MDC1; Mediator of DNA damage checkpoint protein 1 Q14676	EDS(1)DT(1)DVDDSRPPGRPAEVHLER
-1.24	0.00118	RAB1A; Ras-related protein Rab-1A P62820	IQST(0.81)PVK
-1.23	0.00361	ANLN; Anillin Q9NQW6	GNWS(1)AEK
-1.22	0.00737	NFIA; Nuclear factor 1 B1AKN5	SGFSSPS(0.97)PSQTSSLGTAFTQHHR
-1.19	0.00036	DBNL; Drebrin-like protein Q9UJU6	YQEQGGEAS(0.99)PQRTWEQQEVVSR
-1.17	0.00672	RAVER1; Ribonucleoprotein PTB-binding 1 A0A087WZ13	AIGS(0.84)PLGSGEGLLGLS(1)PGPNGHSHLLK
-1.13	0.00350	HAUS6; HAUS augmin-like complex subunit 6 Q7Z4H7	NQIPRT(1)PENLITEIR
-1.08	0.00061	TPR; Nucleoprotein TPR P12270	EGVQGPLNVS(0.96)LSEEGK
-1.04	0.00399	AHNAK; Neuroblast differentiation-associated protein AHNAK Q09666	SRVDIETPNLEGLTGPRLGS(0.99)PSGK

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-1.03	0.00182	SRRM2; Serine/arginine repetitive matrix protein 2 Q9UQ35	QGSIT ^S (0.7)PQANEQSV ^T (0.94)PQRR
-1.02	0.00250	DKC1; H/ACA ribonucleoprotein complex subunit DKC1 O60832	^S (1)LPPEEDVAEIQHAEFLIKPESK
-1.01	0.00496	CHD3; Chromodomain-helicase-DNA-binding protein 3 H7C3H7	GRPPAQALGPAAS(1)PPPS(1)PPLGPSLG
-1.01	0.00048	CRYBG1; Beta/gamma crystallin domain-containing protein 1 A0A0J9YWL0	DTCVQS(1)PISSFPCTDLK
-0.817	0.00246	GATAD2A; Transcriptional repressor p66-alpha Q86YP4	TSAQANSTPTSVASVVTSAES(0.99)PASR
-0.70	0.00021	RAD18; E3 ubiquitin-protein ligase RAD18 Q9NS91	NHLLQFALES(1)PAKS(0.99)PASSSSK

Supplementary Table S4. Significantly decreased phosphopeptide relative abundance level in A431/CCKBR cells after EBRT. MS2-based quantification shown as log₂ ratio, $P < 0.05$.

LOG ₂ RATIO: ¹⁷⁷ Lu-PP-F11N/CON	P-value	UniProt	PROTEIN
5.27	2.6E-06	A0A0C4DH73	IGKV1-12; Protein IGKV1-12
4.44	2.5E-05	Q9BQ67	GRWD1; Glutamate-rich WD repeat-containing protein 1
3.37	0.0001	P52594	AGFG1; Arf-GAP domain and FG repeat-containing protein 1
2.47	3.2E-05	O43815	STRN; Striatin
2.41	2.6E-05	Q7Z4H3	HDDC2; HD domain-containing protein 2
2.25	0.001	Q13751	LAMB3; Laminin subunit beta-3
2.16	9.5E-05	P53539	FOSB; Protein fosB
1.82	0.0001	P53814	SMTN; Smoothelin
1.65	6.3E-05	H3BRB3	KIF22; Kinesin-like protein
1.64	0.0005	Q15750	TAB1; TGF-beta-activated kinase 1 and MAP3K7-binding protein 1
1.62	0.0002	O96005	CLPT1; Cleft lip and palate transmembrane protein
1.46	0.0001	I3VM54	KDM2A; Lysine-specific demethylase 2A
1.09	0.0010	Q7Z4H7	HAUS6; HAUS augmin-like complex subunit 6
1.01	0.0003	O00622	CYR61; Protein CYR61
1.00	0.0141	Q86YV9	HPS6; Hermansky-Pudlak syndrome 6 protein
0.94	0.0118	Q5QP56	BCL2L1; Bcl-2-like protein 1
0.86	0.0121	Q02952	AKA12; A-kinase anchor protein 12
0.84	0.0077	Q02040	AK17A; A-kinase anchor protein 17A
0.821	0.0010	S4R3V8	LSR; Lipolysis-stimulated lipoprotein receptor
-1.46	0.0002	Q15018	FAM175B; BRISC complex subunit Abro1
-1.55	0.0065	Q92667	AKAP1; A-kinase anchor protein 1, mitochondrial
-1.60	0.0002	Q9Y6B6	SAR1B; GTP-binding protein SAR1b
-1.97	6.0E-05	Q5HYI8	RABL3; Rab-like protein 3
-2.55	0.0005	P35580	MYH10; Myosin-10
-2.60	0.0002	Q8WUY1	THEM6; Protein THEM6

Supplementary Table S5. Significant changes in relative total protein abundance levels after treatment with [¹⁷⁷Lu]Lu-PP-F11N in A431/CCKBR cell. MS2-based quantification shown as log₂ ratio, $P < 0.05$

Supplementary Table S6

LOG ₂ RATIO: EBRT/CON	P-value	UniProt	PROTEIN
1.55	0.0032	Q15392	DHCR24; Delta(24)-sterol reductase
1.39	0.0019	H7BZV4	ARL6IP4; ADP-ribosylation factor-like protein 6-interacting protein 4
1.32	0.0131	P23786	CPT2; Carnitine O-palmitoyltransferase 2, mitochondrial
0.80	0.0069	E9PL01	SPCS2; Signal peptidase complex subunit 2
0.69	0.0017	P14927	UQCRB; Cytochrome b-c1 complex subunit 7
0.68	0.0014	Q9NRN7	AASDHPPT;
0.60	0.0023	Q8IZP0	ABI1; Abl interactor 1
-0.87027	0.0091	Q14165	MLEC; Malectin
-0.89371	0.0007	Q9BVL2	NUP58; Nucleoporin p58/p45
-1.15661	0.0062	Q7Z4H3	HDCC2; HD domain-containing protein 2
-1.79024	0.0001	Q9UPN7	PPP6R1; Serine/threonine-protein phosphatase 6 regulatory subunit 1
-1.7997	0.0036	Q92882	OSTF1; Osteoclast-stimulating factor 1
-1.83217	0.0003	Q8N983	MRPL43; 39S ribosomal protein L43, mitochondrial
-1.90071	0.0024	Q86W92	PPFIBP1; Liprin-beta-1
-2.06716	0.0008	P16435	POR; NADPH-cytochrome P450 reductase

Supplementary Table S6. Significant changes in relative total protein abundance levels after EBRT in A431/CCKBR cells. MS2-based quantification shown as log₂ ratio, $P < 0.05$.

Supplementary Table S7. Comparative analysis of cellular response to TRT with [¹⁷⁷Lu]Lu-PP-F11N and EBRT. Bioinformatics analysis of the protein groups with altered expression or phosphorylation levels in response to PRRT or EBRT identified by proteomics and phosphoproteomics analysis. Fold Enrichments (Fold En.) for identified biological processes (GOTERM) or pathways (BIOCARTA, KEGG PATHWAYS) were scored for terms with $P < 0.01$ in a group of at least 3 proteins.

TRT (¹⁷⁷ Lu-PP-F11N)	P-value Fold En.	EBRT	P-value Fold En.
DNA damage response, repair and nucleus structure			
Cellular response to DNA damage stimulus GOTERM_BP (DDX39A, RAD18, YAP1DTL, MAPK1, TP53, UBA1, USP10)	5.0E-3 3.8	Cellular response to DNA damage stimulus GOTERM_BP (APC, DDX39A, RAD18, RAD50, YAP1, AATF, CHEK1, CHEK2, RNF168, TOP2A, TP53BP1, TP53)	3.5E-4 3.8
DNA damage response, signal transduction by p53 class mediator GOTERM_BP (FOXO3, TP53, USP10)	9.6E-3 19.9	DNA damage response, signal transduction by p53 class mediator GOTERM_BP (GTSE1, CHEK2, NPM1, PML, TNKS1BP1, TP53)	2.5E-3 6.3
DNA damage response, detection of DNA damage GOTERM_BP (RAD18, DTL, RFC1, RPA1)	5.5E-3 11.0	Double-strand break repair via nonhomologous end joining GOTERM_BP (RAD50, HIST3H3, MDC1, RIF1, RNF168, TP53BP1, UIMC1)	3.8E-4 7.3
Translesion synthesis GOTERM_BP (DTL, RFC1, RPA1, USP10)	5.5E-3 11.0	Double-strand break repair via homologous recombination GOTERM_BP (RAD50, RAD51AP1, NUCKS1, PALB2, RPA1, SFPQ)	5.3E-3 5.3
Nucleosome assembly - GOTERM_BP (HIST1H1B, HIST1H1D, HIST2H3A, MCM2, NPM1, SART3)	6.9E-3 5.0	Base-excision repair GOTERM_BP (HUWE1, HMGA1, NTHL1, RPA1, TP53)	1.9E-3 9.4
Sister chromatid cohesion GOTERM_BP (AHCTF1, RANBP2, CENPC, CENPF, KIF22, RPS27)	3.8E-3 5.8	Interstrand cross-link repair GOTERM_BP (RAD51AP1, NUCKS1, RPA1, RNF168, USP1)	6.4E-3 6.7
Nuclear pore complex assembly - GOTERM_BP (AHCTF1, NUP153, NUP93)	5.2E-3 27.1	Nuclear pore complex assembly - GOTERM_BP (NUP107, NUP153, NUP98, RTN4, TPR)	1.6E-5 29.8
		DNA replication GOTERM_BP (POLE, GINS2, RAD50, UPF1, CHEK1, RRM2, CHAF1A, DUT, KAT7, MCM2, MCM4, MCM6, NFIA, NFIC, NUP98, RPA1)	1.4E-8 6.8
RNA processing, transport and metabolism			
mRNA splicing, via spliceosome GOTERM_BP (DDX39A, POLR2A, FIP1L1, HNRNPH1, HNRNPU, RAVR1, SRRM1, SRRM2, SF3B2, SART3, TRA2A)	8.1E-5 4.9	mRNA splicing, via spliceosome GOTERM_BP (DDX39A, ELAVL1, POLR2A, SNW1, YBX1, CAS3, HNRNPA1, HNRNPM, NONO, PABPN1, PCBP1, RAVR1, SRRM1, SRRM2, SPEN, SYNCRIP, TRA2A, TRA2B)	5.2E-8 5.3
mRNA export from nucleus GOTERM_BP (AGFG1, FIP1L1, DDX39A, RANBP2, NUP153, NUP50, NUP93, SRRM1)	6.5E-5 7.9	mRNA export from nucleus GOTERM_BP (DDX39A, UPF1, CAS3, NUP107, NUP153, NUP58, NUP98, SRRM1, TPR)	1.4E-4 5.9
tRNA export from nucleus GOTERM_BP (RANBP2, NUP153, NUP50, NUP93)	3.9E-3 12.4	tRNA export from nucleus GOTERM_BP (NUP107, NUP153, NUP58, NUP98, TPR)	1.3E-3 10.2
RNA transport KEGG_PATHWAY (RANBP2, RGPD5, EIF4G1, NUP153, NUP50, NUP93, RPP30, SRRM1, TGS1)	8.1E-4 4.4	rRNA processing GOTERM_BP (ARL6IP4, DDX47, IWS1, KHSRP, RBM15B, RBMXL1, ADAR, ACIN1, CAS3, HNRNPA1, NONO, PRPF38B, SRRM1, SFPQ, THRAP3)	6.2E-7 5.5
Gene silencing by RNA GOTERM_BP (RANBP2, POLR2A, HIST2H3A, NUP153, NUP50, NUP93)	5.2E-3 5.4	rRNA processing GOTERM_BP (DDX47, DDX21, DIS3L2, UTP14A, UTP18, CCDC86, DKC1, EXOSC10, NOLC1, RRP1B, RPL29)	1.6E-3 3.4
Nuclear-transcribed mRNA catabolic process, nonsense-mediated decay GOTERM_BP (DCP1A, EIF4G1, RPL19, RPL3, RPS27, RPS6)	6.9E-3 5.0	Negative regulation of transcription GOTERM_BP (BCLAF1, GATAD2A, JUN, MYBBP1A, RB1, RBM15B, SNW1, SP100, ATF7IP, CBX3, CBX5, HMGA1, NONO, NACCI, PML, SPEN, SFPQ, TRIM28, TP53, UIMC1)	2.3E-4 2.6
		RNA polymerase III transcription KEGG_PATHWAY (ADAR, NONO, SFPQ)	7.7E-3 20.3
		mRNA surveillance pathway KEGG_PATHWAY (UPF1, ACIN1, CAS3, PABPN1, PPP2R5A, SRRM1)	9.4E-3 4.6
Cell cycle regulation			
Mitotic nuclear division GOTERM_BP (HAUS6, NSUN2, ARHGEF2, ANLN, CENPC, CENPF, KIF22, PPP1R12A, RPS6, SKA3, ZC3HC1)	2.0E-4 4.4	Mitotic nuclear division GOTERM_BP (DIS3L2, HAUS6, PBK, TPX2, ANLN, CDC26, CDCA3, DYNCL1L1, ENSA, NEDD1, NUMA1, NOLC1, TPR)	4.2E-4 3.4
Mitotic nuclear envelope disassembly GOTERM_BP (RANBP2, NUP153, NUP50, NUP93)	9.6E-3 9.0	Mitotic nuclear envelope disassembly GOTERM_BP (NUP107, NUP153, NUP58, NUP98, TPR)	4.4E-3 7.5
Mitotic cell cycle GOTERM_BP (CENPC, CENPF, FAM175B, PAK2)	7.9E-3 9.7	Cell cycle GOTERM_BP (RB1, CDC26, CHEK1, CHEK2, MCM2, MCM4, MCM6, TP53)	1.9E-3 4.5
		G2/M transition of mitotic cell cycle - GOTERM_BP (HAUS6, RBM8A, TPX2, CCP110, CEP152, CHEK1, CHEK2, CLASP1, ENSA, HMMR, NEDD1, PCM1)	7.8E-6 5.7
		G1/S transition of mitotic cell cycle GOTERM_BP (POLE, RB1, MCM2, MCM4, MCM6, RPA1, RRM2)	4.6E-3 4.5
		Mitotic cytokinesis GOTERM_BP (APC, RACGAP1, ANLN, CHMP4B)	9.4E-3 9.0
Signal transduction pathways			
TGF-beta receptor signaling pathway - GOTERM_BP (FOS, JUN, TAB1, CGN, PXN, ZYX)	2.3E-3 6.5	Ras protein signal transduction GOTERM_BP (DHCR24, CRKL, JUN, RB1, SHC1, MAPK14, RREB1, TRIM28, TP53)	1.1E-5 8.4
ErbB signaling pathway KEGG_PATHWAY (ABL2, JUN, SOS1, EGFR, MAPK1, PAK2)	3.3E-3 5.9	Regulation of signal transduction by p53 class mediator GOTERM_BP (RAD50, TPX2, CHEK1, CHEK2, CHD3, CHD4, MTA2, MAPK14, PML, RPA1, TP53)	2.0E-5 5.8
Angiotensin II mediated activation of JNK via Pyk2 BIOCARTA (JUN, SOS1, CALM1, EGFR, MAPK1)	3.8E-3 7.2	ATM Signaling Pathway - KEGG_PATHWAY (JUN, RAD50, CHEK1, CHEK2, TP53)	2.6E-3 8.1
Signaling of Hepatocyte Growth Factor Receptor BIOCARTA (FOS, JUN, SOS1, MAPK1, PXN)	5.3E-3 6.6	Links between Pyk2 and Map Kinases - KEGG_PATHWAY (CRKL, JUN, SHC1, MAPK14, MAP2K2)	7.6E-3 6.0
Integrin Signaling Pathway BIOCARTA (FOS, JUN, SOS1, MAPK1, PXN)	5.8E-3 6.5		
Estrogen signaling pathway - KEGG_PATHWAY (FOS, JUN, SOS1, CALM1, EGFR, MAPK1)	5.7E-3 5.1		
TOR signaling GOTERM_BP (LARP1, CCDC88A, RPS6)	8.4E-3 21.3		
MAPK signaling pathway - KEGG_PATHWAY (FOS, JUN, SOS1, TAB1, EGFR, MAPK1, PAK2, STMN1, TP53)	8.8E-3 3.0		
Regulation of Rho protein signal transduction GOTERM_BP (FGD1, ARHGEF1, ARHGEF5, ARHGEF2, SOS1)	8.9E-3 6.1		
Cell morphology, adhesion and phenotype			
Cell-cell adhesion GOTERM_BP (BAG3, LIMA1, LARP1, SLK, ANLN, CGN, CTTN, EIF4G1, FAM129B, LAD1, MARK2, PAK2, PFKF, PPP1R13L, RSL1D1, TJP1, TJP2)	1.4E-8 6.2	Cell-cell adhesion GOTERM_BP (AHNAK, CDC42EP1, CRKL, LASP1, MKL2, NDRG1, PDLIM1, PDLIM5, PPF1BP1, RAB1A, ARHGEF16, VAPB, ABI1, ANLN, ATXN2L, CAST, CHMP4B, CTTN, DBNL, EIF4G1, GOLGA2, HDLBP, LAD1, MARK2, PCBP1, PTPN1, RTN4, RSL1D1, RPL29, TNKS1BP1, TMPO, TJP2, ZC3HAV1)	1.4E-19 8.0
Regulation of actin cytoskeleton KEGG_PATHWAY (FGD1, ARHGEF1, SOS1, EGFR, ITGB4, MAPK1, PAK2, PXN, PPP1R12A)	2.9E-3 3.6	Actin cytoskeleton reorganization GOTERM_BP (RICTOR, SHC1, CTTN, EPS8, PTPN1, SIPA1L1)	7.1E-4 8.4
Regulation of cytoskeleton organization GOTERM_BP (ARHGEF5, MARK2, MAPK1, STMN1)	8.5E-4 20.9		
Focal adhesion KEGG_PATHWAY (JUN, SOS1, EGFR, ITGB4, LAMB3, MAPK1, PAK2, PXN, PPP1R12A, ZYX)	6.0E-4 4.1		
Tight junction KEGG_PATHWAY (CGN, CLDN4, CTTN, MYH10, TJAP1, TJP1, TJP2)	4.9E-4 6.8		
Cell proliferation GOTERM_BP (BCL2L1, LARP1, ARHGEF1, YAP1, CENPF, CCKBR, CYR61, DKC1, EGFR, FAM83B, MYH10, RPS27, TP53)	3.2E-4 3.5		
Transport and protein modifications			
Regulation of glucose transport GOTERM_BP (RANBP2, NUP153, NUP50, NUP93)	4.3E-3 12.0	Regulation of glucose transport GOTERM_BP (NUP107, NUP153, NUP58, NUP98, TPR)	1.5E-3 9.9
Protein sumoylation GOTERM_BP (RANBP2, HDAC7, MDC1, NUP153, NUP50, NUP93, RPA1, TP53)	1.7E-4 6.8	Protein sumoylation GOTERM_BP (SP100, CBX8, MDC1, NUP107, NUP153, NUP58, NUP98, PML, RPA1, RNF168, TOP2A, TPR, TRIM28, TP53BP1, TP53)	2.8E-9 8.4
Proteoglycans in cancer KEGG_PATHWAY (ARHGEF1, SOS1, CTTN, EGFR, MAPK1, PXN, PPP1R12A, RPS6, TP53)	2.1E-3 3.8	Protein import into nucleus GOTERM_BP (ADAR, KPNA2, KPNA3, NUP107, NUP153, NUP58, PPP1R10, TPR)	2.7E-5 9.0